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RELEASE 12

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Table of contents

intro . . . . . Introduction to base reference manual 1

about . . . . . Display information about your Stata 6
adoupdate . . . . . Update user-written ado-files 7
alpha . . . . . Compute interitem correlations (covariances) and Cronbach's alpha 11
ameans . . . . . Arithmetic, geometric, and harmonic means 18
anova . . . . . Analysis of variance and covariance 22
anova postestimation . . . . . Postestimation tools for anova 62
areg . . . . . Linear regression with a large dummy-variable set 78
areg postestimation . . . . . Postestimation tools for areg 84
asclogit . . . . . Alternative-specific conditional logit (McFadden's choice) model 86
asclogit postestimation . . . . . Postestimation tools for asclogit 96
asmprobit . . . . . Alternative-specific multinomial probit regression 103
asmprobit postestimation . . . . . Postestimation tools for asmprobit 127
asroprobit . . . . . Alternative-specific rank-ordered probit regression 137
asroprobit postestimation . . . . . Postestimation tools for asroprobit 149

BIC note . . . . . Calculating and interpreting BIC 157
binreg . . . . . Generalized linear models: Extensions to the binomial family 162
binreg postestimation . . . . . Postestimation tools for binreg 174
biprobit . . . . . Bivariate probit regression 178
biprobit postestimation . . . . . Postestimation tools for biprobit 185
bitest . . . . . Binomial probability test 188
bootstrap . . . . . Bootstrap sampling and estimation 193
bootstrap postestimation . . . . . Postestimation tools for bootstrap 215
boxcox . . . . . Box–Cox regression models 219
boxcox postestimation . . . . . Postestimation tools for boxcox 229
brier . . . . . Brier score decomposition 231
bsample . . . . . Sampling with replacement 237
bstat . . . . . Report bootstrap results 244

centile . . . . . Report centile and confidence interval 251
ci . . . . . Confidence intervals for means, proportions, and counts 257
clogit . . . . . Conditional (fixed-effects) logistic regression 269
clogit postestimation . . . . . Postestimation tools for clogit 285
cloglog . . . . . Complementary log-log regression 290
cloglog postestimation . . . . . Postestimation tools for cloglog 299
cnsreg . . . . . Constrained linear regression 302
cnsreg postestimation . . . . . Postestimation tools for cnsreg 308
constraint . . . . . Define and list constraints 311
contrast . . . . . Contrasts and linear hypothesis tests after estimation 314
contrast postestimation . . . . . Postestimation tools for contrast 377
copyright . . . . . Display copyright information 379
copyright boost . . . . . Boost copyright notification 380
copyright freetype . . . . . FreeType copyright notification 381
copyright icu . . . . . ICU copyright notification 384
copyright jagpdf . . . . . JagPDF copyright notification 385
copyright lapack . . . . . LAPACK copyright notification 386
copyright libpng . . . . . libpng copyright notification 387
copyright scintilla . . . . . Scintilla copyright notification 389
copyright ttf2pt1 . . . . . ttf2pt1 copyright notification 390

copyright zlib . . . . . zlib copyright notification 392
correlate . . . . . Correlations (covariances) of variables or coefficients 393
cumul . . . . . Cumulative distribution 401
cusum . . . . . Graph cumulative spectral distribution 405

db . . . . . Launch dialog 409
diagnostic plots . . . . . Distributional diagnostic plots 411
display . . . . . Substitute for a hand calculator 423
do . . . . . Execute commands from a file 424
doedit . . . . . Edit do-files and other text files 425
dotplot . . . . . Comparative scatterplots 426
dstdize . . . . . Direct and indirect standardization 433
dydx . . . . . Calculate numeric derivatives and integrals 452

eform_option . . . . . Displaying exponentiated coefficients 458
eivreg . . . . . Errors-in-variables regression 459
eivreg postestimation . . . . . Postestimation tools for eivreg 464
error messages . . . . . Error messages and return codes 466
estat . . . . . Postestimation statistics 467
estimates . . . . . Save and manipulate estimation results 475
estimates describe . . . . . Describe estimation results 479
estimates for . . . . . Repeat postestimation command across models 481
estimates notes . . . . . Add notes to estimation results 483
estimates replay . . . . . Redisplay estimation results 485
estimates save . . . . . Save and use estimation results 487
estimates stats . . . . . Model statistics 491
estimates store . . . . . Store and restore estimation results 493
estimates table . . . . . Compare estimation results 496
estimates title . . . . . Set title for estimation results 502
estimation options . . . . . Estimation options 503
exit . . . . . Exit Stata 506
exlogistic . . . . . Exact logistic regression 507
exlogistic postestimation . . . . . Postestimation tools for exlogistic 525
expoisson . . . . . Exact Poisson regression 529
expoisson postestimation . . . . . Postestimation tools for expoisson 541

fracpoly . . . . . Fractional polynomial regression 543
fracpoly postestimation . . . . . Postestimation tools for fracpoly 558
frontier . . . . . Stochastic frontier models 562
frontier postestimation . . . . . Postestimation tools for frontier 576
fvrevar . . . . . Factor-variables operator programming command 578
fvset . . . . . Declare factor-variable settings 581

gllamm . . . . . Generalized linear and latent mixed models 587
glm . . . . . Generalized linear models 589
glm postestimation . . . . . Postestimation tools for glm 623
glogit . . . . . Logit and probit regression for grouped data 629
glogit postestimation . . . . . Postestimation tools for glogit, gprobit, blogit, and bprobit 640
gmm . . . . . Generalized method of moments estimation 642
gmm postestimation . . . . . Postestimation tools for gmm 699
grmeanby . . . . . Graph means and medians by categorical variables 703

hausman . . . . . Hausman specification test 706

heckman . . . . . Heckman selection model 715
heckman postestimation . . . . . Postestimation tools for heckman 732
heckprob . . . . . Probit model with sample selection 738
heckprob postestimation . . . . . Postestimation tools for heckprob 746
help . . . . . Display online help 751
hetprob . . . . . Heteroskedastic probit model 753
hetprob postestimation . . . . . Postestimation tools for hetprob 760
histogram . . . . . Histograms for continuous and categorical variables 763
hsearch . . . . . Search help files 773

inequality . . . . . Inequality measures 777
intreg . . . . . Interval regression 780
intreg postestimation . . . . . Postestimation tools for intreg 790
ivprobit . . . . . Probit model with continuous endogenous regressors 793
ivprobit postestimation . . . . . Postestimation tools for ivprobit 806
ivregress . . . . . Single-equation instrumental-variables regression 810
ivregress postestimation . . . . . Postestimation tools for ivregress 826
ivtobit . . . . . Tobit model with continuous endogenous regressors 843
ivtobit postestimation . . . . . Postestimation tools for ivtobit 853

jackknife . . . . . Jackknife estimation 857
jackknife postestimation . . . . . Postestimation tools for jackknife 869

kappa . . . . . Interrater agreement 870
kdensity . . . . . Univariate kernel density estimation 884
ksmirnov . . . . . Kolmogorov–Smirnov equality-of-distributions test 894
kwallis . . . . . Kruskal–Wallis equality-of-populations rank test 899

ladder . . . . . Ladder of powers 902
level . . . . . Set default confidence level 909
lincom . . . . . Linear combinations of estimators 911
linktest . . . . . Specification link test for single-equation models 918
lnskew0 . . . . . Find zero-skewness log or Box–Cox transform 924
log . . . . . Echo copy of session to file 928
logistic . . . . . Logistic regression, reporting odds ratios 932
logistic postestimation . . . . . Postestimation tools for logistic 943
logit . . . . . Logistic regression, reporting coefficients 970
logit postestimation . . . . . Postestimation tools for logit 983
loneway . . . . . Large one-way ANOVA, random effects, and reliability 989
lowess . . . . . Lowess smoothing 995
lpoly . . . . . Kernel-weighted local polynomial smoothing 1001
lrtest . . . . . Likelihood-ratio test after estimation 1011
lv . . . . . Letter-value displays 1021

margins . . . . . Marginal means, predictive margins, and marginal effects 1027
margins postestimation . . . . . Postestimation tools for margins 1080
margins, contrast . . . . . Contrasts of margins 1082
margins, pwcompare . . . . . Pairwise comparisons of margins 1094
marginsplot . . . . . Graph results from margins (profile plots, etc.) 1099
matsize . . . . . Set the maximum number of variables in a model 1130
maximize . . . . . Details of iterative maximization 1132
mean . . . . . Estimate means 1139
mean postestimation . . . . . Postestimation tools for mean 1150

meta . . . . . Meta-analysis 1152
mfp . . . . . Multivariable fractional polynomial models 1153
mfp postestimation . . . . . Postestimation tools for mfp 1164
misstable . . . . . Tabulate missing values 1165
mkspline . . . . . Linear and restricted cubic spline construction 1174
ml . . . . . Maximum likelihood estimation 1180
mlogit . . . . . Multinomial (polytomous) logistic regression 1207
mlogit postestimation . . . . . Postestimation tools for mlogit 1221
more . . . . . The —more— message 1232
mprobit . . . . . Multinomial probit regression 1234
mprobit postestimation . . . . . Postestimation tools for mprobit 1241
mvreg . . . . . Multivariate regression 1244
mvreg postestimation . . . . . Postestimation tools for mvreg 1251

nbreg . . . . . Negative binomial regression 1253
nbreg postestimation . . . . . Postestimation tools for nbreg and gnbreg 1265
nestreg . . . . . Nested model statistics 1269
net . . . . . Install and manage user-written additions from the Internet 1275
net search . . . . . Search the Internet for installable packages 1293
netio . . . . . Control Internet connections 1297
news . . . . . Report Stata news 1300
nl . . . . . Nonlinear least-squares estimation 1301
nl postestimation . . . . . Postestimation tools for nl 1321
nlcom . . . . . Nonlinear combinations of estimators 1323
nlogit . . . . . Nested logit regression 1334
nlogit postestimation . . . . . Postestimation tools for nlogit 1356
nlsur . . . . . Estimation of nonlinear systems of equations 1361
nlsur postestimation . . . . . Postestimation tools for nlsur 1383
nptrend . . . . . Test for trend across ordered groups 1385

ologit . . . . . Ordered logistic regression 1389
ologit postestimation . . . . . Postestimation tools for ologit 1398
oneway . . . . . One-way analysis of variance 1402
oprobit . . . . . Ordered probit regression 1412
oprobit postestimation . . . . . Postestimation tools for oprobit 1418
orthog . . . . . Orthogonalize variables and compute orthogonal polynomials 1422

pcorr . . . . . Partial and semipartial correlation coefficients 1429
permute . . . . . Monte Carlo permutation tests 1432
pk . . . . . Pharmacokinetic (biopharmaceutical) data 1442
pkcollapse . . . . . Generate pharmacokinetic measurement dataset 1450
pkcross . . . . . Analyze crossover experiments 1453
pkequiv . . . . . Perform bioequivalence tests 1462
pkexamine . . . . . Calculate pharmacokinetic measures 1469
pkshape . . . . . Reshape (pharmacokinetic) Latin-square data 1475
pksumm . . . . . Summarize pharmacokinetic data 1483
poisson . . . . . Poisson regression 1488
poisson postestimation . . . . . Postestimation tools for poisson 1497
predict . . . . . Obtain predictions, residuals, etc., after estimation 1503
predictnl . . . . . Obtain nonlinear predictions, standard errors, etc., after estimation 1514
probit . . . . . Probit regression 1526
probit postestimation . . . . . Postestimation tools for probit 1538

proportion ..... Estimate proportions 1542
proportion postestimation ..... Postestimation tools for proportion 1547
prtest ..... One- and two-sample tests of proportions 1548
pwcompare ..... Pairwise comparisons 1553
pwcompare postestimation ..... Postestimation tools for pwcompare 1581
pwmean ..... Pairwise comparisons of means 1583
pwmean postestimation ..... Postestimation tools for pwmean 1593

qc ..... Quality control charts 1595
qreg ..... Quantile regression 1610
qreg postestimation ..... Postestimation tools for qreg, iqreg, sqreg, and bsqreg 1630
query ..... Display system parameters 1632

ranksum ..... Equality tests on unmatched data 1639
ratio ..... Estimate ratios 1645
ratio postestimation ..... Postestimation tools for ratio 1654
reg3 ..... Three-stage estimation for systems of simultaneous equations 1655
reg3 postestimation ..... Postestimation tools for reg3 1676
regress ..... Linear regression 1679
regress postestimation ..... Postestimation tools for regress 1704
regress postestimation time series ..... Postestimation tools for regress with time series 1749
#review ..... Review previous commands 1759
roc ..... Receiver operating characteristic (ROC) analysis 1760
roccomp ..... Tests of equality of ROC areas 1762
rocfit ..... Parametric ROC models 1774
rocfit postestimation ..... Postestimation tools for rocfit 1781
rocreg ..... Receiver operating characteristic (ROC) regression 1785
rocreg postestimation ..... Postestimation tools for rocreg 1837
rocregplot ..... Plot marginal and covariate-specific ROC curves after rocreg 1852
roctab ..... Nonparametric ROC analysis 1871
rologit ..... Rank-ordered logistic regression 1881
rologit postestimation ..... Postestimation tools for rologit 1898
rreg ..... Robust regression 1900
rreg postestimation ..... Postestimation tools for rreg 1907
runtest ..... Test for random order 1909

sampsi ..... Sample size and power for means and proportions 1915
saved results ..... Saved results 1926
scobit ..... Skewed logistic regression 1931
scobit postestimation ..... Postestimation tools for scobit 1940
sdtest ..... Variance-comparison tests 1943
search ..... Search Stata documentation 1950
serrbar ..... Graph standard error bar chart 1956
set ..... Overview of system parameters 1959
set cformat ..... Format settings for coefficient tables 1971
set_defaults ..... Reset system parameters to original Stata defaults 1974
set emptycells ..... Set what to do with empty cells in interactions 1976
set seed ..... Specify initial value of random-number seed 1977
set showbaselevels ..... Display settings for coefficient tables 1982
signrank ..... Equality tests on matched data 1986
simulate ..... Monte Carlo simulations 1992
sj ..... Stata Journal and STB installation instructions 1999

sktest . . . Skewness and kurtosis test for normality 2002
slogit . . . Stereotype logistic regression 2007
slogit postestimation . . . Postestimation tools for slogit 2021
smooth . . . Robust nonlinear smoother 2025
spearman . . . Spearman's and Kendall's correlations 2033
spikeplot . . . Spike plots and rootograms 2042
ssc . . . Install and uninstall packages from SSC 2046
stem . . . Stem-and-leaf displays 2053
stepwise . . . Stepwise estimation 2057
suest . . . Seemingly unrelated estimation 2067
summarize . . . Summary statistics 2085
sunflower . . . Density-distribution sunflower plots 2094
sureg . . . Zellner's seemingly unrelated regression 2100
sureg postestimation . . . Postestimation tools for sureg 2108
swilk . . . Shapiro–Wilk and Shapiro–Francia tests for normality 2111
symmetry . . . Symmetry and marginal homogeneity tests 2115

table . . . Tables of summary statistics 2123
tabstat . . . Display table of summary statistics 2133
tabulate oneway . . . One-way tables of frequencies 2138
tabulate twoway . . . Two-way tables of frequencies 2146
tabulate, summarize() . . . One- and two-way tables of summary statistics 2162
test . . . Test linear hypotheses after estimation 2167
testnl . . . Test nonlinear hypotheses after estimation 2186
tetrachoric . . . Tetrachoric correlations for binary variables 2195
tnbreg . . . Truncated negative binomial regression 2205
tnbreg postestimation . . . Postestimation tools for tnbreg 2213
tobit . . . Tobit regression 2217
tobit postestimation . . . Postestimation tools for tobit 2224
total . . . Estimate totals 2229
total postestimation . . . Postestimation tools for total 2235
tpoisson . . . Truncated Poisson regression 2237
tpoisson postestimation . . . Postestimation tools for tpoisson 2244
translate . . . Print and translate logs 2247
treatreg . . . Treatment-effects model 2257
treatreg postestimation . . . Postestimation tools for treatreg 2269
truncreg . . . Truncated regression 2272
truncreg postestimation . . . Postestimation tools for truncreg 2279
ttest . . . Mean-comparison tests 2282

update . . . Update Stata 2291

vce_option . . . Variance estimators 2294
view . . . View files and logs 2299
vwls . . . Variance-weighted least squares 2303
vwls postestimation . . . Postestimation tools for vwls 2309

which . . . Display location and version for an ado-file 2311

xi . . . Interaction expansion 2313

zinb . . . Zero-inflated negative binomial regression 2324
zinb postestimation . . . Postestimation tools for zinb 2331
zip . . . Zero-inflated Poisson regression 2334

zip postestimation . . . . . Postestimation tools for zip 2340

Author index 2343
Subject index 2357

Cross-referencing the documentation

When reading this manual, you will find references to other Stata manuals. For example,

[U] **26 Overview of Stata estimation commands**
[XT] **xtabond**
[D] **reshape**

The first example is a reference to chapter 26, *Overview of Stata estimation commands*, in the *User's Guide*; the second is a reference to the `xtabond` entry in the *Longitudinal-Data/Panel-Data Reference Manual*; and the third is a reference to the `reshape` entry in the *Data-Management Reference Manual*.

All the manuals in the Stata Documentation have a shorthand notation:

[GSM]	*Getting Started with Stata for Mac*
[GSU]	*Getting Started with Stata for Unix*
[GSW]	*Getting Started with Stata for Windows*
[U]	*Stata User's Guide*
[R]	*Stata Base Reference Manual*
[D]	*Stata Data-Management Reference Manual*
[G]	*Stata Graphics Reference Manual*
[XT]	*Stata Longitudinal-Data/Panel-Data Reference Manual*
[MI]	*Stata Multiple-Imputation Reference Manual*
[MV]	*Stata Multivariate Statistics Reference Manual*
[P]	*Stata Programming Reference Manual*
[SEM]	*Stata Structural Equation Modeling Reference Manual*
[SVY]	*Stata Survey Data Reference Manual*
[ST]	*Stata Survival Analysis and Epidemiological Tables Reference Manual*
[TS]	*Stata Time-Series Reference Manual*
[I]	*Stata Quick Reference and Index*
[M]	*Mata Reference Manual*

Detailed information about each of these manuals may be found online at

http://www.stata-press.com/manuals/

Title

intro — Introduction to base reference manual

Description

This entry describes the organization of the reference manuals.

Remarks

The complete list of reference manuals is as follows:

[R]	*Stata Base Reference Manual*
	Volume 1, A–F
	Volume 2, G–M
	Volume 3, N–R
	Volume 4, S–Z
[D]	*Stata Data-Management Reference Manual*
[G]	*Stata Graphics Reference Manual*
[XT]	*Stata Longitudinal-Data/Panel-Data Reference Manual*
[MI]	*Stata Multiple-Imputation Reference Manual*
[MV]	*Stata Multivariate Statistics Reference Manual*
[P]	*Stata Programming Reference Manual*
[SEM]	*Stata Structural Equation Modeling Reference Manual*
[SVY]	*Stata Survey Data Reference Manual*
[ST]	*Stata Survival Analysis and Epidemiological Tables Reference Manual*
[TS]	*Stata Time-Series Reference Manual*
[I]	*Stata Quick Reference and Index*
[M]	*Mata Reference Manual*

When we refer to "reference manuals", we mean all manuals listed above.

When we refer to the *Base Reference Manual*, we mean just the four-volume *Base Reference Manual*, known as [R].

When we refer to the specialty manuals, we mean all the manuals listed above except [R] and [I], the *Stata Quick Reference and Index*.

Detailed information about each of these manuals can be found online at

http://www.stata-press.com/manuals/

Arrangement of the reference manuals

Each manual contains the following sections:

- Table of contents.
  At the beginning of volume 1 of [R], the *Base Reference Manual*, is a table of contents for the four volumes.
- Cross-referencing the documentation.
  This section lists all the manuals and explains how they are cross-referenced.
- Introduction.
  This entry—usually called intro—provides an overview of the manual. In the specialty manuals, this introduction suggests entries that you might want to read first and provides information about new features.

  Each specialty manual contains an overview of the commands described in it.
- Entries.
  Entries are arranged in alphabetical order. Most entries describe Stata commands, but some entries discuss concepts, and others provide overviews.

  Entries that describe estimation commands are followed by an entry discussing postestimation commands that are available for use after the estimation command. For example, the **xtlogit** entry in the [XT] manual is followed by the **xtlogit postestimation** entry.
- Index.
  At the end of each manual is an index. The index for the entire four-volume *Base Reference Manual* is found at the end of the fourth volume.

The *Quick Reference and Index*, [I], contains a combined index for all the manuals and a subject table of contents for all the manuals and the *User's Guide*. It also contains quick-reference information on many subjects, such as the estimation commands.

To find information and commands quickly, use Stata's `search` command; see [R] **search** (see the entry `search` in the [R] manual). You can broaden your search to the Internet by using `search, all` to find commands and extensions written by Stata users.

Arrangement of each entry

Entries in the Stata reference manuals, except the [M] and [SEM] manuals, generally contain the following sections, which are explained below:

Syntax
Menu
Description
Options
Remarks
Saved results
Methods and formulas
References
Also see

Syntax

A command's syntax diagram shows how to type the command, indicates all possible options, and gives the minimal allowed abbreviations for all the items in the command. For instance, the syntax diagram for the `summarize` command is

`summarize` [*varlist*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`detail`	display additional statistics
`meanonly`	suppress the display; calculate only the mean; programmer's option
`format`	use variable's display format
`separator(#)`	draw separator line after every # variables; default is `separator(5)`
display_options	control spacing and base and empty cells

varlist may contain factor variables; see [U] **11.4.3 Factor variables**.
varlist may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`by` is allowed; see [D] **by**.
`aweights`, `fweights`, and `iweights` are allowed. However, `iweights` may not be used with the `detail` option; see [U] **11.1.6 weight**.

Items in the `typewriter-style font` should be typed exactly as they appear in the diagram, although they may be abbreviated. `Underlining` indicates the shortest abbreviations where abbreviations are allowed. For instance, `summarize` may be abbreviated `su`, `sum`, `summ`, etc., or it may be spelled out completely. Items in the typewriter font that are not underlined may not be abbreviated.

Square brackets denote optional items. In the syntax diagram above, *varlist*, *if*, *in*, *weight*, and the *options* are optional.

The *options* are listed in a table immediately following the diagram, along with a brief description of each.

Items typed in *italics* represent arguments for which you are to substitute variable names, observation numbers, and the like.

The diagrams use the following symbols:

#	Indicates a literal number, for example, `5`; see [U] **12.2 Numbers**.
[ ]	Anything enclosed in brackets is optional.
{ }	At least one of the items enclosed in braces must appear.
|	The vertical bar separates alternatives.
%fmt	Any Stata format, for example, `%8.2f`; see [U] **12.5 Formats: Controlling how data are displayed**.
depvar	The dependent variable in an estimation command; see [U] **20 Estimation and postestimation commands**.
exp	Any algebraic expression, for example, `(5+myvar)/2`; see [U] **13 Functions and expressions**.
filename	Any filename; see [U] **11.6 Filenaming conventions**.

indepvars The independent variables in an estimation command; see [U] **20 Estimation and postestimation commands**.

newvar A variable that will be created by the current command; see [U] **11.4.2 Lists of new variables**.

numlist A list of numbers; see [U] **11.1.8 numlist**.

oldvar A previously created variable; see [U] **11.4.1 Lists of existing variables**.

options A list of options; see [U] **11.1.7 options**.

range An observation range, for example, `5/20`; see [U] **11.1.4 in range**.

"*string*" Any string of characters enclosed in double quotes; see [U] **12.4 Strings**.

varlist A list of variable names; see [U] **11.4 varlists**. If *varlist* allows factor variables, a note to that effect will be shown below the syntax diagram; see [U] **11.4.3 Factor variables**. If *varlist* allows time-series operators, a note to that effect will be shown below the syntax diagram; see [U] **11.4.4 Time-series varlists**.

varname A variable name; see [U] **11.3 Naming conventions**.

weight A [*wgttype*=*exp*] modifier; see [U] **11.1.6 weight** and [U] **20.22 Weighted estimation**.

xvar The variable to be displayed on the horizontal axis.

yvar The variable to be displayed on the vertical axis.

The *Syntax* section will indicate whether factor variables or time-series operators may be used with a command. `summarize` allows factor variables and time-series operators.

If a command allows prefix commands, this will be indicated immediately following the table of options. `summarize` allows `by`.

If a command allows weights, the types of weights allowed will be specified, with the default weight listed first. `summarize` allows `aweights`, `fweights`, and `iweights`, and if the type of weight is not specified, the default is `aweights`.

Menu

A menu indicates how the dialog box for the command may be accessed using the menu system.

Description

Following the syntax diagram is a brief description of the purpose of the command.

Options

If the command allows any options, they are explained here, and for dialog users the location of the options in the dialog is indicated. For instance, in the **logistic** entry in this manual, the *Options* section looks like this:

Model

. . .

SE/Robust

. . .

Reporting

...

Maximization

...

Remarks

The explanations under *Description* and *Options* are exceedingly brief and technical; they are designed to provide a quick summary. The remarks explain in English what the preceding technical jargon means. Examples are used to illustrate the command.

Saved results

Commands are classified as e-class, r-class, s-class, or n-class, according to whether they save calculated results in `e()`, `r()`, `s()`, or not at all. These results can then be used in subroutines by other programs (ado-files). Such saved results are documented here; see [U] **18.8 Accessing results calculated by other programs** and [U] **18.9 Accessing results calculated by estimation commands**.

Methods and formulas

The techniques and formulas used in obtaining the results are described here as tersely and technically as possible. If a command is implemented as an ado-file, that is indicated here.

References

Published sources are listed that either were directly referenced in the preceding text or might be of interest.

Also see

Other manual entries relating to this entry are listed that might also interest you.

Also see

[U] **1.1 Getting Started with Stata**

Title

about — Display information about your Stata

Syntax

```
about
```

Menu

Help > About

Description

`about` displays information about your version of Stata.

Remarks

`about` displays information about the release number, flavor, serial number, and license for your Stata. If you are running Stata for Windows, information about memory is also displayed:

```
. about

Stata/MP 12.0 for Windows (64-bit x86-64)
Revision 24 Aug 2011
Copyright 1985-2011 StataCorp LP

Total physical memory:     8388608 KB
Available physical memory:  937932 KB

10-user 32-core Stata network perpetual license:
       Serial number:  5012041234
         Licensed to:  Alan R. Riley
                       StataCorp
```

Also see

[R] **which** — Display location and version for an ado-file

[U] **5 Flavors of Stata**

Title

adoupdate — Update user-written ado-files

Syntax

`adoupdate` [*pkglist*] [`,` *options*]

options	Description
`update`	perform update; default is to list packages that have updates, but not to update them
`all`	include packages that might have updates; default is to list or update only packages that are known to have updates
`ssconly`	check only packages obtained from SSC; default is to check all installed packages
`dir(`*dir*`)`	check packages installed in *dir*; default is to check those installed in PLUS
`verbose`	provide output to assist in debugging network problems

Description

User-written additions to Stata are called packages. These packages can add remarkable abilities to Stata. Packages are found and installed by using `ssc`, `findit`, and `net`; see [R] **ssc**, [R] **search**, and [R] **net**.

User-written packages are updated by their developers, just as official Stata software is updated by StataCorp.

To determine whether your official Stata software is up to date, and to update it if it is not, you use `update`; see [R] **update**.

To determine whether your user-written additions are up to date, and to update them if they are not, you use `adoupdate`.

Options

`update` specifies that packages with updates be updated. The default is simply to list the packages that could be updated without actually performing the update.

The first time you `adoupdate`, do not specify this option. Once you see `adoupdate` work, you will be more comfortable with it. Then type

```
. adoupdate, update
```

The packages that can be updated will be listed and updated.

`all` is rarely specified. Sometimes, `adoupdate` cannot determine whether a package you previously installed has been updated. `adoupdate` can determine that the package is still available over the web but is unsure whether the package has changed. Usually, the package has not changed, but if you want to be certain that you are using the latest version, reinstall from the source.

Specifying `all` does this. Typing

```
. adoupdate, all
```

adds such packages to the displayed list as needing updating but does not update them. Typing

```
. adoupdate, update all
```

lists such packages and updates them.

`ssconly` is a popular option. Many packages are available from the Statistical Software Components (SSC) archive—often called the Boston College Archive—which is provided at http://repec.org. Many users find most of what they want there. See [R] **ssc** for more information on the SSC.

`ssconly` specifies that `adoupdate` check only packages obtained from that source. Specifying this option is popular because SSC always provides distribution dates, and so `adoupdate` can be certain whether an update exists.

`dir(`*dir*`)` specifies which installed packages be checked. The default is `dir(PLUS)`, and that is probably correct. If you are responsible for maintaining a large system, however, you may have previously installed packages in `dir(SITE)`, where they are shared across users. See [P] **sysdir** for an explanation of these directory codewords. You may also specify an actual directory name, such as `C:\mydir`.

`verbose` is specified when you suspect network problems. It provides more detailed output that may help you diagnose the problem.

Remarks

Do not confuse `adoupdate` with `update`. Use `adoupdate` to update user-written files. Use `update` to update the components (including ado-files) of the official Stata software. To use either command, you must be connected to the Internet.

Remarks are presented under the following headings:

Using adoupdate
Possible problem the first time you run adoupdate and the solution
Notes for developers

Using adoupdate

The first time you try `adoupdate`, type

```
. adoupdate
```

That is, do not specify the `update` option. `adoupdate` without `update` produces a report but does not update any files. The first time you run `adoupdate`, you may see messages such as

```
. adoupdate
  (note:  package utx was installed more than once; older copy removed)
  (remaining output omitted)
```

Having the same packages installed multiple times is common; `adoupdate` cleans that up.

The second time you run `adoupdate`, pick one package to update. Suppose that the report indicates that package `st0008` has an update available. Type

```
. adoupdate st0008, update
```

You can specify one or many packages after the `adoupdate` command. You can even use wildcards such as `st*` to mean all packages that start with `st` or `st*8` to mean all packages that start with `st` and end with `8`. You can do that with or without the `update` option.

Finally, you can let adoupdate update all your user-written additions:

```
. adoupdate, update
```

Possible problem the first time you run adoupdate and the solution

The first time you run adoupdate, you might get many duplicate messages:

```
. adoupdate
  (note: package ___ installed more than once; older copy removed)
  (note: package ___ installed more than once; older copy removed)
  (note: package ___ installed more than once; older copy removed)
  ...
  (note: package ___ installed more than once; older copy removed)
  (remaining output omitted)
```

Some users have hundreds of duplicates. You might even see the same package name repeated more than once:

```
(note: package stylus installed more than once; older copy removed)
(note: package stylus installed more than once; older copy removed)
```

That means that the package was duplicated twice.

Stata tolerates duplicates, and you did nothing wrong when you previously installed and updated packages. adoupdate, however, needs the duplicates removed, mainly so that it does not keep checking the same files.

The solution is to just let adoupdate run. adoupdate will run faster next time, when there are no (or just a few) duplicates.

Notes for developers

adoupdate reports whether an installed package is up to date by comparing its distribution date with that of the package available over the web.

If you are distributing software, include the line

```
d Distribution-Date: date
```

somewhere in your .pkg file. The capitalization of Distribution-Date does not matter, but include the hyphen and the colon as shown. Code the date in either of two formats:

all numeric:	*yyyymmdd*, for example, 20110701
Stata standard:	*ddMONyyyy*, for example, 01jul2011

Saved results

adoupdate saves the following in r():

Macros

r(pkglist) a space-separated list of package names that need updating (update not specified) or that were updated (update specified)

Methods and formulas

`adoupdate` is implemented as an ado-file.

Also see

[R] **ssc** — Install and uninstall packages from SSC

[R] **search** — Search Stata documentation

[R] **net** — Install and manage user-written additions from the Internet

[R] **update** — Update Stata

Title

alpha — Compute interitem correlations (covariances) and Cronbach's alpha

Syntax

`alpha` *varlist* [*if*] [*in*] [, *options*]

options	Description
Options	
`asis`	take sign of each item as is
`casewise`	delete cases with missing values
`detail`	list individual interitem correlations and covariances
`generate(`*newvar*`)`	save the generated scale in *newvar*
`item`	display item-test and item-rest correlations
`label`	include variable labels in output table
`min(#)`	must have at least # observations for inclusion
`reverse(`*varlist*`)`	reverse signs of these variables
`std`	standardize items in the scale to mean 0, variance 1

`by` is allowed; see [D] **by**.

Menu

Statistics > Multivariate analysis > Cronbach's alpha

Description

`alpha` computes the interitem correlations or covariances for all pairs of variables in *varlist* and Cronbach's α statistic for the scale formed from them. At least two variables must be specified with `alpha`.

Options

Options

`asis` specifies that the sense (sign) of each item be taken as presented in the data. The default is to determine the sense empirically and reverse the scorings for any that enter negatively.

`casewise` specifies that cases with missing values be deleted listwise. The default is pairwise computation of covariances and correlations.

`detail` lists the individual interitem correlations and covariances.

`generate(`*newvar*`)` specifies that the scale constructed from *varlist* be stored in *newvar*. Unless `asis` is specified, the sense of items entering negatively is automatically reversed. If `std` is also specified, the scale is constructed by using standardized (mean 0, variance 1) values of the individual items. Unlike most Stata commands, `generate()` does not use casewise deletion. A score is created for every observation for which there is a response to at least one item (one variable in *varlist* is not missing). The summative score is divided by the number of items over which the sum is calculated.

`item` specifies that item-test and item-rest correlations and the effects of removing an item from the scale be displayed. `item` is valid only when more than two variables are specified in *varlist*.

`label` requests that the detailed output table be displayed in a compact format that enables the inclusion of variable labels.

`min(#)` specifies that only cases with at least # observations be included in the computations. `casewise` is a shorthand for `min(`*k*`)`, where *k* is the number of variables in *varlist*.

`reverse(`*varlist*`)` specifies that the signs (directions) of the variables (items) in *varlist* be reversed. Any variables specified in `reverse()` that are not also included in `alpha`'s *varlist* are ignored.

`std` specifies that the items in the scale be standardized (mean 0, variance 1) before summing.

Remarks

Cronbach's alpha (Cronbach 1951) assesses the reliability of a summative rating (Likert 1932) scale composed of the variables (called *items*) specified. The set of items is often called a *test* or *battery*. A scale is simply the sum of the individual item scores, reversing the scoring for statements that have negative correlations with the factor (for example, attitude) being measured. Scales can be formed by using the raw item scores or standardized item scores.

The reliability α is defined as the square of the correlation between the measured scale and the underlying factor. If you think of a test as being composed of a random sample of items from a hypothetical domain of items designed to measure the same thing, α represents the expected correlation of one test with an alternative form containing the same number of items. The square root of α is the estimated correlation of a test with errorless true scores (Nunnally and Bernstein 1994, 235).

In addition to reporting α, `alpha` generates the summative scale from the items (variables) specified and automatically reverses the sense of any when necessary. Stata's decision can be overridden by specifying the `reverse(`*varlist*`)` option.

Because it concerns reliability in measuring an unobserved factor, α is related to factor analysis. The test should be designed to measure one factor, and, because the scale will be composed of an unweighted sum, the factor loadings should all contribute roughly equal information to the score. Both of these assumptions can be verified with `factor`; see [MV] **factor**. Equality of factor loadings can also be assessed by using the `item` option.

▷ Example 1

To illustrate `alpha`, we apply it, first without and then with the `item` option, to the automobile dataset after randomly introducing missing values:

```
. use http://www.stata-press.com/data/r12/automiss
(1978 Automobile Data)
. alpha price headroom rep78 trunk weight length turn displ, std
Test scale = mean(standardized items)
Reversed item: rep78
Average interitem correlation:      0.5251
Number of items in the scale:            8
Scale reliability coefficient:      0.8984
```

The scale derived from our somewhat arbitrarily chosen automobile items (variables) appears to be reasonable because the estimated correlation between it and the underlying factor it measures is $\sqrt{0.8984} \approx 0.9478$ and the estimated correlation between this battery of eight items and all other eight-item batteries from the same domain is 0.8984. Because the "items" are not on the same scale,

it is important that `std` was specified so that the scale and its reliability were based on the sum of standardized variables. We could obtain the scale in a new variable called `sc` with the `gen(sc)` option.

Though the scale appears reasonable, we include the `item` option to determine if all the items fit the scale:

```
. alpha price headroom rep78 trunk weight length turn displ, std item
Test scale = mean(standardized items)
```

Item	Obs	Sign	item-test correlation	item-rest correlation	average interitem correlation	alpha
price	70	+	0.5260	0.3719	0.5993	0.9128
headroom	66	+	0.6716	0.5497	0.5542	0.8969
rep78	61	-	0.4874	0.3398	0.6040	0.9143
trunk	69	+	0.7979	0.7144	0.5159	0.8818
weight	64	+	0.9404	0.9096	0.4747	0.8635
length	69	+	0.9382	0.9076	0.4725	0.8625
turn	66	+	0.8678	0.8071	0.4948	0.8727
displacement	63	+	0.8992	0.8496	0.4852	0.8684
Test scale					0.5251	0.8984

"Test" denotes the additive scale; here 0.5251 is the average interitem correlation, and 0.8984 is the alpha coefficient for a test scale based on all items.

"Obs" shows the number of nonmissing values of the items; "Sign" indicates the direction in which an item variable entered the scale; "`-`" denotes that the item was reversed. The remaining four columns in the table provide information on the effect of one item on the scale.

Column four gives the item-test correlations. Apart from the sign of the correlation for items that entered the scale in reversed order, these correlations are the same numbers as those computed by the commands

```
. alpha price headroom rep78 trunk weight length turn displ, std gen(sc)
. pwcorr sc price headroom rep78 trunk weight length turn displ
```

Typically, the item-test correlations should be roughly the same for all items. Item-test correlations may not be adequate to detect items that fit poorly because the poorly fitting items may distort the scale. Accordingly, it may be more useful to consider item-rest correlations (Nunnally and Bernstein 1994), that is, the correlation between an item and the scale that is formed by all other items. The average interitem correlations (covariances if `std` is omitted) of all items, excluding one, are shown in column six. Finally, column seven gives Cronbach's α for the test scale, which consists of all but the one item.

Here neither the `price` item nor the `rep78` item seems to fit well in the scale in all respects. The item-test and item-rest correlations of `price` and `rep78` are much lower than those of the other items. The average interitem correlation increases substantially by removing either `price` or `rep78`; apparently, they do not correlate strongly with the other items. Finally, we see that Cronbach's α coefficient will increase from 0.8984 to 0.9128 if the `price` item is dropped, and it will increase from 0.8984 to 0.9143 if `rep78` is dropped. For well-fitting items, we would of course expect that α decreases by shortening the test.

◁

▷ Example 2

The variable names for the automobile data are reasonably informative. This may not always be true; items in batteries commonly used to measure personality traits, attitudes, values, etc., are usually named with indexed names such as `item12a`, `item12b`, etc. The `label` option forces `alpha` to produce the same statistical information in a more compact format that leaves room to include variable (item) labels. In this compact format, `alpha` excludes the number of nonmissing values of the items, displays the statistics using fewer digits, and uses somewhat cryptic headers:

```
. alpha price headroom rep78 trunk weight length turn displ, std item label detail
Test scale = mean(standardized items)
```

Items	S	it-cor	ir-cor	ii-cor	alpha	label
price	+	0.526	0.372	0.599	0.913	Price
headroom	+	0.672	0.550	0.554	0.897	Headroom (in.)
rep78	-	0.487	0.340	0.604	0.914	Repair Record 1978
trunk	+	0.798	0.714	0.516	0.882	Trunk space (cu. ft.)
weight	+	0.940	0.910	0.475	0.863	Weight (lbs.)
length	+	0.938	0.908	0.473	0.862	Length (in.)
turn	+	0.868	0.807	0.495	0.873	Turn Circle (ft.)
displacement	+	0.899	0.850	0.485	0.868	Displacement (cu. in.)
Test scale				0.525	0.898	mean(standardized items)

```
Interitem correlations (reverse applied) (obs=pairwise, see below)
```

	price	headroom	rep78	trunk
price	1.0000			
headroom	0.1174	1.0000		
rep78	-0.0479	0.1955	1.0000	
trunk	0.2748	0.6841	0.2777	1.0000
weight	0.5093	0.5464	0.3624	0.6486
length	0.4511	0.5823	0.3162	0.7404
turn	0.3528	0.4067	0.4715	0.5900
displacement	0.5537	0.5166	0.3391	0.6471

	weight	length	turn	displacement
weight	1.0000			
length	0.9425	1.0000		
turn	0.8712	0.8589	1.0000	
displacement	0.8753	0.8422	0.7723	1.0000

```
Pairwise number of observations
```

	price	headroom	rep78	trunk
price	70			
headroom	62	66		
rep78	59	54	61	
trunk	65	61	59	69
weight	60	56	52	60
length	66	61	58	64
turn	62	58	56	62
displacement	59	58	51	58

	weight	length	turn	displacement
weight	64			
length	60	69		
turn	57	61	66	
displacement	54	58	56	63

Because the `detail` option was also specified, the interitem correlation matrix was printed, together with the number of observations used for each entry (because these varied across the matrix). Note the negative sign attached to `rep78` in the output, indicating the sense in which it entered the scale.

Better-looking output with less-cryptic headers is produced if the linesize is set to a value of at least 100:

```
. set linesize 100
. alpha price headroom rep78 trunk weight length turn displ, std item label
Test scale = mean(standardized items)
```

Item	Obs	Sign	item-test corr.	item-rest corr.	interitem corr.	alpha	Label
price	70	+	0.5260	0.3719	0.5993	0.9128	Price
headroom	62	+	0.6716	0.5497	0.5542	0.8969	Headroom (in.)
rep78	59	-	0.4874	0.3398	0.6040	0.9143	Repair Record 1978
trunk	65	+	0.7979	0.7144	0.5159	0.8818	Trunk space (cu. ft.)
weight	60	+	0.9404	0.9096	0.4747	0.8635	Weight (lbs.)
length	66	+	0.9382	0.9076	0.4725	0.8625	Length (in.)
turn	62	+	0.8678	0.8071	0.4948	0.8727	Turn Circle (ft.)
displacement	59	+	0.8992	0.8496	0.4852	0.8684	Displacement (cu. in.)
Test scale					0.5251	0.8984	mean(standardized items)

◁

Users of `alpha` require some standard for judging values of α. We paraphrase Nunnally and Bernstein (1994, 265): In the early stages of research, modest reliability of 0.70 or higher will suffice; values in excess of 0.80 often waste time and funds. In contrast, where measurements on individuals are of interest, a reliability of 0.80 may not be nearly high enough. Even with a reliability of 0.90, the standard error of measurement is almost one-third as large as the standard deviation of test scores; a reliability of 0.90 is the minimum that should be tolerated, and a reliability of 0.95 should be considered the desirable standard.

Saved results

`alpha` saves the following in `r()`:

Scalars

`r(alpha)`	scale reliability coefficient
`r(k)`	number of items in the scale
`r(cov)`	average interitem covariance
`r(rho)`	average interitem correlation if `std` is specified

Matrices

`r(Alpha)`	scale reliability coefficient
`r(ItemTestCorr)`	item-test correlation
`r(ItemRestCorr)`	item-rest correlation
`r(MeanInterItemCov)`	average interitem covariance
`r(MeanInterItemCorr)`	average interitem correlation if `std` is specified

If the `item` option is specified, results are saved as row matrices for the `k` subscales when one variable is removed.

Methods and formulas

`alpha` is implemented as an ado-file.

Let x_i, $i = 1, \ldots, k$, be the variables over which α is to be calculated. Let s_i be the sign with which x_i enters the scale. If `asis` is specified, $s_i = 1$ for all i. Otherwise, principal-factor analysis is performed on x_i, and the first factor's score is predicted; see [MV] **factor**. s_i is -1 if correlation of the x_i and the predicted score is negative and $+1$ otherwise.

Let r_{ij} be the correlation between x_i and x_j, c_{ij} be the covariance, and n_{ij} be the number of observations used in calculating the correlation or covariance. The average correlation is

$$\overline{r} = \frac{\sum_{i=2}^{k}\sum_{j=1}^{i-1} s_i s_j n_{ij} r_{ij}}{\sum_{i=2}^{k}\sum_{j=1}^{i-1} n_{ij}}$$

and the average covariance similarly is

$$\overline{c} = \frac{\sum_{i=2}^{k}\sum_{j=1}^{i-1} s_i s_j n_{ij} c_{ij}}{\sum_{i=2}^{k}\sum_{j=1}^{i-1} n_{ij}}$$

Let c_{ii} denote the variance of x_i, and define the average variance as

$$\overline{v} = \frac{\sum_{i=1}^{k} n_{ii} c_{ii}}{\sum_{i=1}^{k} n_{ii}}$$

If `std` is specified, the scale reliability α is calculated as defined by the general form of the Spearman–Brown Prophecy Formula (Nunnally and Bernstein 1994, 232; Allen and Yen 1979, 85–88):

$$\alpha = \frac{k\overline{r}}{1 + (k-1)\overline{r}}$$

This expression corresponds to α under the assumption that the summative rating is the sum of the standardized variables (Nunnally and Bernstein 1994, 234). If `std` is not specified, α is defined (Nunnally and Bernstein 1994, 232 and 234) as

$$\alpha = \frac{k\overline{c}}{\overline{v} + (k-1)\overline{c}}$$

Let x_{ij} reflect the value of item i in the jth observation. If `std` is specified, the jth value of the scale computed from the k x_{ij} items is

$$S_j = \frac{1}{k_j}\sum_{i=1}^{k} s_i S(x_{ij})$$

where $S()$ is the function that returns the standardized (mean 0, variance 1) value if x_{ij} is not missing and returns zero if x_{ij} is missing. k_j is the number of nonmissing values in x_{ij}, $i = 1, \ldots, k$. If `std` is not specified, $S()$ is the function that returns x_{ij} or returns missing if x_{ij} is missing.

Lee Joseph Cronbach (1916–2001) was an American psychometrician and educational psychologist who worked principally on measurement theory, program evaluation, and instruction. He taught and researched at the State College of Washington, the University of Chicago, the University of Illinois, and Stanford University. Cronbach's initial paper on alpha led to a theory of test reliability.

Acknowledgment

This improved version of `alpha` was written by Jeroen Weesie, Department of Sociology, Utrecht University, The Netherlands.

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Also see

[MV] **factor** — Factor analysis

Title

ameans — Arithmetic, geometric, and harmonic means

Syntax

`ameans` [*varlist*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Main	
`add(#)`	add # to each variable in *varlist*
`only`	add # only to variables with nonpositive values
`level(#)`	set confidence level; default is `level(95)`

`by` is allowed; see [D] **by**.

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Arith./geometric/harmonic means

Description

`ameans` computes the arithmetic, geometric, and harmonic means, with their corresponding confidence intervals, for each variable in *varlist* or for all the variables in the data if *varlist* is not specified. `gmeans` and `hmeans` are synonyms for `ameans`.

If you simply want arithmetic means and corresponding confidence intervals, see [R] **ci**.

Options

Main

`add(#)` adds the value # to each variable in *varlist* before computing the means and confidence intervals. This option is useful when analyzing variables with nonpositive values.

`only` modifies the action of the `add(#)` option so that it adds # only to variables with at least one nonpositive value.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

Remarks

▷ Example 1

We have a dataset containing 8 observations on a variable named `x`. The eight values are 5, 4, −4, −5, 0, 0, *missing*, and 7.

```
. ameans x
```

Variable	Type	Obs	Mean	[95% Conf.	Interval]
x	Arithmetic	7	1	-3.204405	5.204405
	Geometric	3	5.192494	2.57899	10.45448
	Harmonic	3	5.060241	3.023008	15.5179

```
. ameans x, add(5)
```

Variable	Type	Obs	Mean	[95% Conf.	Interval]	
x	Arithmetic	7	6	1.795595	10.2044	*
	Geometric	6	5.477226	2.1096	14.22071	*
	Harmonic	6	3.540984	.	.	*

```
(*) 5 was added to the variables prior to calculating the results.
Missing values in confidence intervals for harmonic mean indicate
that confidence interval is undefined for corresponding variables.
Consult Reference Manual for details.
```

The number of observations displayed for the arithmetic mean is the number of nonmissing observations. The number of observations displayed for the geometric and harmonic means is the number of nonmissing, positive observations. Specifying the `add(5)` option produces 3 more positive observations. The confidence interval for the harmonic mean is not reported; see *Methods and formulas* below.

◁

Saved results

`ameans` saves the following in `r()`:

Scalars

`r(N)`	number of nonmissing observations; used for arithmetic mean
`r(N_pos)`	number of nonmissing positive observations; used for geometric and harmonic means
`r(mean)`	arithmetic mean
`r(lb)`	lower bound of confidence interval for arithmetic mean
`r(ub)`	upper bound of confidence interval for arithmetic mean
`r(Var)`	variance of untransformed data
`r(mean_g)`	geometric mean
`r(lb_g)`	lower bound of confidence interval for geometric mean
`r(ub_g)`	upper bound of confidence interval for geometric mean
`r(Var_g)`	variance of $\ln x_i$
`r(mean_h)`	harmonic mean
`r(lb_h)`	lower bound of confidence interval for harmonic mean
`r(ub_h)`	upper bound of confidence interval for harmonic mean
`r(Var_h)`	variance of $1/x_i$

Methods and formulas

`ameans` is implemented as an ado-file.

See Armitage, Berry, and Matthews (2002) or Snedecor and Cochran (1989). For a history of the concept of the mean, see Plackett (1958).

When restricted to the same set of values (that is, to positive values), the arithmetic mean ($\overline{x}$) is greater than or equal to the geometric mean, which in turn is greater than or equal to the harmonic mean. Equality holds only if all values within a sample are equal to a positive constant.

The arithmetic mean and its confidence interval are identical to those provided by `ci`; see [R] **ci**.

To compute the geometric mean, `ameans` first creates $u_j = \ln x_j$ for all positive x_j. The arithmetic mean of the u_j and its confidence interval are then computed as in `ci`. Let $\overline{u}$ be the resulting mean, and let $[\,L, U\,]$ be the corresponding confidence interval. The geometric mean is then $\exp(\overline{u})$, and its confidence interval is $[\,\exp(L), \exp(U)\,]$.

The same procedure is followed for the harmonic mean, except that then $u_j = 1/x_j$. The harmonic mean is then $1/\overline{u}$, and its confidence interval is $[\,1/U, 1/L\,]$ if L is greater than zero. If L is not greater than zero, this confidence interval is not defined, and missing values are reported.

When weights are specified, `ameans` applies the weights to the transformed values, $u_j = \ln x_j$ and $u_j = 1/x_j$, respectively, when computing the geometric and harmonic means. For details on how the weights are used to compute the mean and variance of the u_j, see [R] **summarize**. Without weights, the formula for the geometric mean reduces to

$$\exp\Big\{\frac{1}{n}\sum_j \ln(x_j)\Big\}$$

Without weights, the formula for the harmonic mean is

$$\frac{n}{\sum_j \frac{1}{x_j}}$$

Acknowledgments

This improved version of `ameans` is based on the `gmci` command (Carlin, Vidmar, and Ramalheira 1998) and was written by John Carlin, University of Melbourne, Australia; Suzanna Vidmar, University of Melbourne, Australia; and Carlos Ramalheira, Coimbra University Hospital, Portugal.

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Also see

[R] **ci** — Confidence intervals for means, proportions, and counts

[R] **mean** — Estimate means

[R] **summarize** — Summary statistics

[SVY] **svy estimation** — Estimation commands for survey data

Title

anova — Analysis of variance and covariance

Syntax

`anova` *varname* [`termlist`] [*if*] [*in*] [*weight*] [`,` *options*]

where *termlist* is a factor-variable list (see [U] **11.4.3 Factor variables**) with the following additional features:

- Variables are assumed to be categorical; use the `c.` factor-variable operator to override this.
- The `|` symbol (indicating nesting) may be used in place of the `#` symbol (indicating interaction).
- The `/` symbol is allowed after a term and indicates that the following term is the error term for the preceding terms.

options	Description
Model	
`repeated(`*varlist*`)`	variables in *term*s that are repeated-measures variables
`partial`	use partial (or marginal) sums of squares
`sequential`	use sequential sums of squares
`noconstant`	suppress constant term
`dropemptycells`	drop empty cells from the design matrix
Adv. model	
`bse(`*term*`)`	between-subjects error term in repeated-measures ANOVA
`bseunit(`*varname*`)`	variable representing lowest unit in the between-subjects error term
`grouping(`*varname*`)`	grouping variable for computing pooled covariance matrix

`bootstrap`, `by`, `jackknife`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.
`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > ANOVA/MANOVA > Analysis of variance and covariance

Description

The `anova` command fits analysis-of-variance (ANOVA) and analysis-of-covariance (ANCOVA) models for balanced and unbalanced designs, including designs with missing cells; for repeated-measures ANOVA; and for factorial, nested, or mixed designs.

The `regress` command (see [R] **regress**) will display the coefficients, standard errors, etc., of the regression model underlying the last run of `anova`.

If you want to fit one-way ANOVA models, you may find the `oneway` or `loneway` command more convenient; see [R] **oneway** and [R] **loneway**. If you are interested in MANOVA or MANCOVA, see [MV] **manova**.

Options

Model

`repeated(`*varlist*`)` indicates the names of the categorical variables in the *term*s that are to be treated as repeated-measures variables in a repeated-measures ANOVA or ANCOVA.

`partial` presents the ANOVA table using partial (or marginal) sums of squares. This setting is the default. Also see the `sequential` option.

`sequential` presents the ANOVA table using sequential sums of squares.

`noconstant` suppresses the constant term (intercept) from the ANOVA or regression model.

`dropemptycells` drops empty cells from the design matrix. If `c(emptycells)` is set to `keep` (see [R] **set emptycells**), this option temporarily resets it to `drop` before running the ANOVA model. If `c(emptycells)` is already set to `drop`, this option does nothing.

Adv. model

`bse(`*term*`)` indicates the between-subjects error term in a repeated-measures ANOVA. This option is needed only in the rare case when the `anova` command cannot automatically determine the between-subjects error term.

`bseunit(`*varname*`)` indicates the variable representing the lowest unit in the between-subjects error term in a repeated-measures ANOVA. This option is rarely needed because the `anova` command automatically selects the first variable listed in the between-subjects error term as the default for this option.

`grouping(`*varname*`)` indicates a variable that determines which observations are grouped together in computing the covariance matrices that will be pooled and used in a repeated-measures ANOVA. This option is rarely needed because the `anova` command automatically selects the combination of all variables except the first (or as specified in the `bseunit()` option) in the between-subjects error term as the default for grouping observations.

Remarks

Remarks are presented under the following headings:

Introduction
One-way ANOVA
Two-way ANOVA
N-way ANOVA
Weighted data
ANCOVA
Nested designs
Mixed designs
Latin-square designs
Repeated-measures ANOVA

Introduction

`anova` uses least squares to fit the linear models known as ANOVA or ANCOVA (henceforth referred to simply as ANOVA models).

If your interest is in one-way ANOVA, you may find the `oneway` command to be more convenient; see [R] **oneway**.

Structural equation modeling provides a more general framework for fitting ANOVA models; see the *Stata Structural Equation Modeling Reference Manual*.

ANOVA was pioneered by Fisher. It features prominently in his texts on statistical methods and his design of experiments (1925, 1935). Many books discuss ANOVA; see, for instance, Altman (1991); van Belle et al. (2004); Cobb (1998); Snedecor and Cochran (1989); or Winer, Brown, and Michels (1991). For a classic source, see Scheffé (1959). Kennedy and Gentle (1980) discuss ANOVA's computing problems. Edwards (1985) is concerned primarily with the relationship between multiple regression and ANOVA. Acock (2010, chap. 9) illustrates his discussion with Stata output. Repeated-measures ANOVA is discussed in Winer, Brown, and Michels (1991); Kuehl (2000); and Milliken and Johnson (2009). Pioneering work in repeated-measures ANOVA can be found in Box (1954); Geisser and Greenhouse (1958); Huynh and Feldt (1976); and Huynh (1978).

One-way ANOVA

`anova`, entered without options, performs and reports standard ANOVA. For instance, to perform a one-way layout of a variable called `endog` on `exog`, you would type `anova endog exog`.

▷ Example 1

We run an experiment varying the amount of fertilizer used in growing apple trees. We test four concentrations, using each concentration in three groves of 12 trees each. Later in the year, we measure the average weight of the fruit.

If all had gone well, we would have had 3 observations on the average weight for each of the four concentrations. Instead, two of the groves were mistakenly leveled by a confused man on a large bulldozer. We are left with the following data:

```
. use http://www.stata-press.com/data/r12/apple
(Apple trees)
. list, abbrev(10) sepby(treatment)
```

	treatment	weight
1.	1	117.5
2.	1	113.8
3.	1	104.4
4.	2	48.9
5.	2	50.4
6.	2	58.9
7.	3	70.4
8.	3	86.9
9.	4	87.7
10.	4	67.3

To obtain one-way ANOVA results, we type

```
. anova weight treatment
                          Number of obs =      10     R-squared     =  0.9147
                          Root MSE      = 9.07002     Adj R-squared =  0.8721

                   Source | Partial SS    df       MS           F     Prob > F
--------------------------+----------------------------------------------------
                    Model |  5295.54433     3  1765.18144       21.46     0.0013
                          |
                treatment |  5295.54433     3  1765.18144       21.46     0.0013
                          |
                 Residual |  493.591667     6  82.2652778
--------------------------+----------------------------------------------------
                    Total |    5789.136     9  643.237333
```

We find significant (at better than the 1% level) differences among the four concentrations.

Although the output is a usual ANOVA table, let's run through it anyway. Above the table is a summary of the underlying regression. The model was fit on 10 observations, and the root mean squared error (`Root MSE`) is 9.07. The R^2 for the model is 0.9147, and the adjusted R^2 is 0.8721.

The first line of the table summarizes the model. The sum of squares (`Partial SS`) for the model is 5295.5 with 3 degrees of freedom (`df`). This line results in a mean square (`MS`) of $5295.5/3 \approx 1765.2$. The corresponding F statistic is 21.46 and has a significance level of 0.0013. Thus the model appears to be significant at the 0.13% level.

The next line summarizes the first (and only) term in the model, `treatment`. Because there is only one term, the line is identical to that for the overall model.

The third line summarizes the residual. The residual sum of squares is 493.59 with 6 degrees of freedom, resulting in a mean squared error of 82.27. The square root of this latter number is reported as the `Root MSE`.

The model plus the residual sum of squares equals the total sum of squares, which is reported as 5789.1 in the last line of the table. This is the total sum of squares of `weight` after removal of the mean. Similarly, the model plus the residual degrees of freedom sum to the total degrees of freedom, 9. Remember that there are 10 observations. Subtracting 1 for the mean, we are left with 9 total degrees of freedom.

◁

❑ Technical note

Rather than using the `anova` command, we could have performed this analysis by using the `oneway` command. Example 1 in [R] **oneway** repeats this same analysis. You may wish to compare the output.

❑

Type `regress` to see the underlying regression model corresponding to an ANOVA model fit using the `anova` command.

▷ Example 2

Returning to the apple tree experiment, we found that the fertilizer concentration appears to significantly affect the average weight of the fruit. Although that finding is interesting, we next want to know which concentration appears to grow the heaviest fruit. One way to find out is by examining the underlying regression coefficients.

```
. regress, baselevels
      Source |       SS       df       MS              Number of obs =      10
-------------+------------------------------           F(  3,     6) =   21.46
       Model |  5295.54433     3  1765.18144            Prob > F      =  0.0013
    Residual |  493.591667     6  82.2652778            R-squared     =  0.9147
-------------+------------------------------           Adj R-squared =  0.8721
       Total |    5789.136     9  643.237333            Root MSE      =    9.07

------------------------------------------------------------------------------
      weight |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   treatment |
           1 |          0  (base)
           2 |  -59.16667   7.405641    -7.99   0.000    -77.28762   -41.04572
           3 |     -33.25   8.279758    -4.02   0.007    -53.50984   -12.99016
           4 |      -34.4   8.279758    -4.15   0.006    -54.65984   -14.14016
             |
       _cons |      111.9   5.236579    21.37   0.000     99.08655    124.7134
------------------------------------------------------------------------------
```

See [R] **regress** for an explanation of how to read this table. The `baselevels` option of `regress` displays a row indicating the base category for our categorical variable, `treatment`. In summary, we find that concentration 1, the base (omitted) group, produces significantly heavier fruits than concentration 2, 3, and 4; concentration 2 produces the lightest fruits; and concentrations 3 and 4 appear to be roughly equivalent.

◁

▷ Example 3

We previously typed `anova weight treatment` to produce and display the ANOVA table for our apple tree experiment. Typing `regress` displays the regression coefficients. We can redisplay the ANOVA table by typing `anova` without arguments:

```
. anova
                           Number of obs =      10     R-squared     =  0.9147
                           Root MSE      = 9.07002     Adj R-squared =  0.8721

                  Source | Partial SS    df       MS           F     Prob > F
-------------------------+------------------------------------------------------
                   Model |  5295.54433     3  1765.18144       21.46     0.0013
                         |
               treatment |  5295.54433     3  1765.18144       21.46     0.0013
                         |
                Residual |  493.591667     6  82.2652778
-------------------------+------------------------------------------------------
                   Total |    5789.136     9  643.237333
```

◁

Two-way ANOVA

You can include multiple explanatory variables with the `anova` command, and you can specify interactions by placing '`#`' between the variable names. For instance, typing `anova y a b` performs a two-way layout of `y` on `a` and `b`. Typing `anova y a b a#b` performs a full two-way factorial layout. The shorthand `anova y a##b` does the same.

With the default partial sums of squares, when you specify interacted terms, the order of the terms does not matter. Typing `anova y a b a#b` is the same as typing `anova y b a b#a`.

▷ Example 4

The classic two-way factorial ANOVA problem, at least as far as computer manuals are concerned, is a two-way ANOVA design from Afifi and Azen (1979).

Fifty-eight patients, each suffering from one of three different diseases, were randomly assigned to one of four different drug treatments, and the change in their systolic blood pressure was recorded. Here are the data:

	Disease 1	Disease 2	Disease 3
Drug 1	42, 44, 36 13, 19, 22	33, 26, 33 21	31, –3, 25 25, 24
Drug 2	28, 23, 34 42, 13	34, 33, 31 36	3, 26, 28 32, 4, 16
Drug 3	1, 29, 19	11, 9, 7 1, –6	21, 1, 9 3
Drug 4	24, 9, 22 –2, 15	27, 12, 12 –5, 16, 15	22, 7, 25 5, 12

Let's assume that we have entered these data into Stata and stored the data as `systolic.dta`. Below we `use` the data, `list` the first 10 observations, `summarize` the variables, and `tabulate` the control variables:

```
. use http://www.stata-press.com/data/r12/systolic
(Systolic Blood Pressure Data)
. list in 1/10
```

	drug	disease	systolic
1.	1	1	42
2.	1	1	44
3.	1	1	36
4.	1	1	13
5.	1	1	19
6.	1	1	22
7.	1	2	33
8.	1	2	26
9.	1	2	33
10.	1	2	21

```
. summarize
```

Variable	Obs	Mean	Std. Dev.	Min	Max
drug	58	2.5	1.158493	1	4
disease	58	2.017241	.8269873	1	3
systolic	58	18.87931	12.80087	-6	44

```
. tabulate drug disease
```

	Patient's Disease			
Drug Used	1	2	3	Total
1	6	4	5	15
2	5	4	6	15
3	3	5	4	12
4	5	6	5	16
Total	19	19	20	58

Each observation in our data corresponds to one patient, and for each patient we record `drug`, `disease`, and the increase in the systolic blood pressure, `systolic`. The tabulation reveals that the data are not balanced—there are not equal numbers of patients in each `drug`–`disease` cell. Stata does not require that the data be balanced. We can perform a two-way factorial ANOVA by typing

```
. anova systolic drug disease drug#disease
```

```
                   Number of obs =      58     R-squared     =  0.4560
                   Root MSE      = 10.5096     Adj R-squared =  0.3259
```

Source	Partial SS	df	MS	F	Prob > F
Model	4259.33851	11	387.212591	3.51	0.0013
drug	2997.47186	3	999.157287	9.05	0.0001
disease	415.873046	2	207.936523	1.88	0.1637
drug#disease	707.266259	6	117.87771	1.07	0.3958
Residual	5080.81667	46	110.452536		
Total	9340.15517	57	163.862371		

Although Stata's `table` command does not perform ANOVA, it can produce useful summary tables of your data (see [R] **table**):

```
. table drug disease, c(mean systolic) row col f(%8.2f)
```

Drug Used	Patient's Disease 1	2	3	Total
1	29.33	28.25	20.40	26.07
2	28.00	33.50	18.17	25.53
3	16.33	4.40	8.50	8.75
4	13.60	12.83	14.20	13.50
Total	22.79	18.21	15.80	18.88

These are simple means and are not influenced by our `anova` model. More useful is the `margins` command (see [R] **margins**) that provides marginal means and adjusted predictions. Because `drug` is the only significant factor in our ANOVA, we now examine the adjusted marginal means for `drug`.

```
. margins drug, asbalanced
Adjusted predictions                            Number of obs   =         58
Expression   : Linear prediction, predict()
at           : drug             (asbalanced)
               disease          (asbalanced)
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
drug						
1	25.99444	2.751008	9.45	0.000	20.60257	31.38632
2	26.55556	2.751008	9.65	0.000	21.16368	31.94743
3	9.744444	3.100558	3.14	0.002	3.667462	15.82143
4	13.54444	2.637123	5.14	0.000	8.375778	18.71311

These adjusted marginal predictions are not equal to the simple drug means (see the total column from the `table` command); they are based upon predictions from our ANOVA model. The `asbalanced` option of `margins` corresponds with the interpretation of the F statistic produced by ANOVA—each cell is given equal weight regardless of its sample size (see the following three technical notes). You

can omit the asbalanced option and obtain predictive margins that take into account the unequal sample sizes of the cells.

```
. margins drug
Predictive margins                              Number of obs   =         58
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
drug						
1	25.89799	2.750533	9.42	0.000	20.50704	31.28893
2	26.41092	2.742762	9.63	0.000	21.0352	31.78664
3	9.722989	3.099185	3.14	0.002	3.648697	15.79728
4	13.55575	2.640602	5.13	0.000	8.380261	18.73123

◁

❑ Technical note

How do you interpret the significance of terms like drug and disease in unbalanced data? If you are familiar with SAS, the sums of squares and the F statistic reported by Stata correspond to SAS type III sums of squares. (Stata can also calculate sequential sums of squares, but we will postpone that topic for now.)

Let's think in terms of the following table:

	Disease 1	Disease 2	Disease 3	
Drug 1	μ_{11}	μ_{12}	μ_{13}	$\mu_{1\cdot}$
Drug 2	μ_{21}	μ_{22}	μ_{23}	$\mu_{2\cdot}$
Drug 3	μ_{31}	μ_{32}	μ_{33}	$\mu_{3\cdot}$
Drug 4	μ_{41}	μ_{42}	μ_{43}	$\mu_{4\cdot}$
	$\mu_{\cdot 1}$	$\mu_{\cdot 2}$	$\mu_{\cdot 3}$	$\mu_{\cdot\cdot}$

In this table, μ_{ij} is the mean increase in systolic blood pressure associated with drug i and disease j, while $\mu_{i\cdot}$ is the mean for drug i, $\mu_{\cdot j}$ is the mean for disease j, and $\mu_{\cdot\cdot}$ is the overall mean.

If the data are balanced, meaning that there are equal numbers of observations going into the calculation of each mean μ_{ij}, the row means, $\mu_{i\cdot}$, are given by

$$\mu_{i\cdot} = \frac{\mu_{i1} + \mu_{i2} + \mu_{i3}}{3}$$

In our case, the data are not balanced, but we define the $\mu_{i\cdot}$ according to that formula anyway. The test for the main effect of drug is the test that

$$\mu_{1\cdot} = \mu_{2\cdot} = \mu_{3\cdot} = \mu_{4\cdot}$$

To be absolutely clear, the F test of the term drug, called the *main effect* of drug, is formally equivalent to the test of the three constraints:

$$\frac{\mu_{11}+\mu_{12}+\mu_{13}}{3} = \frac{\mu_{21}+\mu_{22}+\mu_{23}}{3}$$

$$\frac{\mu_{11}+\mu_{12}+\mu_{13}}{3} = \frac{\mu_{31}+\mu_{32}+\mu_{33}}{3}$$

$$\frac{\mu_{11}+\mu_{12}+\mu_{13}}{3} = \frac{\mu_{41}+\mu_{42}+\mu_{43}}{3}$$

In our data, we obtain a significant F statistic of 9.05 and thus reject those constraints.

❑

❑ Technical note

Stata can display the symbolic form underlying the test statistics it presents, as well as display other test statistics and their symbolic forms; see *Obtaining symbolic forms* in [R] **anova postestimation**. Here is the result of requesting the symbolic form for the main effect of `drug` in our data:

```
. test drug, symbolic
drug
           1  -(r2+r3+r4)
           2   r2
           3   r3
           4   r4
disease
           1  0
           2  0
           3  0
drug#disease
        1  1  -1/3 (r2+r3+r4)
        1  2  -1/3 (r2+r3+r4)
        1  3  -1/3 (r2+r3+r4)
        2  1   1/3 r2
        2  2   1/3 r2
        2  3   1/3 r2
        3  1   1/3 r3
        3  2   1/3 r3
        3  3   1/3 r3
        4  1   1/3 r4
        4  2   1/3 r4
        4  3   1/3 r4
_cons          0
```

This says exactly what we said in the previous technical note.

❑

❑ Technical note

Saying that there is no main effect of a variable is not the same as saying that it has no effect at all. Stata's ability to perform ANOVA on unbalanced data can easily be put to ill use.

For example, consider the following table of the probability of surviving a bout with one of two diseases according to the drug administered to you:

	Disease 1	Disease 2
Drug 1	1	0
Drug 2	0	1

If you have disease 1 and are administered drug 1, you live. If you have disease 2 and are administered drug 2, you live. In all other cases, you die.

This table has no main effects of either drug or disease, although there is a large interaction effect. You might now be tempted to reason that because there is only an interaction effect, you would be indifferent between the two drugs in the absence of knowledge about which disease infects you. Given an equal chance of having either disease, you reason that it does not matter which drug is administered to you—either way, your chances of surviving are 0.5.

You may not, however, have an equal chance of having either disease. If you knew that disease 1 was 100 times more likely to occur in the population, and if you knew that you had one of the two diseases, you would express a strong preference for receiving drug 1.

When you calculate the significance of main effects on unbalanced data, you must ask yourself why the data are unbalanced. If the data are unbalanced for random reasons and you are making predictions for a balanced population, the test of the main effect makes perfect sense. If, however, the data are unbalanced because the underlying populations are unbalanced and you are making predictions for such unbalanced populations, the test of the main effect may be practically—if not statistically—meaningless.

❑

▷ Example 5

Stata can perform ANOVA not only on unbalanced populations, but also on populations that are so unbalanced that entire cells are missing. For instance, using our systolic blood pressure data, let's refit the model eliminating the drug 1–disease 1 cell. Because `anova` follows the same syntax as all other Stata commands, we can explicitly specify the data to be used by typing the `if` qualifier at the end of the `anova` command. Here we want to use the data that are not for drug 1 and disease 1:

```
. anova systolic drug##disease if !(drug==1 & disease==1)
                          Number of obs =      52     R-squared     =  0.4545
                          Root MSE      = 10.1615     Adj R-squared =  0.3215
                 Source | Partial SS    df       MS           F     Prob > F
------------------------+----------------------------------------------------
                  Model |  3527.95897    10  352.795897        3.42     0.0025
                        |
                   drug |  2686.57832     3  895.526107        8.67     0.0001
                disease |  327.792598     2  163.896299        1.59     0.2168
           drug#disease |  703.007602     5   140.60152        1.36     0.2586
                        |
               Residual |  4233.48333    41  103.255691
------------------------+----------------------------------------------------
                  Total |  7761.44231    51  152.185143
```

Here we used `drug##disease` as a shorthand for `drug disease drug#disease`.

◁

❑ Technical note

The test of the main effect of drug in the presence of missing cells is more complicated than that for unbalanced data. Our underlying tableau now has the following form:

	Disease 1	Disease 2	Disease 3	
Drug 1		μ_{12}	μ_{13}	
Drug 2	μ_{21}	μ_{22}	μ_{23}	$\mu_{2\cdot}$
Drug 3	μ_{31}	μ_{32}	μ_{33}	$\mu_{3\cdot}$
Drug 4	μ_{41}	μ_{42}	μ_{43}	$\mu_{4\cdot}$
		$\mu_{\cdot 2}$	$\mu_{\cdot 3}$	

The hole in the drug 1–disease 1 cell indicates that the mean is unobserved. Considering the main effect of drug, the test is unchanged for the rows in which all the cells are defined:

$$\mu_{2\cdot} = \mu_{3\cdot} = \mu_{4\cdot}$$

The first row, however, requires special attention. Here we want the average outcome for drug 1, which is averaged only over diseases 2 and 3, to be equal to the average values of all other drugs averaged over those same two diseases:

$$\frac{\mu_{12} + \mu_{13}}{2} = \frac{\big(\mu_{22} + \mu_{23}\big)/2 + \big(\mu_{32} + \mu_{33}\big)/2 + \big(\mu_{42} + \mu_{43}\big)/2}{3}$$

Thus the test contains three constraints:

$$\begin{aligned}
\frac{\mu_{21} + \mu_{22} + \mu_{23}}{3} &= \frac{\mu_{31} + \mu_{32} + \mu_{33}}{3} \\
\frac{\mu_{21} + \mu_{22} + \mu_{23}}{3} &= \frac{\mu_{41} + \mu_{42} + \mu_{43}}{3} \\
\frac{\mu_{12} + \mu_{13}}{2} &= \frac{\mu_{22} + \mu_{23} + \mu_{32} + \mu_{33} + \mu_{42} + \mu_{43}}{6}
\end{aligned}$$

❑

Stata can calculate two types of sums of squares, *partial* and *sequential*. If you do not specify which sums of squares to calculate, Stata calculates partial sums of squares. The technical notes above have gone into great detail about the definition and use of partial sums of squares. Use the `sequential` option to obtain sequential sums of squares.

❑ Technical note

Before we illustrate sequential sums of squares, consider one more feature of the partial sums. If you know how such things are calculated, you may worry that the terms must be specified in some particular order, that Stata would balk or, even worse, produce different results if you typed, say, `anova drug#disease drug disease` rather than `anova drug disease drug#disease`. We assure you that is not the case.

When you type a model, Stata internally reorganizes the terms, forms the cross-product matrix, inverts it, converts the result to an upper-Hermite form, and then performs the hypothesis tests. As a final touch, Stata reports the results in the same order that you typed the terms.

❑

▷ Example 6

We wish to estimate the effects on systolic blood pressure of drug and disease by using sequential sums of squares. We want to introduce disease first, then drug, and finally, the interaction of drug and disease:

```
. anova systolic disease drug disease#drug, sequential
                          Number of obs =      58     R-squared     =  0.4560
                          Root MSE      = 10.5096     Adj R-squared =  0.3259
```

Source	Seq. SS	df	MS	F	Prob > F
Model	4259.33851	11	387.212591	3.51	0.0013
disease	488.639383	2	244.319691	2.21	0.1210
drug	3063.43286	3	1021.14429	9.25	0.0001
disease#drug	707.266259	6	117.87771	1.07	0.3958
Residual	5080.81667	46	110.452536		
Total	9340.15517	57	163.862371		

The F statistic on `disease` is now 2.21. When we fit this same model by using partial sums of squares, the statistic was 1.88.

◁

N-way ANOVA

You may include high-order interaction terms, such as a third-order interaction between the variables `A`, `B`, and `C`, by typing `A#B#C`.

▷ Example 7

We wish to determine the operating conditions that maximize yield for a manufacturing process. There are three temperature settings, two chemical supply companies, and two mixing methods under investigation. Three observations are obtained for each combination of these three factors.

```
. use http://www.stata-press.com/data/r12/manuf
(manufacturing process data)
. describe
Contains data from http://www.stata-press.com/data/r12/manuf.dta
  obs:            36                          manufacturing process data
 vars:             4                          2 Jan 2011 13:28
 size:           144
```

variable name	storage type	display format	value label	variable label
temperature	byte	%9.0g	temp	machine temperature setting
chemical	byte	%9.0g	supplier	chemical supplier
method	byte	%9.0g	meth	mixing method
yield	byte	%9.0g		product yield

```
Sorted by:
```

We wish to perform a three-way factorial ANOVA. We could type

```
. anova yield temp chem temp#chem meth temp#meth chem#meth temp#chem#meth
```

but prefer to use the ## factor-variable operator for brevity.

```
. anova yield temp##chem##meth
```

```
                          Number of obs =      36     R-squared     =  0.5474
                          Root MSE      = 2.62996     Adj R-squared =  0.3399
```

Source	Partial SS	df	MS	F	Prob > F
Model	200.75	11	18.25	2.64	0.0227
temperature	30.5	2	15.25	2.20	0.1321
chemical	12.25	1	12.25	1.77	0.1958
temperature#chemical	24.5	2	12.25	1.77	0.1917
method	42.25	1	42.25	6.11	0.0209
temperature#method	87.5	2	43.75	6.33	0.0062
chemical#method	.25	1	.25	0.04	0.8508
temperature#chemical# method	3.5	2	1.75	0.25	0.7785
Residual	166	24	6.91666667		
Total	366.75	35	10.4785714		

The interaction between temperature and method appears to be the important story in these data. A table of means for this interaction is given below.

```
. table method temp, c(mean yield) row col f(%8.2f)
```

mixing method	machine temperature setting low	medium	high	Total
stir	7.50	6.00	6.00	6.50
fold	5.50	9.00	11.50	8.67
Total	6.50	7.50	8.75	7.58

Here our ANOVA is balanced (each cell has the same number of observations), and we obtain the same values as in the table above (but with additional information such as confidence intervals) by using the `margins` command. Because our ANOVA is balanced, using the `asbalanced` option with `margins` would not produce different results. We request the predictive margins for the two terms that appear significant in our ANOVA: `temperature#method` and `method`.

```
. margins temperature#method method
Predictive margins                                Number of obs   =         36
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
temperature# method						
1 1	7.5	1.073675	6.99	0.000	5.395636	9.604364
1 2	5.5	1.073675	5.12	0.000	3.395636	7.604364
2 1	6	1.073675	5.59	0.000	3.895636	8.104364
2 2	9	1.073675	8.38	0.000	6.895636	11.10436
3 1	6	1.073675	5.59	0.000	3.895636	8.104364
3 2	11.5	1.073675	10.71	0.000	9.395636	13.60436
method						
1	6.5	.6198865	10.49	0.000	5.285045	7.714955
2	8.666667	.6198865	13.98	0.000	7.451711	9.881622

We decide to use the folding method of mixing and a high temperature in our manufacturing process.

◁

Weighted data

Like all estimation commands, `anova` can produce estimates on weighted data. See [U] **11.1.6 weight** for details on specifying the weight.

▷ Example 8

We wish to investigate the prevalence of byssinosis, a form of pneumoconiosis that can afflict workers exposed to cotton dust. We have data on 5,419 workers in a large cotton mill. We know whether each worker smokes, his or her race, and the dustiness of the work area. The variables are

`smokes`	smoker or nonsmoker in the last five years
`race`	white or other
`workplace`	1 (most dusty), 2 (less dusty), 3 (least dusty)

We wish to fit an ANOVA model explaining the prevalence of byssinosis according to a full factorial model of `smokes`, `race`, and `workplace`.

The data are unbalanced. Moreover, although we have data on 5,419 workers, the data are grouped according to the explanatory variables, along with some other variables, resulting in 72 observations. For each observation, we know the number of workers in the group (`pop`), the prevalence of byssinosis (`prob`), and the values of the three explanatory variables. Thus we wish to fit a three-way factorial model on grouped data.

We begin by showing a bit of the data, which are from Higgins and Koch (1977).

```
. use http://www.stata-press.com/data/r12/byssin
(Byssinosis incidence)
. describe
Contains data from http://www.stata-press.com/data/r12/byssin.dta
  obs:            72                          Byssinosis incidence
 vars:             5                          19 Dec 2010 07:04
 size:           864
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
smokes          int    %8.0g       smokes     Smokes
race            int    %8.0g       race       Race
workplace       int    %8.0g       workplace
                                               Dustiness of workplace
pop             int    %8.0g                  Population size
prob            float  %9.0g                  Prevalence of byssinosis
-------------------------------------------------------------------------------
Sorted by:
. list in 1/5, abbrev(10) divider
```

	smokes	race	workplace	pop	prob
1.	yes	white	most	40	.075
2.	yes	white	less	74	0
3.	yes	white	least	260	.0076923
4.	yes	other	most	164	.152439
5.	yes	other	less	88	0

The first observation in the data represents a group of 40 white workers who smoke and work in a "most" dusty work area. Of those 40 workers, 7.5% have byssinosis. The second observation represents a group of 74 white workers who also smoke but who work in a "less" dusty environment. None of those workers has byssinosis.

Almost every Stata command allows weights. Here we want to weight the data by `pop`. We can, for instance, make a table of the number of workers by their smoking status and race:

```
. tabulate smokes race [fw=pop]
```

	Race		
Smokes	other	white	Total
no	799	1,431	2,230
yes	1,104	2,085	3,189
Total	1,903	3,516	5,419

The `[fw=pop]` at the end of the `tabulate` command tells Stata to count each observation as representing `pop` persons. When making the tally, `tabulate` treats the first observation as representing 40 workers, the second as representing 74 workers, and so on.

Similarly, we can make a table of the dustiness of the workplace:

```
. tabulate workplace [fw=pop]
```

Dustiness of workplace	Freq.	Percent	Cum.
least	3,450	63.66	63.66
less	1,300	23.99	87.65
most	669	12.35	100.00
Total	5,419	100.00	

We can discover the average incidence of byssinosis among these workers by typing

```
. summarize prob [fw=pop]
```

Variable	Obs	Mean	Std. Dev.	Min	Max
prob	5419	.0304484	.0567373	0	.287037

We discover that 3.04% of these workers have byssinosis. Across all cells, the byssinosis rates vary from 0 to 28.7%. Just to prove that there might be something here, let's obtain the average incidence rates according to the dustiness of the workplace:

```
. table workplace smokes race [fw=pop], c(mean prob)
```

Dustiness of workplace	Race and Smokes			
	other		white	
	no	yes	no	yes
least	.0107527	.0101523	.0081549	.0162774
less	.02	.0081633	.0136612	.0143149
most	.0820896	.1679105	.0833333	.2295082

Let's now fit the ANOVA model.

```
. anova prob workplace smokes race workplace#smokes workplace#race
> smokes#race workplace#smokes#race [aweight=pop]
(sum of wgt is   5.4190e+03)
```

Number of obs = 65 R-squared = 0.8300
Root MSE = .025902 Adj R-squared = 0.7948

Source	Partial SS	df	MS	F	Prob > F
Model	.173646538	11	.015786049	23.53	0.0000
workplace	.097625175	2	.048812588	72.76	0.0000
smokes	.013030812	1	.013030812	19.42	0.0001
race	.001094723	1	.001094723	1.63	0.2070
workplace#smokes	.019690342	2	.009845171	14.67	0.0000
workplace#race	.001352516	2	.000676258	1.01	0.3718
smokes#race	.001662874	1	.001662874	2.48	0.1214
workplace#smokes#race	.000950841	2	.00047542	0.71	0.4969
Residual	.035557766	53	.000670901		
Total	.209204304	64	.003268817		

Of course, if we want to see the underlying regression, we could type `regress`.

Above we examined simple means of the cells of `workplace#smokes#race`. Our ANOVA shows `workplace`, `smokes`, and their interaction as being the only significant factors in our model. We now examine the predictive marginal mean byssinosis rates for these terms.

```
. margins workplace#smokes workplace smokes
Predictive margins                              Number of obs   =         65
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
workplace# smokes						
1 1	.0090672	.0062319	1.45	0.146	-.003147	.0212814
1 2	.0141264	.0053231	2.65	0.008	.0036934	.0245595
2 1	.0158872	.009941	1.60	0.110	-.0035967	.0353711
2 2	.0121546	.0087353	1.39	0.164	-.0049663	.0292756
3 1	.0828966	.0182151	4.55	0.000	.0471957	.1185975
3 2	.2078768	.012426	16.73	0.000	.1835222	.2322314
workplace						
1	.0120701	.0040471	2.98	0.003	.0041379	.0200022
2	.0137273	.0065685	2.09	0.037	.0008533	.0266012
3	.1566225	.0104602	14.97	0.000	.1361208	.1771241
smokes						
1	.0196915	.0050298	3.91	0.000	.0098332	.0295498
2	.0358626	.0041949	8.55	0.000	.0276408	.0440844

Smoking combined with the most dusty workplace produces the highest byssinosis rates.

◁

Ronald Aylmer Fisher (1890–1962) (Sir Ronald from 1952) studied mathematics at Cambridge. Even before he finished his studies, he had published on statistics. He worked as a statistician at Rothamsted Experimental Station (1919–1933), as professor of eugenics at University College London (1933–1943), as professor of genetics at Cambridge (1943–1957), and in retirement at the CSIRO Division of Mathematical Statistics in Adelaide. His many fundamental and applied contributions to statistics and genetics mark him as one of the greatest statisticians of all time, including original work on tests of significance, distribution theory, theory of estimation, fiducial inference, and design of experiments.

ANCOVA

You can include multiple explanatory variables with the `anova` command, but unless you explicitly state otherwise by using the `c.` factor-variable operator, all the variables are interpreted as *categorical variables*. Using the `c.` operator, you can designate variables as *continuous* and thus perform ANCOVA.

▷ Example 9

We have census data recording the death rate (`drate`) and median age (`age`) for each state. The dataset also includes the region of the country in which each state is located (`region`):

```
. use http://www.stata-press.com/data/r12/census2
(1980 Census data by state)
. summarize drate age region
```

Variable	Obs	Mean	Std. Dev.	Min	Max
drate	50	84.3	13.07318	40	107
age	50	29.5	1.752549	24	35
region	50	2.66	1.061574	1	4

`age` is coded in integral years from 24 to 35, and `region` is coded from 1 to 4, with 1 standing for the Northeast, 2 for the North Central, 3 for the South, and 4 for the West.

When we examine the data more closely, we discover large differences in the death rate across regions of the country:

```
. tabulate region, summarize(drate)
```

Census region	Summary of Death Rate Mean	Std. Dev.	Freq.
NE	93.444444	7.0553368	9
N Cntrl	88.916667	5.5833899	12
South	88.3125	8.5457104	16
West	68.769231	13.342625	13
Total	84.3	13.073185	50

Naturally, we wonder if these differences might not be explained by differences in the median ages of the populations. To find out, we fit a regression model (via `anova`) of `drate` on `region` and `age`. In the `anova` example below, we treat `age` as a categorical variable.

```
. anova drate region age
```

```
                   Number of obs =      50     R-squared     =  0.7927
                   Root MSE      =  6.7583     Adj R-squared =  0.7328
```

Source	Partial SS	df	MS	F	Prob > F
Model	6638.86529	11	603.533208	13.21	0.0000
region	1320.00973	3	440.003244	9.63	0.0001
age	2237.24937	8	279.656171	6.12	0.0000
Residual	1735.63471	38	45.6745977		
Total	8374.5	49	170.908163		

We have the answer to our question: differences in median ages do not eliminate the differences in death rates across the four regions. The ANOVA table summarizes the two terms in the model, `region` and `age`. The `region` term contains 3 degrees of freedom, and the `age` term contains 8 degrees of freedom. Both are significant at better than the 1% level.

The `age` term contains 8 degrees of freedom. Because we did not explicitly indicate that `age` was to be treated as a continuous variable, it was treated as *categorical*, meaning that unique coefficients were estimated for each level of age. The only clue of this labeling is that the number of degrees of freedom associated with the `age` term exceeds 1. The labeling becomes more obvious if we review the regression coefficients:

```
. regress, baselevels
```

Source	SS	df	MS		
Model	6638.86529	11	603.533208	Number of obs	= 50
Residual	1735.63471	38	45.6745977	F(11, 38)	= 13.21
				Prob > F	= 0.0000
				R-squared	= 0.7927
				Adj R-squared	= 0.7328
Total	8374.5	49	170.908163	Root MSE	= 6.7583

drate	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
region						
1	0	(base)				
2	.4428387	3.983664	0.11	0.912	-7.621668	8.507345
3	-.2964637	3.934766	-0.08	0.940	-8.261981	7.669054
4	-13.37147	4.195344	-3.19	0.003	-21.8645	-4.878439
age						
24	0	(base)				
26	-15	9.557677	-1.57	0.125	-34.34851	4.348506
27	14.30833	7.857378	1.82	0.076	-1.598099	30.21476
28	12.66011	7.495513	1.69	0.099	-2.51376	27.83399
29	18.861	7.28918	2.59	0.014	4.104825	33.61717
30	20.87003	7.210148	2.89	0.006	6.273847	35.46621
31	29.91307	8.242741	3.63	0.001	13.22652	46.59963
32	27.02853	8.509432	3.18	0.003	9.802089	44.25498
35	38.925	9.944825	3.91	0.000	18.79275	59.05724
_cons	68.37147	7.95459	8.60	0.000	52.26824	84.47469

The `regress` command displayed the `anova` model as a regression table. We used the `baselevels` option to display the dropped level (or base) for each term.

If we want to treat `age` as a continuous variable, we must prepend `c.` to `age` in our `anova`.

```
. anova drate region c.age
```

Number of obs	= 50	R-squared	= 0.7203
Root MSE	= 7.21483	Adj R-squared	= 0.6954

Source	Partial SS	df	MS	F	Prob > F
Model	6032.08254	4	1508.02064	28.97	0.0000
region	1645.66228	3	548.554092	10.54	0.0000
age	1630.46662	1	1630.46662	31.32	0.0000
Residual	2342.41746	45	52.0537213		
Total	8374.5	49	170.908163		

The `age` term now has 1 degree of freedom. The regression coefficients are

```
. regress, baselevels
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  4,    45) =   28.97
       Model |  6032.08254     4  1508.02064            Prob > F      =  0.0000
    Residual |  2342.41746    45  52.0537213            R-squared     =  0.7203
-------------+------------------------------           Adj R-squared =  0.6954
       Total |     8374.5    49  170.908163            Root MSE      =  7.2148

------------------------------------------------------------------------------
       drate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      region |
          1 |          0  (base)
          2 |   1.792526   3.375925     0.53   0.598    -5.006935    8.591988
          3 |   .6979912    3.18154     0.22   0.827     -5.70996    7.105942
          4 |  -13.37578   3.723447    -3.59   0.001    -20.87519   -5.876377
            |
        age |   3.922947   .7009425     5.60   0.000     2.511177    5.334718
      _cons |  -28.60281   21.93931    -1.30   0.199    -72.79085    15.58524
------------------------------------------------------------------------------
```

Although we started analyzing these data to explain the regional differences in death rate, let's focus on the effect of age for a moment. In our first model, each level of `age` had a unique death rate associated with it. For instance, the predicted death rate in a north central state with a median age of 28 was

$$0.44 + 12.66 + 68.37 \approx 81.47$$

whereas the predicted death rate from our current model is

$$1.79 + 3.92 \times 28 - 28.60 \approx 82.95$$

Our previous model had an R^2 of 0.7927, whereas our current model has an R^2 of 0.7203. This "small" loss of predictive power accompanies a gain of 7 degrees of freedom, so we suspect that the continuous-age model is as good as the discrete-age model.

◁

❑ Technical note

There is enough information in the two ANOVA tables to attach a statistical significance to our suspicion that the loss of predictive power is offset by the savings in degrees of freedom. Because the continuous-age model is nested within the discrete-age model, we can perform a standard Chow test. For those of us who know such formulas off the top of our heads, the F statistic is

$$\frac{(2342.41746 - 1735.63471)/7}{45.6745977} = 1.90$$

There is, however, a better way.

We can find out whether our continuous model is as good as our discrete model by putting `age` in the model twice: once as a continuous variable and once as a categorical variable. The categorical variable will then measure deviations around the straight line implied by the continuous variable, and the F test for the significance of the categorical variable will test whether those deviations are jointly zero.

```
. anova drate region c.age age
                          Number of obs =      50     R-squared     =  0.7927
                          Root MSE      =  6.7583     Adj R-squared =  0.7328
```

Source	Partial SS	df	MS	F	Prob > F
Model	6638.86529	11	603.533208	13.21	0.0000
region	1320.00973	3	440.003244	9.63	0.0001
age	699.74137	1	699.74137	15.32	0.0004
age	606.782747	7	86.6832496	1.90	0.0970
Residual	1735.63471	38	45.6745977		
Total	8374.5	49	170.908163		

We find that the F test for the significance of the (categorical) `age` variable is 1.90, just as we calculated above. It is significant at the 9.7% level. If we hold to a 5% significance level, we cannot reject the null hypothesis that the effect of `age` is linear.

❑

▷ Example 10

In our census data, we still find significant differences across the regions after controlling for the median age of the population. We might now wonder whether the regional differences are differences in level—independent of age—or are instead differences in the regional effects of age. Just as we can interact categorical variables with other categorical variables, we can interact categorical variables with continuous variables.

```
. anova drate region c.age region#c.age
                          Number of obs =      50     R-squared     =  0.7365
                          Root MSE      = 7.24852     Adj R-squared =  0.6926
```

Source	Partial SS	df	MS	F	Prob > F
Model	6167.7737	7	881.110529	16.77	0.0000
region	188.713602	3	62.9045339	1.20	0.3225
age	873.425599	1	873.425599	16.62	0.0002
region#age	135.691162	3	45.2303874	0.86	0.4689
Residual	2206.7263	42	52.5411023		
Total	8374.5	49	170.908163		

The `region#c.age` term in our model measures the differences in slopes across the regions. We cannot reject the null hypothesis that there are no such differences. The `region` effect is now "insignificant". This status does not mean that there are no regional differences in death rates because each test is a *marginal* or *partial* test. Here, with `region#c.age` included in the model, `region` is being tested at the point where `age` is zero. Apart from this value not existing in the dataset, it is also a long way from the mean value of `age`, so the test of `region` at this point is meaningless (although it is valid if you acknowledge what is being tested).

To obtain a more sensible test of `region`, we can subtract the mean from the `age` variable and use this in the model.

```
. quietly summarize age
. generate mage = age - r(mean)
```

```
. anova drate region c.mage region#c.mage
                          Number of obs =      50     R-squared     =  0.7365
                          Root MSE      = 7.24852     Adj R-squared =  0.6926
```

Source	Partial SS	df	MS	F	Prob > F
Model	6167.7737	7	881.110529	16.77	0.0000
region	1166.14735	3	388.715783	7.40	0.0004
mage	873.425599	1	873.425599	16.62	0.0002
region#mage	135.691162	3	45.2303874	0.86	0.4689
Residual	2206.7263	42	52.5411023		
Total	8374.5	49	170.908163		

`region` is significant when tested at the mean of the `age` variable.

◁

Remember that we can specify interactions by typing *varname*`#`*varname*. We have seen examples of interacting categorical variables with categorical variables and, in the examples above, a categorical variable (`region`) with a continuous variable (`age` or `mage`).

We can also interact continuous variables with continuous variables. To include an $\texttt{age}^2$ term in our model, we could type `c.age#c.age`. If we also wanted to interact the categorical variable `region` with the $\texttt{age}^2$ term, we could type `region#c.age#c.age` (or even `c.age#region#c.age`).

Nested designs

In addition to specifying interaction terms, nested terms can also be specified in an ANOVA. A vertical bar is used to indicate nesting: `A|B` is read as `A` nested within `B`. `A|B|C` is read as `A` nested within `B`, which is nested within `C`. `A|B#C` is read as `A` is nested within the interaction of `B` and `C`. `A#B|C` is read as the interaction of `A` and `B`, which is nested within `C`.

Different error terms can be specified for different parts of the model. The forward slash is used to indicate that the next term in the model is the error term for what precedes it. For instance, `anova y A / B|A` indicates that the F test for `A` is to be tested by using the mean square from `B|A` in the denominator. Error terms (terms following the slash) are generally not tested unless they are themselves followed by a slash. Residual error is the default error term.

For example, consider *A* `/` *B* `/` *C*, where *A*, *B*, and *C* may be arbitrarily complex terms. Then `anova` will report *A* tested by *B* and *B* tested by *C*. If we add one more slash on the end to form *A* `/` *B* `/` *C* `/`, then `anova` will also report *C* tested by the residual error.

▷ Example 11

We have collected data from a manufacturer that is evaluating which of five different brands of machinery to buy to perform a particular function in an assembly line. Twenty assembly-line employees were selected at random for training on these machines, with four employees assigned to learn a particular machine. The output from each employee (operator) on the brand of machine for which he trained was measured during four trial periods. In this example, the operator is nested within machine. Because of sickness and employee resignations, the final data are not balanced. The following table gives the mean output and sample size for each machine and operator combination.

```
. use http://www.stata-press.com/data/r12/machine, clear
(machine data)
```

```
. table machine operator, c(mean output n output) col f(%8.2f)
```

five brands of machine	operator nested in machine 1	2	3	4	Total
1	9.15	9.48	8.27	8.20	8.75
	2	4	3	4	13
2	15.03	11.55	11.45	11.52	12.47
	3	2	2	4	11
3	11.27	10.13	11.13		10.84
	3	3	3		9
4	16.10	18.97	15.35	16.60	16.65
	3	3	4	3	13
5	15.30	14.35	10.43		13.63
	4	4	3		11

Assuming that `operator` is random (that is, we wish to infer to the larger population of possible operators) and `machine` is fixed (that is, only these five machines are of interest), the typical test for `machine` uses `operator` nested within `machine` as the error term. `operator` nested within `machine` can be tested by residual error. Our earlier warning concerning designs with either unplanned missing cells or unbalanced cell sizes, or both, also applies to interpreting the ANOVA results from this unbalanced nested example.

```
. anova output machine / operator|machine /
                          Number of obs =      57     R-squared     =  0.8661
                          Root MSE      = 1.47089     Adj R-squared =  0.8077
```

Source	Partial SS	df	MS	F	Prob > F
Model	545.822288	17	32.1071934	14.84	0.0000
machine	430.980792	4	107.745198	13.82	0.0001
operator|machine	101.353804	13	7.79644648		
operator|machine	101.353804	13	7.79644648	3.60	0.0009
Residual	84.3766582	39	2.16350406		
Total	630.198947	56	11.2535526		

`operator|machine` is preceded by a slash, indicating that it is the error term for the terms before it (here `machine`). `operator|machine` is also followed by a slash that indicates it should be tested with residual error. The output lists the `operator|machine` term twice, once as the error term for machine, and again as a term tested by residual error. A line is placed in the ANOVA table to separate the two. In general, a dividing line is placed in the output to separate the terms into groups that are tested with the same error term. The overall model is tested by residual error and is separated from the rest of the table by a blank line at the top of the table.

The results indicate that the machines are not all equal and that there are significant differences between operators.

◁

▷ Example 12

Your company builds and operates sewage treatment facilities. You want to compare two particulate solutions during the particulate reduction step of the sewage treatment process. For each solution, two area managers are randomly selected to implement and oversee the change to the new treatment process in two of their randomly chosen facilities. Two workers at each of these facilities are trained to operate the new process. A measure of particulate reduction is recorded at various times during the month at each facility for each worker. The data are described below.

```
. use http://www.stata-press.com/data/r12/sewage
(Sewage treatment)
. describe
Contains data from http://www.stata-press.com/data/r12/sewage.dta
  obs:            64                          Sewage treatment
 vars:             5                          9 May 2011 12:43
 size:           320
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
particulate     byte   %9.0g                  particulate reduction
solution        byte   %9.0g                  2 particulate solutions
manager         byte   %9.0g                  2 managers per solution
facility        byte   %9.0g                  2 facilities per manager
worker          byte   %9.0g                  2 workers per facility
-------------------------------------------------------------------------------
Sorted by:  solution  manager  facility  worker
```

You want to determine if the two particulate solutions provide significantly different particulate reduction. You would also like to know if `manager`, `facility`, and `worker` are significant effects. `solution` is a fixed factor, whereas `manager`, `facility`, and `worker` are random factors.

In the following `anova` command, we use abbreviations for the variable names, which can sometimes make long ANOVA model statements easier to read.

```
. anova particulate s / m|s / f|m|s / w|f|m|s /, dropemptycells
                          Number of obs =      64     R-squared     =  0.6338
                          Root MSE      = 12.7445     Adj R-squared =  0.5194
```

Source	Partial SS	df	MS	F	Prob > F
Model	13493.6094	15	899.573958	5.54	0.0000
solution	7203.76563	1	7203.76563	17.19	0.0536
manager|solution	838.28125	2	419.140625		
manager|solution	838.28125	2	419.140625	0.55	0.6166
facility|manager|solution	3064.9375	4	766.234375		
facility|manager|solution	3064.9375	4	766.234375	2.57	0.1193
worker|facility|manager|solution	2386.625	8	298.328125		
worker|facility|manager|solution	2386.625	8	298.328125	1.84	0.0931
Residual	7796.25	48	162.421875		
Total	21289.8594	63	337.934276		

While solution is not declared significant at the 5% significance level, it is near enough to that threshold to warrant further investigation (see example 3 in [R] **anova postestimation** for a continuation of the analysis of these data).

◁

❑ Technical note

Why did we use the dropemptycells option with the previous anova? By default, Stata retains empty cells when building the design matrix and currently treats | and # the same in how it determines the possible number of cells. Retaining empty cells in an ANOVA with nested terms can cause your design matrix to become too large. In example 12, there are $1024 = 2 \times 4 \times 8 \times 16$ cells that are considered possible for the worker|facility|manager|solution term because the worker, facility, and manager variables are uniquely numbered. With the dropemptycells option, the worker|facility|manager|solution term requires just 16 columns in the design matrix (corresponding to the 16 unique workers).

Why did we not use the dropemptycells option in example 11, where operator is nested in machine? If you look at the table presented at the beginning of that example, you will see that operator is compactly instead of uniquely numbered (you need both operator number and machine number to determine the operator). Here the dropemptycells option would have only reduced our design matrix from 26 columns down to 24 columns (because there were only 3 operators instead of 4 for machines 3 and 5).

We suggest that you specify dropemptycells when there are nested terms in your ANOVA. You could also use the set emptycells drop command to accomplish the same thing; see [R] **set**.

❑

Mixed designs

An ANOVA can consist of both nested and crossed terms. A split-plot ANOVA design provides an example.

▷ Example 13

Two reading programs and three skill-enhancement techniques are under investigation. Ten classes of first-grade students were randomly assigned so that five classes were taught with one reading program and another five classes were taught with the other. The 30 students in each class were divided into six groups with 5 students each. Within each class, the six groups were divided randomly so that each of the three skill-enhancement techniques was taught to two of the groups within each class. At the end of the school year, a reading assessment test was administered to all the students. In this split-plot ANOVA, the whole-plot treatment is the two reading programs, and the split-plot treatment is the three skill-enhancement techniques.

```
. use http://www.stata-press.com/data/r12/reading
(Reading experiment data)
```

```
. describe
Contains data from http://www.stata-press.com/data/r12/reading.dta
  obs:           300                          Reading experiment data
 vars:             5                          9 Mar 2011 18:57
 size:         1,500                           (_dta has notes)
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
score           byte   %9.0g                  reading score
program         byte   %9.0g                  reading program
class           byte   %9.0g                  class nested in program
skill           byte   %9.0g                  skill enhancement technique
group           byte   %9.0g                  group nested in class and skill
-------------------------------------------------------------------------------
Sorted by:
```

In this split-plot ANOVA, the error term for `program` is `class` nested within `program`. The error term for `skill` and the `program` by `skill` interaction is the `class` by `skill` interaction nested within `program`. Other terms are also involved in the model and can be seen below.

Our `anova` command is too long to fit on one line of this manual. Where we have chosen to break the command into multiple lines is arbitrary. If we were typing this command into Stata, we would just type along and let Stata automatically wrap across lines, as necessary.

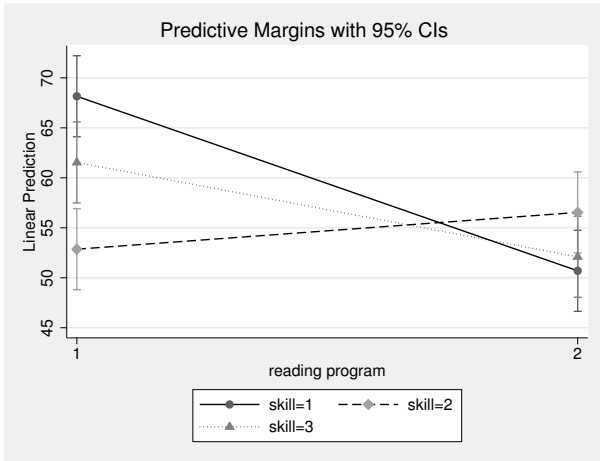
```
. anova score prog / class|prog skill prog#skill / class#skill|prog
> / group|class#skill|prog /, dropemptycells
                          Number of obs =     300     R-squared     =  0.3738
                          Root MSE      = 14.6268     Adj R-squared =  0.2199
                  Source | Partial SS    df       MS           F     Prob > F
-------------------------+------------------------------------------------------
                   Model |  30656.5167    59  519.601977       2.43     0.0000
                         |
                 program |     4493.07     1     4493.07       8.73     0.0183
           class|program |  4116.61333     8  514.576667
-------------------------+------------------------------------------------------
                   skill |  1122.64667     2  561.323333       1.54     0.2450
            program#skill |     5694.62     2     2847.31       7.80     0.0043
      class#skill|program |  5841.46667    16  365.091667
-------------------------+------------------------------------------------------
      class#skill|program |  5841.46667    16  365.091667       1.17     0.3463
       group|class#skill| |
                 program |      9388.1    30  312.936667
-------------------------+------------------------------------------------------
       group|class#skill| |
                 program |      9388.1    30  312.936667       1.46     0.0636
                         |
                Residual |     51346.4   240  213.943333
-------------------------+------------------------------------------------------
                   Total |  82002.9167   299  274.257246
```

The `program#skill` term is significant, as is the `program` term. Let's look at the predictive margins for these two terms and at a `marginsplot` for the first term.

```
. margins, within(program skill)
Predictive margins                                Number of obs   =        300
Expression   : Linear prediction, predict()
within       : program skill
Empty cells  : reweight
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
program# skill						
1 1	68.16	2.068542	32.95	0.000	64.10573	72.21427
1 2	52.86	2.068542	25.55	0.000	48.80573	56.91427
1 3	61.54	2.068542	29.75	0.000	57.48573	65.59427
2 1	50.7	2.068542	24.51	0.000	46.64573	54.75427
2 2	56.54	2.068542	27.33	0.000	52.48573	60.59427
2 3	52.1	2.068542	25.19	0.000	48.04573	56.15427

```
. marginsplot, plot2opts(lp(dash) m(D)) plot3opts(lp(dot) m(T))
  Variables that uniquely identify margins: program skill
```




```
. margins, within(program)
Predictive margins                                Number of obs   =        300
Expression   : Linear prediction, predict()
within       : program
Empty cells  : reweight
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
program						
1	60.85333	1.194273	50.95	0.000	58.5126	63.19407
2	53.11333	1.194273	44.47	0.000	50.7726	55.45407

Because our ANOVA involves nested terms, we used the `within()` option of `margins`; see [R] **margins**.

skill 2 produces a low score when combined with program 1 and a high score when combined with program 2, demonstrating the interaction between the reading program and the skill-enhancement technique. You might conclude that the first reading program and the first skill-enhancement technique perform best when combined. However, notice the overlapping confidence interval for the first reading program and the third skill-enhancement technique.

◁

❑ Technical note

There are several valid ways to write complicated anova terms. In the reading experiment example (example 13), we had a term group|class#skill|program. This term can be read as group nested within both class and skill and further nested within program. You can also write this term as group|class#skill#program or group|program#class#skill or group|skill#class|program, etc. All variations will produce the same result. Some people prefer having only one '|' in a term and would use group|class#skill#program, which is read as group nested within class, skill, and program.

❑

Gertrude Mary Cox (1900–1978) was born on a farm near Dayton, Iowa. Initially intending to become superintendent of an orphanage, she enrolled at Iowa State College. There she majored in mathematics and attained the college's first Master's degree in statistics. After working on her PhD in psychological statistics for two years at the University of California–Berkeley, she decided to go back to Iowa State to work with George W. Snedecor. There she pursued her interest in and taught a course in design of experiments. That work led to her collaboration with W. G. Cochran, which produced a classic text. In 1940, when Snedecor shared with her his list of men he was nominating to head the statistics department at North Carolina State College, she wanted to know why she had not been included. He added her name, she won the position, and she built an outstanding department at North Carolina State. Cox retired early so she could work at the Research Triangle Institute in North Carolina. She consulted widely, served as editor of *Biometrics*, and was elected to the National Academy of Sciences.

Latin-square designs

You can use anova to analyze a Latin-square design. Consider the following example, published in Snedecor and Cochran (1989).

▷ Example 14

Data from a Latin-square design are as follows:

Row	Column 1	Column 2	Column 3	Column 4	Column 5
1	257(B)	230(E)	279(A)	287(C)	202(D)
2	245(D)	283(A)	245(E)	280(B)	260(C)
3	182(E)	252(B)	280(C)	246(D)	250(A)
4	203(A)	204(C)	227(D)	193(E)	259(B)
5	231(C)	271(D)	266(B)	334(A)	338(E)

In Stata, the data might appear as follows:

```
. use http://www.stata-press.com/data/r12/latinsq
. list
```

	row	c1	c2	c3	c4	c5
1.	1	257	230	279	287	202
2.	2	245	283	245	280	260
3.	3	182	252	280	246	250
4.	4	203	204	227	193	259
5.	5	231	271	266	334	338

Before `anova` can be used on these data, the data must be organized so that the outcome measurement is in one column. `reshape` is inadequate for this task because there is information about the treatments in the sequence of these observations. `pkshape` is designed to reshape this type of data; see [R] **pkshape**.

```
. pkshape row row c1-c5, order(beacd daebc ebcda acdeb cdbae)
. list
```

	sequence	outcome	treat	carry	period
1.	1	257	1	0	1
2.	2	245	5	0	1
3.	3	182	2	0	1
4.	4	203	3	0	1
5.	5	231	4	0	1
6.	1	230	2	1	2
7.	2	283	3	5	2
8.	3	252	1	2	2
9.	4	204	4	3	2
10.	5	271	5	4	2
11.	1	279	3	2	3
12.	2	245	2	3	3
13.	3	280	4	1	3
14.	4	227	5	4	3
15.	5	266	1	5	3
16.	1	287	4	3	4
17.	2	280	1	2	4
18.	3	246	5	4	4
19.	4	193	2	5	4
20.	5	334	3	1	4
21.	1	202	5	4	5
22.	2	260	4	1	5
23.	3	250	3	5	5
24.	4	259	1	2	5
25.	5	338	2	3	5

```
. anova outcome sequence period treat
                          Number of obs =      25     R-squared     =  0.6536
                          Root MSE      = 32.4901     Adj R-squared =  0.3073

                 Source | Partial SS    df       MS           F     Prob > F
------------------------+----------------------------------------------------
                  Model |    23904.08    12  1992.00667       1.89     0.1426
                        |
                sequence |    13601.36     4     3400.34       3.22     0.0516
                  period |     6146.16     4     1536.54       1.46     0.2758
                   treat |     4156.56     4     1039.14       0.98     0.4523
                        |
                Residual |    12667.28    12  1055.60667
------------------------+----------------------------------------------------
                   Total |    36571.36    24  1523.80667
```

These methods will work with any type of Latin-square design, including those with replicated measurements. For more information, see [R] **pk**, [R] **pkcross**, and [R] **pkshape**.

Repeated-measures ANOVA

One approach for analyzing repeated-measures data is to use multivariate ANOVA (MANOVA); see [MV] **manova**. In this approach, the data are placed in wide form (see [D] **reshape**), and the repeated measures enter the MANOVA as dependent variables.

A second approach for analyzing repeated measures is to use `anova`. However, one of the underlying assumptions for the F tests in ANOVA is independence of observations. In a repeated-measures design, this assumption is almost certainly violated or is at least suspect. In a repeated-measures ANOVA, the subjects (or whatever the experimental units are called) are observed for each level of one or more of the other categorical variables in the model. These variables are called the repeated-measure variables. Observations from the same subject are likely to be correlated.

The approach used in repeated-measures ANOVA to correct for this lack of independence is to apply a correction to the degrees of freedom of the F test for terms in the model that involve repeated measures. This correction factor, ϵ, lies between the reciprocal of the degrees of freedom for the repeated term and 1. Box (1954) provided the pioneering work in this area. Milliken and Johnson (2009) refer to the lower bound of this correction factor as Box's conservative correction factor. Winer, Brown, and Michels (1991) call it simply the conservative correction factor.

Geisser and Greenhouse (1958) provide an estimate for the correction factor called the Greenhouse–Geisser ϵ. This value is estimated from the data. Huynh and Feldt (1976) show that the Greenhouse–Geisser ϵ tends to be conservatively biased. They provide a revised correction factor called the Huynh–Feldt ϵ. When the Huynh–Feldt ϵ exceeds 1, it is set to 1. Thus there is a natural ordering for these correction factors:

$$\text{Box's conservative } \epsilon \leq \text{Greenhouse–Geisser } \epsilon \leq \text{Huynh–Feldt } \epsilon \leq 1$$

A correction factor of 1 is the same as no correction.

`anova` with the `repeated()` option computes these correction factors and displays the revised test results in a table that follows the standard ANOVA table. In the resulting table, H-F stands for Huynh–Feldt, G-G stands for Greenhouse–Geisser, and Box stands for Box's conservative ϵ.

▷ Example 15

This example is taken from table 4.3 of Winer, Brown, and Michels (1991). The reaction time for five subjects each tested with four drugs was recorded in the variable `score`. Here is a table of the data (see [P] **tabdisp** if you are unfamiliar with `tabdisp`):

```
. use http://www.stata-press.com/data/r12/t43, clear
(T4.3 -- Winer, Brown, Michels)
. tabdisp person drug, cellvar(score)
```

person	drug 1	2	3	4
1	30	28	16	34
2	14	18	10	22
3	24	20	18	30
4	38	34	20	44
5	26	28	14	30

`drug` is the repeated variable in this simple repeated-measures ANOVA example. The ANOVA is specified as follows:

```
. anova score person drug, repeated(drug)
                          Number of obs =      20     R-squared     =  0.9244
                          Root MSE      = 3.06594     Adj R-squared =  0.8803

                   Source | Partial SS    df       MS           F     Prob > F
--------------------------+----------------------------------------------------
                    Model |       1379     7        197       20.96     0.0000
                          |
                   person |      680.8     4        170.2     18.11     0.0001
                     drug |      698.2     3  232.733333     24.76     0.0000
                          |
                 Residual |      112.8    12          9.4
--------------------------+----------------------------------------------------
                    Total |     1491.8    19  78.5157895

Between-subjects error term:  person
                     Levels:  5          (4 df)
     Lowest b.s.e. variable:  person
Repeated variable: drug
                                        Huynh-Feldt epsilon        =  1.0789
                                        *Huynh-Feldt epsilon reset to 1.0000
                                        Greenhouse-Geisser epsilon =  0.6049
                                        Box's conservative epsilon =  0.3333

                                                  ------------ Prob > F ------------
                   Source |      df       F      Regular     H-F      G-G       Box
--------------------------+----------------------------------------------------
                     drug |       3     24.76     0.0000    0.0000   0.0006    0.0076
                 Residual |      12
--------------------------+----------------------------------------------------
```

Here the Huynh–Feldt ϵ is 1.0789, which is larger than 1. It is reset to 1, which is the same as making no adjustment to the standard test computed in the main ANOVA table. The Greenhouse–Geisser ϵ is 0.6049, and its associated p-value is computed from an F ratio of 24.76 using 1.8147 ($= 3\epsilon$) and 7.2588 ($= 12\epsilon$) degrees of freedom. Box's conservative ϵ is set equal to the reciprocal of the degrees of freedom for the repeated term. Here it is 1/3, so Box's conservative test is computed using 1 and 4 degrees of freedom for the observed F ratio of 24.76.

Even for Box's conservative ϵ, `drug` is significant with a p-value of 0.0076. The following table gives the predictive marginal mean `score` (that is, response time) for each of the four drugs:

```
. margins drug
Predictive margins                                Number of obs   =         20
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
drug						
1	26.4	1.371131	19.25	0.000	23.71263	29.08737
2	25.6	1.371131	18.67	0.000	22.91263	28.28737
3	15.6	1.371131	11.38	0.000	12.91263	18.28737
4	32	1.371131	23.34	0.000	29.31263	34.68737

The ANOVA table for this example provides an F test for `person`, but you should ignore it. An appropriate test for `person` would require replication (that is, multiple measurements for `person` and `drug` combinations). Also, without replication there is no test available for investigating the interaction between `person` and `drug`.

◁

▷ Example 16

Table 7.7 of Winer, Brown, and Michels (1991) provides another repeated-measures ANOVA example. There are four dial shapes and two methods for calibrating dials. Subjects are nested within calibration method, and an accuracy score is obtained. The data are shown below.

```
. use http://www.stata-press.com/data/r12/t77
(T7.7 -- Winer, Brown, Michels)
. tabdisp shape subject calib, cell(score)
```

4 dial shapes	2 methods for calibrating dials and subject nested in calib: 1			2		
	1	2	3	1	2	3
1	0	3	4	4	5	7
2	0	1	3	2	4	5
3	5	5	6	7	6	8
4	3	4	2	8	6	9

The calibration method and dial shapes are fixed factors, whereas subjects are random. The appropriate test for calibration method uses the nested subject term as the error term. Both the dial shape and the interaction between dial shape and calibration method are tested with the dial shape by subject interaction nested within calibration method. Here we drop this term from the `anova` command, and it becomes residual error. The dial shape is the repeated variable because each subject is tested with all four dial shapes. Here is the `anova` command that produces the desired results:

```
. anova score calib / subject|calib shape calib#shape, repeated(shape)
                          Number of obs =      24     R-squared     =  0.8925
                          Root MSE      = 1.11181     Adj R-squared =  0.7939

                  Source | Partial SS    df       MS           F     Prob > F
-------------------------+----------------------------------------------------
                   Model |     123.125    11  11.1931818       9.06     0.0003
                         |
                   calib |  51.0416667     1  51.0416667      11.89     0.0261
            subject|calib |  17.1666667     4  4.29166667
-------------------------+----------------------------------------------------
                   shape |  47.4583333     3  15.8194444      12.80     0.0005
              calib#shape |  7.45833333     3  2.48611111       2.01     0.1662
                         |
                Residual |  14.8333333    12  1.23611111
-------------------------+----------------------------------------------------
                   Total |  137.958333    23  5.99818841

Between-subjects error term:  subject|calib
                     Levels:  6          (4 df)
         Lowest b.s.e. variable:  subject
         Covariance pooled over:  calib     (for repeated variable)
Repeated variable: shape
                                     Huynh-Feldt epsilon        =  0.8483
                                     Greenhouse-Geisser epsilon =  0.4751
                                     Box's conservative epsilon =  0.3333

                                              ------------ Prob > F ------------
                  Source |     df       F    Regular     H-F      G-G       Box
-------------------------+----------------------------------------------------
                   shape |      3   12.80     0.0005    0.0011   0.0099    0.0232
              calib#shape |      3    2.01     0.1662    0.1791   0.2152    0.2291
                Residual |     12
-------------------------+----------------------------------------------------
```

The repeated-measure ϵ corrections are applied to any terms that are tested in the main ANOVA table and have the repeated variable in the term. These ϵ corrections are given in a table below the main ANOVA table. Here the repeated-measures tests for `shape` and `calib#shape` are presented.

Calibration method is significant, as is dial shape. The interaction between calibration method and dial shape is not significant. The repeated-measure ϵ corrections do not change these conclusions, but they do change the significance level for the tests on `shape` and `calib#shape`. Here, though, unlike in the previous example, the Huynh–Feldt ϵ is less than 1.

Here are the predictive marginal mean scores for calibration method and dial shapes. Because the interaction was not significant, we request only the `calib` and `shape` predictive margins.

```
. margins, within(calib)
Predictive margins                                Number of obs   =         24
Expression   : Linear prediction, predict()
within       : calib
Empty cells  : reweight

------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       calib |
           1 |          3   .3209506     9.35   0.000     2.370948    3.629052
           2 |   5.916667   .3209506    18.43   0.000     5.287615    6.545718
------------------------------------------------------------------------------
```

```
. margins, within(shape)
Predictive margins                                Number of obs   =         24
Expression   : Linear prediction, predict()
within       : shape
Empty cells  : reweight
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
shape						
1	3.833333	.4538926	8.45	0.000	2.94372	4.722947
2	2.5	.4538926	5.51	0.000	1.610387	3.389613
3	6.166667	.4538926	13.59	0.000	5.277053	7.05628
4	5.333333	.4538926	11.75	0.000	4.44372	6.222947

◁

❑ Technical note

The computation of the Greenhouse–Geisser and Huynh–Feldt epsilons in a repeated-measures ANOVA requires the number of levels and degrees of freedom for the between-subjects error term, as well as a value computed from a pooled covariance matrix. The observations are grouped based on all but the lowest-level variable in the between-subjects error term. The covariance over the repeated variables is computed for each resulting group, and then these covariance matrices are pooled. The dimension of the pooled covariance matrix is the number of levels of the repeated variable (or combination of levels for multiple repeated variables). In example 16, there are four levels of the repeated variable (`shape`), so the resulting covariance matrix is 4×4.

The `anova` command automatically attempts to determine the between-subjects error term and the lowest-level variable in the between-subjects error term to group the observations for computation of the pooled covariance matrix. `anova` issues an error message indicating that the `bse()` or `bseunit()` option is required when `anova` cannot determine them. You may override the default selections of `anova` by specifying the `bse()`, `bseunit()`, or `grouping()` option. The term specified in the `bse()` option must be a term in the ANOVA model.

The default selection for the between-subjects error term (the `bse()` option) is the interaction of the nonrepeated categorical variables in the ANOVA model. The first variable listed in the between-subjects error term is automatically selected as the lowest-level variable in the between-subjects error term but can be overridden with the `bseunit(`*varname*`)` option. *varname* is often a term, such as subject or subsample within subject, and is most often listed first in the term because of the nesting notation of ANOVA. This term makes sense in most repeated-measures ANOVA designs when the terms of the model are written in standard form. For instance, in example 16, there were three categorical variables (`subject`, `calib`, and `shape`), with `shape` being the repeated variable. Here `anova` looked for a term involving only `subject` and `calib` to determine the between-subjects error term. It found `subject|calib` as the term with six levels and 4 degrees of freedom. `anova` then picked `subject` as the default for the `bseunit()` option (the lowest variable in the between-subjects error term) because it was listed first in the term.

The grouping of observations proceeds, based on the different combinations of values of the variables in the between-subjects error term, excluding the lowest level variable (as found by default or as specified with the `bseunit()` option). You may specify the `grouping()` option to change the default grouping used in computing the pooled covariance matrix.

The between-subjects error term, number of levels, degrees of freedom, lowest variable in the term, and grouping information are presented after the main ANOVA table and before the rest of the repeated-measures output.

❑

▷ Example 17

Data with two repeated variables are given in table 7.13 of Winer, Brown, and Michels (1991). The accuracy scores of subjects making adjustments to three dials during three different periods are recorded. Three subjects are exposed to a certain noise background level, whereas a different set of three subjects is exposed to a different noise background level. Here is a table of accuracy scores for the `noise`, `subject`, `period`, and `dial` variables:

```
. use http://www.stata-press.com/data/r12/t713
(T7.13 -- Winer, Brown, Michels)
. tabdisp subject dial period, by(noise) cell(score) stubwidth(11)
```

noise background and subject nested in noise	10 minute time periods and dial								
	1			2			3		
	1	2	3	1	2	3	1	2	3
1									
1	45	53	60	40	52	57	28	37	46
2	35	41	50	30	37	47	25	32	41
3	60	65	75	58	54	70	40	47	50
2									
1	50	48	61	25	34	51	16	23	35
2	42	45	55	30	37	43	22	27	37
3	56	60	77	40	39	57	31	29	46

`noise`, `period`, and `dial` are fixed, whereas `subject` is random. Both `period` and `dial` are repeated variables. The ANOVA for this example is specified next.

```
. anova score noise / subject|noise period noise#period
> / period#subject|noise  dial noise#dial / dial#subject|noise
> period#dial noise#period#dial, repeated(period dial)
```

```
                          Number of obs =      54     R-squared     =  0.9872
                          Root MSE      = 2.81859     Adj R-squared =  0.9576
```

Source	Partial SS	df	MS	F	Prob > F
Model	9797.72222	37	264.803303	33.33	0.0000
noise	468.166667	1	468.166667	0.75	0.4348
subject|noise	2491.11111	4	622.777778		
period	3722.33333	2	1861.16667	63.39	0.0000
noise#period	333	2	166.5	5.67	0.0293
period#subject|noise	234.888889	8	29.3611111		
dial	2370.33333	2	1185.16667	89.82	0.0000
noise#dial	50.3333333	2	25.1666667	1.91	0.2102
dial#subject|noise	105.555556	8	13.1944444		
period#dial	10.6666667	4	2.66666667	0.34	0.8499
noise#period#dial	11.3333333	4	2.83333333	0.36	0.8357
Residual	127.111111	16	7.94444444		
Total	9924.83333	53	187.261006		

```
Between-subjects error term:  subject|noise
                     Levels:  6          (4 df)
       Lowest b.s.e. variable:  subject
       Covariance pooled over:  noise     (for repeated variables)
Repeated variable: period
                                  Huynh-Feldt epsilon        =  1.0668
                                  *Huynh-Feldt epsilon reset to 1.0000
                                  Greenhouse-Geisser epsilon =  0.6476
                                  Box's conservative epsilon =  0.5000
```

			Prob > F			
Source	df	F	Regular	H-F	G-G	Box
period	2	63.39	0.0000	0.0000	0.0003	0.0013
noise#period	2	5.67	0.0293	0.0293	0.0569	0.0759
period#subject|noise	8					

```
Repeated variable: dial
                                  Huynh-Feldt epsilon        =  2.0788
                                  *Huynh-Feldt epsilon reset to 1.0000
                                  Greenhouse-Geisser epsilon =  0.9171
                                  Box's conservative epsilon =  0.5000
```

			Prob > F			
Source	df	F	Regular	H-F	G-G	Box
dial	2	89.82	0.0000	0.0000	0.0000	0.0007
noise#dial	2	1.91	0.2102	0.2102	0.2152	0.2394
dial#subject|noise	8					

```
Repeated variables: period#dial
                                    Huynh-Feldt epsilon        =  1.3258
                                    *Huynh-Feldt epsilon reset to 1.0000
                                    Greenhouse-Geisser epsilon =  0.5134
                                    Box's conservative epsilon =  0.2500
                                                 ------------ Prob > F ------------
              Source |  df      F    Regular     H-F      G-G       Box
---------------------+-------------------------------------------------------------
         period#dial |   4    0.34   0.8499    0.8499   0.7295    0.5934
    noise#period#dial |   4    0.36   0.8357    0.8357   0.7156    0.5825
            Residual |  16
---------------------+-------------------------------------------------------------
```

For each repeated variable and for each combination of interactions of repeated variables, there are different ϵ correction values. The `anova` command produces tables for each applicable combination.

The two most significant factors in this model appear to be `dial` and `period`. The `noise` by `period` interaction may also be significant, depending on the correction factor you use. Below is a table of predictive margins for the accuracy score for dial, period, and noise by period.

```
. margins, within(dial)
Predictive margins                              Number of obs   =         54
Expression   : Linear prediction, predict()
within       : dial
Empty cells  : reweight
------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        dial |
           1 |   37.38889   .6643478    56.28   0.000     36.08679    38.69099
           2 |   42.22222   .6643478    63.55   0.000     40.92012    43.52432
           3 |   53.22222   .6643478    80.11   0.000     51.92012    54.52432
------------------------------------------------------------------------------

. margins, within(period)
Predictive margins                              Number of obs   =         54
Expression   : Linear prediction, predict()
within       : period
Empty cells  : reweight
------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      period |
           1 |   54.33333   .6643478    81.78   0.000     53.03124    55.63543
           2 |      44.5    .6643478    66.98   0.000      43.1979     45.8021
           3 |         34   .6643478    51.18   0.000      32.6979     35.3021
------------------------------------------------------------------------------
```

```
. margins, within(noise period)
Predictive margins                                Number of obs   =         54
Expression   : Linear prediction, predict()
within       : noise period
Empty cells  : reweight
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
noise#period						
1 1	53.77778	.9395297	57.24	0.000	51.93633	55.61922
1 2	49.44444	.9395297	52.63	0.000	47.603	51.28589
1 3	38.44444	.9395297	40.92	0.000	36.603	40.28589
2 1	54.88889	.9395297	58.42	0.000	53.04744	56.73033
2 2	39.55556	.9395297	42.10	0.000	37.71411	41.397
2 3	29.55556	.9395297	31.46	0.000	27.71411	31.397

Dial shape 3 produces the highest score, and scores decrease over the periods.

◁

Example 17 had two repeated-measurement variables. Up to four repeated-measurement variables may be specified in the `anova` command.

Saved results

`anova` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(mss)`	model sum of squares
`e(df_m)`	model degrees of freedom
`e(rss)`	residual sum of squares
`e(df_r)`	residual degrees of freedom
`e(r2)`	R-squared
`e(r2_a)`	adjusted R-squared
`e(F)`	F statistic
`e(rmse)`	root mean squared error
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(ss_#)`	sum of squares for term #
`e(df_#)`	numerator degrees of freedom for term #
`e(ssdenom_#)`	denominator sum of squares for term # (when using nonresidual error)
`e(dfdenom_#)`	denominator degrees of freedom for term # (when using nonresidual error)
`e(F_#)`	F statistic for term # (if computed)
`e(N_bse)`	number of levels of the between-subjects error term
`e(df_bse)`	degrees of freedom for the between-subjects error term
`e(box#)`	Box's conservative epsilon for a particular combination of repeated variables (`repeated()` only)
`e(gg#)`	Greenhouse–Geisser epsilon for a particular combination of repeated variables (`repeated()` only)
`e(hf#)`	Huynh–Feldt epsilon for a particular combination of repeated variables (`repeated()` only)
`e(rank)`	rank of `e(V)`

Macros

e(cmd)	anova
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(varnames)	names of the right-hand-side variables
e(term_#)	term #
e(errorterm_#)	error term for term # (when using nonresidual error)
e(sstype)	type of sum of squares; sequential or partial
e(repvars)	names of repeated variables (repeated() only)
e(repvar#)	names of repeated variables for a particular combination (repeated() only)
e(model)	ols
e(wtype)	weight type
e(wexp)	weight expression
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators
e(Srep)	covariance matrix based on repeated measures (repeated() only)

Functions

e(sample)	marks estimation sample

Methods and formulas

anova is implemented as an ado-file.

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Also see

[R] **anova postestimation** — Postestimation tools for anova

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **loneway** — Large one-way ANOVA, random effects, and reliability

[R] **oneway** — One-way analysis of variance

[R] **regress** — Linear regression

[MV] **manova** — Multivariate analysis of variance and covariance

Stata Structural Equation Modeling Reference Manual

Title

anova postestimation — Postestimation tools for anova

Description

The following postestimation commands are of special interest after `anova`:

Command	Description
`dfbeta`	DFBETA influence statistics
`estat hettest`	tests for heteroskedasticity
`estat imtest`	information matrix test
`estat ovtest`	Ramsey regression specification-error test for omitted variables
`estat szroeter`	Szroeter's rank test for heteroskedasticity
`estat vif`	variance inflation factors for the independent variables
`acprplot`	augmented component-plus-residual plot
`avplot`	added-variable plot
`avplots`	all added-variable plots in one image
`cprplot`	component-plus-residual plot
`lvr2plot`	leverage-versus-squared-residual plot
`rvfplot`	residual-versus-fitted plot
`rvpplot`	residual-versus-predictor plot

For information about these commands, see [R] **regress postestimation**.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation commands

In addition to the common estat commands (see [R] **estat**), estat hettest, estat imtest, estat ovtest, estat szroeter, and estat vif are also available. dfbeta is also available. The syntax for dfbeta and these estat commands is the same as after regress; see [R] **regress postestimation**.

In addition to the standard syntax of test (see [R] **test**), test after anova has three additionally allowed syntaxes; see below. test performs Wald tests of expressions involving the coefficients of the underlying regression model. Simple and composite linear hypotheses are possible.

Syntax for predict

predict after anova follows the same syntax as predict after regress and can provide predictions, residuals, standardized residuals, Studentized residuals, the standard error of the residuals, the standard error of the prediction, the diagonal elements of the projection (hat) matrix, and Cook's D. See [R] **regress postestimation** for details.

Syntax for test after anova

In addition to the standard syntax of test (see [R] **test**), test after anova also allows the following:

```
test, test(matname) [mtest[(opt)] matvlc(matname)]                    syntax a

test, showorder                                                       syntax b

test [term [term ...]] [/ term [term ...]] [, symbolic]               syntax c
```

syntax a test expression involving the coefficients of the underlying regression model; you provide information as a matrix

syntax b show underlying order of design matrix, which is useful when constructing *matname* argument of the test() option

syntax c test effects and show symbolic forms

Menu

Statistics > Linear models and related > ANOVA/MANOVA > Test linear hypotheses after anova

Options for test after anova

test(*matname*) is required with syntax a of test. The rows of *matname* specify linear combinations of the underlying design matrix of the ANOVA that are to be jointly tested. The columns correspond to the underlying design matrix (including the constant if it has not been suppressed). The column and row names of *matname* are ignored.

A listing of the constraints imposed by the test() option is presented before the table containing the tests. You should examine this table to verify that you have applied the linear combinations you desired. Typing test, showorder allows you to examine the ordering of the columns for the design matrix from the ANOVA.

`mtest`[`(`*opt*`)`] specifies that tests are performed for each condition separately. *opt* specifies the method for adjusting p-values for multiple testing. Valid values for *opt* are

`bonferroni`	Bonferroni's method
`holm`	Holm's method
`sidak`	Šidák's method
`noadjust`	no adjustment is to be made

Specifying `mtest` with no argument is equivalent to `mtest(noadjust)`.

`matvlc(`*matname*`)`, a programmer's option, saves the variance–covariance matrix of the linear combinations involved in the suite of tests. For the test $\mathbf{Lb} = \mathbf{c}$, what is returned in *matname* is $\mathbf{L}V\mathbf{L}'$, where V is the estimated variance–covariance matrix of $\mathbf{b}$.

`showorder` causes `test` to list the definition of each column in the design matrix. `showorder` is not allowed with any other option.

`symbolic` requests the symbolic form of the test rather than the test statistic. When this option is specified with no terms (`test, symbolic`), the symbolic form of the estimable functions is displayed.

Remarks

Remarks are presented under the following headings:

Testing effects
Obtaining symbolic forms
Testing coefficients and contrasts of margins

See examples 4, 7, 8, 13, 15, 16, and 17 in [R] **anova** for examples that use the `margins` command.

Testing effects

After fitting a model using `anova`, you can test for the significance of effects in the ANOVA table, as well as for effects that are not reported in the ANOVA table, by using the `test` or `contrast` command. You follow `test` or `contrast` by the list of effects that you wish to test. By default, these commands use the residual mean squared error in the denominator of the F ratio. You can specify other error terms by using the slash notation, just as you would with `anova`. See [R] **contrast** for details on this command.

▷ Example 1

Recall our byssinosis example (example 8) in [R] **anova**:

```
. anova prob workplace smokes race workplace#smokes workplace#race
> smokes#race workplace#smokes#race [aweight=pop]
(sum of wgt is   5.4190e+03)
                          Number of obs =      65     R-squared     =  0.8300
                          Root MSE      = .025902     Adj R-squared =  0.7948
```

Source	Partial SS	df	MS	F	Prob > F
Model	.173646538	11	.015786049	23.53	0.0000
workplace	.097625175	2	.048812588	72.76	0.0000
smokes	.013030812	1	.013030812	19.42	0.0001
race	.001094723	1	.001094723	1.63	0.2070
workplace#smokes	.019690342	2	.009845171	14.67	0.0000
workplace#race	.001352516	2	.000676258	1.01	0.3718
smokes#race	.001662874	1	.001662874	2.48	0.1214
workplace#smokes#race	.000950841	2	.00047542	0.71	0.4969
Residual	.035557766	53	.000670901		
Total	.209204304	64	.003268817		

We can easily obtain a test on a particular term from the ANOVA table. Here are two examples:

```
. test smokes
```

Source	Partial SS	df	MS	F	Prob > F
smokes	.013030812	1	.013030812	19.42	0.0001
Residual	.035557766	53	.000670901		

```
. test smokes#race
```

Source	Partial SS	df	MS	F	Prob > F
smokes#race	.001662874	1	.001662874	2.48	0.1214
Residual	.035557766	53	.000670901		

Both of these tests use residual error by default and agree with the ANOVA table produced earlier.

We could have performed these same tests with `contrast`:

```
. contrast smokes
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
smokes	1	19.42	0.0001
Residual	53		

```
. contrast smokes#race
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
smokes#race	1	2.48	0.1214
Residual	53		

❑ Technical note

After `anova`, you can use the '`/`' syntax in `test` or `contrast` to perform tests with a variety of non-$\sigma^2\mathbf{I}$ error structures. However, in most unbalanced models, the mean squares are not independent and do not have equal expectations under the null hypothesis. Also, be warned that you assume responsibility for the validity of the test statistic.

❑

▷ Example 2

We return to the nested ANOVA example (example 11) in [R] **anova**, where five brands of machinery were compared in an assembly line. We can obtain appropriate tests for the nested terms using `test`, even if we had run the `anova` command without initially indicating the proper error terms.

```
. use http://www.stata-press.com/data/r12/machine
(machine data)
. anova output machine operator|machine
                          Number of obs =      57     R-squared     =  0.8661
                          Root MSE      = 1.47089     Adj R-squared =  0.8077
                  Source |  Partial SS    df       MS           F     Prob > F
-------------------------+----------------------------------------------------
                   Model |  545.822288    17  32.1071934       14.84     0.0000
                         |
                 machine |  430.980792     4  107.745198       49.80     0.0000
         operator|machine |  101.353804    13  7.79644648        3.60     0.0009
                         |
                Residual |  84.3766582    39  2.16350406
-------------------------+----------------------------------------------------
                   Total |  630.198947    56  11.2535526
```

In this ANOVA table, `machine` is tested with residual error. With this particular nested design, the appropriate error term for testing `machine` is `operator` nested within `machine`, which is easily obtained from `test`.

```
. test machine / operator|machine
                  Source |  Partial SS    df       MS           F     Prob > F
-------------------------+----------------------------------------------------
                 machine |  430.980792     4  107.745198       13.82     0.0001
         operator|machine |  101.353804    13  7.79644648
```

This result from `test` matches what we obtained from our `anova` command.

◁

▷ Example 3

The other nested ANOVA example (example 12) in [R] **anova** was based on the sewage data. The ANOVA table is presented here again. As before, we will use abbreviations of variable names in typing the commands.

```
. use http://www.stata-press.com/data/r12/sewage
(Sewage treatment)
```

```
. anova particulate s / m|s / f|m|s / w|f|m|s /, dropemptycells
                          Number of obs =      64     R-squared     =  0.6338
                          Root MSE      = 12.7445     Adj R-squared =  0.5194
```

Source	Partial SS	df	MS	F	Prob > F
Model	13493.6094	15	899.573958	5.54	0.0000
solution	7203.76563	1	7203.76563	17.19	0.0536
manager|solution	838.28125	2	419.140625		
manager|solution	838.28125	2	419.140625	0.55	0.6166
facility|manager|solution	3064.9375	4	766.234375		
facility|manager|solution	3064.9375	4	766.234375	2.57	0.1193
worker|facility|manager|solution	2386.625	8	298.328125		
worker|facility|manager|solution	2386.625	8	298.328125	1.84	0.0931
Residual	7796.25	48	162.421875		
Total	21289.8594	63	337.934276		

In practice, it is often beneficial to pool nonsignificant nested terms to increase the power of tests on remaining terms. One rule of thumb is to allow the pooling of a term whose p-value is larger than 0.25. In this sewage example, the p-value for the test of `manager` is 0.6166. This value indicates that the manager effect is negligible and might be ignored. Currently, `solution` is tested by `manager|solution`, which has only 2 degrees of freedom. If we pool the `manager` and `facility` terms and use this pooled estimate as the error term for `solution`, we would have a term with 6 degrees of freedom.

Below are two tests: a test of `solution` with the pooled `manager` and `facility` terms and a test of this pooled term by `worker`.

```
. test s / m|s f|m|s
```

Source	Partial SS	df	MS	F	Prob > F
solution	7203.76563	1	7203.76563	11.07	0.0159
manager|solution facility|manager|solution	3903.21875	6	650.536458		

```
. test m|s f|m|s / w|f|m|s
```

Source	Partial SS	df	MS	F	Prob > F
manager|solution facility|manager|solution	3903.21875	6	650.536458	2.18	0.1520
worker|facility|manager|solution	2386.625	8	298.328125		

In the first test, we included two terms after the forward slash (`m|s` and `f|m|s`). `test` after `anova` allows multiple terms both before and after the slash. The terms before the slash are combined and are then tested by the combined terms that follow the slash (or residual error if no slash is present).

The p-value for `solution` using the pooled term is 0.0159. Originally, it was 0.0536. The increase in the power of the test is due to the increase in degrees of freedom for the pooled error term.

We can get identical results if we drop `manager` from the `anova` model. (This dataset has unique numbers for each facility so that there is no confusion of facilities when `manager` is dropped.)

```
. anova particulate s / f|s / w|f|s /, dropemptycells
                          Number of obs =      64     R-squared     =  0.6338
                          Root MSE      = 12.7445     Adj R-squared =  0.5194
```

Source	Partial SS	df	MS	F	Prob > F
Model	13493.6094	15	899.573958	5.54	0.0000
solution	7203.76563	1	7203.76563	11.07	0.0159
facility|solution	3903.21875	6	650.536458		
facility|solution	3903.21875	6	650.536458	2.18	0.1520
worker|facility|solution	2386.625	8	298.328125		
worker|facility|solution	2386.625	8	298.328125	1.84	0.0931
Residual	7796.25	48	162.421875		
Total	21289.8594	63	337.934276		

This output agrees with our earlier `test` results. ◁

In the following example, two terms from the `anova` are jointly tested (pooled).

▷ Example 4

In example 10 of [R] **anova**, we fit the model `anova drate region c.mage region#c.mage`. Now we use the `contrast` command to test for the overall significance of `region`.

```
. contrast region region#c.mage, overall
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
region	3	7.40	0.0004
region#c.mage	3	0.86	0.4689
Overall	6	5.65	0.0002
Residual	42		

The overall F statistic associated with the `region` and `region#c.mage` terms is 5.65, and it is significant at the 0.02% level.

In the ANOVA output, the `region` term, by itself, had a sum of squares of 1166.15, which, based on 3 degrees of freedom, yielded an F statistic of 7.40 and a significance level of 0.0004. This is the same test that is reported by `contrast` in the row labeled `region`. Likewise, the test from the ANOVA output for the `region#c.mage` term is reproduced in the second row of the `contrast` output. ◁

Obtaining symbolic forms

`test` can produce the symbolic form of the estimable functions and symbolic forms for particular tests.

▷ Example 5

After fitting an ANOVA model, we type `test, symbolic` to obtain the symbolic form of the estimable functions. For instance, returning to our blood pressure data introduced in example 4 of [R] **anova**, let's begin by reestimating `systolic` on `drug`, `disease`, and `drug#disease`:

```
. use http://www.stata-press.com/data/r12/systolic, clear
(Systolic Blood Pressure Data)
. anova systolic drug##disease
                          Number of obs =      58     R-squared     =  0.4560
                          Root MSE      = 10.5096     Adj R-squared =  0.3259
                 Source | Partial SS    df       MS           F     Prob > F
------------------------+----------------------------------------------------
                  Model |  4259.33851    11  387.212591       3.51     0.0013
                        |
                   drug |  2997.47186     3  999.157287       9.05     0.0001
                disease |  415.873046     2  207.936523       1.88     0.1637
           drug#disease |  707.266259     6   117.87771       1.07     0.3958
                        |
                Residual |  5080.81667    46  110.452536
------------------------+----------------------------------------------------
                   Total |  9340.15517    57  163.862371
```

To obtain the symbolic form of the estimable functions, type

```
. test, symbolic
drug
           1  -(r2+r3+r4-r0)
           2   r2
           3   r3
           4   r4
disease
           1  -(r6+r7-r0)
           2   r6
           3   r7
drug#disease
        1  1  -(r2+r3+r4+r6+r7-r12-r13-r15-r16-r18-r19-r0)
        1  2   r6 - (r12+r15+r18)
        1  3   r7 - (r13+r16+r19)
        2  1   r2 - (r12+r13)
        2  2   r12
        2  3   r13
        3  1   r3 - (r15+r16)
        3  2   r15
        3  3   r16
        4  1   r4 - (r18+r19)
        4  2   r18
        4  3   r19
_cons           r0
```

◁

▷ Example 6

To obtain the symbolic form for a particular test, we type `test` *term* [*term* ...], `symbolic`. For instance, the symbolic form for the test of the main effect of `drug` is

```
. test drug, symbolic
drug
           1  -(r2+r3+r4)
           2   r2
           3   r3
           4   r4
disease
           1  0
           2  0
           3  0
drug#disease
        1  1  -1/3 (r2+r3+r4)
        1  2  -1/3 (r2+r3+r4)
        1  3  -1/3 (r2+r3+r4)
        2  1   1/3 r2
        2  2   1/3 r2
        2  3   1/3 r2
        3  1   1/3 r3
        3  2   1/3 r3
        3  3   1/3 r3
        4  1   1/3 r4
        4  2   1/3 r4
        4  3   1/3 r4
_cons          0
```

If we omit the `symbolic` option, we instead see the result of the test:

```
. test drug
```

Source	Partial SS	df	MS	F	Prob > F
drug	2997.47186	3	999.157287	9.05	0.0001
Residual	5080.81667	46	110.452536		

◁

Testing coefficients and contrasts of margins

The `test` command allows you to perform tests directly on the coefficients of the underlying regression model. For instance, the coefficient on the third `drug` and the second `disease` is referred to as `3.drug#2.disease`. This could also be written as `i3.drug#i2.disease`, or `_b[3.drug#2.disease]`, or even `_coef[i3.drug#i2.disease]`; see [U] **13.5 Accessing coefficients and standard errors**.

▷ Example 7

Let's begin by testing whether the coefficient on the third `drug` is equal to the coefficient on the fourth in our blood pressure data. We have already fit the model `anova systolic drug##disease` (equivalent to `anova systolic drug disease drug#disease`), and you can see the results of that estimation in example 5. Even though we have performed many tasks since we fit the model, Stata still remembers, and we can perform tests at any time.

```
. test 3.drug = 4.drug
 ( 1)  3.drug - 4.drug = 0
       F(  1,    46) =    0.13
            Prob > F =    0.7234
```

We find that the two coefficients are not significantly different, at least at any significance level smaller than 73%.

For more complex tests, the `contrast` command often provides a more concise way to specify the test we are interested in and prevents us from having to write the tests in terms of the regression coefficients. With `contrast`, we instead specify our tests in terms of differences in the marginal means for the levels of a particular factor. For example, if we want to compare the third and fourth drugs, we can test the difference in the mean impact on systolic blood pressure separately for each disease using the `@` operator. We also use the reverse adjacent operator, `ar.`, to compare the fourth level of drug with the previous level.

```
. contrast ar4.drug@disease
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
drug@disease			
(4 vs 3) 1	1	0.13	0.7234
(4 vs 3) 2	1	1.76	0.1917
(4 vs 3) 3	1	0.65	0.4230
Joint	3	0.85	0.4761
Residual	46		

	Contrast	Std. Err.	[95% Conf.	Interval]
drug@disease				
(4 vs 3) 1	-2.733333	7.675156	-18.18262	12.71595
(4 vs 3) 2	8.433333	6.363903	-4.376539	21.24321
(4 vs 3) 3	5.7	7.050081	-8.491077	19.89108

None of the individual contrasts shows significant differences between the third drug and the fourth drug. Likewise, the overall F statistic is 0.85, which is hardly significant. We cannot reject the hypothesis that the third drug has the same effect as the fourth drug.

◁

❑ Technical note

Alternatively, we could have specified these tests based on the coefficients of the underlying regression model using the `test` command. We would have needed to perform tests on the coefficients for `drug` and for the coefficients on `drug` interacted with `disease` in order to test for differences in the means mentioned above. To do this, we start with our previous `test` command:

```
. test 3.drug = 4.drug
```

Notice that the F statistic for this test is equivalent to the test labeled `(4 vs 3) 1` in the `contrast` output. Let's now add the constraint that the coefficient on the third drug interacted with the third disease is equal to the coefficient on the fourth drug, again interacted with the third disease. We do that by typing the new constraint and adding the `accumulate` option:

```
. test 3.drug#3.disease = 4.drug#3.disease, accumulate
 ( 1)  3.drug - 4.drug = 0
 ( 2)  3.drug#3.disease - 4.drug#3.disease = 0
       F(  2,    46) =    0.39
            Prob > F =    0.6791
```

So far, our test includes the equality of the two drug coefficients, along with the equality of the two drug coefficients when interacted with the third disease. Now we add two more equations, one for each of the remaining two diseases:

```
. test 3.drug#2.disease = 4.drug#2.disease, accumulate
 ( 1)  3.drug - 4.drug = 0
 ( 2)  3.drug#3.disease - 4.drug#3.disease = 0
 ( 3)  3.drug#2.disease - 4.drug#2.disease = 0
       F(  3,    46) =    0.85
            Prob > F =    0.4761
. test 3.drug#1.disease = 4.drug#1.disease, accumulate
 ( 1)  3.drug - 4.drug = 0
 ( 2)  3.drug#3.disease - 4.drug#3.disease = 0
 ( 3)  3.drug#2.disease - 4.drug#2.disease = 0
 ( 4)  3o.drug#1b.disease - 4o.drug#1b.disease = 0
       Constraint 4 dropped
       F(  3,    46) =    0.85
            Prob > F =    0.4761
```

The overall F statistic reproduces the one from the joint test in the `contrast` output.

You may notice that we also got the message "Constraint 4 dropped". For the technically inclined, this constraint was unnecessary, given the normalization of the model. If we specify all the constraints involved in our test or use `contrast`, we need not worry about the normalization because Stata handles this automatically.

❑

The `test()` option of `test` provides another alternative for testing coefficients. Instead of spelling out each coefficient involved in the test, a matrix representing the test provides the needed information. `test, showorder` shows the order of the terms in the ANOVA corresponding to the order of the columns for the matrix argument of `test()`.

▷ Example 8

We repeat the last test of example 7 above with the `test()` option. First, we view the definition and order of the columns underlying the ANOVA performed on the systolic data.

```
. test, showorder
 Order of columns in the design matrix
      1: (drug==1)
      2: (drug==2)
      3: (drug==3)
      4: (drug==4)
      5: (disease==1)
      6: (disease==2)
      7: (disease==3)
      8: (drug==1)*(disease==1)
      9: (drug==1)*(disease==2)
     10: (drug==1)*(disease==3)
     11: (drug==2)*(disease==1)
     12: (drug==2)*(disease==2)
     13: (drug==2)*(disease==3)
     14: (drug==3)*(disease==1)
     15: (drug==3)*(disease==2)
     16: (drug==3)*(disease==3)
     17: (drug==4)*(disease==1)
     18: (drug==4)*(disease==2)
     19: (drug==4)*(disease==3)
     20: _cons
```

Columns 1–4 correspond to the four levels of `drug`. Columns 5–7 correspond to the three levels of `disease`. Columns 8–19 correspond to the interaction of `drug` and `disease`. The last column corresponds to `_cons`, the constant in the model.

We construct the matrix `dr3vs4` with the same four constraints as the last test shown in example 7 and then use the `test(dr3vs4)` option to perform the test.

```
. mat dr3vs4 = (0,0,1,-1,  0,0,0,  0,0,0,0,0,0,0,0,0, 0, 0, 0,  0 \
>               0,0,0, 0,  0,0,0,  0,0,0,0,0,0,0,0,1, 0, 0,-1,  0 \
>               0,0,0, 0,  0,0,0,  0,0,0,0,0,0,0,1,0, 0,-1, 0,  0 \
>               0,0,0, 0,  0,0,0,  0,0,0,0,0,0,1,0,0,-1, 0, 0,  0)
. test, test(dr3vs4)
 ( 1)  3.drug - 4.drug = 0
 ( 2)  3.drug#3.disease - 4.drug#3.disease = 0
 ( 3)  3.drug#2.disease - 4.drug#2.disease = 0
 ( 4)  3o.drug#1b.disease - 4o.drug#1b.disease = 0
       Constraint 4 dropped
       F(  3,    46) =    0.85
            Prob > F =    0.4761
```

Here the effort involved with spelling out the coefficients is similar to that of constructing a matrix and using it in the `test()` option. When the test involving coefficients is more complicated, the `test()` option may be more convenient than specifying the coefficients directly in `test`. However, as previously demonstrated, `contrast` may provide an even simpler method for testing the same hypothesis.

◁

After fitting an ANOVA model, various contrasts (1-degree-of-freedom tests comparing different levels of a categorical variable) are often of interest. `contrast` can perform each 1-degree-of-freedom test in addition to the combined test, even in cases in which the contrasts do not correspond to one of the contrast operators.

▷ Example 9

Rencher and Schaalje (2008) illustrate 1-degree-of-freedom contrasts for an ANOVA comparing the net weight of cans filled by five machines (labeled `A`–`E`). The data were originally obtained from Ostle and Mensing (1975). Rencher and Schaalje use a cell-means ANOVA model approach for this problem. We could do the same by using the `noconstant` option of `anova`; see [R] **anova**. Instead, we obtain the same results by using the standard overparameterized ANOVA approach (that is, we keep the constant in the model).

```
. use http://www.stata-press.com/data/r12/canfill
(Can Fill Data)
. list, sepby(machine)
```

	machine	weight
1.	A	11.95
2.	A	12.00
3.	A	12.25
4.	A	12.10
5.	B	12.18
6.	B	12.11
7.	C	12.16
8.	C	12.15
9.	C	12.08
10.	D	12.25
11.	D	12.30
12.	D	12.10
13.	E	12.10
14.	E	12.04
15.	E	12.02
16.	E	12.02

```
. anova weight machine
```

```
                   Number of obs =      16     R-squared     =  0.4123
                   Root MSE      = .087758     Adj R-squared =  0.1986
```

Source	Partial SS	df	MS	F	Prob > F
Model	.059426993	4	.014856748	1.93	0.1757
machine	.059426993	4	.014856748	1.93	0.1757
Residual	.084716701	11	.007701518		
Total	.144143694	15	.00960958		

The four 1-degree-of-freedom tests of interest among the five machines are `A` and `D` versus `B`, `C`, and `E`; `B` and `E` versus `C`; `A` versus `D`; and `B` versus `E`. We can specify these tests as user-defined contrasts by placing the corresponding contrast coefficients into positions related to the five levels of machine as described in *User-defined contrasts* of [R] **contrast**.

```
. contrast {machine 3 -2 -2  3 -2}
>          {machine 0  1 -2  0  1}
>          {machine 1  0  0 -1  0}
>          {machine 0  1  0  0 -1}, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
machine			
(1)	1	0.75	0.4055
(2)	1	0.31	0.5916
(3)	1	4.47	0.0582
(4)	1	1.73	0.2150
Joint	4	1.93	0.1757
Residual	11		

`contrast` produces a 1-degree-of-freedom test for each of the specified contrasts as well as a joint test. We included the `noeffects` option so that the table displaying the values of the individual contrasts with their confidence intervals was suppressed.

The significance values above are not adjusted for multiple comparisons. We could have produced the Bonferroni-adjusted significance values by using the `mcompare(bonferroni)` option.

```
. contrast {machine 3 -2 -2  3 -2}
>          {machine 0  1 -2  0  1}
>          {machine 1  0  0 -1  0}
>          {machine 0  1  0  0 -1}, mcompare(bonferroni) noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F	Bonferroni P>F
machine				
(1)	1	0.75	0.4055	1.0000
(2)	1	0.31	0.5916	1.0000
(3)	1	4.47	0.0582	0.2329
(4)	1	1.73	0.2150	0.8601
Joint	4	1.93	0.1757	
Residual	11			

```
Note: Bonferroni-adjusted p-values are reported for tests
      on individual contrasts only.
```

◁

▷ Example 10

Here there are two factors, `A` and `B`, each with three levels. The levels are quantitative so that linear and quadratic contrasts are of interest.

```
. use http://www.stata-press.com/data/r12/twowaytrend
. anova Y A B A#B
```

Source	Partial SS	df	MS	F	Prob > F
Model	2578.55556	8	322.319444	45.09	0.0000
A	2026.72222	2	1013.36111	141.77	0.0000
B	383.722222	2	191.861111	26.84	0.0000
A#B	168.111111	4	42.0277778	5.88	0.0015
Residual	193	27	7.14814815		
Total	2771.55556	35	79.1873016		

Number of obs = 36 R-squared = 0.9304
Root MSE = 2.6736 Adj R-squared = 0.9097

We can use the `p.` contrast operator to obtain the 1-degree-of-freedom tests for the linear and quadratic effects of `A` and `B`.

```
. contrast p.A p.B, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
A			
(linear)	1	212.65	0.0000
(quadratic)	1	70.88	0.0000
Joint	2	141.77	0.0000
B			
(linear)	1	26.17	0.0000
(quadratic)	1	27.51	0.0000
Joint	2	26.84	0.0000
Residual	27		

All the above tests appear to be significant. In addition to presenting the 1-degree-of-freedom tests, the combined tests for `A` and `B` are produced and agree with the original ANOVA results.

Now we explore the interaction between `A` and `B`.

```
. contrast p.A#p1.B, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
A#B			
(linear) (linear)	1	17.71	0.0003
(quadratic) (linear)	1	0.07	0.7893
Joint	2	8.89	0.0011
Residual	27		

The 2-degrees-of-freedom test of the interaction of `A` with the linear components of `B` is significant at the 0.0011 level. But, when we examine the two 1-degree-of-freedom tests that compose this result,

the significance is due to the linear A by linear B contrast (significance level of 0.0003). A significance value of 0.7893 for the quadratic A by linear B indicates that this factor is not significant for these data.

```
. contrast p.A#p2.B, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
A#B			
(linear) (quadratic)	1	2.80	0.1058
(quadratic) (quadratic)	1	2.94	0.0979
Joint	2	2.87	0.0741
Residual	27		

The test of A with the quadratic components of B does not fall below the 0.05 significance level. ◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

References

Ostle, B., and R. W. Mensing. 1975. *Statistics in Research*. 3rd ed. Ames, IA: Iowa State University Press.

Rencher, A. C., and G. B. Schaalje. 2008. *Linear Models in Statistics*. 2nd ed. New York: Wiley.

Also see

[R] **anova** — Analysis of variance and covariance

[R] **regress postestimation** — Postestimation tools for regress

[U] **20 Estimation and postestimation commands**

Title

areg — Linear regression with a large dummy-variable set

Syntax

`areg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] , `absorb(`*varname*`)` [*options*]

options	Description
Model	
* `absorb(`*varname*`)`	categorical variable to be absorbed
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `ols`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`coeflegend`	display legend instead of statistics

*`absorb(`*varname*`)` is required.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `jackknife`, `mi estimate`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweight`s are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`aweights`, `fweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Other > Linear regression absorbing one cat. variable

Description

`areg` fits a linear regression absorbing one categorical factor. `areg` is designed for datasets with many groups, but not a number of groups that increases with the sample size. See the `xtreg, fe` command in [XT] **xtreg** for an estimator that handles the case in which the number of groups increases with the sample size.

Options

Model

`absorb(`*varname*`)` specifies the categorical variable, which is to be included in the regression as if it were specified by dummy variables. `absorb()` is required.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(ols)`, the default, uses the standard variance estimator for ordinary least-squares regression.

Exercise caution when using the `vce(cluster` *clustvar*`)` option with `areg`. The effective number of degrees of freedom for the robust variance estimator is $n_g - 1$, where n_g is the number of clusters. Thus the number of levels of the `absorb()` variable should not exceed the number of clusters.

Reporting

`level(#)`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `areg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Suppose that you have a regression model that includes among the explanatory variables a large number, k, of mutually exclusive and exhaustive dummies:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{d}_1\gamma_1 + \mathbf{d}_2\gamma_2 + \cdots + \mathbf{d}_k\gamma_k + \boldsymbol{\epsilon}$$

For instance, the dummy variables, $\mathbf{d}_i$, might indicate countries in the world or states of the United States. One solution would be to fit the model with `regress`, but this solution is possible only if k is small enough so that the total number of variables (the number of columns of $\mathbf{X}$ plus the number of $\mathbf{d}_i$'s plus one for $\mathbf{y}$) is sufficiently small—meaning less than `matsize` (see [R] **matsize**). For problems with more variables than the largest possible value of `matsize` (100 for Small Stata, 800 for Stata/IC, and 11,000 for Stata/SE and Stata/MP), `regress` will not work. `areg` provides a way of obtaining estimates of $\boldsymbol{\beta}$—but not the γ_i's—in these cases. The effects of the dummy variables are said to be absorbed.

▷ Example 1

So that we can compare the results produced by `areg` with Stata's other regression commands, we will fit a model in which k is small. `areg`'s real use, however, is when k is large.

In our automobile data, we have a variable called `rep78` that is coded 1, 2, 3, 4, and 5, where 1 means poor and 5 means excellent. Let's assume that we wish to fit a regression of `mpg` on `weight`, `gear_ratio`, and `rep78` (parameterized as a set of dummies).

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight gear_ratio b5.rep78
```

Source	SS	df	MS	Number of obs =	69
				F(6, 62) =	21.31
Model	1575.97621	6	262.662702	Prob > F =	0.0000
Residual	764.226686	62	12.3262369	R-squared =	0.6734
				Adj R-squared =	0.6418
Total	2340.2029	68	34.4147485	Root MSE =	3.5109

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0051031	.0009206	-5.54	0.000	-.0069433	-.003263
gear_ratio	.901478	1.565552	0.58	0.567	-2.228015	4.030971
rep78						
1	-2.036937	2.740728	-0.74	0.460	-7.515574	3.4417
2	-2.419822	1.764338	-1.37	0.175	-5.946682	1.107039
3	-2.557432	1.370912	-1.87	0.067	-5.297846	.1829814
4	-2.788389	1.395259	-2.00	0.050	-5.577473	.0006939
_cons	36.23782	7.01057	5.17	0.000	22.22389	50.25175

To fit the `areg` equivalent, we type

```
. areg mpg weight gear_ratio, absorb(rep78)
```

Linear regression, absorbing indicators

Number of obs	=		69
F(2, 62)	=		41.64
Prob > F	=		0.0000
R-squared	=		0.6734
Adj R-squared	=		0.6418
Root MSE	=		3.5109

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0051031	.0009206	-5.54	0.000	-.0069433	-.003263
gear_ratio	.901478	1.565552	0.58	0.567	-2.228015	4.030971
_cons	34.05889	7.056383	4.83	0.000	19.95338	48.1644
rep78	F(4, 62) =		1.117	0.356	(5 categories)	

Both `regress` and `areg` display the same R^2 values, root mean squared error, and—for `weight` and `gear_ratio`—the same parameter estimates, standard errors, t statistics, significance levels, and confidence intervals. `areg`, however, does not report the coefficients for `rep78`, and, in fact, they are not even calculated. This computational trick makes the problem manageable when k is large. `areg` reports a test that the coefficients associated with `rep78` are jointly zero. Here this test has a significance level of 35.6%. This F test for `rep78` is the same that we would obtain after `regress` if we were to specify `test 1.rep78 2.rep78 3.rep78 4.rep78`; see [R] **test**.

The model F tests reported by `regress` and `areg` also differ. The `regress` command reports a test that all coefficients except that of the constant are equal to zero; thus, the dummies are included in this test. The `areg` output shows a test that all coefficients excluding the dummies and the constant are equal to zero. This is the same test that can be obtained after `regress` by typing `test weight gear_ratio`.

◁

❑ Technical note

areg is designed for datasets with many groups, but not a number that grows with the sample size. Consider two different samples from the U.S. population. In the first sample, we have 10,000 individuals and we want to include an indicator for each of the 50 states, whereas in the second sample we have 3 observations on each of 10,000 individuals and we want to include an indicator for each individual. areg was designed for datasets similar to the first sample in which we have a fixed number of groups, the 50 states. In the second sample, the number of groups, which is the number of individuals, grows as we include more individuals in the sample. For an estimator designed to handle the case in which the number of groups grows with the sample size, see the xtreg, fe command in [XT] **xtreg**.

Although the point estimates produced by areg and xtreg, fe are the same, the estimated VCEs differ when cluster() is specified because the commands make different assumptions about whether the number of groups increases with the sample size.

❑

❑ Technical note

The intercept reported by areg deserves some explanation because, given k mutually exclusive and exhaustive dummies, it is arbitrary. areg identifies the model by choosing the intercept that makes the prediction calculated at the means of the independent variables equal to the mean of the dependent variable: $\overline{\mathbf{y}} = \overline{\mathbf{x}}\,\widehat{\boldsymbol{\beta}}$.

```
. predict yhat
(option xb assumed; fitted values)
. summarize mpg yhat if rep78 != .
```

Variable	Obs	Mean	Std. Dev.	Min	Max
mpg	69	21.28986	5.866408	12	41
yhat	69	21.28986	4.383224	11.58643	28.07367

We had to include if rep78 < . in our summarize command because we have missing values in our data. areg automatically dropped those missing values (as it should) in forming the estimates, but predict with the xb option will make predictions for cases with missing rep78 because it does not know that rep78 is really part of our model.

These predicted values do not include the absorbed effects (that is, the $\mathbf{d}_i\gamma_i$). For predicted values that include these effects, use the xbd option of predict (see [R] **areg postestimation**) or see [XT] **xtreg**.

❑

▷ Example 2

areg, vce(robust) is a Huberized version of areg; see [P] **_robust**. Just as areg is equivalent to using regress with dummies, areg, vce(robust) is equivalent to using regress, vce(robust) with dummies. You can use areg, vce(robust) when you expect heteroskedastic or nonnormal errors. areg, vce(robust), like ordinary regression, assumes that the observations are independent, unless the vce(cluster *clustvar*) option is specified. If the vce(cluster *clustvar*) option is specified, this independence assumption is relaxed and only the clusters identified by equal values of *clustvar* are assumed to be independent.

Assume that we were to collect data by randomly sampling 10,000 doctors (from 100 hospitals) and then sampling 10 patients of each doctor, yielding a total dataset of 100,000 patients in a cluster sample. If in some regression we wished to include effects of the hospitals to which the doctors belonged, we would want to include a dummy variable for each hospital, adding 100 variables to our model. `areg` could fit this model by

```
. areg depvar patient_vars, absorb(hospital) vce(cluster doctor)
```

◁

Saved results

`areg` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(tss)`	total sum of squares
`e(df_m)`	model degrees of freedom
`e(rss)`	residual sum of squares
`e(df_r)`	residual degrees of freedom
`e(r2)`	R-squared
`e(r2_a)`	adjusted R-squared
`e(df_a)`	degrees of freedom for absorbed effect
`e(rmse)`	root mean squared error
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(F)`	F statistic
`e(F_absorb)`	F statistic for absorbed effect (when `vce(robust)` is not specified)
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`areg`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(absvar)`	name of `absorb` variable
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(clustvar)`	name of cluster variable
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(datasignature)`	the checksum
`e(datasignaturevars)`	variables used in calculation of checksum
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(marginsnotok)`	predictions disallowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(Cns)`	constraints matrix
`e(V)`	variance–covariance matrix of the estimators
`e(V_modelbased)`	model-based variance

Functions

`e(sample)`	marks estimation sample

Methods and formulas

areg is implemented as an ado-file.

areg begins by recalculating *depvar* and *indepvars* to have mean 0 within the groups specified by absorb(). The overall mean of each variable is then added back in. The adjusted *depvar* is then regressed on the adjusted *indepvars* with regress, yielding the coefficient estimates. The degrees of freedom of the variance–covariance matrix of the coefficients is then adjusted to account for the absorbed variables—this calculation yields the same results (up to numerical roundoff error) as if the matrix had been calculated directly by the formulas given in [R] **regress**.

areg with vce(robust) or vce(cluster *clustvar*) works similarly, calling _robust after regress to produce the Huber/White/sandwich estimator of the variance or its clustered version. See [P] **_robust**, particularly *Introduction* and *Methods and formulas*. The model F test uses the robust variance estimates. There is, however, no simple computational means of obtaining a robust test of the absorbed dummies; thus this test is not displayed when the vce(robust) or vce(cluster *clustvar*) option is specified.

The number of groups specified in absorb() are included in the degrees of freedom used in the finite-sample adjustment of the cluster–robust VCE estimator. This statement is only valid if the number of groups is small relative to the sample size. (Technically, the number of groups must remain fixed as the sample size grows.) For an estimator that allows the number of groups to grow with the sample size, see the xtreg, fe command in [XT] **xtreg**.

Reference

Blackwell, J. L., III. 2005. Estimation and testing of fixed-effect panel-data systems. *Stata Journal* 5: 202–207.

Also see

[R] **areg postestimation** — Postestimation tools for areg

[R] **regress** — Linear regression

[MI] **estimation** — Estimation commands for use with mi estimate

[XT] **xtreg** — Fixed-, between-, and random-effects and population-averaged linear models

[U] **20 Estimation and postestimation commands**

Title

areg postestimation — Postestimation tools for areg

Description

The following postestimation commands are available after `areg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic]
```

where $y_j = \mathbf{x}_j\mathbf{b} + d_{\text{absorbvar}} + e_j$ and *statistic* is

statistic	Description
Main	
`xb`	$\mathbf{x}_j\mathbf{b}$, fitted values; the default
`stdp`	standard error of the prediction
`dresiduals`	$d_{\text{absorbvar}} + e_j = y_j - \mathbf{x}_j\mathbf{b}$
* `xbd`	$\mathbf{x}_j\mathbf{b} + d_{\text{absorbvar}}$
* `d`	$d_{\text{absorbvar}}$
* `residuals`	residual
* `score`	score; equivalent to `residuals`

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the prediction of $\mathbf{x}_j\mathbf{b}$, the fitted values, by using the average effect of the absorbed variable. Also see `xbd` below.

`stdp` calculates the standard error of $\mathbf{x}_j\mathbf{b}$.

`dresiduals` calculates $y_j - \mathbf{x}_j\mathbf{b}$, which are the residuals plus the effect of the absorbed variable.

`xbd` calculates $\mathbf{x}_j\mathbf{b} + d_{\text{absorbvar}}$, which are the fitted values including the individual effects of the absorbed variable.

`d` calculates $d_{\text{absorbvar}}$, the individual coefficients for the absorbed variable.

`residuals` calculates the residuals, that is, $y_j - (\mathbf{x}_j\mathbf{b} + d_{\text{absorbvar}})$.

`score` is a synonym for `residuals`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **areg** — Linear regression with a large dummy-variable set

[U] **20 Estimation and postestimation commands**

Title

asclogit — Alternative-specific conditional logit (McFadden's choice) model

Syntax

```
asclogit depvar [indepvars] [if] [in] [weight], case(varname)
    alternatives(varname) [options]
```

options	Description
Model	
* `case(`*varname*`)`	use *varname* to identify cases
* `alternatives(`*varname*`)`	use *varname* to identify the alternatives available for each case
`casevars(`*varlist*`)`	case-specific variables
`basealternative(`*# | lbl | str*`)`	alternative to normalize location
`noconstant`	suppress alternative-specific constant terms
`altwise`	use alternativewise deletion instead of casewise deletion
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`or`	report odds ratios
`noheader`	do not display the header on the coefficient table
`nocnsreport`	do not display constraints
display_options	control column formats and line width
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

* `case(`*varname*`)` and `alternatives(`*varname*`)` are required.

`bootstrap`, `by`, `jackknife`, `statsby`, and `xi` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`fweights`, `iweights`, and `pweights` are allowed (see [U] **11.1.6 weight**), but they are interpreted to apply to cases as a whole, not to individual observations. See *Use of weights* in [R] **clogit**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Categorical outcomes > Alternative-specific conditional logit

Description

`asclogit` fits McFadden's choice model, which is a specific case of the more general conditional logistic regression model (McFadden 1974). `asclogit` requires multiple observations for each case (individual or decision), where each observation represents an alternative that may be chosen. The cases are identified by the variable specified in the `case()` option, whereas the alternatives are identified by the variable specified in the `alternatives()` option. The outcome or chosen alternative is identified by a value of 1 in *depvar*, whereas zeros indicate the alternatives that were not chosen. There can be multiple alternatives chosen for each case.

`asclogit` allows two types of independent variables: alternative-specific variables and case-specific variables. Alternative-specific variables vary across both cases and alternatives and are specified in *indepvars*. Case-specific variables vary only across cases and are specified in the `casevars()` option.

See [R] **clogit** for a more general application of conditional logistic regression. For example, `clogit` would be used when you have grouped data where each observation in a group may be a different individual, but all individuals in a group have a common characteristic. You may use `clogit` to obtain the same estimates as `asclogit` by specifying the `case()` variable as the `group()` variable in `clogit` and generating variables that interact the `casevars()` in `asclogit` with each alternative (in the form of an indicator variable), excluding the interaction variable associated with the base alternative. `asclogit` takes care of this data-management burden for you. Also, for `clogit`, each record (row in your data) is an observation, whereas in `asclogit` each case, consisting of several records (the alternatives) in your data, is an observation. This last point is important because `asclogit` will drop observations, by default, in a casewise fashion. That is, if there is at least one missing value in any of the variables for each record of a case, the entire case is dropped from estimation. To use alternativewise deletion, specify the `altwise` option and only the records with missing values will be dropped from estimation.

Options

Model

`case(`*varname*`)` specifies the numeric variable that identifies each case. `case()` is required and must be integer valued.

`alternatives(`*varname*`)` specifies the variable that identifies the alternatives for each case. The number of alternatives can vary with each case; the maximum number of alternatives cannot exceed the limits of `tabulate oneway`; see [R] **tabulate oneway**. `alternatives()` is required and may be a numeric or a string variable.

`casevars(`*varlist*`)` specifies the case-specific numeric variables. These are variables that are constant for each case. If there are a maximum of J alternatives, there will be $J - 1$ sets of coefficients associated with the `casevars()`.

`basealternative(`*# | lbl | str*`)` specifies the alternative that normalizes the latent-variable location (the level of utility). The base alternative may be specified as a number, label, or string depending on the storage type of the variable indicating alternatives. The default is the alternative with the highest frequency.

If `vce(bootstrap)` or `vce(jackknife)` is specified, you must specify the base alternative. This is to ensure that the same model is fit with each call to `asclogit`.

`noconstant` suppresses the $J-1$ alternative-specific constant terms.

`altwise` specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion; that is, the entire group of observations making up a case is deleted if any missing values are encountered. This option does not apply to observations that are marked out by the `if` or `in` qualifier or the `by` prefix.

`offset(`*varname*`)`, `constraints(`*numlist* | *matname*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`or` reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. `or` may be specified at estimation or when replaying previously estimated results.

`noheader` prevents the coefficient table header from being displayed.

`nocnsreport`; see [R] **estimation options**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

`technique(bhhh)` is not allowed.

The initial estimates must be specified as `from(`*matname* `[ , copy ])`, where *matname* is the matrix containing the initial estimates and the `copy` option specifies that only the position of each element in *matname* is relevant. If `copy` is not specified, the column stripe of *matname* identifies the estimates.

The following option is available with `asclogit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

`asclogit` fits McFadden's choice model (McFadden [1974]; for a brief introduction, see Greene [2012, sec. 18.2] or Cameron and Trivedi [2010, sec. 15.5]). In this model, we have a set of unordered alternatives indexed by $1, 2, \ldots, J$. Let y_{ij}, $j = 1, \ldots, J$, be an indicator variable for the alternative actually chosen by the ith individual (case). That is, $y_{ij} = 1$ if individual i chose alternative j and $y_{ij} = 0$ otherwise. The independent variables come in two forms: alternative specific and case specific. Alternative-specific variables vary among the alternatives (as well as cases), and case-specific

variables vary only among cases. Assume that we have p alternative-specific variables so that for case i we have a $J \times p$ matrix, $\mathbf{X}_i$. Further, assume that we have q case-specific variables so that we have a $1 \times q$ vector $\mathbf{z}_i$ for case i. Our random-utility model can then be expressed as

$$\mathbf{u}_i = \mathbf{X}_i\boldsymbol{\beta} + (\mathbf{z}_i\mathbf{A})' + \boldsymbol{\epsilon}_i$$

Here $\boldsymbol{\beta}$ is a $p \times 1$ vector of alternative-specific regression coefficients and $\mathbf{A} = (\boldsymbol{\alpha}_1, \ldots, \boldsymbol{\alpha}_J)$ is a $q \times J$ matrix of case-specific regression coefficients. The elements of the $J \times 1$ vector $\boldsymbol{\epsilon}_i$ are independent Type I (Gumbel-type) extreme-value random variables with mean γ (the Euler–Mascheroni constant, approximately 0.577) and variance $\pi^2/6$. We must fix one of the $\boldsymbol{\alpha}_j$ to the constant vector to normalize the location. We set $\boldsymbol{\alpha}_k = 0$, where k is specified by the `basealternative()` option. The vector $\mathbf{u}_i$ quantifies the utility that the individual gains from the J alternatives. The alternative chosen by individual i is the one that maximizes utility.

▷ Example 1

We have data on 295 consumers and their choice of automobile. Each consumer chose among an American, Japanese, or European car; the variable `car` indicates the nationality of the car for each alternative. We want to explore the relationship between the choice of `car` to the consumer's sex (variable `sex`) and income (variable `income` in thousands of dollars). We also have information on the number of dealerships of each nationality in the consumer's city in the variable `dealer` that we want to include as a regressor. We assume that consumers' preferences are influenced by the number of dealerships in an area but that the number of dealerships is not influenced by consumer preferences (which we admit is a rather strong assumption). The variable `dealer` is an alternative-specific variable ($\mathbf{X}_i$ is a 3×1 vector in our previous notation), and `sex` and `income` are case-specific variables ($\mathbf{z}_i$ is a 1×2 vector). Each consumer's chosen car is indicated by the variable `choice`.

Let's list some of the data.

```
. use http://www.stata-press.com/data/r12/choice
. list id car choice dealer sex income in 1/12, sepby(id)
```

	id	car	choice	dealer	sex	income
1.	1	American	0	18	male	46.7
2.	1	Japan	0	8	male	46.7
3.	1	Europe	1	5	male	46.7
4.	2	American	1	17	male	26.1
5.	2	Japan	0	6	male	26.1
6.	2	Europe	0	2	male	26.1
7.	3	American	1	12	male	32.7
8.	3	Japan	0	6	male	32.7
9.	3	Europe	0	2	male	32.7
10.	4	American	0	18	female	49.2
11.	4	Japan	1	7	female	49.2
12.	4	Europe	0	4	female	49.2

We see, for example, that the first consumer, a male earning \$46,700 per year, chose to purchase a European car even though there are more American and Japanese car dealers in his area. The fourth consumer, a female earning \$49,200 per year, purchased a Japanese car.

We now fit our model.

```
. asclogit choice dealer, case(id) alternatives(car) casevars(sex income)
Iteration 0:   log likelihood = -273.55685
Iteration 1:   log likelihood = -252.75109
Iteration 2:   log likelihood = -250.78555
Iteration 3:   log likelihood =  -250.7794
Iteration 4:   log likelihood =  -250.7794

Alternative-specific conditional logit          Number of obs      =       885
Case variable: id                               Number of cases    =       295
Alternative variable: car                       Alts per case: min =         3
                                                               avg =       3.0
                                                               max =         3
                                                Wald chi2(5)       =     15.86
Log likelihood =  -250.7794                     Prob > chi2        =    0.0072
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
car						
dealer	.0680938	.0344465	1.98	0.048	.00058	.1356076
American	(base alternative)					
Japan						
sex	-.5346039	.3141564	-1.70	0.089	-1.150339	.0811314
income	.0325318	.012824	2.54	0.011	.0073973	.0576663
_cons	-1.352189	.6911829	-1.96	0.050	-2.706882	.0025049
Europe						
sex	.5704109	.4540247	1.26	0.209	-.3194612	1.460283
income	.032042	.0138676	2.31	0.021	.004862	.0592219
_cons	-2.355249	.8526681	-2.76	0.006	-4.026448	-.6840501

Displaying the results as odds ratios makes interpretation easier.

```
. asclogit, or noheader
```

choice	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
car						
dealer	1.070466	.0368737	1.98	0.048	1.00058	1.145232
American	(base alternative)					
Japan						
sex	.5859013	.1840647	-1.70	0.089	.3165294	1.084513
income	1.033067	.013248	2.54	0.011	1.007425	1.059361
_cons	.2586735	.1787907	-1.96	0.050	.0667446	1.002508
Europe						
sex	1.768994	.8031669	1.26	0.209	.7265404	4.307178
income	1.032561	.0143191	2.31	0.021	1.004874	1.061011
_cons	.0948699	.0808925	-2.76	0.006	.0178376	.5045693

These results indicate that men (sex = 1) are less likely to pick a Japanese car over an American car than women (odds ratio 0.59) but that men are more likely to choose a European car over an American car (odds ratio 1.77). Raising a person's income increases the likelihood that he or she purchases a Japanese or European car; interestingly, the effect of higher income is about the same for these two types of cars.

◁

Daniel Little McFadden was born in 1937 in North Carolina. He studied physics, psychology, and economics at the University of Minnesota and has taught economics at Pittsburgh, Berkeley, MIT, and the University of Southern California. His contributions to logit models were triggered by a student's project on freeway routing decisions, and his work consistently links economic theory and applied problems. In 2000, he shared the Nobel Prize in Economics with James J. Heckman.

❑ Technical note

McFadden's choice model is related to multinomial logistic regression (see [R] **mlogit**). If all the independent variables are case specific, then the two models are identical. We verify this supposition by running the previous example without the alternative-specific variable, `dealer`.

```
. asclogit choice, case(id) alternatives(car) casevars(sex income) nolog
Alternative-specific conditional logit          Number of obs      =        885
Case variable: id                               Number of cases    =        295
Alternative variable: car                       Alts per case: min =          3
                                                               avg =        3.0
                                                               max =          3
                                                Wald chi2(4)      =      12.53
Log likelihood = -252.72012                     Prob > chi2       =     0.0138
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
American	(base alternative)					
Japan						
sex	-.4694799	.3114939	-1.51	0.132	-1.079997	.141037
income	.0276854	.0123666	2.24	0.025	.0034472	.0519236
_cons	-1.962652	.6216804	-3.16	0.002	-3.181123	-.7441807
Europe						
sex	.5388441	.4525279	1.19	0.234	-.3480942	1.425782
income	.0273669	.013787	1.98	0.047	.000345	.0543889
_cons	-3.180029	.7546837	-4.21	0.000	-4.659182	-1.700876

To run `mlogit`, we must rearrange the dataset. `mlogit` requires a dependent variable that indicates the choice—1, 2, or 3—for each individual. We will use `car` as our dependent variable for those observations that represent the choice actually chosen.

```
. keep if choice == 1
(590 observations deleted)
. mlogit car sex income
Iteration 0:   log likelihood =  -259.1712
Iteration 1:   log likelihood = -252.81165
Iteration 2:   log likelihood = -252.72014
Iteration 3:   log likelihood = -252.72012
Multinomial logistic regression                 Number of obs   =        295
                                                LR chi2(4)      =      12.90
                                                Prob > chi2     =     0.0118
Log likelihood = -252.72012                     Pseudo R2       =     0.0249
```

car	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
American	(base outcome)					
Japan						
sex	-.4694798	.3114939	-1.51	0.132	-1.079997	.1410371
income	.0276854	.0123666	2.24	0.025	.0034472	.0519236
_cons	-1.962651	.6216803	-3.16	0.002	-3.181122	-.7441801
Europe						
sex	.5388443	.4525278	1.19	0.234	-.348094	1.425783
income	.027367	.013787	1.98	0.047	.000345	.0543889
_cons	-3.18003	.7546837	-4.21	0.000	-4.659182	-1.700877

The results are the same except for the model statistic: `asclogit` uses a Wald test and `mlogit` uses a likelihood-ratio test. If you prefer the likelihood-ratio test, you can fit the constant-only model for `asclogit` followed by the full model and use [R] **lrtest**. The following example will carry this out.

```
. use http://www.stata-press.com/data/r12/choice, clear
. asclogit choice, case(id) alternatives(car)
. estimates store null
. asclogit choice, case(id) alternatives(car) casevars(sex income)
. lrtest null .
```

❑

❑ Technical note

We force you to explicitly identify the case-specific variables in the `casevars()` option to ensure that the program behaves as you expect. For example, an `if` or `in` qualifier may drop observations in such a way that (what was expected to be) an alternative-specific variable turns into a case-specific variable. Here you would probably want `asclogit` to terminate instead of interacting the variable with the alternative indicators. This situation could also occur if `asclogit` drops cases, or observations if you use the `altwise` option, because of missing values.

❑

Saved results

asclogit saves the following in e():

Scalars

e(N)	number of observations
e(N_case)	number of cases
e(k)	number of parameters
e(k_alt)	number of alternatives
e(k_indvars)	number of alternative-specific variables
e(k_casevars)	number of case-specific variables
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(N_clust)	number of clusters
e(const)	constant indicator
e(i_base)	base alternative index
e(chi2)	χ^2
e(F)	F statistic
e(p)	significance
e(alt_min)	minimum number of alternatives
e(alt_avg)	average number of alternatives
e(alt_max)	maximum number of alternatives
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	asclogit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(indvars)	alternative-specific independent variable
e(casevars)	case-specific variables
e(case)	variable defining cases
e(altvar)	variable defining alternatives
e(alteqs)	alternative equation names
e(alt#)	alternative labels
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald, type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(datasignature)	the checksum
e(datasignaturevars)	variables used in calculation of checksum
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(stats)	alternative statistics
e(altvals)	alternative values
e(altfreq)	alternative frequencies
e(alt_casevars)	indicators for estimated case-specific coefficients—e(k_alt)×e(k_casevars)
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

asclogit is implemented as an ado-file.

In this model, we have a set of unordered alternatives indexed by $1, 2, \ldots, J$. Let y_{ij}, $j = 1, \ldots, J$, be an indicator variable for the alternative actually chosen by the ith individual (case). That is, $y_{ij} = 1$ if individual i chose alternative j and $y_{ij} = 0$ otherwise. The independent variables come in two forms: alternative specific and case specific. Alternative-specific variables vary among the alternatives (as well as cases), and case-specific variables vary only among cases. Assume that we have p alternative-specific variables so that for case i we have a $J \times p$ matrix, $\mathbf{X}_i$. Further, assume that we have q case-specific variables so that we have a $1 \times q$ vector $\mathbf{z}_i$ for case i. The deterministic component of the random-utility model can then be expressed as

$$\begin{aligned}\eta_i &= \mathbf{X}_i\boldsymbol{\beta} + (\mathbf{z}_i\mathbf{A})' \\ &= \mathbf{X}_i\boldsymbol{\beta} + (\mathbf{z}_i \otimes \mathbf{I}_J)\,\mathrm{vec}(\mathbf{A}') \\ &= (\mathbf{X}_i,\ \mathbf{z}_i \otimes \mathbf{I}_J)\begin{pmatrix}\boldsymbol{\beta} \\ \mathrm{vec}(\mathbf{A}')\end{pmatrix} \\ &= \mathbf{X}_i^*\boldsymbol{\beta}^*\end{aligned}$$

As before, $\boldsymbol{\beta}$ is a $p \times 1$ vector of alternative-specific regression coefficients, and $\mathbf{A} = (\boldsymbol{\alpha}_1, \ldots, \boldsymbol{\alpha}_J)$ is a $q \times J$ matrix of case-specific regression coefficients; remember that we must fix one of the $\boldsymbol{\alpha}_j$ to the constant vector to normalize the location. Here $\mathbf{I}_J$ is the $J \times J$ identity matrix, vec() is the vector function that creates a vector from a matrix by placing each column of the matrix on top of the other (see [M-5] **vec( )**), and $\otimes$ is the Kronecker product (see [M-2] **op_kronecker**).

We have rewritten the linear equation so that it is a form that can be used by clogit, namely, $\mathbf{X}_i^*\boldsymbol{\beta}^*$, where

$$\mathbf{X}_i^* = (\mathbf{X}_i,\ \mathbf{z}_i \otimes \mathbf{I}_J)$$

$$\boldsymbol{\beta}^* = \begin{pmatrix}\boldsymbol{\beta} \\ \mathrm{vec}(\mathbf{A}')\end{pmatrix}$$

With this in mind, see *Methods and formulas* in [R] **clogit** for the computational details of the conditional logit model.

This command supports the clustered version of the Huber/White/sandwich estimator of the variance using vce(robust) and vce(cluster *clustvar*). See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. Specifying vce(robust) is equivalent to specifying vce(cluster *casevar*), where *casevar* is the variable that identifies the cases.

References

Cameron, A. C., and P. K. Trivedi. 2010. *Microeconometrics Using Stata*. Rev. ed. College Station, TX: Stata Press.

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

McFadden, D. L. 1974. Conditional logit analysis of qualitative choice behavior. In *Frontiers in Econometrics*, ed. P. Zarembka, 105–142. New York: Academic Press.

Also see

[R] **asclogit postestimation** — Postestimation tools for asclogit

[R] **asmprobit** — Alternative-specific multinomial probit regression

[R] **asroprobit** — Alternative-specific rank-ordered probit regression

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **nlogit** — Nested logit regression

[R] **ologit** — Ordered logistic regression

[U] **20 Estimation and postestimation commands**

Title

asclogit postestimation — Postestimation tools for asclogit

Description

The following postestimation commands are of special interest after `asclogit`:

Commands	Description
`estat alternatives`	alternative summary statistics
`estat mfx`	marginal effects

For information about these commands, see below.

The following standard postestimation commands are also available:

Commands	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`	likelihood-ratio test
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predicted probabilities, estimated linear predictor and its standard error
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation commands

`estat alternatives` displays summary statistics about the alternatives in the estimation sample.

`estat mfx` computes probability marginal effects.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic options]

predict [type] {stub* | newvarlist} [if] [in], scores
```

statistic	Description
Main	
pr	probability that each alternative is chosen; the default
xb	linear prediction
stdp	standard error of the linear prediction

options	Description
Main	
*k(# | observed)	condition on # alternatives per case or on observed number of alternatives
altwise	use alternativewise deletion instead of casewise deletion when computing probabilities
nooffset	ignore the offset() variable specified in asclogit

*k(# | observed) may be used only with pr.

These statistics are available both in and out of sample; type predict ... if e(sample) ... if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

pr computes the probability of choosing each alternative conditioned on each case choosing k() alternatives. This is the default statistic with default k(1); one alternative per case is chosen.

xb computes the linear prediction.

stdp computes the standard error of the linear prediction.

k(# | observed) conditions the probability on # alternatives per case or on the observed number of alternatives. The default is k(1). This option may be used only with the pr option.

altwise specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion. The xb and stdp options always use alternativewise deletion.

nooffset is relevant only if you specified offset(*varname*) for asclogit. It modifies the calculations made by predict so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}\boldsymbol{\beta}$ rather than as $\mathbf{x}\boldsymbol{\beta} + \text{offset}$.

scores calculates the scores for each coefficient in e(b). This option requires a new variable list of length equal to the number of columns in e(b). Otherwise, use the *stub** option to have predict generate enumerated variables with prefix *stub*.

Syntax for estat alternatives

```
estat alternatives
```

Menu

Statistics > Postestimation > Reports and statistics

Syntax for estat mfx

```
estat mfx [if] [in] [, options]
```

options	Description
Main	
varlist(*varlist*)	display marginal effects for *varlist*
at(mean [*atlist*] | median [*atlist*])	calculate marginal effects at these values
k(#)	condition on the number of alternatives chosen to be #
Options	
level(#)	set confidence interval level; default is level(95)
nodiscrete	treat indicator variables as continuous
noesample	do not restrict calculation of means and medians to the estimation sample
nowght	ignore weights when calculating means and medians

Menu

Statistics > Postestimation > Reports and statistics

Options for estat mfx

Main

varlist(*varlist*) specifies the variables for which to display marginal effects. The default is all variables.

at(mean [*atlist*] | median [*atlist*]) specifies the values at which the marginal effects are to be calculated. *atlist* is

[[*alternative*:*variable* = #] [*variable* = #] [*alternative*:*offset* = #] [...]]

The default is to calculate the marginal effects at the means of the independent variables by using the estimation sample, at(mean). If offset() is used during estimation, the means of the offsets (by alternative) are computed by default.

After specifying the summary statistic, you can specify a series of specific values for variables. You can specify values for alternative-specific variables by alternative, or you can specify one value for all alternatives. You can specify only one value for case-specific variables. You specify values for the offset() variable (if present) the same way as for alternative-specific variables. For example, in the choice dataset (car choice), income is a case-specific variable, whereas dealer is an alternative-specific variable. The following would be a legal syntax for estat mfx:

```
. estat mfx, at(mean American:dealer=18 income=40)
```

When `nodiscrete` is not specified, `at(mean` [*atlist*]`)` or `at(median` [*atlist*]`)` has no effect on computing marginal effects for indicator variables, which are calculated as the discrete change in the simulated probability as the indicator variable changes from 0 to 1.

The mean and median computations respect any `if` or `in` qualifiers, so you can restrict the data over which the statistic is computed. You can even restrict the values to a specific case, for example,

```
. estat mfx if case==21
```

`k(#)` computes the probabilities conditioned on # alternatives chosen. The default is one alternative chosen.

Options

`level(#)` sets the confidence level; default is `level(95)`.

`nodiscrete` specifies that indicator variables be treated as continuous variables. An indicator variable is one that takes on the value 0 or 1 in the estimation sample. By default, the discrete change in the simulated probability is computed as the indicator variable changes from 0 to 1.

`noesample` specifies that the whole dataset be considered instead of only those marked in the `e(sample)` defined by the `asclogit` command.

`nowght` specifies that weights be ignored when calculating the medians.

Remarks

Remarks are presented under the following headings:

Predicted probabilities
Obtaining estimation statistics

Predicted probabilities

After fitting a McFadden's choice model with alternative-specific conditional logistic regression, you can use `predict` to obtain the estimated probability of alternative choices given case profiles.

▷ Example 1

In example 1 of [R] **asclogit**, we fit a model of consumer choice of automobile. The alternatives are nationality of the automobile manufacturer: American, Japanese, or European. There is one alternative-specific variable in the model, `dealer`, which contains the number of dealerships of each nationality in the consumer's city. The case-specific variables are `sex`, the consumer's sex, and `income`, the consumer's income in thousands of dollars.

```
. use http://www.stata-press.com/data/r12/choice
. asclogit choice dealer, case(id) alternatives(car) casevars(sex income)
  (output omitted)
. predict p
(option pr assumed; Pr(car))
. predict p2, k(2)
(option pr assumed; Pr(car))
. format p p2 %6.4f
```

```
. list car choice dealer sex income p p2 in 1/9, sepby(id)
```

	car	choice	dealer	sex	income	p	p2
1.	American	0	18	male	46.7	0.6025	0.8589
2.	Japan	0	8	male	46.7	0.2112	0.5974
3.	Europe	1	5	male	46.7	0.1863	0.5437
4.	American	1	17	male	26.1	0.7651	0.9293
5.	Japan	0	6	male	26.1	0.1282	0.5778
6.	Europe	0	2	male	26.1	0.1067	0.4929
7.	American	1	12	male	32.7	0.6519	0.8831
8.	Japan	0	6	male	32.7	0.1902	0.5995
9.	Europe	0	2	male	32.7	0.1579	0.5174

◁

Obtaining estimation statistics

Here we will demonstrate the specialized `estat` subcommands after `asclogit`. Use `estat alternatives` to obtain a table of alternative statistics. The table will contain the alternative values, labels (if any), the number of cases in which each alternative is present, the frequency that the alternative is selected, and the percent selected.

Use `estat mfx` to obtain marginal effects after `asclogit`.

▷ Example 2

We will continue with the automobile choice example, where we first list the alternative statistics and then compute the marginal effects at the mean income in our sample, assuming that there are five automobile dealers for each nationality. We will evaluate the probabilities for females because `sex` is coded 0 for females, and we will be obtaining the discrete change from 0 to 1.

```
. estat alternatives
    Alternatives summary for car
```

index	Alternative value	label	Cases present	Frequency selected	Percent selected
1	1	American	295	192	65.08
2	2	Japan	295	64	21.69
3	3	Europe	295	39	13.22

```
. estat mfx, at(dealer=0 sex=0) varlist(sex income)
Pr(choice = American|1 selected) = .41964329
```

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
casevars							
sex*	.026238	.068311	0.38	0.701	-.107649	.160124	0
income	-.007891	.002674	-2.95	0.003	-.013132	-.00265	42.097

(*) dp/dx is for discrete change of indicator variable from 0 to 1

```
Pr(choice = Japan|1 selected) = .42696187
```

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
casevars							
sex*	-.161164	.079238	-2.03	0.042	-.316468	-.005859	0
income	.005861	.002997	1.96	0.051	-.000014	.011735	42.097

```
(*) dp/dx is for discrete change of indicator variable from 0 to 1
Pr(choice = Europe|1 selected) = .15339484
```

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
casevars							
sex*	.134926	.076556	1.76	0.078	-.015122	.284973	0
income	.00203	.001785	1.14	0.255	-.001469	.00553	42.097

```
(*) dp/dx is for discrete change of indicator variable from 0 to 1
```

The marginal effect of `income` indicates that there is a lower chance for a consumer to buy American automobiles with an increase in income. There is an indication that men have a higher preference for European automobiles than women but a lower preference for Japanese automobiles. We did not include the marginal effects for `dealer` because we view these as nuisance parameters, so we adjusted the probabilities by fixing dealer to a constant, 0.

◁

Saved results

`estat mfx` saves the following in `r()`:

Scalars

`r(pr_`*alt*`)` scalars containing the computed probability of each alternative evaluated at the value that is labeled X in the table output. Here *alt* are the labels in the macro `e(alteqs)`.

Matrices

`r(`*alt*`)` matrices containing the computed marginal effects and associated statistics. There is one matrix for each alternative, where *alt* are the labels in the macro `e(alteqs)`. Column 1 of each matrix contains the marginal effects; column 2, their standard errors; column 3, their z statistics; and columns 4 and 5, the confidence intervals. Column 6 contains the values of the independent variables used to compute the probabilities `r(pr_`*alt*`)`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

The deterministic component of the random-utility model can be expressed as

$$\begin{aligned}\boldsymbol{\eta} &= \mathbf{X}\boldsymbol{\beta} + (\mathbf{z}\mathbf{A})' \\ &= \mathbf{X}\boldsymbol{\beta} + (\mathbf{z} \otimes \mathbf{I}_J)\,\mathrm{vec}(\mathbf{A}') \\ &= (\mathbf{X},\ \mathbf{z} \otimes \mathbf{I}_J) \begin{pmatrix} \boldsymbol{\beta} \\ \mathrm{vec}(\mathbf{A}') \end{pmatrix} \\ &= \mathbf{X}^*\boldsymbol{\beta}^*\end{aligned}$$

where $\mathbf{X}$ is the $J \times p$ matrix containing the alternative-specific covariates, $\mathbf{z}$ is a $1 \times q$ vector of case-specific variables, $\boldsymbol{\beta}$ is a $p \times 1$ vector of alternative-specific regression coefficients, and $\mathbf{A} = (\boldsymbol{\alpha}_1, \ldots, \boldsymbol{\alpha}_J)$ is a $q \times J$ matrix of case-specific regression coefficients (with one of the $\boldsymbol{\alpha}_j$ fixed to the constant). Here $\mathbf{I}_J$ is the $J \times J$ identity matrix, vec() is the vector function that creates a vector from a matrix by placing each column of the matrix on top of the other (see [M-5] **vec( )**), and $\otimes$ is the Kronecker product (see [M-2] **op_kronecker**).

We have rewritten the linear equation so that it is a form that we all recognize, namely, $\boldsymbol{\eta} = \mathbf{X}^*\boldsymbol{\beta}^*$, where

$$\mathbf{X}^* = (\mathbf{X},\ \mathbf{z} \otimes \mathbf{I}_J)$$

$$\boldsymbol{\beta}^* = \begin{pmatrix} \boldsymbol{\beta} \\ \mathrm{vec}(\mathbf{A}') \end{pmatrix}$$

To compute the marginal effects, we use the derivative of the log likelihood $\partial\ell(\mathbf{y}|\boldsymbol{\eta})/\partial\boldsymbol{\eta}$, where $\ell(\mathbf{y}|\boldsymbol{\eta}) = \log \Pr(\mathbf{y}|\boldsymbol{\eta})$ is the log of the probability of the choice indicator vector $\mathbf{y}$ given the linear predictor vector $\boldsymbol{\eta}$. Namely,

$$\begin{aligned}\frac{\partial \Pr(\mathbf{y}|\boldsymbol{\eta})}{\partial \mathrm{vec}(\mathbf{X}^*)'} &= \Pr(\mathbf{y}|\boldsymbol{\eta}) \frac{\partial \ell(\mathbf{y}|\boldsymbol{\eta})}{\partial \boldsymbol{\eta}'} \frac{\partial \boldsymbol{\eta}}{\partial \mathrm{vec}(\mathbf{X}^*)'} \\ &= \Pr(\mathbf{y}|\boldsymbol{\eta}) \frac{\partial \ell(\mathbf{y}|\boldsymbol{\eta})}{\partial \boldsymbol{\eta}'} \left(\boldsymbol{\beta}^{*\prime} \otimes \mathbf{I}_J\right)\end{aligned}$$

The standard errors of the marginal effects are computed using the delta method.

Also see

[R] **asclogit** — Alternative-specific conditional logit (McFadden's choice) model

[U] **20 Estimation and postestimation commands**

Title

asmprobit — Alternative-specific multinomial probit regression

Syntax

```
asmprobit depvar [indepvars] [if] [in] [weight], case(varname)
    alternatives(varname) [options]
```

options	Description
Model	
* `case(`*varname*`)`	use *varname* to identify cases
* `alternatives(`*varname*`)`	use *varname* to identify the alternatives available for each case
`casevars(`*varlist*`)`	case-specific variables
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
Model 2	
`correlation(`*correlation*`)`	correlation structure of the latent-variable errors
`stddev(`*stddev*`)`	variance structure of the latent-variable errors
`structural`	use the structural covariance parameterization; default is the differenced covariance parameterization
`factor(#)`	use the factor covariance structure with dimension #
`noconstant`	suppress the alternative-specific constant terms
`basealternative(`*# | lbl | str*`)`	alternative used for normalizing location
`scalealternative(`*# | lbl | str*`)`	alternative used for normalizing scale
`altwise`	use alternativewise deletion instead of casewise deletion
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`notransform`	do not transform variance–covariance estimates to the standard deviation and correlation metric
`nocnsreport`	do not display constraints
display_options	control column formats and line width

Integration

`intmethod(`*seqtype*`)`	type of quasi- or pseudouniform point set
`intpoints(#)`	number of points in each sequence
`intburn(#)`	starting index in the Hammersley or Halton sequence
`intseed(`*code*`|#)`	pseudouniform random-number seed
`antithetics`	use antithetic draws
`nopivot`	do not use integration interval pivoting
`initbhhh(#)`	use the BHHH optimization algorithm for the first # iterations
`favor(speed|space)`	favor speed or space when generating integration points

Maximization

maximize_options	control the maximization process
`coeflegend`	display legend instead of statistics

correlation	Description
`unstructured`	one correlation parameter for each pair of alternatives; correlations with the `basealternative()` are zero; the default
`exchangeable`	one correlation parameter common to all pairs of alternatives; correlations with the `basealternative()` are zero
`independent`	constrain all correlation parameters to zero
`pattern` *matname*	user-specified matrix identifying the correlation pattern
`fixed` *matname*	user-specified matrix identifying the fixed and free correlation parameters

stddev	Description
`heteroskedastic`	estimate standard deviation for each alternative; standard deviations for `basealternative()` and `scalealternative()` set to one
`homoskedastic`	all standard deviations are one
`pattern` *matname*	user-specified matrix identifying the standard deviation pattern
`fixed` *matname*	user-specified matrix identifying the fixed and free standard deviations

seqtype	Description
`hammersley`	Hammersley point set
`halton`	Halton point set
`random`	uniform pseudorandom point set

*`case(`*varname*`)` and `alternatives(`*varname*`)` are required.
`bootstrap`, `by`, `jackknife`, `statsby`, and `xi` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Categorical outcomes > Alternative-specific multinomial probit

Description

`asmprobit` fits multinomial probit (MNP) models by using maximum simulated likelihood (MSL) implemented by the Geweke–Hajivassiliou–Keane (GHK) algorithm. By estimating the variance–covariance parameters of the latent-variable errors, the model allows you to relax the independence of irrelevant alternatives (IIA) property that is characteristic of the multinomial logistic model.

`asmprobit` requires multiple observations for each case (decision), where each observation represents an alternative that may be chosen. The cases are identified by the variable specified in the `case()` option, whereas the alternatives are identified by the variable specified in the `alternative()` option. The outcome (chosen alternative) is identified by a value of 1 in *depvar*, with 0 indicating the alternatives that were not chosen; only one alternative may be chosen for each case.

`asmprobit` allows two types of independent variables: alternative-specific variables and case-specific variables. Alternative-specific variables vary across both cases and alternatives and are specified in *indepvars*. Case-specific variables vary only across cases and are specified in the `casevars()` option.

Options

Model

`case(`*varname*`)` specifies the variable that identifies each case. This variable identifies the individuals or entities making a choice. `case()` is required.

`alternatives(`*varname*`)` specifies the variable that identifies the alternatives for each case. The number of alternatives can vary with each case; the maximum number of alternatives is 20. `alternatives()` is required.

`casevars(`*varlist*`)` specifies the case-specific variables that are constant for each `case()`. If there are a maximum of J alternatives, there will be $J-1$ sets of coefficients associated with `casevars()`.

`constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

Model 2

`correlation(`*correlation*`)` specifies the correlation structure of the latent-variable errors.

`correlation(unstructured)` is the most general and has $J(J-3)/2+1$ unique correlation parameters. This is the default unless `stdev()` or `structural` are specified.

`correlation(exchangeable)` provides for one correlation coefficient common to all latent variables, except the latent variable associated with the `basealternative()` option.

`correlation(independent)` assumes that all correlations are zero.

`correlation(pattern` *matname*`)` and `correlation(fixed` *matname*`)` give you more flexibility in defining the correlation structure. See *Variance structures* later in this entry for more information.

`stddev(`*stddev*`)` specifies the variance structure of the latent-variable errors.

`stddev(heteroskedastic)` is the most general and has $J-2$ estimable parameters. The standard deviations of the latent-variable errors for the alternatives specified in `basealternative()` and `scalealternative()` are fixed to one.

`stddev(homoskedastic)` constrains all the standard deviations to equal one.

`stddev(pattern` *matname*`)` and `stddev(fixed` *matname*`)` give you added flexibility in defining the standard deviation parameters. See *Variance structures* later in this entry for more information.

`structural` requests the $J \times J$ structural covariance parameterization instead of the default $J-1 \times J-1$ differenced covariance parameterization (the covariance of the latent errors differenced with that of the base alternative). The differenced covariance parameterization will achieve the same MSL regardless of the choice of `basealternative()` and `scalealternative()`. On the other hand, the structural covariance parameterization imposes more normalizations that may bound the model away from its maximum likelihood and thus prevent convergence with some datasets or choices of `basealternative()` and `scalealternative()`.

`factor(#)` requests that the factor covariance structure of dimension # be used. The `factor()` option can be used with the `structural` option but cannot be used with `stddev()` or `correlation()`. A $\# \times J$ (or $\# \times J-1$) matrix, $\mathbf{C}$, is used to factor the covariance matrix as $I + \mathbf{C}'\mathbf{C}$, where I is the identity matrix of dimension J (or $J-1$). The column dimension of $\mathbf{C}$ depends on whether the covariance is structural or differenced. The row dimension of $\mathbf{C}$, #, must be less than or equal to `floor(`$(J(J-1)/2-1)/(J-2)$`)`, because there are only $J(J-1)/2-1$ identifiable variance–covariance parameters. This covariance parameterization may be useful for reducing the number of covariance parameters that need to be estimated.

If the covariance is structural, the column of $\mathbf{C}$ corresponding to the base alternative contains zeros. The column corresponding to the scale alternative has a one in the first row and zeros elsewhere. If the covariance is differenced, the column corresponding to the scale alternative (differenced with the base) has a one in the first row and zeros elsewhere.

`noconstant` suppresses the $J-1$ alternative-specific constant terms.

`basealternative(#` | *lbl* | *str*`)` specifies the alternative used to normalize the latent-variable location (also referred to as the level of utility). The base alternative may be specified as a number, label, or string. The standard deviation for the latent-variable error associated with the base alternative is fixed to one, and its correlations with all other latent-variable errors are set to zero. The default is the first alternative when sorted. If a `fixed` or `pattern` matrix is given in the `stddev()` and `correlation()` options, the `basealternative()` will be implied by the fixed standard deviations and correlations in the matrix specifications. `basealternative()` cannot be equal to `scalealternative()`.

`scalealternative(#` | *lbl* | *str*`)` specifies the alternative used to normalize the latent-variable scale (also referred to as the scale of utility). The scale alternative may be specified as a number, label, or string. The default is to use the second alternative when sorted. If a `fixed` or `pattern` matrix is given in the `stddev()` option, the `scalealternative()` will be implied by the fixed standard deviations in the matrix specification. `scalealternative()` cannot be equal to `basealternative()`.

If a `fixed` or `pattern` matrix is given for the `stddev()` option, the base alternative and scale alternative are implied by the standard deviations and correlations in the matrix specifications, and they need not be specified in the `basealternative()` and `scalealternative()` options.

`altwise` specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion; that is, the entire group of observations making up a case is deleted if any missing values are encountered. This option does not apply to observations that are marked out by the `if` or `in` qualifier or the `by` prefix.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If specifying `vce(bootstrap)` or `vce(jackknife)`, you must also specify `basealternative()` and `scalealternative()`.

Reporting

`level(#)`; see [R] **estimation options**.

`notransform` prevents retransforming the Cholesky-factored variance–covariance estimates to the correlation and standard deviation metric.

This option has no effect if `structural` is not specified because the default differenced variance–covariance estimates have no interesting interpretation as correlations and standard deviations. `notransform` also has no effect if the `correlation()` and `stddev()` options are specified with anything other than their default values. Here it is generally not possible to factor the variance–covariance matrix, so optimization is already performed using the standard deviation and correlation representations.

`nocnsreport`; see [R] **estimation options**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Integration

`intmethod(hammersley | halton | random)` specifies the method of generating the point sets used in the quasi–Monte Carlo integration of the multivariate normal density. `intmethod(hammersley)`, the default, uses the Hammersley sequence; `intmethod(halton)` uses the Halton sequence; and `intmethod(random)` uses a sequence of uniform random numbers.

`intpoints(#)` specifies the number of points to use in the quasi–Monte Carlo integration. If this option is not specified, the number of points is $50 \times J$ if `intmethod(hammersley)` or `intmethod(halton)` is used and $100 \times J$ if `intmethod(random)` is used. Larger values of `intpoints()` provide better approximations of the log likelihood, but at the cost of added computation time.

`intburn(#)` specifies where in the Hammersley or Halton sequence to start, which helps reduce the correlation between the sequences of each dimension. The default is 0. This option may not be specified with `intmethod(random)`.

`intseed(`*code* | `#)` specifies the seed to use for generating the uniform pseudorandom sequence. This option may be specified only with `intmethod(random)`. *code* refers to a string that records the state of the random-number generator `runiform()`; see [R] **set seed**. An integer value # may be used also. The default is to use the current seed value from Stata's uniform random-number generator, which can be obtained from `c(seed)`.

`antithetics` specifies that antithetic draws be used. The antithetic draw for the $J - 1$ vector uniform-random variables, $\mathbf{x}$, is $1 - \mathbf{x}$.

`nopivot` turns off integration interval pivoting. By default, `asmprobit` will pivot the wider intervals of integration to the interior of the multivariate integration. This improves the accuracy of the quadrature estimate. However, discontinuities may result in the computation of numerical second-order derivatives using finite differencing (for the Newton–Raphson optimize technique, `tech(nr)`) when few simulation points are used, resulting in a non–positive-definite Hessian. `asmprobit`

uses the Broyden–Fletcher–Goldfarb–Shanno optimization algorithm, by default, which does not require computing the Hessian numerically using finite differencing.

`initbhhh(#)` specifies that the Berndt–Hall–Hall–Hausman (BHHH) algorithm be used for the initial # optimization steps. This option is the only way to use the BHHH algorithm along with other optimization techniques. The algorithm switching feature of `ml`'s `technique()` option cannot include `bhhh`.

`favor(speed|space)` instructs `asmprobit` to favor either speed or space when generating the integration points. `favor(speed)` is the default. When favoring speed, the integration points are generated once and stored in memory, thus increasing the speed of evaluating the likelihood. This speed increase can be seen when there are many cases or when the user specifies a large number of integration points, `intpoints(#)`. When favoring space, the integration points are generated repeatedly with each likelihood evaluation.

For unbalanced data, where the number of alternatives varies with each case, the estimates computed using `intmethod(random)` will vary slightly between `favor(speed)` and `favor(space)`. This is because the uniform sequences will not be identical, even when initiating the sequences using the same uniform seed, `intseed(`*code*`|#)`. For `favor(speed)`, `ncase` blocks of `intpoints(#)` $\times$ $J-2$ uniform points are generated, where J is the maximum number of alternatives. For `favor(space)`, the column dimension of the matrices of points varies with the number of alternatives that each case has.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**.

The following options may be particularly useful in obtaining convergence with `asmprobit`: `difficult`, `technique(`*algorithm_spec*`)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`.

If `technique()` contains more than one algorithm specification, `bhhh` cannot be one of them. To use the BHHH algorithm with another algorithm, use the `initbhhh()` option and specify the other algorithm in `technique()`.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `asmprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Variance structures

Introduction

The MNP model is used with discrete dependent variables that take on more than two outcomes that do not have a natural ordering. The stochastic error terms are assumed to have a multivariate normal distribution that is heteroskedastic and correlated. Say that you have a set of J unordered

alternatives that are modeled by a regression of both case-specific and alternative-specific covariates. A "case" refers to the information on one decision maker. Underlying the model is the set of J latent variables (utilities),

$$\eta_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\alpha}_j + \xi_{ij} \tag{1}$$

where i denotes cases and j denotes alternatives. $\mathbf{x}_{ij}$ is a $1 \times p$ vector of alternative-specific variables, $\boldsymbol{\beta}$ is a $p \times 1$ vector of parameters, $\mathbf{z}_i$ is a $1 \times q$ vector of case-specific variables, $\boldsymbol{\alpha}_j$ is a $q \times 1$ vector of parameters for the jth alternative, and $\xi_i = (\xi_{i1}, \ldots, \xi_{iJ})$ is distributed multivariate normal with mean zero and covariance matrix $\boldsymbol{\Omega}$. The decision maker selects the alternative whose latent variable is highest.

Because the MNP model allows for a general covariance structure in ξ_{ij}, it does not impose the IIA property inherent in multinomial logistic and conditional logistic models. That is, the MNP model permits the odds of choosing one alternative over another to depend on the remaining alternatives. For example, consider the choice of travel mode between two cities: air, train, bus, or car, as a function of the travel mode cost, travel time (alternative-specific variables), and an individual's income (a case-specific variable). The odds of choosing air travel over a bus may not be independent of the train alternative because both bus and train travel are public ground transportation. That is, the probability of choosing air travel is $\Pr(\eta_{\text{air}} > \eta_{\text{bus}}, \eta_{\text{air}} > \eta_{\text{train}}, \eta_{\text{air}} > \eta_{\text{car}})$, and the two events $\eta_{\text{air}} > \eta_{\text{bus}}$ and $\eta_{\text{air}} > \eta_{\text{train}}$ may be correlated.

An alternative to MNP that will allow a nested correlation structure in ξ_{ij} is the nested logit model (see [R] **nlogit**).

The added flexibility of the MNP model does impose a significant computation burden because of the need to evaluate probabilities from the multivariate normal distribution. These probabilities are evaluated using simulation techniques because a closed-form solution does not exist. See *Methods and formulas* for more information.

Not all the J sets of regression coefficients $\boldsymbol{\alpha}_j$ are identifiable, nor are all $J(J+1)/2$ elements of the variance–covariance matrix $\boldsymbol{\Omega}$. As described by Train (2009, sec. 2.5), the model requires normalization because both the location (level) and scale of the latent variable are irrelevant. Increasing the latent variables by a constant does not change which η_{ij} is the maximum for decision maker i, nor does multiplying them by a constant. To normalize location, we choose an alternative, indexed by k, say, and take the difference between the latent variable k and the $J-1$ others,

$$\begin{aligned} v_{ijk} &= \eta_{ij} - \eta_{ik} \\ &= (\mathbf{x}_{ij} - \mathbf{x}_{ik})\boldsymbol{\beta} + \mathbf{z}_i(\boldsymbol{\alpha}_j - \boldsymbol{\alpha}_k) + \xi_{ij} - \xi_{ik} \\ &= \boldsymbol{\delta}_{ij'}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\gamma}_{j'} + \epsilon_{ij'} \\ &= \lambda_{ij'} + \epsilon_{ij'} \end{aligned} \tag{2}$$

where $j' = j$ if $j < k$ and $j' = j-1$ if $j > k$, so that $j' = 1, \ldots, J-1$. One can now work with the $(J-1) \times (J-1)$ covariance matrix $\boldsymbol{\Sigma}_{(k)}$ for $\boldsymbol{\epsilon}_i' = (\epsilon_{i1}, \ldots, \epsilon_{i,J-1})$. The kth alternative here is the `basealternative()` in `asmprobit`. From (2), the probability that decision maker i chooses alternative k, for example, is

$$\begin{aligned} \Pr(i \text{ chooses } k) &= \Pr(v_{i1k} \le 0, \ldots, v_{i,J-1,k} \le 0) \\ &= \Pr(\epsilon_{i1} \le -\lambda_{i1}, \ldots, \epsilon_{i,J-1} \le -\lambda_{i,J-1}) \end{aligned}$$

To normalize for scale, one of the diagonal elements of $\boldsymbol{\Sigma}_{(k)}$ must be fixed to a constant. In `asmprobit`, this is the error variance for the alternative specified by `scalealternative()`. Thus there are a total of, at most, $J(J-1)/2-1$ identifiable variance–covariance parameters. See *Variance structures* below for more on this issue.

In fact, the model is slightly more general in that not all cases need to have faced all J alternatives. The model allows for situations in which some cases chose among all possible alternatives, whereas other cases were given a choice among a subset of them, and perhaps other cases were given a choice among a different subset. The number of observations for each case is equal to the number of alternatives faced.

The MNP model is often motivated using a random-utility consumer-choice framework. Equation (1) represents the utility that consumer i receives from good j. The consumer purchases the good for which the utility is highest. Because utility is ordinal, all that matters is the ranking of the utilities from the alternatives. Thus one must normalize for location and scale.

▷ Example 1

Application of MNP models is common in the analysis of transportation data. Greene (2012, sec. 18.2.9) uses travel-mode choice data between Sydney and Melbourne to demonstrate estimating parameters of various discrete-choice models. The data contain information on 210 individuals' choices of travel mode. The four alternatives are air, train, bus, and car, with indices 1, 2, 3, and 4, respectively. One alternative-specific variable is `travelcost`, a measure of generalized cost of travel that is equal to the sum of in-vehicle cost and a wagelike measure times the amount of time spent traveling. A second alternative-specific variable is the terminal time, `termtime`, which is zero for car transportation. Household income, `income`, is a case-specific variable.

```
. use http://www.stata-press.com/data/r12/travel
. list id mode choice travelcost termtime income in 1/12, sepby(id)
```

	id	mode	choice	travel~t	termtime	income
1.	1	air	0	70	69	35
2.	1	train	0	71	34	35
3.	1	bus	0	70	35	35
4.	1	car	1	30	0	35
5.	2	air	0	68	64	30
6.	2	train	0	84	44	30
7.	2	bus	0	85	53	30
8.	2	car	1	50	0	30
9.	3	air	0	129	69	40
10.	3	train	0	195	34	40
11.	3	bus	0	149	35	40
12.	3	car	1	101	0	40

The model of travel choice is

$$\eta_{ij} = \beta_1 \texttt{travelcost}_{ij} + \beta_2 \texttt{termtime}_{ij} + \alpha_{1j} \texttt{income}_i + \alpha_{0j} + \xi_{ij}$$

The alternatives can be grouped as air and ground travel. With this in mind, we set the `air` alternative to be the `basealternative()` and choose `train` as the scaling alternative. Because these are the first and second alternatives in the `mode` variable, they are also the defaults.

```
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income)
```

(*output omitted*)

```
Alternative-specific multinomial probit        Number of obs      =       840
Case variable: id                              Number of cases    =       210
Alternative variable: mode                     Alts per case: min =         4
                                                              avg =       4.0
                                                              max =         4
Integration sequence:      Hammersley
Integration points:               200          Wald chi2(5)       =     32.05
Log simulated-likelihood = -190.09418          Prob > chi2        =    0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
mode						
travelcost	-.00977	.0027834	-3.51	0.000	-.0152253	-.0043146
termtime	-.0377095	.0094088	-4.01	0.000	-.0561504	-.0192686
air	(base alternative)					
train						
income	-.0291971	.0089246	-3.27	0.001	-.046689	-.0117052
_cons	.5616376	.3946551	1.42	0.155	-.2118721	1.335147
bus						
income	-.0127503	.0079267	-1.61	0.108	-.0282863	.0027857
_cons	-.0571364	.4791861	-0.12	0.905	-.9963239	.882051
car						
income	-.0049086	.0077486	-0.63	0.526	-.0200957	.0102784
_cons	-1.833393	.8186156	-2.24	0.025	-3.43785	-.2289357
/lnl2_2	-.5502039	.3905204	-1.41	0.159	-1.31561	.2152021
/lnl3_3	-.6005552	.3353292	-1.79	0.073	-1.257788	.0566779
/l2_1	1.131518	.2124817	5.33	0.000	.7150612	1.547974
/l3_1	.9720669	.2352116	4.13	0.000	.5110606	1.433073
/l3_2	.5197214	.2861552	1.82	0.069	-.0411325	1.080575

```
(mode=air is the alternative normalizing location)
(mode=train is the alternative normalizing scale)
. estimates store full
```

By default, the differenced covariance parameterization is used, so the covariance matrix for this model is 3×3. There are two free variances to estimate and three correlations. To help ensure that the covariance matrix remains positive definite, `asmprobit` uses the square root transformation, where it optimizes on the Cholesky-factored variance–covariance. To ensure that the diagonal elements of the Cholesky estimates remain positive, we use the log transformation. The estimates labeled `/lnl2_2` and `/lnl3_3` in the coefficient table are the log-transformed diagonal elements of the Cholesky matrix. The estimates labeled `/l2_1`, `/l3_1`, and `/l3_2` are the off-diagonal entries for elements $(2, 1)$, $(3, 1)$, and $(3, 2)$ of the Cholesky matrix.

Although the transformed parameters of the differenced covariance parameterization are difficult to interpret, you can view them untransformed by using the `estat` command. Typing

```
. estat correlation
```

	train	bus	car
train	1.0000		
bus	0.8909	1.0000	
car	0.7895	0.8951	1.0000

```
Note: correlations are for alternatives differenced with air
```

gives the correlations, and typing

```
. estat covariance
```

	train	bus	car
train	2		
bus	1.600208	1.613068	
car	1.37471	1.399703	1.515884

```
Note: covariances are for alternatives differenced with air
```

gives the (co)variances.

We can reduce the number of covariance parameters in the model by using the factor model by Cameron and Trivedi (2005). For large models with many alternatives, the parameter reduction can be dramatic, but for our example we will use `factor(1)`, a one-dimension factor model, to reduce by 3 the number of parameters associated with the covariance matrix.

```
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income) factor(1)
```

(*output omitted*)

```
Alternative-specific multinomial probit        Number of obs      =       840
Case variable: id                              Number of cases    =       210

Alternative variable: mode                     Alts per case: min =         4
                                                              avg =       4.0
                                                              max =         4

Integration sequence:      Hammersley
Integration points:              200           Wald chi2(5)       =    107.85
Log simulated-likelihood = -196.85094          Prob > chi2        =    0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
mode						
travelcost	-.0093696	.0036329	-2.58	0.010	-.01649	-.0022492
termtime	-.0593173	.0064585	-9.18	0.000	-.0719757	-.0466589
air	(base alternative)					
train						
income	-.0373511	.0098219	-3.80	0.000	-.0566018	-.0181004
_cons	.1092322	.3949529	0.28	0.782	-.6648613	.8833257
bus						
income	-.0158793	.0112239	-1.41	0.157	-.0378777	.0061191
_cons	-1.082181	.4678732	-2.31	0.021	-1.999196	-.1651666
car						
income	.0042677	.0092601	0.46	0.645	-.0138817	.0224171
_cons	-3.765445	.5540636	-6.80	0.000	-4.851389	-2.6795
/c1_2	1.182805	.3060299	3.86	0.000	.5829972	1.782612
/c1_3	1.227705	.3401237	3.61	0.000	.5610747	1.894335

```
(mode=air is the alternative normalizing location)
(mode=train is the alternative normalizing scale)
```

The estimates labeled `/c1_2` and `/c1_3` in the coefficient table are the factor loadings. These factor loadings produce the following differenced covariance estimates:

```
. estat covariance
```

	train	bus	car
train	2		
bus	1.182805	2.399027	
car	1.227705	1.452135	2.507259

```
Note: covariances are for alternatives differenced with air
```

◁

Variance structures

The matrix $\mathbf{\Omega}$ has $J(J+1)/2$ distinct elements because it is symmetric. Selecting a base alternative, normalizing its error variance to one, and constraining the correlations between its error and the other errors reduces the number of estimable parameters by J. Moreover, selecting a scale alternative and normalizing its error variance to one reduces the number by one, as well. Hence, there are at most $m = J(J-1)/2 - 1$ estimable parameters in $\mathbf{\Omega}$.

In practice, estimating all m parameters can be difficult, so one must often place more restrictions on the parameters. The `asmprobit` command provides the `correlation()` option to specify restrictions on the $J(J-3)/2+1$ correlation parameters not already restricted as a result of choosing the base alternatives, and it provides `stddev()` to specify restrictions on the $J-2$ standard deviations not already restricted as a result of choosing the base and scale alternatives.

When the `structural` option is used, `asmprobit` fits the model by assuming that all m parameters can be estimated, which is equivalent to specifying `correlation(unstructured)` and `stddev(heteroskedastic)`. The unstructured correlation structure means that all $J(J-3)/2+1$ of the remaining correlation parameters will be estimated, and the heteroskedastic specification means that all $J-2$ standard deviations will be estimated. With these default settings, the log likelihood is maximized with respect to the Cholesky decomposition of $\boldsymbol{\Omega}$, and then the parameters are transformed to the standard deviation and correlation form.

The `correlation(exchangeable)` option forces the $J(J-3)/2+1$ correlation parameters to be equal, and `correlation(independent)` forces all the correlations to be zero. Using the `stddev(homoskedastic)` option forces all J standard deviations to be one. These options may help in obtaining convergence for a model if the default options do not produce satisfactory results. In fact, when fitting a complex model, it may be advantageous to first fit a simple one and then proceed with removing the restrictions one at a time.

Advanced users may wish to specify alternative variance structures of their own choosing, and the next few paragraphs explain how to do so.

`correlation(pattern` *matname*`)` allows you to give the name of a $J \times J$ matrix that identifies a correlation structure. Sequential positive integers starting at 1 are used to identify each correlation parameter: if there are three correlation parameters, they are identified by 1, 2, and 3. The integers can be repeated to indicate that correlations with the same number should be constrained to be equal. A zero or a missing value (`.`) indicates that the correlation is to be set to zero. `asmprobit` considers only the elements of the matrix *below* the main diagonal.

Suppose that you have a model with four alternatives, numbered 1–4, and alternative 1 is the base. The unstructured and exchangeable correlation structures identified in the 4×4 lower triangular matrices are

unstructured

	1	2	3	4
1	·			
2	0	·		
3	0	1	·	
4	0	2	3	·

exchangeable

	1	2	3	4
1	·			
2	0	·		
3	0	1	·	
4	0	1	1	·

`asmprobit` labels these correlation structures unstructured and exchangeable, even though the correlations corresponding to the base alternative are set to zero. More formally: these terms are appropriate when considering the $(J-1) \times (J-1)$ submatrix $\boldsymbol{\Sigma}_{(k)}$ defined in the *Introduction* above.

You can also use the `correlation(fixed` *matname*`)` option to specify a matrix that specifies fixed and free parameters. Here the free parameters (those that are to be estimated) are identified by a missing value, and nonmissing values represent correlations that are to be taken as given. Below is a correlation structure that would set the correlations of alternative 1 to be 0.5:

	1	2	3	4
1	·			
2	0.5	·		
3	0.5	·	·	
4	0.5	·	·	·

The order of the elements of the `pattern` or `fixed` matrices must be the same as the numeric order of the alternative levels.

To specify the structure of the standard deviations—the diagonal elements of $\boldsymbol{\Omega}$—you can use the `stddev(pattern` *matname*`)` option, where *matname* is a $1 \times J$ matrix. Sequential positive integers starting at 1 are used to identify each standard deviation parameter. The integers can be repeated to indicate that standard deviations with the same number are to be constrained to be equal. A missing value indicates that the corresponding standard deviation is to be set to one. In the four-alternative example mentioned above, suppose that you wish to set the first and second standard deviations to one and that you wish to constrain the third and fourth standard deviations to be equal; the following `pattern` matrix will do that:

$$\begin{array}{c} \\ 1 \end{array} \begin{array}{c} \begin{array}{cccc} 1 & 2 & 3 & 4 \end{array} \\ \begin{pmatrix} \cdot & \cdot & 1 & 1 \end{pmatrix} \end{array}$$

Using the `stddev(fixed` *matname*`)` option allows you to identify the fixed and free standard deviations. Fixed standard deviations are entered as positive real numbers, and free parameters are identified with missing values. For example, to constrain the first and second standard deviations to equal one and to allow the third and fourth to be estimated, you would use this `fixed` matrix:

$$\begin{array}{c} \\ 1 \end{array} \begin{array}{c} \begin{array}{cccc} 1 & 2 & 3 & 4 \end{array} \\ \begin{pmatrix} 1 & 1 & \cdot & \cdot \end{pmatrix} \end{array}$$

When supplying either the `pattern` or the `fixed` matrices, you must ensure that the model is properly scaled. At least two standard deviations must be constant for the model to be scaled. A warning is issued if `asmprobit` detects that the model is not scaled.

The order of the elements of the `pattern` or `fixed` matrices must be the same as the numeric order of the alternative levels.

▷ Example 2

In example 1, we used the differenced covariance parameterization, the default. We now use the `structural` option to view the $J-2$ standard deviation estimates and the $(J-1)(J-2)/2$ correlation estimates. Here we will fix the standard deviations for the `air` and `train` alternatives to 1 and the correlations between `air` and the rest of the alternatives to 0.

```
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income) structural
```

(*output omitted*)

```
Alternative-specific multinomial probit        Number of obs      =       840
Case variable: id                              Number of cases    =       210
Alternative variable: mode                     Alts per case: min =         4
                                                              avg =       4.0
                                                              max =         4
Integration sequence:      Hammersley
Integration points:               200          Wald chi2(5)       =     32.05
Log simulated-likelihood = -190.09418          Prob > chi2        =    0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
mode						
travelcost	-.0097703	.0027834	-3.51	0.000	-.0152257	-.0043149
termtime	-.0377103	.0094092	-4.01	0.000	-.056152	-.0192687
air	(base alternative)					
train						
income	-.0291975	.0089246	-3.27	0.001	-.0466895	-.0117055
_cons	.5616448	.3946529	1.42	0.155	-.2118607	1.33515
bus						
income	-.01275	.0079266	-1.61	0.108	-.0282858	.0027858
_cons	-.0571664	.4791996	-0.12	0.905	-.9963803	.8820476
car						
income	-.0049085	.0077486	-0.63	0.526	-.0200955	.0102785
_cons	-1.833444	.8186343	-2.24	0.025	-3.437938	-.22895
/lnsigma3	-.2447428	.4953363	-0.49	0.621	-1.215584	.7260985
/lnsigma4	-.3309429	.6494493	-0.51	0.610	-1.60384	.9419543
/atanhr3_2	1.01193	.3890994	2.60	0.009	.249309	1.774551
/atanhr4_2	.5786576	.3940461	1.47	0.142	-.1936586	1.350974
/atanhr4_3	.8885204	.5600561	1.59	0.113	-.2091693	1.98621
sigma1	1	(base alternative)				
sigma2	1	(scale alternative)				
sigma3	.7829059	.3878017			.2965368	2.067
sigma4	.7182462	.4664645			.2011227	2.564989
rho3_2	.766559	.1604596			.244269	.9441061
rho4_2	.5216891	.2868027			-.1912734	.874283
rho4_3	.7106622	.277205			-.2061713	.9630403

```
(mode=air is the alternative normalizing location)
(mode=train is the alternative normalizing scale)
```

When comparing this output to that of example 1, we see that we have achieved the same log likelihood. That is, the structural parameterization using `air` as the base alternative and `train` as the scale alternative applied no restrictions on the model. This will not always be the case. We leave it up to you to try different base and scale alternatives, and you will see that not all the different combinations will achieve the same log likelihood. This is not true for the differenced covariance parameterization: it will always achieve the same log likelihood (and the maximum possible likelihood) regardless of the base and scale alternatives. This is why it is the default parameterization.

For an exercise, we can compute the differenced covariance displayed in example 1 by using the following ado-code.

```
. estat covariance
```

	air	train	bus	car
air	1			
train	0	1		
bus	0	.6001436	.6129416	
car	0	.3747012	.399619	.5158776

```
. return list
matrices:
               r(cov) :  4 x 4
. matrix cov = r(cov)
. matrix M = (1,-1,0,0 \ 1,0,-1,0 \ 1,0,0,-1)
. matrix cov1 = M*cov*M'
. matrix list cov1
symmetric cov1[3,3]
           r1         r2         r3
r1          2
r2  1.6001436  1.6129416
r3  1.3747012   1.399619  1.5158776
```

The slight difference in the regression coefficients between the example 1 and example 2 coefficient tables reflects the accuracy of the [M-5] **ghk( )** algorithm using 200 points from the Hammersley sequence.

We now fit the model using the exchangeable correlation matrix and compare the models with a likelihood-ratio test.

```
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income) correlation(exchangeable)
```

(*output omitted*)

```
Alternative-specific multinomial probit        Number of obs      =       840
Case variable: id                              Number of cases    =       210
Alternative variable: mode                     Alts per case: min =         4
                                                              avg =       4.0
                                                              max =         4
Integration sequence:      Hammersley
Integration points:               200          Wald chi2(5)       =     53.60
Log simulated-likelihood =  -190.4679          Prob > chi2        =    0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
mode						
travelcost	-.0084636	.0020452	-4.14	0.000	-.012472	-.0044551
termtime	-.0345394	.0072812	-4.74	0.000	-.0488103	-.0202684
air	(base alternative)					
train						
income	-.0290357	.0083226	-3.49	0.000	-.0453477	-.0127237
_cons	.5517445	.3719913	1.48	0.138	-.177345	1.280834
bus						
income	-.0132562	.0074133	-1.79	0.074	-.0277859	.0012735
_cons	-.0052517	.4337932	-0.01	0.990	-.8554708	.8449673
car						
income	-.0060878	.006638	-0.92	0.359	-.0190981	.0069224
_cons	-1.565918	.6633007	-2.36	0.018	-2.865964	-.265873
/lnsigmaP1	-.3557589	.1972809	-1.80	0.071	-.7424222	.0309045
/lnsigmaP2	-1.308596	.8872957	-1.47	0.140	-3.047663	.4304719
/atanhrP1	1.116589	.3765488	2.97	0.003	.3785667	1.854611
sigma1	1	(base alternative)				
sigma2	1	(scale alternative)				
sigma3	.7006416	.1382232			.4759596	1.031387
sigma4	.2701992	.2397466			.0474697	1.537983
rho3_2	.8063791	.131699			.3614621	.9521783
rho4_2	.8063791	.131699			.3614621	.9521783
rho4_3	.8063791	.131699			.3614621	.9521783

```
(mode=air is the alternative normalizing location)
(mode=train is the alternative normalizing scale)
. lrtest full .
Likelihood-ratio test                                 LR chi2(2)  =      0.75
(Assumption: . nested in full)                        Prob > chi2 =    0.6882
```

The likelihood-ratio test suggests that a common correlation is a plausible hypothesis, but this could be an artifact of the small sample size. The labeling of the standard deviation and correlation estimates has changed from `/lnsigma` and `/atanhr`, in the previous example, to `/lnsigmaP` and `/atanhrP`. The "P" identifies the parameter's index in the pattern matrices used by `asmprobit`. The pattern matrices are saved in `e(stdpattern)` and `e(corpattern)`. ◁

❑ Technical note

Another way to fit the model with the exchangeable correlation structure in example 2 is to use the `constraint` command to define the constraints on the `rho` parameters manually and then apply those.

```
. constraint 1 [atanhr3_2]_cons = [atanhr4_2]_cons
. constraint 2 [atanhr3_2]_cons = [atanhr4_3]_cons
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income) constraints(1 2) structural
```

With this method, however, we must keep track of what parameterization of the `rho`s is used in estimation, and that depends on the options specified.

❑

▷ Example 3

In the last example, we used the `correlation(exchangeable)` option, reducing the number of correlation parameters from three to one. We can explore a two–correlation parameter model by specifying a `pattern` matrix in the `correlation()` option. Suppose that we wish to have the correlation between train and bus be equal to the correlation between bus and car and to have the standard deviations for the bus and car equations be equal. We will use air as the base category and train as the scale category.

```
. matrix define corpat = J(4, 4, .)
. matrix corpat[3,2] = 1
. matrix corpat[4,3] = 1
. matrix corpat[4,2] = 2
. matrix define stdpat = J(1, 4, .)
. matrix stdpat[1,3] = 1
. matrix stdpat[1,4] = 1
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income) correlation(pattern corpat) stddev(pattern stdpat)
Iteration 0:   log simulated-likelihood = -201.33896
Iteration 1:   log simulated-likelihood = -201.00457  (backed up)
Iteration 2:   log simulated-likelihood = -200.80208  (backed up)
Iteration 3:   log simulated-likelihood = -200.79758  (backed up)
Iteration 4:   log simulated-likelihood = -200.55655  (backed up)
Iteration 5:   log simulated-likelihood =  -200.5421  (backed up)
Iteration 6:   log simulated-likelihood = -196.24925
  (output omitted)
Iteration 20:  log simulated-likelihood = -190.12874
Iteration 21:  log simulated-likelihood = -190.12871
Iteration 22:  log simulated-likelihood = -190.12871
Alternative-specific multinomial probit        Number of obs      =       840
Case variable: id                              Number of cases    =       210
Alternative variable: mode                     Alts per case: min =         4
                                                              avg =       4.0
                                                              max =         4
Integration sequence:      Hammersley
Integration points:              200           Wald chi2(5)       =     41.67
Log simulated-likelihood = -190.12871          Prob > chi2        =    0.0000
```

choice	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
mode						
travelcost	-.0100335	.0026203	-3.83	0.000	-.0151692	-.0048979
termtime	-.0385731	.008608	-4.48	0.000	-.0554445	-.0217018
air	(base alternative)					
train						
income	-.029271	.0089739	-3.26	0.001	-.0468595	-.0116824
_cons	.56528	.4008037	1.41	0.158	-.2202809	1.350841
bus						
income	-.0124658	.0080043	-1.56	0.119	-.0281539	.0032223
_cons	-.0741685	.4763422	-0.16	0.876	-1.007782	.859445
car						
income	-.0046905	.0079934	-0.59	0.557	-.0203573	.0109763
_cons	-1.897931	.7912106	-2.40	0.016	-3.448675	-.3471867
/lnsigmaP1	-.197697	.2751269	-0.72	0.472	-.7369359	.3415418
/atanhrP1	.9704403	.3286981	2.95	0.003	.3262038	1.614677
/atanhrP2	.5830923	.3690419	1.58	0.114	-.1402165	1.306401
sigma1	1	(base alternative)				
sigma2	1	(scale alternative)				
sigma3	.8206185	.2257742			.4785781	1.407115
sigma4	.8206185	.2257742			.4785781	1.407115
rho3_2	.7488977	.1443485			.3151056	.9238482
rho4_2	.5249094	.2673598			-.1393048	.863362
rho4_3	.7488977	.1443485			.3151056	.9238482

(mode=air is the alternative normalizing location)
(mode=train is the alternative normalizing scale)

In the call to `asmprobit`, we did not need to specify the `basealternative()` and `scalealternative()` options because they are implied by the specifications of the pattern matrices.

◁

❑ Technical note

If you experience convergence problems, try specifying `nopivot`, increasing `intpoints()`, specifying `antithetics`, specifying `technique(nr)` with `difficult`, or specifying a switching algorithm in the `technique()` option. As a last resort, you can use the `nrtolerance()` and `showtolerance` options. Changing the base and scale alternative in the model specification can also affect convergence if the `structural` option is used.

Because simulation methods are used to obtain multivariate normal probabilities, the estimates obtained have a limited degree of precision. Moreover, the solutions are particularly sensitive to the starting values used. Experimenting with different starting values may help in obtaining convergence, and doing so is a good way to verify previous results.

If you wish to use the BHHH algorithm along with another maximization algorithm, you must specify the `initbhhh(#)` option, where # is the number of BHHH iterations to use before switching to the algorithm specified in `technique()`. The BHHH algorithm uses an outer-product-of-gradients

approximation for the Hessian, and asmprobit must perform the gradient calculations differently than for the other algorithms.

❑

❑ Technical note

If there are no alternative-specific variables in your model, the variance–covariance matrix parameters are not identifiable. For such a model to converge, you would therefore need to use correlation(independent) and stddev(homoskedastic). A better alternative is to use mprobit, which is geared specifically toward models with only case-specific variables. See [R] **mprobit**.

❑

Saved results

asmprobit saves the following in e():

Scalars

e(N)	number of observations
e(N_case)	number of cases
e(k)	number of parameters
e(k_alt)	number of alternatives
e(k_indvars)	number of alternative-specific variables
e(k_casevars)	number of case-specific variables
e(k_sigma)	number of variance estimates
e(k_rho)	number of correlation estimates
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(df_m)	model degrees of freedom
e(ll)	log simulated-likelihood
e(N_clust)	number of clusters
e(const)	constant indicator
e(i_base)	base alternative index
e(i_scale)	scale alternative index
e(mc_points)	number of Monte Carlo replications
e(mc_burn)	starting sequence index
e(mc_antithetics)	antithetics indicator
e(chi2)	χ^2
e(p)	significance
e(fullcov)	unstructured covariance indicator
e(structcov)	1 if structured covariance; 0 otherwise
e(cholesky)	Cholesky-factored covariance indicator
e(alt_min)	minimum number of alternatives
e(alt_avg)	average number of alternatives
e(alt_max)	maximum number of alternatives
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	asmprobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(indvars)	alternative-specific independent variable
e(casevars)	case-specific variables
e(case)	variable defining cases
e(altvar)	variable defining alternatives
e(alteqs)	alternative equation names
e(alt#)	alternative labels
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(correlation)	correlation structure
e(stddev)	variance structure
e(cov_class)	class of the covariance structure
e(chi2type)	Wald, type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(mc_method)	technique used to generate sequences
e(mc_seed)	random-number generator seed
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(datasignature)	the checksum
e(datasignaturevars)	variables used in calculation of checksum
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(mfx_dlg)	program used to implement estat mfx dialog
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(stats)	alternative statistics
e(stdpattern)	variance pattern
e(stdfixed)	fixed and free standard deviations
e(altvals)	alternative values
e(altfreq)	alternative frequencies
e(alt_casevars)	indicators for estimated case-specific coefficients—e(k_alt)×e(k_casevars)
e(corpattern)	correlation structure
e(corfixed)	fixed and free correlations
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

asmprobit is implemented as an ado-file.

The simulated maximum likelihood estimates for the MNP are obtained using ml; see [R] **ml**. The likelihood evaluator implements the GHK algorithm to approximate the multivariate distribution function (Geweke 1989; Hajivassiliou and McFadden 1998; Keane and Wolpin 1994). The technique

is also described in detail by Genz (1992), but Genz describes a more general algorithm where both lower and upper bounds of integration are finite. We briefly describe the GHK simulator and refer you to Bolduc (1999) for the score computations.

As discussed earlier, the latent variables for a J-alternative model are $\eta_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\alpha}_j + \xi_{ij}$, for $j = 1, \ldots, J$, $i = 1, \ldots, n$, and $\boldsymbol{\xi}_i' = (\xi_{i,1}, \ldots, \xi_{i,\mathrm{J}}) \sim \mathrm{MVN}(\mathbf{0}, \boldsymbol{\Omega})$. The experimenter observes alternative k for the ith observation if $k = \arg\max(\eta_{ij}, j = 1, \ldots, J)$. Let

$$\begin{aligned} v_{ij'} &= \eta_{ij} - \eta_{ik} \\ &= (\mathbf{x}_{ij} - \mathbf{x}_{ik})\boldsymbol{\beta} + \mathbf{z}_i(\boldsymbol{\alpha}_j - \boldsymbol{\alpha}_k) + \xi_{ij} - \xi_{ik} \\ &= \boldsymbol{\delta}_{ij'}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\gamma}_{j'} + \epsilon_{ij'} \end{aligned}$$

where $j' = j$ if $j < k$ and $j' = j - 1$ if $j > k$, so that $j' = 1, \ldots, J-1$. Further, $\epsilon_i = (\epsilon_{i1}, \ldots, \epsilon_{i,\mathrm{J}-1}) \sim \mathrm{MVN}(\mathbf{0}, \boldsymbol{\Sigma}_{(k)})$. $\boldsymbol{\Sigma}$ is indexed by k because it depends on the choice made. We denote the deterministic part of the model as $\lambda_{ij'} = \boldsymbol{\delta}_{ij'}\boldsymbol{\beta} + \mathbf{z}_j\boldsymbol{\gamma}_{j'}$, and the probability of this event is

$$\begin{aligned} \Pr(y_i = k) &= \Pr(v_{i1} \le 0, \ldots, v_{i,J-1} \le 0) \\ &= \Pr(\epsilon_{i1} \le -\lambda_{i1}, \ldots, \epsilon_{i,J-1} \le -\lambda_{i,J-1}) \\ &= (2\pi)^{-(J-1)/2} \, |\boldsymbol{\Sigma}_{(k)}|^{-1/2} \int_{-\infty}^{-\lambda_{i1}} \cdots \int_{-\infty}^{-\lambda_{i,J-1}} \exp\left(-\tfrac{1}{2}\mathbf{z}'\boldsymbol{\Sigma}_{(k)}^{-1}\mathbf{z}\right) d\mathbf{z} \end{aligned} \tag{3}$$

Simulated likelihood

For clarity in the discussion that follows, we drop the index denoting case so that for an arbitrary observation $v' = (v_1, \ldots, v_{J-1})$, $\boldsymbol{\lambda}' = (\lambda_1, \ldots, \lambda_{J-1})$, and $\boldsymbol{\epsilon}' = (\epsilon_1, \ldots, \epsilon_{J-1})$.

The Cholesky-factored variance–covariance, $\boldsymbol{\Sigma} = \mathbf{L}\mathbf{L}'$, is lower triangular,

$$\mathbf{L} = \begin{pmatrix} l_{11} & 0 & \ldots & 0 \\ l_{21} & l_{22} & \ldots & 0 \\ \vdots & \vdots & & \vdots \\ l_{J-1,1} & l_{J-1,2} & \ldots & l_{J-1,J-1} \end{pmatrix}$$

and the correlated latent-variable errors can be expressed as linear functions of uncorrelated normal variates, $\epsilon = \mathbf{L}\zeta$, where $\zeta' = (\zeta_1, \ldots, \zeta_{J-1})$ and $\zeta_j \sim$ iid $\mathrm{N}(0, 1)$. We now have $v = \lambda + \mathbf{L}\zeta$, and by defining

$$z_j = \begin{cases} -\dfrac{\lambda_1}{l_{11}} & \text{for } j = 1 \\ -\dfrac{\lambda_j + \sum_{i=1}^{j-1} l_{ji}\zeta_i}{l_{jj}} & \text{for } j = 2, \ldots, J-1 \end{cases} \tag{4}$$

we can express the probability statement (3) as the product of conditional probabilities

$$\begin{aligned} \Pr(y_i = k) = \Pr(\zeta_1 \le z_1) \, &\Pr(\zeta_2 \le z_2 \mid \zeta_1 \le z_1) \cdots \\ &\Pr(\zeta_{J-1} \le z_{J-1} \mid \zeta_1 \le z_1, \ldots, \zeta_{J-2} \le z_{J-2}) \end{aligned}$$

because

$$\begin{aligned}\Pr(v_1 \le 0) &= \Pr(\lambda_1 + l_{11}\zeta_1 \le 0)\\ &= \Pr\left(\zeta_1 \le -\frac{\lambda_1}{l_{11}}\right)\\ \Pr(v_2 \le 0) &= \Pr(\lambda_2 + l_{21}\zeta_1 + l_{22}\zeta_2 \le 0)\\ &= \Pr\left(\zeta_2 \le -\frac{\lambda_2 + l_{21}\zeta_1}{l_{22}} \mid \zeta_1 \le -\frac{\lambda_1}{l_{11}}\right)\\ &\ldots\end{aligned}$$

The Monte Carlo algorithm then must make draws from the truncated standard normal distribution. It does so by generating $J-1$ uniform variates, $\delta_j, j = 1, \ldots, J-1$, and computing

$$\widetilde{\zeta}_j = \begin{cases} \Phi^{-1}\left\{\delta_1 \Phi\left(-\dfrac{\lambda_1}{l_{11}}\right)\right\} & \text{for } j = 1\\ \Phi^{-1}\left\{\delta_j \Phi\left(\dfrac{-\lambda_j - \sum_{i=1}^{j-1} l_{ji}\widetilde{\zeta}_i}{l_{jj}}\right)\right\} & \text{for } j = 2, \ldots, J-1 \end{cases}$$

Define $\widetilde{z}_j$ by replacing $\widetilde{\zeta}_i$ for ζ_i in (4) so that the simulated probability for the lth draw is

$$p_l = \prod_{j=1}^{J-1} \Phi(\widetilde{z}_j)$$

To increase accuracy, the bounds of integration, λ_j, are ordered so that the largest integration intervals are on the inside. The rows and columns of the variance–covariance matrix are pivoted accordingly (Genz 1992).

For a more detailed description of the GHK algorithm in Stata, see Gates (2006).

Repeated draws are made, say, N, and the simulated likelihood for the ith case, denoted $\widehat{L}_i$, is computed as

$$\widehat{L}_i = \frac{1}{N}\sum_{l=1}^{N} p_l$$

The overall simulated log likelihood is $\sum_i \log \widehat{L}_i$.

If the true likelihood is L_i, the error bound on the approximation can be expressed as

$$|\widehat{L}_i - L_i| \le V(L_i) D_N\{(\delta_i)\}$$

where $V(L_i)$ is the total variation of L_i and D_N is the discrepancy, or nonuniformity, of the set of abscissas. For the uniform pseudorandom sequence, δ_i, the discrepancy is of order $O\{(\log\log N/N)^{1/2}\}$. The order of discrepancy can be improved by using quasirandom sequences.

Quasi–Monte Carlo integration is carried out by `asmprobit` by replacing the uniform deviates with either the Halton or the Hammersley sequences. These sequences spread the points more evenly than the uniform random sequence and have a smaller order of discrepancy, $O\left[\{(\log N)^{J-1}\}/N\right]$ and $O\left[\{(\log N)^{J-2}\}/N\right]$, respectively. The Halton sequence of dimension $J-1$ is generated from the first $J-1$ primes, p_k, so that on draw l we have $\mathbf{h}_l = \{r_{p_1}(l), r_{p_2}(l), \ldots, r_{p_{J-1}}(l)\}$, where

$$r_{p_k}(l) = \sum_{j=0}^{q} b_{jk}(l) p_k^{-j-1} \in (0,1)$$

is the radical inverse function of l with base p_k so that $\sum_{j=0}^{q} b_{jk}(l) p_k^j = l$, where $p_k^q \leq l < p_k^{q+1}$ (Fang and Wang 1994).

This function is demonstrated with base $p_3 = 5$ and $l = 33$, which generates $r_5(33)$. Here $q = 2$, $b_{0,3}(33) = 3$, $b_{1,5}(33) = 1$, and $b_{2,5}(33) = 1$, so that $r_5(33) = 3/5 + 1/25 + 1/625$.

The Hammersley sequence uses an evenly spaced set of points with the first $J - 2$ components of the Halton sequence

$$\mathbf{h}_l = \left\{ \frac{2l-1}{2N}, r_{p_1}(l), r_{p_2}(l), \ldots, r_{p_{J-2}}(l) \right\}$$

for $l = 1, \ldots, N$.

For a more detailed description of the Halton and Hammersley sequences, see Drukker and Gates (2006).

Computations for the derivatives of the simulated likelihood are taken from Bolduc (1999). Bolduc gives the analytical first-order derivatives for the log of the simulated likelihood with respect to the regression coefficients and the parameters of the Cholesky-factored variance–covariance matrix. `asmprobit` uses these analytical first-order derivatives and numerical second-order derivatives.

This command supports the clustered version of the Huber/White/sandwich estimator of the variance using `vce(robust)` and `vce(cluster` *clustvar*`)`. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. Specifying `vce(robust)` is equivalent to specifying `vce(cluster` *casevar*`)`, where *casevar* is the variable that identifies the cases.

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Also see

[R] **asmprobit postestimation** — Postestimation tools for asmprobit

[R] **asclogit** — Alternative-specific conditional logit (McFadden's choice) model

[R] **asroprobit** — Alternative-specific rank-ordered probit regression

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **mprobit** — Multinomial probit regression

[U] **20 Estimation and postestimation commands**

Title

asmprobit postestimation — Postestimation tools for asmprobit

Description

The following postestimation commands are of special interest after `asmprobit`:

Command	Description
`estat alternatives`	alternative summary statistics
`estat covariance`	covariance matrix of the latent-variable errors for the alternatives
`estat correlation`	correlation matrix of the latent-variable errors for the alternatives
`estat facweights`	covariance factor weights matrix
`estat mfx`	marginal effects

For information about these commands, see below.

The following standard postestimation commands are also available:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`	likelihood-ratio test
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predicted probabilities, estimated linear predictor and its standard error
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation commands

`estat alternatives` displays summary statistics about the alternatives in the estimation sample and provides a mapping between the index numbers that label the covariance parameters of the model and their associated values and labels for the alternative variable.

`estat covariance` computes the estimated variance–covariance matrix of the latent-variable errors for the alternatives. The estimates are displayed, and the variance–covariance matrix is stored in `r(cov)`.

`estat correlation` computes the estimated correlation matrix of the latent-variable errors for the alternatives. The estimates are displayed, and the correlation matrix is stored in `r(cor)`.

`estat facweights` displays the covariance factor weights matrix and stores it in `r(C)`.

`estat mfx` computes the simulated probability marginal effects.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic altwise]
predict [type] {stub*|newvarlist} [if] [in], scores
```

statistic	Description
Main	
`pr`	probability alternative is chosen; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability that alternative j is chosen in case i.

`xb` calculates the linear prediction $\mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\alpha}_j$ for alternative j and case i.

`stdp` calculates the standard error of the linear predictor.

`altwise` specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion. The `xb` and `stdp` options always use alternativewise deletion.

`scores` calculates the scores for each coefficient in `e(b)`. This option requires a new variable list of length equal to the number of columns in `e(b)`. Otherwise, use the *stub*`*` option to have `predict` generate enumerated variables with prefix *stub*.

Syntax for estat alternatives

```
estat alternatives
```

Menu

Statistics > Postestimation > Reports and statistics

Syntax for estat covariance

```
estat covariance [ , format(%fmt) border(bspec) left(#) ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat covariance

`format(%fmt)` sets the matrix display format. The default is `format(%9.0g)`.

`border(bspec)` sets the matrix display border style. The default is `border(all)`. See [P] **matlist**.

`left(#)` sets the matrix display left indent. The default is `left(2)`. See [P] **matlist**.

Syntax for estat correlation

```
estat correlation [ , format(%fmt) border(bspec) left(#) ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat correlation

`format(%fmt)` sets the matrix display format. The default is `format(%9.4f)`.

`border(bspec)` sets the matrix display border style. The default is `border(all)`. See [P] **matlist**.

`left(#)` sets the matrix display left indent. The default is `left(2)`. See [P] **matlist**.

Syntax for estat facweights

```
estat facweights [ , format(%fmt) border(bspec) left(#) ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat facweights

`format(%fmt)` sets the matrix display format. The default is `format(%9.0f)`.

`border(bspec)` sets the matrix display border style. The default is `border(all)`. See [P] **matlist**.

`left(#)` sets the matrix display left indent. The default is `left(2)`. See [P] **matlist**.

Syntax for estat mfx

```
estat mfx [if] [in] [, options]
```

options	Description
Main	
varlist(*varlist*)	display marginal effects for *varlist*
at(mean [*atlist*] | median [*atlist*])	calculate marginal effects at these values
Options	
level(#)	set confidence interval level; default is level(95)
nodiscrete	treat indicator variables as continuous
noesample	do not restrict calculation of means and medians to the estimation sample
nowght	ignore weights when calculating means and medians

Menu

Statistics > Postestimation > Reports and statistics

Options for estat mfx

Main

varlist(*varlist*) specifies the variables for which to display marginal effects. The default is all variables.

at(mean [*atlist*] | median [*atlist*]) specifies the values at which the marginal effects are to be calculated. *atlist* is

[[*alternative*:*variable* = #] [*variable* = #] [...]]

The default is to calculate the marginal effects at the means of the independent variables at the estimation sample, at(mean).

After specifying the summary statistic, you can specify a series of specific values for variables. You can specify values for alternative-specific variables by alternative, or you can specify one value for all alternatives. You can specify only one value for case-specific variables. For example, in the travel dataset, income is a case-specific variable, whereas termtime and travelcost are alternative-specific variables. The following would be a legal syntax for estat mfx:

```
. estat mfx, at(mean air:termtime=50 travelcost=100 income=60)
```

When nodiscrete is not specified, at(mean [*atlist*]) or at(median [*atlist*]) has no effect on computing marginal effects for indicator variables, which are calculated as the discrete change in the simulated probability as the indicator variable changes from 0 to 1.

The mean and median computations respect any if and in qualifiers, so you can restrict the data over which the means or medians are computed. You can even restrict the values to a specific case; for example,

```
. estat mfx if case==21
```

Options

level(#) specifies the confidence level, as a percentage, for confidence intervals. The default is level(95) or as set by set level; see [U] **20.7 Specifying the width of confidence intervals**.

`nodiscrete` specifies that indicator variables be treated as continuous variables. An indicator variable is one that takes on the value 0 or 1 in the estimation sample. By default, the discrete change in the simulated probability is computed as the indicator variable changes from 0 to 1.

`noesample` specifies that the whole dataset be considered instead of only those marked in the `e(sample)` defined by the `asmprobit` command.

`nowght` specifies that weights be ignored when calculating the means or medians.

Remarks

Remarks are presented under the following headings:

Predicted probabilities
Obtaining estimation statistics
Obtaining marginal effects

Predicted probabilities

After fitting an alternative-specific multinomial probit model, you can use `predict` to obtain the simulated probabilities that an individual will choose each of the alternatives. When evaluating the multivariate normal probabilities via Monte Carlo simulation, `predict` uses the same method to generate the random sequence of numbers as the previous call to `asmprobit`. For example, if you specified `intmethod(Halton)` when fitting the model, `predict` also uses the Halton sequence.

▷ Example 1

In example 1 of [R] **asmprobit**, we fit a model of individuals' travel-mode choices. We can obtain the simulated probabilities that an individual chooses each alternative by using `predict`:

```
. use http://www.stata-press.com/data/r12/travel
. asmprobit choice travelcost termtime, case(id) alternatives(mode)
> casevars(income)
  (output omitted)
. predict prob
(option pr assumed; Pr(mode))
. list id mode prob choice in 1/12, sepby(id)
```

	id	mode	prob	choice
1.	1	air	.1494137	0
2.	1	train	.329167	0
3.	1	bus	.1320298	0
4.	1	car	.3898562	1
5.	2	air	.2565875	0
6.	2	train	.2761054	0
7.	2	bus	.0116135	0
8.	2	car	.4556921	1
9.	3	air	.2098406	0
10.	3	train	.1081824	0
11.	3	bus	.1671841	0
12.	3	car	.5147822	1

◁

Obtaining estimation statistics

Once you have fit a multinomial probit model, you can obtain the estimated variance or correlation matrices for the model alternatives by using the `estat` command.

▷ Example 2

To display the correlations of the errors in the latent-variable equations, we type

```
. estat correlation
```

	train	bus	car
train	1.0000		
bus	0.8909	1.0000	
car	0.7895	0.8951	1.0000

```
Note: correlations are for alternatives differenced with air
```

The covariance matrix can be displayed by typing

```
. estat covariance
```

	train	bus	car
train	2		
bus	1.600208	1.613068	
car	1.37471	1.399703	1.515884

```
Note: covariances are for alternatives differenced with air
```

◁

Obtaining marginal effects

The marginal effects are computed as the derivative of the simulated probability for an alternative with respect to an independent variable. A table of marginal effects is displayed for each alternative, with the table containing the marginal effect for each case-specific variable and the alternative for each alternative-specific variable.

By default, the marginal effects are computed at the means of each continuous independent variable over the estimation sample. For indicator variables, the difference in the simulated probability evaluated at 0 and 1 is computed by default. Indicator variables will be treated as continuous variables if the `nodiscrete` option is used.

▷ Example 3

Continuing with our model from example 1, we obtain the marginal effects for alternatives `air`, `train`, `bus`, and `car` evaluated at the mean values of each independent variable. Recall that the `travelcost` and `termtime` variables are alternative specific, taking on different values for each alternative, so they have a separate marginal effect for each alternative.

```
. estat mfx
```

Pr(choice = air) = .29434926

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
travelcost							
air	-.002688	.000677	-3.97	0.000	-.004015	-.001362	102.65
train	.0009	.000436	2.07	0.039	.000046	.001755	130.2
bus	.000376	.000271	1.39	0.166	-.000155	.000908	115.26
car	.001412	.00051	2.77	0.006	.000412	.002412	95.414
termtime							
air	-.010376	.002711	-3.83	0.000	-.015689	-.005063	61.01
train	.003475	.001639	2.12	0.034	.000264	.006687	35.69
bus	.001452	.001008	1.44	0.150	-.000523	.003427	41.657
car	.005449	.002164	2.52	0.012	.001209	.00969	0
casevars							
income	.003891	.001847	2.11	0.035	.000271	.007511	34.548

Pr(choice = train) = .29531182

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
travelcost							
air	.000899	.000436	2.06	0.039	.000045	.001753	102.65
train	-.004081	.001466	-2.78	0.005	-.006953	-.001208	130.2
bus	.001278	.00063	2.03	0.042	.000043	.002513	115.26
car	.001904	.000887	2.15	0.032	.000166	.003641	95.414
termtime							
air	.003469	.001638	2.12	0.034	.000258	.00668	61.01
train	-.01575	.00247	-6.38	0.000	-.020591	-.010909	35.69
bus	.004934	.001593	3.10	0.002	.001812	.008056	41.657
car	.007348	.002228	3.30	0.001	.00298	.011715	0
casevars							
income	-.00957	.002223	-4.31	0.000	-.013927	-.005214	34.548

Pr(choice = bus) = .08880039

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
travelcost							
air	.00038	.000274	1.39	0.165	-.000157	.000916	102.65
train	.001279	.00063	2.03	0.042	.000044	.002514	130.2
bus	-.003182	.001175	-2.71	0.007	-.005485	-.00088	115.26
car	.001523	.000675	2.26	0.024	.0002	.002847	95.414
termtime							
air	.001466	.001017	1.44	0.149	-.000526	.003459	61.01
train	.004937	.001591	3.10	0.002	.001819	.008055	35.69
bus	-.012283	.002804	-4.38	0.000	-.017778	-.006788	41.657
car	.00588	.002255	2.61	0.009	.001461	.010299	0
casevars							
income	.000435	.001461	0.30	0.766	-.002428	.003298	34.548

```
Pr(choice = car) = .32168607
```

variable	dp/dx	Std. Err.	z	P>|z|	[95% C.I.]		X
travelcost							
air	.00141	.000509	2.77	0.006	.000411	.002408	102.65
train	.001903	.000886	2.15	0.032	.000166	.003641	130.2
bus	.001523	.000675	2.25	0.024	.000199	.002847	115.26
car	-.004836	.001539	-3.14	0.002	-.007853	-.001819	95.414
termtime							
air	.005441	.002161	2.52	0.012	.001205	.009677	61.01
train	.007346	.002228	3.30	0.001	.00298	.011713	35.69
bus	.005879	.002256	2.61	0.009	.001456	.010301	41.657
car	-.018666	.003938	-4.74	0.000	-.026385	-.010948	0
casevars							
income	.005246	.002166	2.42	0.015	.001002	.00949	34.548

First, we note that there is a separate marginal effects table for each alternative and that table begins by reporting the overall probability of choosing the alternative, for example, 0.2944 for air travel. We see in the first table that a unit increase in terminal time for air travel from 61.01 minutes will result in a decrease in probability of choosing air travel (when the probability is evaluated at the mean of all variables) by approximately 0.01, with a 95% confidence interval of about -0.016 to -0.005. Travel cost has a less negative effect of choosing air travel (at the average cost of 102.65). Alternatively, an increase in terminal time and travel cost for train, bus, or car from these mean values will increase the chance for air travel to be chosen. Also, with an increase in income from 34.5, it would appear that an individual would be more likely to choose air or automobile travel over bus or train. (While the marginal effect for bus travel is positive, it is not significant.)

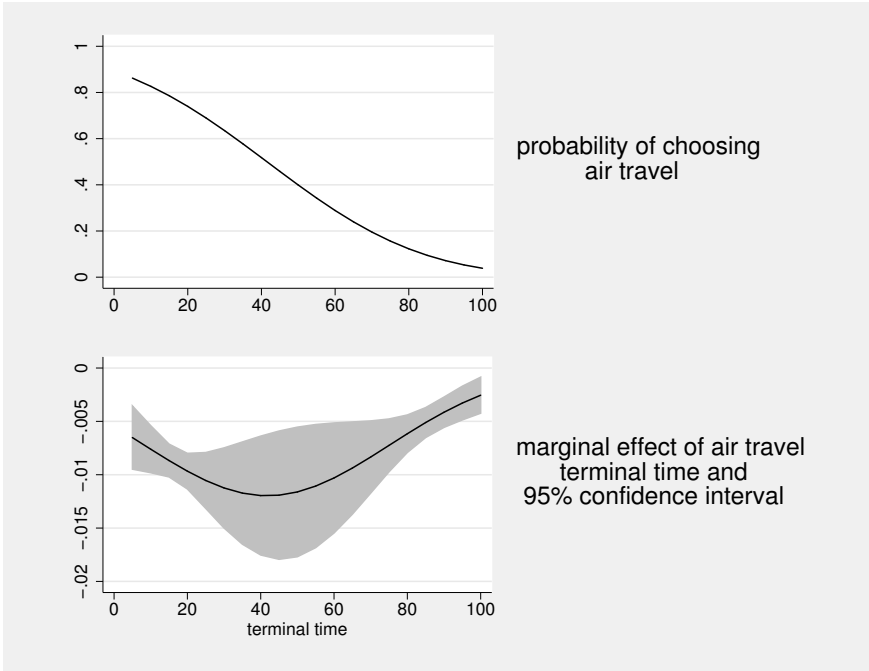
◁

▷ Example 4

Plotting the simulated probability marginal effect evaluated over a range of values for an independent variable may be more revealing than a table of values. Below are the commands for generating the simulated probability marginal effect of air travel for increasing air travel terminal time. We fix all other independent variables at their medians.

```
. qui gen meff = .
. qui gen tt = .
. qui gen lb = .
. qui gen ub = .
. forvalues i=0/19 {
  2.         local termtime = 5+5*`i'
  3.         qui replace tt = `termtime' if _n == `i'+1
  4.         qui estat mfx, at(median air:termtime=`termtime') var(termtime)
  5.         mat air = r(air)
  6.         qui replace meff = air[1,1] if _n == `i'+1
  7.         qui replace lb = air[1,5] if _n == `i'+1
  8.         qui replace ub = air[1,6] if _n == `i'+1
  9.         qui replace prob = r(pr_air) if _n == `i'+1
 10. }
. label variable tt "terminal time"
```

```
. twoway (rarea lb ub tt, pstyle(ci)) (line meff tt, lpattern(solid)), name(meff)
> legend(off) title("  marginal effect of air travel" "terminal time and"
> "95% confidence interval", position(3))
. twoway line prob tt, name(prob) title("  probability of choosing" "air travel",
> position(3)) graphregion(margin(r+9)) ytitle("") xtitle("")
. graph combine prob meff, cols(1) graphregion(margin(l+5 r+5))
```



From the graphs, we see that the simulated probability of choosing air travel decreases in an sigmoid fashion. The marginal effects display the rate of change in the simulated probability as a function of the air travel terminal time. The rate of change in the probability of choosing air travel decreases until the air travel terminal time reaches about 45; thereafter, it increases.

◁

Saved results

`estat mfx` saves the following in `r()`:

Scalars

`r(pr_`*alt*`)` scalars containing the computed probability of each alternative evaluated at the value that is labeled X in the table output. Here *alt* are the labels in the macro `e(alteqs)`.

Matrices

`r(`*alt*`)` matrices containing the computed marginal effects and associated statistics. There is one matrix for each alternative, where *alt* are the labels in the macro `e(alteqs)`. Column 1 of each matrix contains the marginal effects; column 2, their standard errors; columns 3 and 4, their z statistics and the p-values for the z statistics; and columns 5 and 6, the confidence intervals. Column 7 contains the values of the independent variables used to compute the probabilities `r(pr_`*alt*`)`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Marginal effects

The marginal effects are computed as the derivative of the simulated probability with respect to each independent variable. A set of marginal effects is computed for each alternative; thus, for J alternatives, there will be J tables. Moreover, the alternative-specific variables will have J entries, one for each alternative in each table. The details of computing the effects are different for alternative-specific variables and case-specific variables, as well as for continuous and indicator variables.

We use the latent-variable notation of `asmprobit` (see [R] **asmprobit**) for a J-alternative model and, for notational convenience, we will drop any subscripts involving observations. We then have the following linear functions $\eta_j = \mathbf{x}_j\boldsymbol{\beta} + \mathbf{z}\boldsymbol{\alpha}_j$, for $j = 1, \ldots, J$. Let k index the alternative of interest, and then

$$\begin{aligned} v_{j'} &= \eta_j - \eta_k \\ &= (\mathbf{x}_j - \mathbf{x}_k)\boldsymbol{\beta} + \mathbf{z}(\boldsymbol{\alpha}_j - \boldsymbol{\alpha}_k) + \boldsymbol{\epsilon}_{j'} \end{aligned}$$

where $j' = j$ if $j < k$ and $j' = j - 1$ if $j > k$, so that $j' = 1, \ldots, J-1$ and $\boldsymbol{\epsilon}_{j'} \sim \text{MVN}(\mathbf{0}, \boldsymbol{\Sigma})$. Denote $p_k = \Pr(v_1 \leq 0, \ldots, v_{J-1} \leq 0)$ as the simulated probability of choosing alternative k given profile $\mathbf{x}_k$ and $\mathbf{z}$. The marginal effects are then $\partial p_k/\partial \mathbf{x}_k$, $\partial p_k/\partial \mathbf{x}_j$, and $\partial p_k/\partial \mathbf{z}$, where $k = 1, \ldots, J$, $j \neq k$. `asmprobit` analytically computes the first-order derivatives of the simulated probability with respect to the v's, and the marginal effects for $\mathbf{x}$'s and $\mathbf{z}$ are obtained via the chain rule. The standard errors for the marginal effects are computed using the delta method.

Also see

[R] **asmprobit** — Alternative-specific multinomial probit regression

[U] **20 Estimation and postestimation commands**

Title

asroprobit — Alternative-specific rank-ordered probit regression

Syntax

```
asroprobit depvar [indepvars] [if] [in] [weight], case(varname)
    alternatives(varname) [options]
```

options	Description
Model	
* `case(`*varname*`)`	use *varname* to identify cases
* `alternatives(`*varname*`)`	use *varname* to identify the alternatives available for each case
`casevars(`*varlist*`)`	case-specific variables
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
Model 2	
`correlation(`*correlation*`)`	correlation structure of the latent-variable errors
`stddev(`*stddev*`)`	variance structure of the latent-variable errors
`structural`	use the structural covariance parameterization; default is the differenced covariance parameterization
`factor(#)`	use the factor covariance structure with dimension #
`noconstant`	suppress the alternative-specific constant terms
`basealternative(`*# | lbl | str*`)`	alternative used for normalizing location
`scalealternative(`*# | lbl | str*`)`	alternative used for normalizing scale
`altwise`	use alternativewise deletion instead of casewise deletion
`reverse`	interpret the lowest rank in *depvar* as the best; the default is the highest rank is the best
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`notransform`	do not transform variance–covariance estimates to the standard deviation and correlation metric
`nocnsreport`	do not display constraints
display_options	control column formats and line width

Integration

intmethod(*seqtype*)	type of quasi- or pseudouniform sequence
intpoints(#)	number of points in each sequence
intburn(#)	starting index in the Hammersley or Halton sequence
intseed(*code* | #)	pseudouniform random-number seed
antithetics	use antithetic draws
nopivot	do not use integration interval pivoting
initbhhh(#)	use the BHHH optimization algorithm for the first # iterations
favor(speed | space)	favor speed or space when generating integration points

Maximization

maximize_options	control the maximization process
coeflegend	display legend instead of statistics

correlation	Description
unstructured	one correlation parameter for each pair of alternatives; correlations with the basealternative() are zero; the default
exchangeable	one correlation parameter common to all pairs of alternatives; correlations with the basealternative() are zero
independent	constrain all correlation parameters to zero
pattern *matname*	user-specified matrix identifying the correlation pattern
fixed *matname*	user-specified matrix identifying the fixed and free correlation parameters

stddev	Description
heteroskedastic	estimate standard deviation for each alternative; standard deviations for basealternative() and scalealternative() set to one
homoskedastic	all standard deviations are one
pattern *matname*	user-specified matrix identifying the standard deviation pattern
fixed *matname*	user-specified matrix identifying the fixed and free standard deviations

seqtype	Description
hammersley	Hammersley point set
halton	Halton point set
random	uniform pseudorandom point set

*case(*varname*) and alternatives(*varname*) are required.
bootstrap, by, jackknife, statsby, and xi are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Ordinal outcomes > Rank-ordered probit regression

Description

`asroprobit` fits rank-ordered probit (ROP) models by using maximum simulated likelihood (MSL). The model allows you to relax the independence of irrelevant alternatives (IIA) property that is characteristic of the rank-ordered logistic model by estimating the variance–covariance parameters of the latent-variable errors. Each unique identifier in the `case()` variable has multiple alternatives identified in the `alternatives()` variable, and *depvar* contains the ranked alternatives made by each case. Only the order in the ranks, not the magnitude of their differences, is assumed to be relevant. By default, the largest rank indicates the more desirable alternative. Use the `reverse` option if the lowest rank should be interpreted as the more desirable alternative. Tied ranks are allowed, but they increase the computation time because all permutations of the tied ranks are used in computing the likelihood for each case. `asroprobit` allows two types of independent variables: alternative-specific variables, in which the values of each variable vary with each alternative, and case-specific variables, which vary with each case.

The estimation technique of `asroprobit` is nearly identical to that of `asmprobit`, and the two routines share many of the same options; see [R] **asmprobit**.

Options

Model

`case(`*varname*`)` specifies the variable that identifies each case. This variable identifies the individuals or entities making a choice. `case()` is required.

`alternatives(`*varname*`)` specifies the variable that identifies the alternatives available for each case. The number of alternatives can vary with each case; the maximum number of alternatives is 20. `alternatives()` is required.

`casevars(`*varlist*`)` specifies the case-specific variables that are constant for each `case()`. If there are a maximum of J alternatives, there will be $J-1$ sets of coefficients associated with `casevars()`.

`constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

Model 2

`correlation(`*correlation*`)` specifies the correlation structure of the latent-variable errors.

`correlation(unstructured)` is the most general and has $J(J-3)/2+1$ unique correlation parameters. This is the default unless `stddev()` or `structural` are specified.

`correlation(exchangeable)` provides for one correlation coefficient common to all latent variables, except the latent variable associated with the `basealternative()`.

`correlation(independent)` assumes that all correlations are zero.

`correlation(pattern` *matname*`)` and `correlation(fixed` *matname*`)` give you more flexibility in defining the correlation structure. See *Variance structures* in [R] **asmprobit** for more information.

`stddev(`*stddev*`)` specifies the variance structure of the latent-variable errors.

`stddev(heteroskedastic)` is the most general and has $J-2$ estimable parameters. The standard deviations of the latent-variable errors for the alternatives specified in `basealternative()` and `scalealternative()` are fixed to one.

`stddev(homoskedastic)` constrains all the standard deviations to equal one.

`stddev(pattern` *matname*`)` and `stddev(fixed` *matname*`)` give you added flexibility in defining the standard deviation parameters. See *Variance structures* in [R] **asmprobit** for more information.

`structural` requests the $J \times J$ structural covariance parameterization instead of the default $J-1 \times J-1$ differenced covariance parameterization (the covariance of the latent errors differenced with that of the base alternative). The differenced covariance parameterization will achieve the same maximum simulated likelihood regardless of the choice of `basealternative()` and `scalealternative()`. On the other hand, the structural covariance parameterization imposes more normalizations that may bound the model away from its maximum likelihood and thus prevent convergence with some datasets or choices of `basealternative()` and `scalealternative()`.

`factor(#)` requests that the factor covariance structure of dimension # be used. The `factor()` option can be used with the `structural` option but cannot be used with `stddev()` or `correlation()`. A $\# \times J$ (or $\# \times J-1$) matrix, $\mathbf{C}$, is used to factor the covariance matrix as $I + \mathbf{C}'\mathbf{C}$, where I is the identity matrix of dimension J (or $J-1$). The column dimension of $\mathbf{C}$ depends on whether the covariance is structural or differenced. The row dimension of $\mathbf{C}$, #, must be less than or equal to `floor(`$(J(J-1)/2-1)/(J-2)$`)`, because there are only $J(J-1)/2-1$ identifiable variance–covariance parameters. This covariance parameterization may be useful for reducing the number of covariance parameters that need to be estimated.

If the covariance is structural, the column of $\mathbf{C}$ corresponding to the base alternative contains zeros. The column corresponding to the scale alternative has a one in the first row and zeros elsewhere. If the covariance is differenced, the column corresponding to the scale alternative (differenced with the base) has a one in the first row and zeros elsewhere.

`noconstant` suppresses the $J-1$ alternative-specific constant terms.

`basealternative(#` | *lbl* | *str*`)` specifies the alternative used to normalize the latent-variable location (also referred to as the level of utility). The base alternative may be specified as a number, label, or string. The standard deviation for the latent-variable error associated with the base alternative is fixed to one, and its correlations with all other latent-variable errors are set to zero. The default is the first alternative when sorted. If a `fixed` or `pattern` matrix is given in the `stddev()` and `correlation()` options, the `basealternative()` will be implied by the fixed standard deviations and correlations in the matrix specifications. `basealternative()` cannot be equal to `scalealternative()`.

`scalealternative(#` | *lbl* | *str*`)` specifies the alternative used to normalize the latent-variable scale (also referred to as the scale of utility). The scale alternative may be specified as a number, label, or string. The default is to use the second alternative when sorted. If a `fixed` or `pattern` matrix is given in the `stddev()` option, the `scalealternative()` will be implied by the fixed standard deviations in the matrix specification. `scalealternative()` cannot be equal to `basealternative()`.

If a `fixed` or `pattern` matrix is given for the `stddev()` option, the base alternative and scale alternative are implied by the standard deviations and correlations in the matrix specifications, and they need not be specified in the `basealternative()` and `scalealternative()` options.

`altwise` specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion; that is, the entire group of observations making up a case is deleted if any missing values are encountered. This option does not apply to observations that are marked out by the `if` or `in` qualifier or the `by` prefix.

`reverse` directs `asroprobit` to interpret the rank in *depvar* that is smallest in value as the preferred alternative. By default, the rank that is largest in value is the favored alternative.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If specifying `vce(bootstrap)` or `vce(jackknife)`, you must also specify `basealternative()` and `scalealternative()`.

Reporting

`level(#)`; see [R] **estimation options**.

`notransform` prevents retransforming the Cholesky-factored variance–covariance estimates to the correlation and standard deviation metric.

This option has no effect if `structural` is not specified because the default differenced variance–covariance estimates have no interesting interpretation as correlations and standard deviations. `notransform` also has no effect if the `correlation()` and `stddev()` options are specified with anything other than their default values. Here it is generally not possible to factor the variance–covariance matrix, so optimization is already performed using the standard deviation and correlation representations.

`nocnsreport`; see [R] **estimation options**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Integration

`intmethod(hammersley | halton | random)` specifies the method of generating the point sets used in the quasi–Monte Carlo integration of the multivariate normal density. `intmethod(hammersley)`, the default, uses the Hammersley sequence; `intmethod(halton)` uses the Halton sequence; and `intmethod(random)` uses a sequence of uniform random numbers.

`intpoints(#)` specifies the number of points to use in the quasi–Monte Carlo integration. If this option is not specified, the number of points is $50 \times J$ if `intmethod(hammersley)` or `intmethod(halton)` is used and $100 \times J$ if `intmethod(random)` is used. Larger values of `intpoints()` provide better approximations of the log likelihood, but at the cost of added computation time.

`intburn(#)` specifies where in the Hammersley or Halton sequence to start, which helps reduce the correlation between the sequences of each dimension. The default is 0. This option may not be specified with `intmethod(random)`.

`intseed(`*code* | `#)` specifies the seed to use for generating the uniform pseudorandom sequence. This option may be specified only with `intmethod(random)`. *code* refers to a string that records the state of the random-number generator `runiform()`; see [R] **set seed**. An integer value # may be used also. The default is to use the current seed value from Stata's uniform random-number generator, which can be obtained from `c(seed)`.

`antithetics` specifies that antithetic draws be used. The antithetic draw for the $J - 1$ vector uniform-random variables, $\mathbf{x}$, is $1 - \mathbf{x}$.

`nopivot` turns off integration interval pivoting. By default, `asroprobit` will pivot the wider intervals of integration to the interior of the multivariate integration. This improves the accuracy of the quadrature estimate. However, discontinuities may result in the computation of numerical second-order derivatives using finite differencing (for the Newton–Raphson optimize technique, `tech(nr)`) when few simulation points are used, resulting in a non–positive-definite Hessian. `asroprobit`

uses the Broyden–Fletcher–Goldfarb–Shanno optimization algorithm, by default, which does not require computing the Hessian numerically using finite differencing.

`initbhhh(#)` specifies that the Berndt–Hall–Hall–Hausman (BHHH) algorithm be used for the initial # optimization steps. This option is the only way to use the BHHH algorithm along with other optimization techniques. The algorithm switching feature of `ml`'s `technique()` option cannot include `bhhh`.

`favor(speed | space)` instructs `asroprobit` to favor either speed or space when generating the integration points. `favor(speed)` is the default. When favoring speed, the integration points are generated once and stored in memory, thus increasing the speed of evaluating the likelihood. This speed increase can be seen when there are many cases or when the user specifies a large number of integration points, `intpoints(#)`. When favoring space, the integration points are generated repeatedly with each likelihood evaluation.

For unbalanced data, where the number of alternatives varies with each case, the estimates computed using `intmethod(random)` will vary slightly between `favor(speed)` and `favor(space)`. This is because the uniform sequences will not be identical, even when initiating the sequences using the same uniform seed, `intseed(`*code* | `#)`. For `favor(speed)`, `ncase` blocks of `intpoints(#)` $\times$ $J - 2$ uniform points are generated, where J is the maximum number of alternatives. For `favor(space)`, the column dimension of the matrices of points varies with the number of alternatives that each case has.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, [`no`]`log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**.

The following options may be particularly useful in obtaining convergence with `asroprobit`: `difficult`, `technique(`*algorithm_spec*`)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`.

If `technique()` contains more than one algorithm specification, `bhhh` cannot be one of them. To use the BHHH algorithm with another algorithm, use the `initbhhh()` option and specify the other algorithm in `technique()`.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

When specifying `from(`*matname* [`, copy`]`)`, the values in *matname* associated with the latent-variable error variances must be for the log-transformed standard deviations and inverse-hyperbolic tangent-transformed correlations. This option makes using the coefficient vector from a previously fitted `asroprobit` model convenient as a starting point.

The following option is available with `asroprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

The mathematical description and numerical computations of the rank-ordered probit model are similar to that of the multinomial probit model. The only difference is that the dependent variable of the rank-ordered probit model is ordinal, showing preferences among alternatives, as opposed to the binary dependent variable of the multinomial probit model, indicating a chosen alternative. We will describe how the likelihood of a ranking is computed using the latent-variable framework here, but for details of the latent-variable parameterization of these models and the method of maximum simulated likelihood, see [R] **asmprobit**.

Consider the latent-variable parameterization of a J alternative rank-ordered probit model. Using the notation from `asmprobit`, we have variables η_{ij}, $j = 1, \ldots, J$, such that

$$\eta_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\alpha}_j + \xi_{ij}$$

Here the $\mathbf{x}_{ij}$ are the alternative-specific independent variables, the $\mathbf{z}_i$ are the case-specific variables, and the ξ_{ij} are multivariate normal with mean zero and covariance $\boldsymbol{\Omega}$. Without loss of generality, assume that individual i ranks the alternatives in order of the alternative indices $j = 1, 2, \ldots, J$, so the alternative J is the preferred alternative and alternative 1 is the least preferred alternative. The probability of this ranking given $\boldsymbol{\beta}$ and $\boldsymbol{\alpha}_j$ is the probability that $\eta_{i,J-1} - \eta_{i,J} \leq 0$ and $\eta_{i,J-2} - \eta_{i,J-1} \leq 0$, ..., and $\eta_{i,1} - \eta_{i,2} \leq 0$.

▷ Example 1

Long and Freese (2006) provide an example of a rank-ordered logit model with alternative-specific variables. We use this dataset to demonstrate `asroprobit`. The data come from the Wisconsin Longitudinal Study. This is a study of 1957 Wisconsin high school graduates that were asked to rate their relative preference of four job characteristics: esteem, a job other people regard highly; variety, a job that is not repetitive and allows you to do a variety of things; autonomy, a job where your supervisor does not check on you frequently; and security, a job with a low risk of being laid off. The case-specific covariates are gender, `female`, an indicator variable for females, and `score`, a score on a general mental ability test measured in standard deviations. The alternative-specific variables are `high` and `low`, which indicate whether the respondent's current job is high or low in esteem, variety, autonomy, or security. This approach provides three states for a respondent's current job status for each alternative, $(1, 0)$, $(0, 1)$, and $(0, 0)$, using the notation (`high`, `low`). The score $(1, 1)$ is omitted because the respondent's current job cannot be considered both high and low in one of the job characteristics. The $(0, 0)$ score would indicate that the respondent's current job does not rank high or low (is neutral) in a job characteristic. The alternatives are ranked such that 1 is the preferred alternative and 4 is the least preferred.

```
. use http://www.stata-press.com/data/r12/wlsrank
(1992 Wisconsin Longitudinal Study data on job values)
. list id jobchar rank female score high low in 1/12, sepby(id)
```

	id	jobchar	rank	female	score	high	low
1.	1	security	1	1	.0492111	0	0
2.	1	autonomy	4	1	.0492111	0	0
3.	1	variety	1	1	.0492111	0	0
4.	1	esteem	3	1	.0492111	0	0
5.	5	security	2	1	2.115012	1	0
6.	5	variety	2	1	2.115012	1	0
7.	5	esteem	2	1	2.115012	1	0
8.	5	autonomy	1	1	2.115012	0	0
9.	7	autonomy	1	0	1.701852	1	0
10.	7	variety	1	0	1.701852	0	1
11.	7	esteem	4	0	1.701852	0	0
12.	7	security	1	0	1.701852	0	0

The three cases listed have tied ranks. `asroprobit` will allow ties, but at the cost of increased computation time. To evaluate the likelihood of the first observation, `asroprobit` must compute

$$\Pr(\texttt{esteem} = 3,\ \texttt{variety} = 1,\ \texttt{autonomy} = 4,\ \texttt{security} = 2) +$$
$$\Pr(\texttt{esteem} = 3,\ \texttt{variety} = 2,\ \texttt{autonomy} = 4,\ \texttt{security} = 1)$$

and both of these probabilities are estimated using simulation. In fact, the full dataset contains 7,237 tied ranks and `asroprobit` takes a great deal of time to estimate the parameters. For exposition, we estimate the rank-ordered probit model by using the cases without ties. These cases are marked in the variable `noties`.

The model of job preference is

$$\eta_{ij} = \beta_1 \texttt{high}_{ij} + \beta_2 \texttt{low}_{ij} \; + \; \alpha_{1j}\texttt{female}_i + \alpha_{2j}\texttt{score}_i + \alpha_{0j} + \xi_{ij}$$

for $j = 1, 2, 3, 4$. The base alternative will be `esteem`, so $\alpha_{01} = \alpha_{11} = \alpha_{21} = 0$.

```
. asroprobit rank high low if noties, case(id) alternatives(jobchar)
> casevars(female score) reverse
note: variable high has 107 cases that are not alternative-specific: there is
      no within-case variability
note: variable low has 193 cases that are not alternative-specific: there is
      no within-case variability
Iteration 0:   log simulated-likelihood = -1103.2768
Iteration 1:   log simulated-likelihood = -1089.3361  (backed up)
  (output omitted)
Alternative-specific rank-ordered probit       Number of obs      =       1660
Case variable: id                              Number of cases    =        415
Alternative variable: jobchar                  Alts per case: min =          4
                                                              avg =        4.0
                                                              max =          4
Integration sequence:      Hammersley
Integration points:               200          Wald chi2(8)       =      34.01
Log simulated-likelihood = -1080.2206          Prob > chi2        =     0.0000
```

rank	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
jobchar						
high	.3741029	.0925685	4.04	0.000	.192672	.5555337
low	-.0697443	.1093317	-0.64	0.524	-.2840305	.1445419
esteem	(base alternative)					
variety						
female	.1351487	.1843088	0.73	0.463	-.2260899	.4963873
score	.1405482	.0977567	1.44	0.151	-.0510515	.3321479
_cons	1.735016	.1451343	11.95	0.000	1.450558	2.019474
autonomy						
female	.2561828	.1679565	1.53	0.127	-.0730059	.5853715
score	.1898853	.0875668	2.17	0.030	.0182575	.361513
_cons	.7009797	.1227336	5.71	0.000	.4604262	.9415333
security						
female	.232622	.2057547	1.13	0.258	-.1706497	.6358938
score	-.1780076	.1102115	-1.62	0.106	-.3940181	.038003
_cons	1.343766	.1600059	8.40	0.000	1.030161	1.657372
/lnl2_2	.1805151	.0757296	2.38	0.017	.0320878	.3289424
/lnl3_3	.4843091	.0793343	6.10	0.000	.3288168	.6398014
/l2_1	.6062037	.1169368	5.18	0.000	.3770117	.8353957
/l3_1	.4509217	.1431183	3.15	0.002	.1704151	.7314283
/l3_2	.2289447	.1226081	1.87	0.062	-.0113627	.4692521

```
(jobchar=esteem is the alternative normalizing location)
(jobchar=variety is the alternative normalizing scale)
```

We specified the `reverse` option because a rank of 1 is the highest preference. The variance–covariance estimates are for the Cholesky-factored variance–covariance for the latent-variable errors differenced with that of alternative `esteem`. We can view the estimated correlations by entering

```
. estat correlation
```

	variety	autonomy	security
variety	1.0000		
autonomy	0.4516	1.0000	
security	0.2652	0.2399	1.0000

```
Note: correlations are for alternatives differenced with esteem
```

and typing

```
. estat covariance
```

	variety	autonomy	security
variety	2		
autonomy	.8573015	1.80229	
security	.6376996	.5475882	2.890048

```
Note: covariances are for alternatives differenced with esteem
```

gives the (co)variances. [R] **mprobit** explains that if the latent-variable errors are independent, then the correlations in the differenced parameterization should be ∼0.5 and the variances should be ∼2.0, which seems to be the case here.

The coefficient estimates for the probit models can be difficult to interpret because of the normalization for location and scale. The regression estimates for the case-specific variables will be relative to the base alternative and the regression estimates for both the case-specific and alternative-specific variables are affected by the scale normalization. The more pronounced the heteroskedasticity and correlations, the more pronounced the resulting estimate differences when choosing alternatives to normalize for location and scale. However, when using the differenced covariance structure, you will obtain the same model likelihood regardless of which alternatives you choose as the base and scale alternatives. For model interpretation, you can examine the estimated probabilities and marginal effects by using postestimation routines `predict` and `estat mfx`. See [R] **asroprobit postestimation**. ◁

Saved results

asroprobit saves the following in e():

Scalars

e(N)	number of observations
e(N_case)	number of cases
e(N_ties)	number of ties
e(k)	number of parameters
e(k_alt)	number of alternatives
e(k_indvars)	number of alternative-specific variables
e(k_casevars)	number of case-specific variables
e(k_sigma)	number of variance estimates
e(k_rho)	number of correlation estimates
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(df_m)	model degrees of freedom
e(ll)	log simulated-likelihood
e(N_clust)	number of clusters
e(const)	constant indicator
e(i_base)	base alternative index
e(i_scale)	scale alternative index
e(mc_points)	number of Monte Carlo replications
e(mc_burn)	starting sequence index
e(mc_antithetics)	antithetics indicator
e(reverse)	1 if minimum rank is best, 0 if maximum rank is best
e(chi2)	χ^2
e(p)	significance
e(fullcov)	unstructured covariance indicator
e(structcov)	1 if structured covariance; 0 otherwise
e(cholesky)	Cholesky-factored covariance indicator
e(alt_min)	minimum number of alternatives
e(alt_avg)	average number of alternatives
e(alt_max)	maximum number of alternatives
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	asroprobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(indvars)	alternative-specific independent variable
e(casevars)	case-specific variables
e(case)	variable defining cases
e(altvar)	variable defining alternatives
e(alteqs)	alternative equation names
e(alt#)	alternative labels
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(correlation)	correlation structure
e(stddev)	variance structure
e(chi2type)	Wald, type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(mc_method)	Hammersley, Halton, or uniform random; technique to generate sequences
e(mc_seed)	random-number generator seed
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(datasignature)	the checksum
e(datasignaturevars)	variables used in calculation of checksum
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(mfx_dlg)	program used to implement estat mfx dialog
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(stats)	alternative statistics
e(stdpattern)	variance pattern
e(stdfixed)	fixed and free standard deviations
e(altvals)	alternative values
e(altfreq)	alternative frequencies
e(alt_casevars)	indicators for estimated case-specific coefficients—e(k_alt)×e(k_casevars)
e(corpattern)	correlation structure
e(corfixed)	fixed and free correlations
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

asroprobit is implemented as an ado-file.

From a computational perspective, asroprobit is similar to asmprobit and the two programs share many numerical tools. Therefore, we will use the notation from *Methods and formulas* in [R] **asmprobit** to discuss the rank-ordered probit probability model.

The latent variables for a J-alternative model are $\eta_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\alpha}_j + \xi_{ij}$, for $j = 1, \ldots, J$, $i = 1, \ldots, n$, and $\boldsymbol{\xi}_i' = (\xi_{i,1}, \ldots, \xi_{i,\mathrm{J}}) \sim \mathrm{MVN}(\mathbf{0}, \boldsymbol{\Omega})$. Without loss of generality, assume for the ith observation that an individual ranks the alternatives in the order of their numeric indices, $\mathbf{y}_i = (J, J-1, \ldots, 1)$, so the first alternative is the most preferred and the last alternative is the least preferred. We can then difference the latent variables such that

$$\begin{aligned} v_{ik} &= \eta_{i,k+1} - \eta_{i,k} \\ &= (\mathbf{x}_{i,k+1} - \mathbf{x}_{i,k})\boldsymbol{\beta} + \mathbf{z}_i(\boldsymbol{\alpha}_{k+1} - \boldsymbol{\alpha}_k) + \xi_{i,k+1} - \xi_{ik} \\ &= \boldsymbol{\delta}_{ik}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\gamma}_k + \epsilon_{ik} \end{aligned}$$

for $k = 1, \ldots, J-1$ and where $\epsilon_i = (\epsilon_{i1}, \ldots, \epsilon_{i,\mathrm{J}-1}) \sim \mathrm{MVN}(\mathbf{0}, \boldsymbol{\Sigma}_{(i)})$. $\boldsymbol{\Sigma}$ is indexed by i because it is specific to the ranking of individual i. We denote the deterministic part of the model as $\lambda_{ik} = \boldsymbol{\delta}_{ik}\boldsymbol{\beta} + \mathbf{z}_j\boldsymbol{\gamma}_k$, and the probability of this event is

$$\begin{aligned} \Pr(\mathbf{y}_i) &= \Pr(v_{i1} \le 0, \ldots, v_{i,J-1} \le 0) \\ &= \Pr(\epsilon_{i1} \le -\lambda_{i1}, \ldots, \epsilon_{i,J-1} \le -\lambda_{i,J-1}) \\ &= (2\pi)^{-(J-1)/2} \, |\boldsymbol{\Sigma}_{(i)}|^{-1/2} \int_{-\infty}^{-\lambda_{i1}} \cdots \int_{-\infty}^{-\lambda_{i,J-1}} \exp\left(-\tfrac{1}{2}\mathbf{z}'\boldsymbol{\Sigma}_{(i)}^{-1}\mathbf{z}\right) d\mathbf{z} \end{aligned}$$

The integral has the same form as (3) of *Methods and formulas* in [R] **asmprobit**. See [R] **asmprobit** for details on evaluating this integral numerically by using simulation.

`asroprobit` handles tied ranks by enumeration. For k tied ranks, it will generate $k!$ rankings, where ! is the factorial operator $k! = k(k-1)(k-2)\cdots(2)(1)$. For two sets of tied ranks of size k_1 and k_2, `asroprobit` will generate $k_1!k_2!$ rankings. The total probability is the sum of the probability of each ranking. For example, if there are two tied ranks such that $\mathbf{y}_i = (J, J, J-2, \ldots, 1)$, then `asroprobit` will evaluate $\Pr(\mathbf{y}_i) = \Pr(\mathbf{y}_i^{(1)}) + \Pr(\mathbf{y}_i^{(2)})$, where $\mathbf{y}_i^{(1)} = (J, J-1, J-2, \ldots, 1)$ and $\mathbf{y}_i^{(2)} = (J-1, J, J-2, \ldots, 1)$.

This command supports the clustered version of the Huber/White/sandwich estimator of the variance using `vce(robust)` and `vce(cluster` *clustvar*`)`. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. Specifying `vce(robust)` is equivalent to specifying `vce(cluster` *casevar*`)`, where *casevar* is the variable that identifies the cases.

Reference

Long, J. S., and J. Freese. 2006. *Regression Models for Categorical Dependent Variables Using Stata*. 2nd ed. College Station, TX: Stata Press.

Also see

[R] **asroprobit postestimation** — Postestimation tools for asroprobit

[R] **asmprobit** — Alternative-specific multinomial probit regression

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **mprobit** — Multinomial probit regression

[R] **oprobit** — Ordered probit regression

[U] **20 Estimation and postestimation commands**

Title

asroprobit postestimation — Postestimation tools for asroprobit

Description

The following postestimation commands are of special interest after `asroprobit`:

Command	Description
`estat alternatives`	alternative summary statistics
`estat covariance`	covariance matrix of the latent-variable errors for the alternatives
`estat correlation`	correlation matrix of the latent-variable errors for the alternatives
`estat facweights`	covariance factor weights matrix
`estat mfx`	marginal effects

For information about these commands, see below.

The following standard postestimation commands are also available:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`	likelihood-ratio test
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predicted probabilities, estimated linear predictor and its standard error
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation commands

`estat alternatives` displays summary statistics about the alternatives in the estimation sample. The command also provides a mapping between the index numbers that label the covariance parameters of the model and their associated values and labels for the alternative variable.

`estat covariance` computes the estimated variance–covariance matrix of the latent-variable errors for the alternatives. The estimates are displayed, and the variance–covariance matrix is stored in `r(cov)`.

`estat correlation` computes the estimated correlation matrix of the latent-variable errors for the alternatives. The estimates are displayed, and the correlation matrix is stored in `r(cor)`.

`estat facweights` displays the covariance factor weights matrix and stores it in `r(C)`.

`estat mfx` computes marginal effects of a simulated probability of a set of ranked alternatives. The probability is stored in `r(pr)`, the matrix of rankings is stored in `r(ranks)`, and the matrix of marginal-effect statistics is stored in `r(mfx)`.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic altwise]

predict [type] {stub* | newvarlist} [if] [in], scores
```

statistic	Description
Main	
pr	probability of each ranking, by case; the default
pr1	probability that each alternative is preferred
xb	linear prediction
stdp	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of each ranking. For each case, one probability is computed for the ranks in `e(depvar)`.

`pr1` calculates the probability that each alternative is preferred.

`xb` calculates the linear prediction $\mathbf{x}_{ij}\boldsymbol{\beta} + \mathbf{z}_i\boldsymbol{\alpha}_j$ for alternative j and case i.

`stdp` calculates the standard error of the linear predictor.

`altwise` specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion. The `xb` and `stdp` options always use alternativewise deletion.

`scores` calculates the scores for each coefficient in `e(b)`. This option requires a new variable list of length equal to the number of columns in `e(b)`. Otherwise, use the *stub*`*` option to have `predict` generate enumerated variables with prefix *stub*.

Syntax for estat alternatives

```
estat alternatives
```

Menu

Statistics > Postestimation > Reports and statistics

Syntax for estat covariance

```
estat covariance [ , format(%fmt) border(bspec) left(#) ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat covariance

`format(%fmt)` sets the matrix display format. The default is `format(%9.0g)`.

`border(bspec)` sets the matrix display border style. The default is `border(all)`. See [P] **matlist**.

`left(#)` sets the matrix display left indent. The default is `left(2)`. See [P] **matlist**.

Syntax for estat correlation

```
estat correlation [ , format(%fmt) border(bspec) left(#) ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat correlation

`format(%fmt)` sets the matrix display format. The default is `format(%9.4f)`.

`border(bspec)` sets the matrix display border style. The default is `border(all)`. See [P] **matlist**.

`left(#)` sets the matrix display left indent. The default is `left(2)`. See [P] **matlist**.

Syntax for estat facweights

```
estat facweights [ , format(%fmt) border(bspec) left(#) ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat facweights

`format(%fmt)` sets the matrix display format. The default is `format(%9.0f)`.

`border(bspec)` sets the matrix display border style. The default is `border(all)`. See [P] **matlist**.

`left(#)` sets the matrix display left indent. The default is `left(2)`. See [P] **matlist**.

Syntax for estat mfx

```
estat mfx [if] [in] [, options]
```

options	Description
Main	
varlist(*varlist*)	display marginal effects for *varlist*
at(median [*atlist*])	calculate marginal effects at these values
rank(*ranklist*)	calculate marginal effects for the simulated probability of these ranked alternatives
Options	
level(#)	set confidence interval level; default is level(95)
nodiscrete	treat indicator variables as continuous
noesample	do not restrict calculation of the medians to the estimation sample
nowght	ignore weights when calculating medians

Menu

Statistics > Postestimation > Reports and statistics

Options for estat mfx

Main

varlist(*varlist*) specifies the variables for which to display marginal effects. The default is all variables.

at(median [*atlist*]) specifies the values at which the marginal effects are to be calculated. *atlist* is

[[*alternative*:*variable* = #] [*variable* = #] [...]])

The marginal effects are calculated at the medians of the independent variables.

After specifying the summary statistic, you can specify specific values for variables. You can specify values for alternative-specific variables by alternative, or you can specify one value for all alternatives. You can specify only one value for case-specific variables. For example, in the wlsrank dataset, female and score are case-specific variables, whereas high and low are alternative-specific variables. The following would be a legal syntax for estat mfx:

```
. estat mfx, at(median high=0 esteem:high=1 low=0 security:low=1 female=1)
```

When nodiscrete is not specified, at(median [*atlist*]) has no effect on computing marginal effects for indicator variables, which are calculated as the discrete change in the simulated probability as the indicator variable changes from 0 to 1.

The median computations respect any if or in qualifiers, so you can restrict the data over which the medians are computed. You can even restrict the values to a specific case, for example,

```
. estat mfx if case==13
```

rank(*ranklist*) specifies the ranks for the alternatives. *ranklist* is

alternative = # *alternative* = # [...])

The default is to rank the calculated latent variables. Alternatives excluded from `rank()` are omitted from the analysis. You must therefore specify at least two alternatives in `rank()`. You may have tied ranks in the rank specification. Only the order in the ranks is relevant.

Options

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`nodiscrete` specifies that indicator variables be treated as continuous variables. An indicator variable is one that takes on the value 0 or 1 in the estimation sample. By default, the discrete change in the simulated probability is computed as the indicator variable changes from 0 to 1.

`noesample` specifies that the whole dataset be considered instead of only those marked in the `e(sample)` defined by the `asroprobit` command.

`nowght` specifies that weights be ignored when calculating the medians.

Remarks

Remarks are presented under the following headings:

Predicted probabilities
Obtaining estimation statistics

Predicted probabilities

After fitting an alternative-specific rank-ordered probit model, you can use `predict` to obtain the probabilities of alternative rankings or the probabilities of each alternative being preferred. When evaluating the multivariate normal probabilities via (quasi) Monte Carlo, `predict` uses the same method to generate the (quasi) random sequence of numbers as the previous call to `asroprobit`. For example, if you specified `intmethod(halton)` when fitting the model, `predict` also uses Halton sequences.

▷ Example 1

In example 1 of [R] **asroprobit**, we fit a model of job characteristic preferences. This is a study of 1957 Wisconsin high school graduates that were asked to rate their relative preference of four job characteristics: esteem, a job other people regard highly; variety, a job that is not repetitive and allows you to do a variety of things; autonomy, a job where your supervisor does not check on you frequently; and security, a job with a low risk of being laid off. The case-specific covariates are gender, `female`, an indicator variable for females, and `score`, a score on a general mental ability test measured in standard deviations. The alternative-specific variables are `high` and `low`, which indicate whether the respondent's current job is high or low in esteem, variety, autonomy, or security. This approach provides three states for a respondent's current job status for each alternative, $(1,0)$, $(0,1)$, and $(0,0)$, using the notation (`high`, `low`). The score $(1,1)$ is omitted because the respondent's current job cannot be considered both high and low in one of the job characteristics. The $(0,0)$ score would indicate that the respondent's current job does not rank high or low (is neutral) in a job characteristic. The alternatives are ranked such that 1 is the preferred alternative and 4 is the least preferred.

We can obtain the probabilities of the observed alternative rankings, the `pr` option, and the probability of each alternative being preferred, the `pr1` option, by using `predict`:

```
. use http://www.stata-press.com/data/r12/wlsrank
(1992 Wisconsin Longitudinal Study data on job values)
. asroprobit rank high low if noties, case(id) alternatives(jobchar)
> casevars(female score) reverse
  (output omitted)
. keep if e(sample)
(11244 observations deleted)
. predict prob, pr
. predict prob1, pr1
. list id jobchar prob prob1 rank female score high low in 1/12
```

	id	jobchar	prob	prob1	rank	female	score	high	low
1.	13	security	.0421807	.2784269	3	0	.3246512	0	1
2.	13	autonomy	.0421807	.1029036	1	0	.3246512	0	0
3.	13	variety	.0421807	.6026725	2	0	.3246512	1	0
4.	13	esteem	.0421807	.0160111	4	0	.3246512	0	1
5.	19	autonomy	.0942025	.1232488	4	1	.0492111	0	0
6.	19	esteem	.0942025	.0140261	3	1	.0492111	0	0
7.	19	security	.0942025	.4601368	1	1	.0492111	1	0
8.	19	variety	.0942025	.4025715	2	1	.0492111	0	0
9.	22	esteem	.1414177	.0255264	4	1	1.426412	1	0
10.	22	variety	.1414177	.4549441	1	1	1.426412	0	0
11.	22	security	.1414177	.2629494	3	1	1.426412	0	0
12.	22	autonomy	.1414177	.2566032	2	1	1.426412	1	0

The `prob` variable is constant for each case because it contains the probability of the ranking in the `rank` variable. On the other hand, the `prob1` variable contains the estimated probability of each alternative being preferred. For each case, the sum of the values in `prob1` will be approximately 1.0. They do not add up to exactly 1.0 because of approximations due to the GHK algorithm.

◁

Obtaining estimation statistics

For examples of the specialized `estat` subcommands `covariance` and `correlation`, see [R] **asmprobit postestimation**. The entry also has a good example of computing marginal effects after `asmprobit` that is applicable to `asroprobit`. Below we will elaborate further on marginal effects after `asroprobit` where we manipulate the `rank()` option.

▷ Example 2

We will continue with the preferred job characteristics example where we first compute the marginal effects for case `id` = 13.

```
. estat mfx if id==13, rank(security=3 autonomy=1 variety=2 esteem=4)

Pr(esteem=4 variety=2 autonomy=1 security=3) = .04218068
```

variable	dp/dx	Std. Err.	z	P>|z|	[	95% C.I.	]	X
high*								
esteem	-.008713	.001964	-4.44	0.000	-.012562	-.004864		0
variety	-.009102	.003127	-2.91	0.004	-.015231	-.002973		1
autonomy	.025535	.007029	3.63	0.000	.011758	.039313		0
security	-.003745	.001394	-2.69	0.007	-.006477	-.001013		0
low*								
esteem	.001614	.002646	0.61	0.542	-.003572	.0068		1
variety	.001809	.003012	0.60	0.548	-.004094	.007712		0
autonomy	-.003849	.006104	-0.63	0.528	-.015813	.008115		0
security	.000582	.000985	0.59	0.554	-.001348	.002513		1
casevars								
female*	.009767	.009064	1.08	0.281	-.007998	.027533		0
score	.008587	.004488	1.91	0.056	-.00021	.017384		.32465

```
(*) dp/dx is for discrete change of indicator variable from 0 to 1
```

Next we compute the marginal effects for the probability that autonomy is preferred given the profile of case `id` = 13.

```
. estat mfx if id==13, rank(security=2 autonomy=1 variety=2 esteem=2)

Pr(esteem=3 variety=4 autonomy=1 security=2) +
Pr(esteem=4 variety=3 autonomy=1 security=2) +
Pr(esteem=2 variety=4 autonomy=1 security=3) +
Pr(esteem=4 variety=2 autonomy=1 security=3) +
Pr(esteem=2 variety=3 autonomy=1 security=4) +
Pr(esteem=3 variety=2 autonomy=1 security=4) = .10276103
```

variable	dp/dx	Std. Err.	z	P>|z|	[	95% C.I.	]	X
high*								
esteem	-.003524	.001258	-2.80	0.005	-.005989	-.001059		0
variety	-.036203	.00894	-4.05	0.000	-.053724	-.018681		1
autonomy	.057279	.013801	4.15	0.000	.030231	.084328		0
security	-.0128	.002665	-4.80	0.000	-.018024	-.007576		0
low*								
esteem	.000518	.000833	0.62	0.534	-.001116	.002151		1
variety	.006409	.010588	0.61	0.545	-.014343	.027161		0
autonomy	-.008818	.013766	-0.64	0.522	-.035799	.018163		0
security	.002314	.003697	0.63	0.531	-.004932	.009561		1
casevars								
female*	.013839	.021607	0.64	0.522	-.028509	.056188		0
score	.017917	.011062	1.62	0.105	-.003764	.039598		.32465

```
(*) dp/dx is for discrete change of indicator variable from 0 to 1
```

The probability computed by `estat mfx` matches the probability computed by `predict, pr1` only within three digits. This outcome is because of how the computation is carried out and the numeric inaccuracy of the GHK simulator using a Hammersley point set of length 200. The computation carried out by `estat mfx` literally computes all six probabilities listed in the header of the MFX table and sums them. The computation by `predict, pr1` is the same as `predict` after `asmprobit` (multinomial probit): it computes the probability that `autonomy` is chosen, thus requiring only one

call to the GHK simulator. Hence, there is a difference in the reported values even though the two probability statements are equivalent.

◁

Saved results

`estat mfx` saves the following in `r()`:

Scalars

`r(pr)` scalar containing the computed probability of the ranked alternatives.

Matrices

`r(ranks)` column vector containing the alternative ranks. The rownames identify the alternatives.

`r(mfx)` matrix containing the computed marginal effects and associated statistics. Column 1 of the matrix contains the marginal effects; column 2, their standard errors; column 3, their z statistics; and columns 4 and 5, the confidence intervals. Column 6 contains the values of the independent variables used to compute the probabilities `r(pr)`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **asroprobit** — Alternative-specific rank-ordered probit regression

[R] **asmprobit** — Alternative-specific multinomial probit regression

[U] **20 Estimation and postestimation commands**

Title

BIC note — Calculating and interpreting BIC

Description

This entry discusses a statistical issue that arises when using the Bayesian information criterion (BIC) to compare models.

Stata calculates BIC, assuming $N =$ `e(N)`—we will explain—but sometimes it would be better if a different N were used. Commands that calculate BIC have an `n()` option, allowing you to specify the N to be used.

In summary,

1. If you are comparing results estimated by the same estimation command, using the default BIC calculation is probably fine. There is an issue, but most researchers would ignore it.
2. If you are comparing results estimated by different estimation commands, you need to be on your guard.
    a. If the different estimation commands share the same definitions of observations, independence, and the like, you are back in case 1.
    b. If they differ in these regards, you need to think about the value of N that should be used. For example, `logit` and `xtlogit` differ in that the former assumes independent observations and the latter, independent panels.
    c. If estimation commands differ in the events being used over which the likelihood function is calculated, the information criteria may not be comparable at all. We say information *criteria* because this would apply equally to the Akaike information criterion (AIC), as well as to BIC. For instance, `streg` and `stcox` produce such incomparable results. The events used by `streg` are the actual survival times, whereas the events used by `stcox` are failures within risk pools, conditional on the times at which failures occurred.

Remarks

Remarks are presented under the following headings:

Background
The problem of determining N
The problem of conformable likelihoods
The first problem does not arise with AIC; the second problem does
Calculating BIC correctly

Background

The AIC and the BIC are two popular measures for comparing maximum likelihood models. AIC and BIC are defined as

$$\text{AIC} = -2 \times \ln(\text{likelihood}) + 2 \times k$$

$$\text{BIC} = -2 \times \ln(\text{likelihood}) + \ln(N) \times k$$

where

$$k = \text{number of parameters estimated}$$

$$N = \text{number of observations}$$

We are going to discuss AIC along with BIC because AIC has some of the problems that BIC has, but not all.

AIC and BIC can be viewed as measures that combine fit and complexity. Fit is measured negatively by $-2 \times \ln(\text{likelihood})$; the larger the value, the worse the fit. Complexity is measured positively, either by $2 \times k$ (AIC) or $\ln(N) \times k$ (BIC).

Given two models fit on the same data, the model with the smaller value of the information criterion is considered to be better.

There is substantial literature on these measures: see Akaike (1974); Raftery (1995); Sakamoto, Ishiguro, and Kitagawa (1986); and Schwarz (1978).

When Stata calculates the above measures, it uses the rank of `e(V)` for k and it uses `e(N)` for N. `e(V)` and `e(N)` are Stata notation for results stored by the estimation command. `e(V)` is the variance–covariance matrix of the estimated parameters, and `e(N)` is the number of observations in the dataset used in calculating the result.

The problem of determining N

The difference between AIC and BIC is that AIC uses the constant 2 to weight k, whereas BIC uses $\ln(N)$.

Determining what value of N should be used is problematic. Despite appearances, the definition "N is the number of observations" is not easy to make operational. N does not appear in the likelihood function itself, N is not the output of a standard statistical formula, and what is an observation is often subjective.

▷ Example 1

Often what is meant by N is obvious. Consider a simple logit model. What is meant by N is the number of observations that are statistically independent and that corresponds to M, the number of observations in the dataset used in the calculation. We will write $N = M$.

But now assume that the same dataset has a grouping variable and the data are thought to be clustered within group. To keep the problem simple, let's pretend that there are G groups and m observations within group, so that $M = G \times m$. Because you are worried about intragroup correlation, you fit your model with `xtlogit`, grouping on the grouping variable. Now you wish to calculate BIC. What is the N that should be used? $N = M$ or $N = G$?

That is a deep question. If the observations really are independent, then you should use $N = M$. If the observations within group are not just correlated but are duplicates of one another, and they had to be so, then you should use $N = G$. Between those two extremes, you should probably use a number between N and G, but determining what that number should be from measured correlations is difficult. Using $N = M$ is conservative in that, if anything, it overweights complexity. Conservativeness, however, is subjective, too: using $N = G$ could be considered more conservative in that fewer constraints are being placed on the data.

When the estimated correlation is high, our reaction would be that using $N = G$ is probably more reasonable. Our first reaction, however, would be that using BIC to compare models is probably a misuse of the measure.

Stata uses $N = M$. An informal survey of web-based literature suggests that $N = M$ is the popular choice.

There is another reason, not so good, to choose $N = M$. It makes across-model comparisons more likely to be valid when performed without thinking about the issue. Say that you wish to compare the `logit` and `xtlogit` results. Thus you need to calculate

$$\text{BIC}_p = -2 \times \ln(\text{likelihood}_p) + \ln(N_p) \times k$$

$$\text{BIC}_x = -2 \times \ln(\text{likelihood}_x) + \ln(N_x) \times k$$

Whatever N you use, you must use the same N in both formulas. Stata's choice of $N = M$ at least meets that test.

◁

▷ Example 2

In the above example, using $N = M$ is reasonable. Now let's look at when using $N = M$ is wrong, even if popular.

Consider a model fit by `stcox`. Using $N = M$ is certainly wrong if for no other reason than M is not even a well-defined number. The same data can be represented by different datasets with different numbers of observations. For example, in one dataset, there might be 1 observation per subject. In another, the same subjects could have two records each, the first recording the first half of the time at risk and the second recording the remaining part. All statistics calculated by Stata on either dataset would be the same, but M would be different.

Deciding on the right definition, however, is difficult. Viewed one way, N in the Cox regression case should be the number of risk pools, R, because the Cox regression calculation is made on the basis of the independent risk pools. Viewed another way, N should be the number of subjects, N_{subj}, because, even though the likelihood function is based on risk pools, the parameters estimated are at the subject level.

You can decide which argument you prefer.

For parametric survival models, in single-record data, $N = M$ is unambiguously correct. For multirecord data, there is an argument for $N = M$ and for $N = N_{\text{subj}}$.

◁

The problem of conformable likelihoods

The problem of conformable likelihoods does not concern N. Researchers sometimes use information criteria such as BIC and AIC to make comparisons across models. For that to be valid, the likelihoods must be conformable; that is, the likelihoods must all measure the same thing.

It is common to think of the likelihood function as the $\Pr(\text{data} \mid \text{parameters})$, but in fact, the likelihood is

$$\Pr(\text{particular events in the data} \mid \text{parameters})$$

You must ensure that the events are the same.

For instance, they are not the same in the semiparametric Cox regression and the various parametric survival models. In Cox regression, the events are, at each failure time, that the subjects observed to fail in fact failed, given that failures occurred at those times. In the parametric models, the events are that each subject failed exactly when the subject was observed to fail.

The formula for AIC and BIC is

$$\text{measure} = -2 \times \ln(\text{likelihood}) + \text{complexity}$$

When you are comparing models, if the likelihoods are measuring different events, even if the models obtain estimates of the same parameters, differences in the information measures are irrelevant.

The first problem does not arise with AIC; the second problem does

Regardless of model, the problem of defining N never arises with AIC because N is not used in the AIC calculation. AIC uses a constant 2 to weight complexity as measured by k, rather than $\ln(N)$.

For both AIC and BIC, however, the likelihood functions must be conformable; that is, they must be measuring the same event.

Calculating BIC correctly

When using BIC to compare results, and especially when using BIC to compare results from different models, you should think carefully about how N should be defined. Then specify that number by using the `n()` option:

```
. estimates stats full sub, n(74)
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
full	102	-45.03321	-20.59083	4	49.18167	58.39793
sub	102	-45.03321	-27.17516	3	60.35031	67.26251

Note: N = 74 used in calculating BIC

Both `estimates stats` and `estat ic` allow the `n()` option; see [R] **estimates stats** and [R] **estat**.

Methods and formulas

AIC and BIC are defined as

$$\text{AIC} = -2 \times \ln(\text{likelihood}) + 2 \times k$$

$$\text{BIC} = -2 \times \ln(\text{likelihood}) + \ln(N) \times k$$

where k is the model degrees of freedom calculated as the rank of variance–covariance matrix of the parameters `e(V)` and N is the number of observations used in estimation or, more precisely, the number of independent terms in the likelihood. Operationally, N is defined as `e(N)` unless the `n()` option is specified.

References

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Also see

[R] **estat** — Postestimation statistics

[R] **estimates stats** — Model statistics

Title

binreg — Generalized linear models: Extensions to the binomial family

Syntax

`binreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
`or`	use logit link and report odds ratios
`rr`	use log link and report risk ratios
`hr`	use log-complement link and report health ratios
`rd`	use identity link and report risk differences
`n(#|`*varname*`)`	use # or *varname* for number of trials
`exposure(`*varname*`)`	include ln(*varname*) in model with coefficient constrained to 1
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
`mu(`*varname*`)`	use *varname* as the initial estimate for the mean of *depvar*
`init(`*varname*`)`	synonym for `mu(`*varname*`)`
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `eim`, `robust`, `cluster` *clustvar*, `oim`, `opg`, `bootstrap`, `jackknife`, `hac` *kernel*, `jackknife1`, or `unbiased`
`t(`*varname*`)`	variable name corresponding to time
`vfactor(#)`	multiply variance matrix by scalar #
`disp(#)`	quasi-likelihood multiplier
`scale(x2|dev|#)`	set the scale parameter; default is `scale(1)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`coefficients`	report nonexponentiated coefficients
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
`irls`	use iterated, reweighted least-squares optimization; the default
`ml`	use maximum likelihood optimization
maximize_options	control the maximization process; seldom used
`fisher(#)`	Fisher scoring steps
`search`	search for good starting values
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`bootstrap`, `by`, `jackknife`, `mi estimate`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.
`vce(bootstrap)`, `vce(jackknife)`, and `vce(jackknife1)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.
`fweights`, `aweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Generalized linear models > GLM for the binomial family

Description

`binreg` fits generalized linear models for the binomial family. It estimates odds ratios, risk ratios, health ratios, and risk differences. The available links are

Option	Implied link	Parameter
`or`	`logit`	odds ratios = exp(β)
`rr`	`log`	risk ratios = exp(β)
`hr`	`log complement`	health ratios = exp(β)
`rd`	`identity`	risk differences = β

Estimates of odds, risk, and health ratios are obtained by exponentiating the appropriate coefficients. The `or` option produces the same results as Stata's `logistic` command, and `or coefficients` yields the same results as the `logit` command. When no link is specified, `or` is assumed.

Options

Model

`noconstant`; see [R] **estimation options**.

`or` requests the logit link and results in odds ratios if `coefficients` is not specified.

`rr` requests the log link and results in risk ratios if `coefficients` is not specified.

`hr` requests the log-complement link and results in health ratios if `coefficients` is not specified.

`rd` requests the identity link and results in risk differences.

`n(#|`*varname*`)` specifies either a constant integer to use as the denominator for the binomial family or a variable that holds the denominator for each observation.

`exposure(`*varname*`)`, `offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**. `constraints(`*constraints*`)` and `collinear` are not allowed with `irls`.

`mu(`*varname*`)` specifies *varname* containing an initial estimate for the mean of *depvar*. This option can be useful if you encounter convergence difficulties. `init(`*varname*`)` is a synonym.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification, that allow for intragroup correlation, that are derived from asymptotic theory, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(eim)`, the default, uses the expected information matrix (EIM) for the variance estimator.

`binreg` also allows the following:

`vce(hac` *kernel* [*#*]`)` specifies that a heteroskedasticity- and autocorrelation-consistent (HAC) variance estimate be used. HAC refers to the general form for combining weighted matrices to form the variance estimate. There are three kernels built into `binreg`. *kernel* is a user-written program or one of

`nwest` | `gallant` | `anderson`

If *#* is not specified, $N - 2$ is assumed.

`vce(jackknife1)` specifies that the one-step jackknife estimate of variance be used.

`vce(unbiased)` specifies that the unbiased sandwich estimate of variance be used.

`t(`*varname*`)` specifies the variable name corresponding to time; see [TS] **tsset**. `binreg` does not always need to know `t()`, though it does if `vce(hac ...)` is specified. Then you can either specify the time variable with `t()`, or you can `tsset` your data before calling `binreg`. When the time variable is required, `binreg` assumes that the observations are spaced equally over time.

`vfactor(#)` specifies a scalar by which to multiply the resulting variance matrix. This option allows users to match output with other packages, which may apply degrees of freedom or other small-sample corrections to estimates of variance.

`disp(#)` multiplies the variance of *depvar* by *#* and divides the deviance by *#*. The resulting distributions are members of the quasilikelihood family.

`scale(x2` | `dev` | `#)` overrides the default scale parameter. This option is allowed only with Hessian (information matrix) variance estimates.

By default, `scale(1)` is assumed for the discrete distributions (binomial, Poisson, and negative binomial), and `scale(x2)` is assumed for the continuous distributions (Gaussian, gamma, and inverse Gaussian).

`scale(x2)` specifies that the scale parameter be set to the Pearson chi-squared (or generalized chi-squared) statistic divided by the residual degrees of freedom, which was recommended by McCullagh and Nelder (1989) as a good general choice for continuous distributions.

`scale(dev)` sets the scale parameter to the deviance divided by the residual degrees of freedom. This option provides an alternative to `scale(x2)` for continuous distributions and overdispersed or underdispersed discrete distributions.

`scale(#)` sets the scale parameter to *#*.

Reporting

`level(#)`, `noconstant`; see [R] **estimation options**.

`coefficients` displays the nonexponentiated coefficients and corresponding standard errors and confidence intervals. This option has no effect when the `rd` option is specified, because it always presents the nonexponentiated coefficients.

`nocnsreport`; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

irls requests iterated, reweighted least-squares (IRLS) optimization of the deviance instead of Newton–Raphson optimization of the log likelihood. This option is the default.

ml requests that optimization be carried out by using Stata's ml command; see [R] **ml**.

maximize_options: technique(*algorithm_spec*), [no]log, trace, gradient, showstep, hessian, showtolerance, difficult, iterate(#), tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization method to ml, with technique() set to something other than BHHH, changes the *vcetype* to vce(oim). Specifying technique(bhhh) changes *vcetype* to vce(opg).

fisher(#) specifies the number of Newton–Raphson steps that should use the Fisher scoring Hessian or EIM before switching to the observed information matrix (OIM). This option is available only if ml is specified and is useful only for Newton–Raphson optimization.

search specifies that the command search for good starting values. This option is available only if ml is specified and is useful only for Newton–Raphson optimization.

The following option is available with binreg but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

Wacholder (1986) suggests methods for estimating risk ratios and risk differences from prospective binomial data. These estimates are obtained by selecting the proper link functions in the generalized linear-model framework. (See *Methods and formulas* for details; also see [R] **glm**.)

▷ Example 1

Wacholder (1986) presents an example, using data from Wright et al. (1983), of an investigation of the relationship between alcohol consumption and the risk of a low-birthweight baby. Covariates examined included whether the mother smoked (yes or no), mother's social class (three levels), and drinking frequency (light, moderate, or heavy). The data for the 18 possible categories determined by the covariates are illustrated below.

Let's first describe the data and list a few observations.

```
. use http://www.stata-press.com/data/r12/binreg
. list
```

	cat	d	n	alc	smo	soc
1.	1	11	84	3	1	1
2.	2	5	79	2	1	1
3.	3	11	169	1	1	1
4.	4	6	28	3	2	1
5.	5	3	13	2	2	1
6.	6	1	26	1	2	1
7.	7	4	22	3	1	2
8.	8	3	25	2	1	2
9.	9	12	162	1	1	2
10.	10	4	17	3	2	2
11.	11	2	7	2	2	2
12.	12	6	38	1	2	2
13.	13	0	14	3	1	3
14.	14	1	18	2	1	3
15.	15	12	91	1	1	3
16.	16	7	19	3	2	3
17.	17	2	18	2	2	3
18.	18	8	70	1	2	3

Each observation corresponds to one of the 18 covariate structures. The number of low-birthweight babies from `n` in each category is given by the `d` variable.

We begin by estimating risk ratios:

```
. binreg d i.soc i.alc i.smo, n(n) rr
Iteration 1:   deviance =   14.2879
Iteration 2:   deviance =    13.607
Iteration 3:   deviance =  13.60503
Iteration 4:   deviance =  13.60503
Generalized linear models                         No. of obs      =         18
Optimization     : MQL Fisher scoring             Residual df     =         12
                   (IRLS EIM)                     Scale parameter =          1
Deviance         =   13.6050268                   (1/df) Deviance =   1.133752
Pearson          =  11.51517095                   (1/df) Pearson  =   .9595976
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(u/n)                 [Log]
                                                  BIC             = -21.07943
```

d	Risk Ratio	EIM Std. Err.	z	P>|z|	[95% Conf.	Interval]
soc						
2	1.340001	.3127382	1.25	0.210	.848098	2.11721
3	1.349487	.3291488	1.23	0.219	.8366715	2.176619
alc						
2	1.191157	.3265354	0.64	0.523	.6960276	2.038503
3	1.974078	.4261751	3.15	0.002	1.293011	3.013884
2.smo	1.648444	.332875	2.48	0.013	1.109657	2.448836
_cons	.0630341	.0128061	-13.61	0.000	.0423297	.0938656

By default, Stata reports the risk ratios (the exponentiated regression coefficients) estimated by the model. We can see that the risk ratio comparing heavy drinkers with light drinkers, after adjusting for smoking and social class, is 1.974078. That is, mothers who drink heavily during their pregnancy have approximately twice the risk of delivering low-birthweight babies as mothers who are light drinkers.

The nonexponentiated coefficients can be obtained with the `coefficients` option:

```
. binreg d i.soc i.alc i.smo, n(n) rr coefficients

Iteration 1:   deviance =   14.2879
Iteration 2:   deviance =    13.607
Iteration 3:   deviance =  13.60503
Iteration 4:   deviance =  13.60503

Generalized linear models                         No. of obs      =        18
Optimization     : MQL Fisher scoring             Residual df     =        12
                   (IRLS EIM)                     Scale parameter =         1
Deviance         =   13.6050268                   (1/df) Deviance =  1.133752
Pearson          =  11.51517095                   (1/df) Pearson  =  .9595976

Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(u/n)                 [Log]

                                                  BIC             = -21.07943
```

d	EIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
soc						
2	.2926702	.2333866	1.25	0.210	-.1647591	.7500994
3	.2997244	.2439066	1.23	0.219	-.1783238	.7777726
alc						
2	.1749248	.274133	0.64	0.523	-.362366	.7122156
3	.6801017	.2158856	3.15	0.002	.2569737	1.10323
2.smo	.4998317	.2019329	2.48	0.013	.1040505	.8956129
_cons	-2.764079	.2031606	-13.61	0.000	-3.162266	-2.365891

Risk differences are obtained with the `rd` option:

```
. binreg d i.soc i.alc i.smo, n(n) rd
Iteration 1:   deviance =  18.67277
Iteration 2:   deviance =  14.94364
Iteration 3:   deviance =   14.9185
Iteration 4:   deviance =  14.91762
Iteration 5:   deviance =  14.91758
Iteration 6:   deviance =  14.91758
Iteration 7:   deviance =  14.91758
Generalized linear models                         No. of obs      =         18
Optimization     : MQL Fisher scoring             Residual df     =         12
                   (IRLS EIM)                     Scale parameter =          1
Deviance         =  14.91758277                   (1/df) Deviance =  1.243132
Pearson          =  12.60353235                   (1/df) Pearson  =  1.050294
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = u/n                     [Identity]
                                                  BIC             = -19.76688
```

d	EIM Risk Diff.	EIM Std. Err.	z	P>|z|	[95% Conf.	Interval]
soc						
2	.0263817	.0232124	1.14	0.256	-.0191137	.0718771
3	.0365553	.0268668	1.36	0.174	-.0161026	.0892132
alc						
2	.0122539	.0257713	0.48	0.634	-.0382569	.0627647
3	.0801291	.0302878	2.65	0.008	.020766	.1394921
2.smo	.0542415	.0270838	2.00	0.045	.0011582	.1073248
_cons	.059028	.0160693	3.67	0.000	.0275327	.0905232

The risk difference between heavy drinkers and light drinkers is simply the value of the coefficient for `3.alc` $= 0.0801291$. Because the risk differences are obtained directly from the coefficients estimated by using the identity link, the `coefficients` option has no effect here.

Health ratios are obtained with the `hr` option. The health ratios (exponentiated coefficients for the log-complement link) are reported directly.

```
. binreg d i.soc i.alc i.smo, n(n) hr
Iteration 1:   deviance =  21.15233
Iteration 2:   deviance =  15.16467
Iteration 3:   deviance =  15.13205
Iteration 4:   deviance =  15.13114
Iteration 5:   deviance =  15.13111
Iteration 6:   deviance =  15.13111
Iteration 7:   deviance =  15.13111
Generalized linear models                         No. of obs      =         18
Optimization     : MQL Fisher scoring             Residual df     =         12
                   (IRLS EIM)                     Scale parameter =          1
Deviance         =  15.13110545                   (1/df) Deviance =   1.260925
Pearson          =  12.84203917                   (1/df) Pearson  =    1.07017
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(1-u/n)               [Log complement]
                                                  BIC             = -19.55336
```

d	HR	EIM Std. Err.	z	P>|z|	[95% Conf.	Interval]
soc						
2	.9720541	.024858	-1.11	0.268	.9245342	1.022017
3	.9597182	.0290412	-1.36	0.174	.9044535	1.01836
alc						
2	.9871517	.0278852	-0.46	0.647	.9339831	1.043347
3	.9134243	.0325726	-2.54	0.011	.8517631	.9795493
2.smo	.9409983	.0296125	-1.93	0.053	.8847125	1.000865
_cons	.9409945	.0163084	-3.51	0.000	.9095674	.9735075

(HR) Health ratios

To see the nonexponentiated coefficients, we can specify the `coefficients` option. ◁

Saved results

`binreg, irls` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_eq_model)`	number of equations in overall model test
`e(df_m)`	model degrees of freedom
`e(df)`	residual degrees of freedom
`e(phi)`	model scale parameter
`e(disp)`	dispersion parameter
`e(bic)`	model BIC
`e(N_clust)`	number of clusters
`e(deviance)`	deviance
`e(deviance_s)`	scaled deviance
`e(deviance_p)`	Pearson deviance
`e(deviance_ps)`	scaled Pearson deviance
`e(dispers)`	dispersion
`e(dispers_s)`	scaled dispersion
`e(dispers_p)`	Pearson dispersion
`e(dispers_ps)`	scaled Pearson dispersion
`e(vf)`	factor set by `vfactor()`, `1` if not set
`e(rank)`	rank of `e(V)`
`e(rc)`	return code

Macros

`e(cmd)`	`binreg`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(eform)`	`eform()` option implied by `or`, `rr`, `hr`, or `rd`
`e(varfunc)`	program to calculate variance function
`e(varfunct)`	variance title
`e(varfuncf)`	variance function
`e(link)`	program to calculate link function
`e(linkt)`	link title
`e(linkf)`	link function
`e(m)`	number of binomial trials
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title_fl)`	family–link title
`e(clustvar)`	name of cluster variable
`e(offset)`	linear offset variable
`e(cons)`	`noconstant` or not set
`e(hac_kernel)`	HAC kernel
`e(hac_lag)`	HAC lag
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(opt)`	type of optimization
`e(opt1)`	optimization title, line 1
`e(opt2)`	optimization title, line 2
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(marginsok)`	predictions allowed by `margins`
`e(marginsnotok)`	predictions disallowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

binreg, ml saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(df)	residual degrees of freedom
e(phi)	model scale parameter
e(aic)	model AIC, if ml
e(bic)	model BIC
e(ll)	log likelihood, if ml
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance of model test
e(deviance)	deviance
e(deviance_s)	scaled deviance
e(deviance_p)	Pearson deviance
e(deviance_ps)	scaled Pearson deviance
e(dispers)	dispersion
e(dispers_s)	scaled dispersion
e(dispers_p)	Pearson dispersion
e(dispers_ps)	scaled Pearson dispersion
e(vf)	factor set by vfactor(), 1 if not set
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	binreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(eform)	eform() option implied by or, rr, hr, or rd
e(varfunc)	program to calculate variance function
e(varfunct)	variance title
e(varfuncf)	variance function
e(link)	program to calculate link function
e(linkt)	link title
e(linkf)	link function
e(m)	number of binomial trials
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(title_fl)	family–link title
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(cons)	noconstant or not set
e(hac_kernel)	HAC kernel
e(hac_lag)	HAC lag
e(chi2type)	Wald; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(opt1)	optimization title, line 1
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

binreg is implemented as an ado-file.

Let π_i be the probability of success for the ith observation, $i = 1, \ldots, N$, and let $X\beta$ be the linear predictor. The link function relates the covariates of each observation to its respective probability through the linear predictor.

In logistic regression, the logit link is used:

$$\ln\left(\frac{\pi}{1-\pi}\right) = X\beta$$

The regression coefficient β_k represents the change in the logarithm of the odds associated with a one-unit change in the value of the X_k covariate; thus $\exp(\beta_k)$ is the ratio of the odds associated with a change of one unit in X_k.

For risk differences, the identity link $\pi = X\beta$ is used. The regression coefficient β_k represents the risk difference associated with a change of one unit in X_k. When using the identity link, you can obtain fitted probabilities outside the interval $(0, 1)$. As suggested by Wacholder, at each iteration, fitted probabilities are checked for range conditions (and put back in range if necessary). For example, if the identity link results in a fitted probability that is smaller than 1e–4, the probability is replaced with 1e–4 before the link function is calculated.

A similar adjustment is made for the logarithmic link, which is used for estimating the risk ratio, $\ln(\pi) = X\beta$, where $\exp(\beta_k)$ is the risk ratio associated with a change of one unit in X_k, and for the log-complement link used to estimate the probability of no disease or health, where $\exp(\beta_k)$ represents the "health ratio" associated with a change of one unit in X_k.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

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Also see

[R] **binreg postestimation** — Postestimation tools for binreg

[R] **glm** — Generalized linear models

[MI] **estimation** — Estimation commands for use with mi estimate

[U] **20 Estimation and postestimation commands**

Title

binreg postestimation — Postestimation tools for binreg

Description

The following postestimation commands are available after `binreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic options]
```

statistic	Description
Main	
`mu`	expected value of y; the default
`xb`	linear prediction $\eta = \mathbf{x}\widehat{\boldsymbol{\beta}}$
`eta`	synonym for `xb`
`stdp`	standard error of the linear prediction
`anscombe`	Anscombe (1953) residuals
`cooksd`	Cook's distance
`deviance`	deviance residuals
`hat`	diagonals of the "hat" matrix as an analog to simple linear regression
`likelihood`	weighted average of the standardized deviance and standard Pearson residuals
`pearson`	Pearson residuals
`response`	differences between the observed and fitted outcomes
`score`	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$
`working`	working residuals

options	Description
Options	
`nooffset`	modify calculations to ignore the offset variable
`adjusted`	adjust deviance residual to speed up convergence
`standardized`	multiply residual by the factor $(1-h)^{1/2}$
`studentized`	multiply residual by one over the square root of the estimated scale parameter
`modified`	modify denominator of residual to be a reasonable estimate of the variance of *depvar*

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`mu`, the default, specifies that `predict` calculate the expected value of y, equal to $g^{-1}(\mathbf{x}\widehat{\boldsymbol{\beta}})$ [$ng^{-1}(\mathbf{x}\widehat{\boldsymbol{\beta}})$ for the binomial family].

`xb` calculates the linear prediction $\eta = \mathbf{x}\widehat{\boldsymbol{\beta}}$.

`eta` is a synonym for `xb`.

`stdp` calculates the standard error of the linear prediction.

`anscombe` calculates the Anscombe (1953) residuals to produce residuals that closely follow a normal distribution.

`cooksd` calculates Cook's distance, which measures the aggregate change in the estimated coefficients when each observation is left out of the estimation.

`deviance` calculates the deviance residuals, which are recommended by McCullagh and Nelder (1989) and others as having the best properties for examining goodness of fit of a GLM. They are approximately normally distributed if the model is correct and may be plotted against the fitted values or against a covariate to inspect the model's fit. Also see the `pearson` option below.

`hat` calculates the diagonals of the "hat" matrix as an analog to simple linear regression.

`likelihood` calculates a weighted average of the standardized deviance and standardized Pearson (described below) residuals.

`pearson` calculates the Pearson residuals, which often have markedly skewed distributions for nonnormal family distributions. Also see the `deviance` option above.

`response` calculates the differences between the observed and fitted outcomes.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

`working` calculates the working residuals, which are response residuals weighted according to the derivative of the link function.

Options

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `binreg`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`adjusted` adjusts the deviance residual to make the convergence to the limiting normal distribution faster. The adjustment deals with adding to the deviance residual a higher-order term depending on the variance function family. This option is allowed only when `deviance` is specified.

`standardized` requests that the residual be multiplied by the factor $(1 - h)^{-1/2}$, where h is the diagonal of the hat matrix. This step is done to take into account the correlation between *depvar* and its predicted value.

`studentized` requests that the residual be multiplied by one over the square root of the estimated scale parameter.

`modified` requests that the denominator of the residual be modified to be a reasonable estimate of the variance of *depvar*. The base residual is multiplied by the factor $(k/w)^{-1/2}$, where k is either one or the user-specified dispersion parameter and w is the specified weight (or one if left unspecified).

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

References

Anscombe, F. J. 1953. Contribution of discussion paper by H. Hotelling "New light on the correlation coefficient and its transforms". *Journal of the Royal Statistical Society, Series B* 15: 229–230.

McCullagh, P., and J. A. Nelder. 1989. *Generalized Linear Models*. 2nd ed. London: Chapman & Hall/CRC.

Also see

[R] **binreg** — Generalized linear models: Extensions to the binomial family

[U] **20 Estimation and postestimation commands**

Title

biprobit — Bivariate probit regression

Syntax

Bivariate probit regression

```
biprobit depvar1 depvar2 [indepvars] [if] [in] [weight] [, options]
```

Seemingly unrelated bivariate probit regression

```
biprobit equation1 equation2 [if] [in] [weight] [, su_options]
```

where *equation*$_1$ and *equation*$_2$ are specified as

```
( [eqname:] depvar [=] [indepvars] [ , noconstant offset(varname) ] )
```

options	Description
Model	
noconstant	suppress constant term
partial	fit partial observability model
offset1(*varname*)	offset variable for first equation
offset2(*varname*)	offset variable for second equation
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
noskip	perform likelihood-ratio test
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

su_options	Description
Model	
partial	fit partial observability model
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
noskip	perform likelihood-ratio test
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar$_1$, *depvar*$_2$, *indepvars*, and *depvar* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
bootstrap, by, jackknife, rolling, statsby, and svy are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
vce(), noskip, and weights are not allowed with the svy prefix; see [SVY] **svy**.
pweights, fweights, and iweights are allowed; see [U] **11.1.6 weight**.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

biprobit

Statistics > Binary outcomes > Bivariate probit regression

seemingly unrelated biprobit

Statistics > Binary outcomes > Seemingly unrelated bivariate probit regression

Description

biprobit fits maximum-likelihood two-equation probit models—either a bivariate probit or a seemingly unrelated probit (limited to two equations).

Options

Model

`noconstant`; see [R] **estimation options**.

`partial` specifies that the partial observability model be fit. This particular model commonly has poor convergence properties, so we recommend that you use the `difficult` option if you want to fit the Poirier partial observability model; see [R] **maximize**.

This model computes the product of the two dependent variables so that you do not have to replace each with the product.

`offset1(`*varname*`)`, `offset2(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`noskip` specifies that a full maximum-likelihood model with only a constant for the regression equation be fit. This model is not displayed but is used as the base model to compute a likelihood-ratio test for the model test statistic displayed in the estimation header. By default, the overall model test statistic is an asymptotically equivalent Wald test of all the parameters in the regression equation being zero (except the constant). For many models, this option can substantially increase estimation time.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `biprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

For a good introduction to the bivariate probit models, see Greene (2012, 738–752) and Pindyck and Rubinfeld (1998). Poirier (1980) explains the partial observability model. Van de Ven and Van Pragg (1981) explain the probit model with sample selection; see [R] **heckprob** for details.

▷ Example 1

We use the data from Pindyck and Rubinfeld (1998, 332). In this dataset, the variables are whether children attend private school (`private`), number of years the family has been at the present residence (`years`), log of property tax (`logptax`), log of income (`loginc`), and whether the head of the household voted for an increase in property taxes (`vote`).

We wish to model the bivariate outcomes of whether children attend private school and whether the head of the household voted for an increase in property tax based on the other covariates.

```
. use http://www.stata-press.com/data/r12/school
. biprobit private vote years logptax loginc
Fitting comparison equation 1:
Iteration 0:   log likelihood = -31.967097
Iteration 1:   log likelihood = -31.452424
Iteration 2:   log likelihood = -31.448958
Iteration 3:   log likelihood = -31.448958
Fitting comparison equation 2:
Iteration 0:   log likelihood = -63.036914
Iteration 1:   log likelihood = -58.534843
Iteration 2:   log likelihood = -58.497292
Iteration 3:   log likelihood = -58.497288
Comparison:    log likelihood = -89.946246
Fitting full model:
Iteration 0:   log likelihood = -89.946246
Iteration 1:   log likelihood = -89.258897
Iteration 2:   log likelihood = -89.254028
Iteration 3:   log likelihood = -89.254028
Bivariate probit regression                     Number of obs   =         95
                                                Wald chi2(6)    =       9.59
Log likelihood = -89.254028                     Prob > chi2     =     0.1431
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
private						
years	-.0118884	.0256778	-0.46	0.643	-.0622159	.0384391
logptax	-.1066962	.6669782	-0.16	0.873	-1.413949	1.200557
loginc	.3762037	.5306484	0.71	0.478	-.663848	1.416255
_cons	-4.184694	4.837817	-0.86	0.387	-13.66664	5.297253
vote						
years	-.0168561	.0147834	-1.14	0.254	-.0458309	.0121188
logptax	-1.288707	.5752266	-2.24	0.025	-2.416131	-.1612839
loginc	.998286	.4403565	2.27	0.023	.1352031	1.861369
_cons	-.5360573	4.068509	-0.13	0.895	-8.510188	7.438073
/athrho	-.2764525	.2412099	-1.15	0.252	-.7492153	.1963102
rho	-.2696186	.2236753			-.6346806	.1938267

```
Likelihood-ratio test of rho=0:     chi2(1) =  1.38444    Prob > chi2 = 0.2393
```

The output shows several iteration logs. The first iteration log corresponds to running the univariate probit model for the first equation, and the second log corresponds to running the univariate probit for the second model. If $\rho = 0$, the sum of the log likelihoods from these two models will equal the log likelihood of the bivariate probit model; this sum is printed in the iteration log as the comparison log likelihood.

The final iteration log is for fitting the full bivariate probit model. A likelihood-ratio test of the log likelihood for this model and the comparison log likelihood is presented at the end of the output. If we had specified the `vce(robust)` option, this test would be presented as a Wald test instead of as a likelihood-ratio test.

We could have fit the same model by using the seemingly unrelated syntax as

```
. biprobit (private=years logptax loginc) (vote=years logptax loginc)
```

◁

Saved results

`biprobit` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_aux)`	number of auxiliary parameters
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model (`noskip` only)
`e(ll_c)`	log likelihood, comparison model
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(chi2_c)`	χ^2 for comparison test
`e(p)`	significance
`e(rho)`	ρ
`e(rank)`	rank of `e(V)`
`e(rank0)`	rank of `e(V)` for constant-only model
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

`e(cmd)`	`biprobit`
`e(cmdline)`	command as typed
`e(depvar)`	names of dependent variables
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(clustvar)`	name of cluster variable
`e(offset1)`	offset for first equation
`e(offset2)`	offset for second equation
`e(chi2type)`	`Wald` or `LR`; type of model χ^2 test
`e(chi2_ct)`	`Wald` or `LR`; type of model χ^2 test corresponding to `e(chi2_c)`
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(opt)`	type of optimization
`e(which)`	`max` or `min`; whether optimizer is to perform maximization or minimization
`e(ml_method)`	type of `ml` method
`e(user)`	name of likelihood-evaluator program
`e(technique)`	maximization technique
`e(properties)`	`b V`
`d(predict)`	program used to implement `predict`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

biprobit is implemented as an ado-file.

The log likelihood, $\ln L$, is given by

$$\begin{aligned}
\xi_j^{\beta} &= x_j\beta + \text{offset}_j^{\beta} \\
\xi_j^{\gamma} &= z_j\gamma + \text{offset}_j^{\gamma} \\
q_{1j} &= \begin{cases} 1 & \text{if } y_{1j} \neq 0 \\ -1 & \text{otherwise} \end{cases} \\
q_{2j} &= \begin{cases} 1 & \text{if } y_{2j} \neq 0 \\ -1 & \text{otherwise} \end{cases} \\
\rho_j^{*} &= q_{1j}q_{2j}\rho \\
\ln L &= \sum_{j=1}^{n} w_j \ln\Phi_2\left(q_{1j}\xi_j^{\beta}, q_{2j}\xi_j^{\gamma}, \rho_j^{*}\right)
\end{aligned}$$

where $\Phi_2()$ is the cumulative bivariate normal distribution function (with mean $[\,0\ \ 0\,]'$) and w_j is an optional weight for observation j. This derivation assumes that

$$\begin{aligned}
y_{1j}^{*} &= x_j\beta + \epsilon_{1j} + \text{offset}_j^{\beta} \\
y_{2j}^{*} &= z_j\gamma + \epsilon_{2j} + \text{offset}_j^{\gamma} \\
E(\epsilon_1) &= E(\epsilon_2) = 0 \\
\text{Var}(\epsilon_1) &= \text{Var}(\epsilon_2) = 1 \\
\text{Cov}(\epsilon_1, \epsilon_2) &= \rho
\end{aligned}$$

where y_{1j}^{*} and y_{2j}^{*} are the unobserved latent variables; instead, we observe only $y_{ij} = 1$ if $y_{ij}^{*} > 0$ and $y_{ij} = 0$ otherwise (for $i = 1, 2$).

In the maximum likelihood estimation, ρ is not directly estimated, but atanh ρ is

$$\text{atanh}\,\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

From the form of the likelihood, if $\rho = 0$, then the log likelihood for the bivariate probit models is equal to the sum of the log likelihoods of the two univariate probit models. A likelihood-ratio test may therefore be performed by comparing the likelihood of the full bivariate model with the sum of the log likelihoods for the univariate probit models.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`biprobit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

De Luca, G. 2008. SNP and SML estimation of univariate and bivariate binary-choice models. *Stata Journal* 8: 190–220.

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

Hardin, J. W. 1996. sg61: Bivariate probit models. *Stata Technical Bulletin* 33: 15–20. Reprinted in *Stata Technical Bulletin Reprints*, vol. 6, pp. 152–158. College Station, TX: Stata Press.

Heckman, J. 1979. Sample selection bias as a specification error. *Econometrica* 47: 153–161.

Pindyck, R. S., and D. L. Rubinfeld. 1998. *Econometric Models and Economic Forecasts*. 4th ed. New York: McGraw–Hill.

Poirier, D. J. 1980. Partial observability in bivariate probit models. *Journal of Econometrics* 12: 209–217.

Van de Ven, W. P. M. M., and B. M. S. Van Pragg. 1981. The demand for deductibles in private health insurance: A probit model with sample selection. *Journal of Econometrics* 17: 229–252.

Also see

[R] **biprobit postestimation** — Postestimation tools for biprobit

[R] **mprobit** — Multinomial probit regression

[R] **probit** — Probit regression

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

biprobit postestimation — Postestimation tools for biprobit

Description

The following postestimation commands are available after `biprobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_eq1 newvar_eq2 newvar_athrho} [if] [in], scores
```

statistic	Description
Main	
p11	$\Phi_2(\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, \rho)$, predicted probability $\Pr(y_{1j}=1, y_{2j}=1)$; the default
p10	$\Phi_2(\mathbf{x}_j\mathbf{b}, -\mathbf{z}_j\mathbf{g}, -\rho)$, predicted probability $\Pr(y_{1j}=1, y_{2j}=0)$
p01	$\Phi_2(-\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, -\rho)$, predicted probability $\Pr(y_{1j}=0, y_{2j}=1)$
p00	$\Phi_2(-\mathbf{x}_j\mathbf{b}, -\mathbf{z}_j\mathbf{g}, \rho)$, predicted probability $\Pr(y_{1j}=0, y_{2j}=0)$
pmarg1	$\Phi(\mathbf{x}_j\mathbf{b})$, marginal success probability for equation 1
pmarg2	$\Phi(\mathbf{z}_j\mathbf{g})$, marginal success probability for equation 2
pcond1	$\Phi_2(\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, \rho)/\Phi(\mathbf{z}_j\mathbf{g})$, conditional probability of success for equation 1
pcond2	$\Phi_2(\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, \rho)/\Phi(\mathbf{x}_j\mathbf{b})$, conditional probability of success for equation 2
xb1	$\mathbf{x}_j\mathbf{b}$, linear prediction for equation 1
xb2	$\mathbf{z}_j\mathbf{g}$, linear prediction for equation 2
stdp1	standard error of the linear prediction for equation 1
stdp2	standard error of the linear prediction for equation 2

where $\Phi()$ is the standard normal-distribution function and $\Phi_2()$ is the bivariate standard normal-distribution function.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

p11, the default, calculates the bivariate predicted probability $\Pr(y_{1j}=1, y_{2j}=1)$.

p10 calculates the bivariate predicted probability $\Pr(y_{1j}=1, y_{2j}=0)$.

p01 calculates the bivariate predicted probability $\Pr(y_{1j}=0, y_{2j}=1)$.

p00 calculates the bivariate predicted probability $\Pr(y_{1j}=0, y_{2j}=0)$.

pmarg1 calculates the univariate (marginal) predicted probability of success $\Pr(y_{1j}=1)$.

pmarg2 calculates the univariate (marginal) predicted probability of success $\Pr(y_{2j}=1)$.

pcond1 calculates the conditional (on success in equation 2) predicted probability of success $\Pr(y_{1j}=1, y_{2j}=1)/\Pr(y_{2j}=1)$.

pcond2 calculates the conditional (on success in equation 1) predicted probability of success $\Pr(y_{1j}=1, y_{2j}=1)/\Pr(y_{1j}=1)$.

`xb1` calculates the probit linear prediction $\mathbf{x}_j\mathbf{b}$.

`xb2` calculates the probit linear prediction $\mathbf{z}_j\mathbf{g}$.

`stdp1` calculates the standard error of the linear prediction for equation 1.

`stdp2` calculates the standard error of the linear prediction for equation 2.

`nooffset` is relevant only if you specified `offset1(`*varname*`)` or `offset2(`*varname*`)` for `biprobit`. It modifies the calculations made by `predict` so that they ignore the offset variables; the linear predictions are treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_{1\text{j}}$ and $\mathbf{z}_j\boldsymbol{\gamma}$ rather than as $\mathbf{z}_j\boldsymbol{\gamma} + \text{offset}_{2\text{j}}$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\mathbf{z}_j\boldsymbol{\gamma})$.

The third new variable will contain $\partial \ln L/\partial(\text{atanh}\,\rho)$.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **biprobit** — Bivariate probit regression

[U] **20 Estimation and postestimation commands**

Title

bitest — Binomial probability test

Syntax

Binomial probability test

`bitest` *varname*`==` $\#_p$ [*if*] [*in*] [*weight*] [`,` `detail`]

Immediate form of binomial probability test

`bitesti` $\#_N$ $\#_{\text{succ}}$ $\#_p$ [`,` `detail`]

`by` is allowed with `bitest`; see [D] **by**.
`fweights` are allowed with `bitest`; see [U] **11.1.6 weight**.

Menu

bitest

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Binomial probability test

bitesti

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Binomial probability test calculator

Description

`bitest` performs exact hypothesis tests for binomial random variables. The null hypothesis is that the probability of a success on a trial is $\#_p$. The total number of trials is the number of nonmissing values of *varname* (in `bitest`) or $\#_N$ (in `bitesti`). The number of observed successes is the number of 1s in *varname* (in `bitest`) or $\#_{\text{succ}}$ (in `bitesti`). *varname* must contain only 0s, 1s, and missing.

`bitesti` is the immediate form of `bitest`; see [U] **19 Immediate commands** for a general introduction to immediate commands.

Option

Advanced

`detail` shows the probability of the observed number of successes, k_{obs}; the probability of the number of successes on the opposite tail of the distribution that is used to compute the two-sided p-value, k_{opp}; and the probability of the point next to k_{opp}. This information can be safely ignored. See the technical note below for details.

Remarks

Remarks are presented under the following headings:

bitest
bitesti

bitest

▷ Example 1

We test 15 university students for high levels of one measure of visual quickness which, from other evidence, we believe is present in 30% of the nonuniversity population. Included in our data is `quick`, taking on the values 1 ("success") or 0 ("failure") depending on the outcome of the test.

```
. use http://www.stata-press.com/data/r12/quick
. bitest quick == 0.3
```

Variable	N	Observed k	Expected k	Assumed p	Observed p
quick	15	7	4.5	0.30000	0.46667

```
Pr(k >= 7)            = 0.131143  (one-sided test)
Pr(k <= 7)            = 0.949987  (one-sided test)
Pr(k <= 1 or k >= 7) = 0.166410  (two-sided test)
```

The first part of the output reveals that, assuming a true probability of success of 0.3, the expected number of successes is 4.5 and that we observed seven. Said differently, the assumed frequency under the null hypothesis H_0 is 0.3, and the observed frequency is 0.47.

The first line under the table is a one-sided test; it is the probability of observing seven or more successes conditional on $p = 0.3$. It is a test of $H_0: p = 0.3$ versus the alternative hypothesis $H_A: p > 0.3$. Said in English, the alternative hypothesis is that more than 30% of university students score at high levels on this test of visual quickness. The p-value for this hypothesis test is 0.13.

The second line under the table is a one-sided test of H_0 versus the opposite alternative hypothesis $H_A: p < 0.3$.

The third line is the two-sided test. It is a test of H_0 versus the alternative hypothesis $H_A: p \neq 0.3$.

◁

❑ Technical note

The p-value of a hypothesis test is the probability (calculated assuming H_0 is true) of observing any outcome as extreme or more extreme than the observed outcome, with extreme meaning in the direction of the alternative hypothesis. In example 1, the outcomes $k = 8, 9, \ldots, 15$ are clearly "more extreme" than the observed outcome $k_{obs} = 7$ when considering the alternative hypothesis $H_A: p \neq 0.3$. However, outcomes with only a few successes are also in the direction of this alternative hypothesis. For two-sided hypotheses, outcomes with k successes are considered "as extreme or more extreme" than the observed outcome k_{obs} if $\Pr(k) \leq \Pr(k_{obs})$. Here $\Pr(k = 0)$ and $\Pr(k = 1)$ are both less than $\Pr(k = 7)$, so they are included in the two-sided p-value.

The `detail` option allows you to see the probability (assuming that H_0 is true) of the observed successes ($k = 7$) and the probability of the boundary point ($k = 1$) of the opposite tail used for the two-sided p-value.

```
. bitest quick == 0.3, detail
    Variable |        N   Observed k   Expected k   Assumed p   Observed p
-------------+--------------------------------------------------------------
       quick |       15           7          4.5     0.30000      0.46667

  Pr(k >= 7)            = 0.131143  (one-sided test)
  Pr(k <= 7)            = 0.949987  (one-sided test)
  Pr(k <= 1 or k >= 7) = 0.166410  (two-sided test)

  Pr(k == 7)            = 0.081130  (observed)
  Pr(k == 2)            = 0.091560
  Pr(k == 1)            = 0.030520  (opposite extreme)
```

Also shown is the probability of the point next to the boundary point. This probability, namely, $\Pr(k = 2) = 0.092$, is certainly close to the probability of the observed outcome $\Pr(k = 7) = 0.081$, so some people might argue that $k = 2$ should be included in the two-sided p-value. Statisticians (at least some we know) would reply that the p-value is a precisely defined concept and that this is an arbitrary "fuzzification" of its definition. When you compute exact p-values according to the precise definition of a p-value, your type I error is never more than what you say it is—so no one can criticize you for being anticonservative. Including the point $k = 2$ is being overly conservative because it makes the p-value larger yet. But it is your choice; being overly conservative, at least in statistics, is always safe. Know that `bitest` and `bitesti` always keep to the precise definition of a p-value, so if you wish to include this extra point, you must do so by hand or by using the `r()` saved results; see *Saved results* below.

❑

bitesti

▷ Example 2

The binomial test is a function of two statistics and one parameter: N, the number of observations; k_{obs}, the number of observed successes; and p, the assumed probability of a success on a trial. For instance, in a city of $N = 2{,}500{,}000$, we observe $k_{\text{obs}} = 36$ cases of a particular disease when the population rate for the disease is $p = 0.00001$.

```
. bitesti 2500000 36 .00001
        N   Observed k   Expected k   Assumed p   Observed p
------------------------------------------------------------
  2500000          36           25     0.00001      0.00001

  Pr(k >= 36)            = 0.022458  (one-sided test)
  Pr(k <= 36)            = 0.985448  (one-sided test)
  Pr(k <= 14 or k >= 36) = 0.034859  (two-sided test)
```

◁

▷ Example 3

Boice and Monson (1977) present data on breast cancer cases and person-years of observations for women with tuberculosis who were repeatedly exposed to multiple x-ray fluoroscopies and for women with tuberculosis who were not. The data are

	Exposed	Not exposed	Total
Breast cancer	41	15	56
Person-years	28,010	19,017	47,027

We can thus test whether x-ray fluoroscopic examinations are associated with breast cancer; the assumed rate of exposure is $p = 28010/47027$.

```
. bitesti 56 41 28010/47027
        N   Observed k   Expected k   Assumed p   Observed p
------------------------------------------------------------
       56          41     33.35446       0.59562      0.73214

  Pr(k >= 41)            = 0.023830  (one-sided test)
  Pr(k <= 41)            = 0.988373  (one-sided test)
  Pr(k <= 25 or k >= 41) = 0.040852  (two-sided test)
```

◁

Saved results

`bitest` and `bitesti` save the following in `r()`:

Scalars

`r(N)`	number N of trials	`r(k_opp)`	opposite extreme k
`r(P_p)`	assumed probability p of success	`r(P_k)`	probability of observed k (`detail` only)
`r(k)`	observed number k of successes	`r(P_oppk)`	probability of opposite extreme k (`detail` only)
`r(p_l)`	lower one-sided p-value	`r(k_nopp)`	k next to opposite extreme (`detail` only)
`r(p_u)`	upper one-sided p-value	`r(P_noppk)`	probability of k next to opposite extreme (`detail` only)
`r(p)`	two-sided p-value		

Methods and formulas

`bitest` and `bitesti` are implemented as ado-files.

Let N, k_{obs}, and p be, respectively, the number of observations, the observed number of successes, and the assumed probability of success on a trial. The expected number of successes is Np, and the observed probability of success on a trial is k_{obs}/N.

`bitest` and `bitesti` compute exact p-values based on the binomial distribution. The upper one-sided p-value is

$$\Pr(k \geq k_{\text{obs}}) = \sum_{m=k_{\text{obs}}}^{N} \binom{N}{m} p^m (1-p)^{N-m}$$

The lower one-sided p-value is

$$\Pr(k \leq k_{\text{obs}}) = \sum_{m=0}^{k_{\text{obs}}} \binom{N}{m} p^m (1-p)^{N-m}$$

If $k_{\text{obs}} \geq Np$, the two-sided p-value is

$$\Pr(k \leq k_{\text{opp}} \text{ or } k \geq k_{\text{obs}})$$

where k_{opp} is the largest number $\leq Np$ such that $\Pr(k = k_{\text{opp}}) \leq \Pr(k = k_{\text{obs}})$. If $k_{\text{obs}} < Np$, the two-sided p-value is

$$\Pr(k \leq k_{\text{obs}} \text{ or } k \geq k_{\text{opp}})$$

where k_{opp} is the smallest number $\geq Np$ such that $\Pr(k = k_{\text{opp}}) \leq \Pr(k = k_{\text{obs}})$.

References

Boice, J. D., Jr., and R. R. Monson. 1977. Breast cancer in women after repeated fluoroscopic examinations of the chest. *Journal of the National Cancer Institute* 59: 823–832.

Hoel, P. G. 1984. *Introduction to Mathematical Statistics*. 5th ed. New York: Wiley.

Also see

[R] **ci** — Confidence intervals for means, proportions, and counts

[R] **prtest** — One- and two-sample tests of proportions

Title

bootstrap — Bootstrap sampling and estimation

Syntax

`bootstrap` *exp_list* [, *options eform_option*] : *command*

options	Description
Main	
`reps(#)`	perform # bootstrap replications; default is `reps(50)`
Options	
`strata(`*varlist*`)`	variables identifying strata
`size(#)`	draw samples of size #; default is `_N`
`cluster(`*varlist*`)`	variables identifying resampling clusters
`idcluster(`*newvar*`)`	create new cluster ID variable
`saving(`*filename*`, ...)`	save results to *filename*; save statistics in double precision; save results to *filename* every # replications
`bca`	compute acceleration for BC_a confidence intervals
`mse`	use MSE formula for variance estimation
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`notable`	suppress table of results
`noheader`	suppress table header
`nolegend`	suppress table legend
`verbose`	display the full table legend
`nodots`	suppress replication dots
`noisily`	display any output from *command*
`trace`	trace *command*
`title(`*text*`)`	use *text* as title for bootstrap results
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
eform_option	display coefficient table in exponentiated form
Advanced	
`nodrop`	do not drop observations
`nowarn`	do not warn when `e(sample)` is not set
`force`	do not check for *weights* or `svy` commands; seldom used
`reject(`*exp*`)`	identify invalid results
`seed(#)`	set random-number seed to #
`group(`*varname*`)`	ID variable for groups within `cluster()`
`jackknifeopts(`*jkopts*`)`	options for `jackknife`; see [R] **jackknife**
`coeflegend`	display legend instead of statistics

weights are not allowed in *command*.

`group()`, `jackknifeopts()`, and `coeflegend` do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

exp_list contains	(*name*: *elist*)
	elist
	eexp
elist contains	*newvar* = (*exp*)
	(*exp*)
eexp is	*specname*
	[*eqno*]*specname*
specname is	_b
	_b[]
	_se
	_se[]
eqno is	##
	name

exp is a standard Stata expression; see [U] **13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

Menu

Statistics > Resampling > Bootstrap estimation

Description

`bootstrap` performs bootstrap estimation. Typing

```
. bootstrap exp_list, reps(#): command
```

executes *command* multiple times, bootstrapping the statistics in *exp_list* by resampling observations (with replacement) from the data in memory # times. This method is commonly referred to as the nonparametric bootstrap.

command defines the statistical command to be executed. Most Stata commands and user-written programs can be used with `bootstrap`, as long as they follow standard Stata syntax; see [U] **11 Language syntax**. If the `bca` option is supplied, *command* must also work with `jackknife`; see [R] **jackknife**. The `by` prefix may not be part of *command*.

exp_list specifies the statistics to be collected from the execution of *command*. If *command* changes the contents in `e(b)`, *exp_list* is optional and defaults to `_b`.

Because bootstrapping is a random process, if you want to be able to reproduce results, set the random-number seed by specifying the `seed(#)` option or by typing

```
. set seed #
```

where # is a seed of your choosing, before running `bootstrap`; see [R] **set seed**.

Many estimation commands allow the vce(bootstrap) option. For those commands, we recommend using vce(bootstrap) over bootstrap because the estimation command already handles clustering and other model-specific details for you. The bootstrap prefix command is intended for use with nonestimation commands, such as summarize, user-written commands, or functions of coefficients.

bs and bstrap are synonyms for bootstrap.

Options

Main

reps(#) specifies the number of bootstrap replications to be performed. The default is 50. A total of 50–200 replications are generally adequate for estimates of standard error and thus are adequate for normal-approximation confidence intervals; see Mooney and Duval (1993, 11). Estimates of confidence intervals using the percentile or bias-corrected methods typically require 1,000 or more replications.

Options

strata(*varlist*) specifies the variables that identify strata. If this option is specified, bootstrap samples are taken independently within each stratum.

size(#) specifies the size of the samples to be drawn. The default is _N, meaning to draw samples of the same size as the data. If specified, # must be less than or equal to the number of observations within strata().

If cluster() is specified, the default size is the number of clusters in the original dataset. For unbalanced clusters, resulting sample sizes will differ from replication to replication. For cluster sampling, # must be less than or equal to the number of clusters within strata().

cluster(*varlist*) specifies the variables that identify resampling clusters. If this option is specified, the sample drawn during each replication is a bootstrap sample of clusters.

idcluster(*newvar*) creates a new variable containing a unique identifier for each resampled cluster. This option requires that cluster() also be specified.

saving(*filename* [, *suboptions*]) creates a Stata data file (.dta file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

double specifies that the results for each replication be stored as doubles, meaning 8-byte reals. By default, they are stored as floats, meaning 4-byte reals. This option may be used without the saving() option to compute the variance estimates by using double precision.

every(#) specifies that results be written to disk every #th replication. every() should be specified only in conjunction with saving() when *command* takes a long time for each replication. This option will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

replace specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

bca specifies that bootstrap estimate the acceleration of each statistic in *exp_list*. This estimate is used to construct BC_a confidence intervals. Type estat bootstrap, bca to display the BC_a confidence interval generated by the bootstrap command.

mse specifies that bootstrap compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, bootstrap computes the variance by using deviations from the average of the replicates.

Reporting

`level(#)`; see [R] **estimation options**.

`notable` suppresses the display of the table of results.

`noheader` suppresses the display of the table header. This option implies `nolegend`. This option may also be specified when replaying estimation results.

`nolegend` suppresses the display of the table legend. This option may also be specified when replaying estimation results.

`verbose` specifies that the full table legend be displayed. By default, coefficients and standard errors are not displayed. This option may also be specified when replaying estimation results.

`nodots` suppresses display of the replication dots. By default, one dot character is displayed for each successful replication. A red 'x' is displayed if *command* returns an error or if one of the values in *exp_list* is missing.

`noisily` specifies that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`title(`*text*`)` specifies a title to be displayed above the table of bootstrap results. The default title is the title saved in `e(title)` by an estimation command, or if `e(title)` is not filled in, `Bootstrap results` is used. `title()` may also be specified when replaying estimation results.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

eform_option causes the coefficient table to be displayed in exponentiated form; see [R] ***eform_option***.

command determines which of the following are allowed (`eform(`*string*`)` and `eform` are always allowed):

eform_option	Description
`eform(`*string*`)`	use *string* for the column title
`eform`	exponentiated coefficient, *string* is `exp(b)`
`hr`	hazard ratio, *string* is `Haz. Ratio`
`shr`	subhazard ratio, *string* is `SHR`
`irr`	incidence-rate ratio, *string* is `IRR`
`or`	odds ratio, *string* is `Odds Ratio`
`rrr`	relative-risk ratio, *string* is `RRR`

Advanced

`nodrop` prevents observations outside `e(sample)` and the `if` and `in` qualifiers from being dropped before the data are resampled.

`nowarn` suppresses the display of a warning message when *command* does not set `e(sample)`.

`force` suppresses the restriction that *command* not specify weights or be a `svy` command. This is a rarely used option. Use it only if you know what you are doing.

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

`seed(#)` sets the random-number seed. Specifying this option is equivalent to typing the following command prior to calling `bootstrap`:

```
. set seed #
```

The following options are available with `bootstrap` but are not shown in the dialog box:

`group(`*varname*`)` re-creates *varname* containing a unique identifier for each group across the resampled clusters. This option requires that `idcluster()` also be specified.

This option is useful for maintaining unique group identifiers when sampling clusters with replacement. Suppose that cluster 1 contains 3 groups. If the `idcluster(newclid)` option is specified and cluster 1 is sampled multiple times, `newclid` uniquely identifies each copy of cluster 1. If `group(newgroupid)` is also specified, `newgroupid` uniquely identifies each copy of each group.

`jackknifeopts(`*jkopts*`)` identifies options that are to be passed to `jackknife` when it computes the acceleration values for the BC$_a$ confidence intervals; see [R] **jackknife**. This option requires the `bca` option and is mostly used for passing the `eclass`, `rclass`, or `n(#)` option to `jackknife`.

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Regression coefficients
Expressions
Combining bootstrap datasets
A note about macros
Achieved significance level
Bootstrapping a ratio
Warning messages and e(sample)
Bootstrapping statistics from data with a complex structure

Introduction

With few assumptions, bootstrapping provides a way of estimating standard errors and other measures of statistical precision (Efron 1979; Efron and Stein 1981; Efron 1982; Efron and Tibshirani 1986; Efron and Tibshirani 1993; also see Davison and Hinkley [1997]; Guan [2003]; Mooney and Duval [1993]; Poi [2004]; and Stine [1990]). It provides a way to obtain such measures when no formula is otherwise available or when available formulas make inappropriate assumptions. Cameron and Trivedi (2010, chap. 13) discuss many bootstrapping topics and demonstrate how to do them in Stata.

To illustrate bootstrapping, suppose that you have a dataset containing N observations and an estimator that, when applied to the data, produces certain statistics. You draw, with replacement, N observations from the N-observation dataset. In this random drawing, some of the original observations will appear once, some more than once, and some not at all. Using the resampled dataset, you apply

the estimator and collect the statistics. This process is repeated many times; each time, a new random sample is drawn and the statistics are recalculated.

This process builds a dataset of replicated statistics. From these data, you can calculate the standard error by using the standard formula for the sample standard deviation

$$\widehat{\text{se}} = \left\{ \frac{1}{k-1} \sum (\widehat{\theta}_i - \overline{\theta})^2 \right\}^{1/2}$$

where $\widehat{\theta}_i$ is the statistic calculated using the ith bootstrap sample and k is the number of replications. This formula gives an estimate of the standard error of the statistic, according to Hall and Wilson (1991). Although the average, $\overline{\theta}$, of the bootstrapped estimates is used in calculating the standard deviation, it is not used as the estimated value of the statistic itself. Instead, the original observed value of the statistic, $\widehat{\theta}$, is used, meaning the value of the statistic computed using the original N observations.

You might think that $\overline{\theta}$ is a better estimate of the parameter than $\widehat{\theta}$, but it is not. If the statistic is biased, bootstrapping exaggerates the bias. In fact, the bias can be estimated as $\overline{\theta} - \widehat{\theta}$ (Efron 1982, 33). Knowing this, you might be tempted to subtract this estimate of bias from $\widehat{\theta}$ to produce an unbiased statistic. The bootstrap bias estimate has an indeterminate amount of random error, so this unbiased estimator may have greater mean squared error than the biased estimator (Mooney and Duval 1993; Hinkley 1978). Thus $\widehat{\theta}$ is the best point estimate of the statistic.

The logic behind the bootstrap is that all measures of precision come from a statistic's sampling distribution. When the statistic is estimated on a sample of size N from some population, the sampling distribution tells you the relative frequencies of the values of the statistic. The sampling distribution, in turn, is determined by the distribution of the population and the formula used to estimate the statistic.

Sometimes the sampling distribution can be derived analytically. For instance, if the underlying population is distributed normally and you calculate means, the sampling distribution for the mean is also normal but has a smaller variance than that of the population. In other cases, deriving the sampling distribution is difficult, as when means are calculated from nonnormal populations. Sometimes, as in the case of means, it is not too difficult to derive the sampling distribution as the sample size goes to infinity ($N \rightarrow \infty$). However, such asymptotic distributions may not perform well when applied to finite samples.

If you knew the population distribution, you could obtain the sampling distribution by simulation: you could draw random samples of size N, calculate the statistic, and make a tally. Bootstrapping does precisely this, but it uses the observed distribution of the sample in place of the true population distribution. Thus the bootstrap procedure hinges on the assumption that the observed distribution is a good estimate of the underlying population distribution. In return, the bootstrap produces an estimate, called the bootstrap distribution, of the sampling distribution. From this, you can estimate the standard error of the statistic, produce confidence intervals, etc.

The accuracy with which the bootstrap distribution estimates the sampling distribution depends on the number of observations in the original sample and the number of replications in the bootstrap. A crudely estimated sampling distribution is adequate if you are only going to extract, say, a standard error. A better estimate is needed if you want to use the 2.5th and 97.5th percentiles of the distribution to produce a 95% confidence interval. To extract many features simultaneously about the distribution, an even better estimate is needed. Generally, replications on the order of 1,000 produce very good estimates, but only 50–200 replications are needed for estimates of standard errors. See Poi (2004) for a method to choose the number of bootstrap replications.

Regression coefficients

▷ Example 1

Let's say that we wish to compute bootstrap estimates for the standard errors of the coefficients from the following regression:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight gear foreign
```

Source	SS	df	MS	Number of obs =	74
Model	1629.67805	3	543.226016	F(3, 70) =	46.73
Residual	813.781411	70	11.6254487	Prob > F =	0.0000
				R-squared =	0.6670
				Adj R-squared =	0.6527
Total	2443.45946	73	33.4720474	Root MSE =	3.4096

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.006139	.0007949	-7.72	0.000	-.0077245	-.0045536
gear_ratio	1.457113	1.541286	0.95	0.348	-1.616884	4.53111
foreign	-2.221682	1.234961	-1.80	0.076	-4.684735	.2413715
_cons	36.10135	6.285984	5.74	0.000	23.56435	48.63835

To run the bootstrap, we simply prefix the above regression command with the `bootstrap` command (specifying its options before the colon separator). We must set the random-number seed before calling `bootstrap`.

```
. bootstrap, reps(100) seed(1): regress mpg weight gear foreign
(running regress on estimation sample)
Bootstrap replications (100)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................   50
..................................................   100
```

Linear regression

Number of obs	= 74
Replications	= 100
Wald chi2(3)	= 111.96
Prob > chi2	= 0.0000
R-squared	= 0.6670
Adj R-squared	= 0.6527
Root MSE	= 3.4096

mpg	Observed Coef.	Bootstrap Std. Err.	z	P>|z|	Normal-based [95% Conf.	Interval]
weight	-.006139	.0006498	-9.45	0.000	-.0074127	-.0048654
gear_ratio	1.457113	1.297786	1.12	0.262	-1.086501	4.000727
foreign	-2.221682	1.162728	-1.91	0.056	-4.500587	.0572236
_cons	36.10135	4.71779	7.65	0.000	26.85465	45.34805

The displayed confidence interval is based on the assumption that the sampling (and hence bootstrap) distribution is approximately normal (see *Methods and formulas* below). Because this confidence interval is based on the standard error, it is a reasonable estimate if normality is approximately true, even for a few replications. Other types of confidence intervals are available after `bootstrap`; see [R] **bootstrap postestimation**.

We could instead supply names to our expressions when we run bootstrap. For example,

```
. bootstrap diff=(_b[weight]-_b[gear]): regress mpg weight gear foreign
```

would bootstrap a statistic, named diff, equal to the difference between the coefficients on weight and gear_ratio.

◁

Expressions

▷ Example 2

When we use bootstrap, the list of statistics can contain complex expressions, as long as each expression is enclosed in parentheses. For example, to bootstrap the range of a variable x, we could type

```
. bootstrap range=(r(max)-r(min)), reps(1000): summarize x
```

Of course, we could also bootstrap the minimum and maximum and later compute the range.

```
. bootstrap max=r(max) min=r(min), reps(1000) saving(mybs): summarize x
. use mybs, clear
(bootstrap: summarize)
. generate range = max - min
. bstat range, stat(19.5637501)
```

The difference between the maximum and minimum of x in the sample is 19.5637501.

The stat() option to bstat specifies the observed value of the statistic (range) to be summarized. This option is useful when, as shown above, the statistic of ultimate interest is not specified directly to bootstrap but instead is calculated by other means.

Here the observed values of r(max) and r(min) are saved as characteristics of the dataset created by bootstrap and are thus available for retrieval by bstat; see [R] **bstat**. The observed range, however, is unknown to bstat, so it must be specified.

◁

Combining bootstrap datasets

You can combine two datasets from separate runs of bootstrap by using append (see [D] **append**) and then get the bootstrap statistics for the combined datasets by running bstat. The runs must have been performed independently (having different starting random-number seeds), and the original dataset, command, and bootstrap statistics must have been all the same.

A note about macros

In the previous example, we executed the command

```
. bootstrap max=r(max) min=r(min), reps(1000) saving(mybs): summarize x
```

We did not enclose `r(max)` and `r(min)` in single quotes, as we would in most other contexts, because it would not produce what was intended:

```
. bootstrap 'r(max)' 'r(min)', reps(1000) saving(mybs): summarize x
```

To understand why, note that `'r(max)'`, like any reference to a local macro, will evaluate to a literal string containing the contents of `r(max)` *before* `bootstrap` is even executed. Typing the command above would appear to Stata as if we had typed

```
. bootstrap 14.5441234 33.4393293, reps(1000) saving(mybs): summarize x
```

Even worse, the current contents of `r(min)` and `r(max)` could be empty, producing an even more confusing result. To avoid this outcome, refer to statistics by name (for example, `r(max)`) and not by value (for example, `'r(max)'`).

Achieved significance level

▷ Example 3

Suppose that we wish to estimate the *achieved significance level* (ASL) of a test statistic by using the bootstrap. ASL is another name for p-value. An example is

$$\text{ASL} = \Pr\left(\widehat{\theta}^* \geq \widehat{\theta} | H_0\right)$$

for an upper-tailed, alternative hypothesis, where H_0 denotes the null hypothesis, $\widehat{\theta}$ is the observed value of the test statistic, and $\widehat{\theta}^*$ is the random variable corresponding to the test statistic, assuming that H_0 is true.

Here we will compare the mean miles per gallon (`mpg`) between foreign and domestic cars by using the two-sample t test with unequal variances. The following results indicate the p-value to be `0.0034` for the two-sided test using Satterthwaite's approximation. Thus assuming that mean `mpg` is the same for foreign and domestic cars, we would expect to observe a t statistic more extreme (in absolute value) than `3.1797` in about 0.3% of all possible samples of the type that we observed. Thus we have evidence to reject the null hypothesis that the means are equal.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ttest mpg, by(foreign) unequal
Two-sample t test with unequal variances
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
Domestic	52	19.82692	.657777	4.743297	18.50638	21.14747
Foreign	22	24.77273	1.40951	6.611187	21.84149	27.70396
combined	74	21.2973	.6725511	5.785503	19.9569	22.63769
diff		-4.945804	1.555438		-8.120053	-1.771556

```
    diff = mean(Domestic) - mean(Foreign)                         t =  -3.1797
Ho: diff = 0                     Satterthwaite's degrees of freedom =  30.5463
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0017         Pr(|T| > |t|) = 0.0034          Pr(T > t) = 0.9983
```

We also place the value of the test statistic in a scalar for later use.

```
. scalar tobs = r(t)
```

Efron and Tibshirani (1993, 224) describe an alternative to Satterthwaite's approximation that estimates the ASL by bootstrapping the statistic from the test of equal means. Their idea is to recenter the two samples to the combined sample mean so that the data now conform to the null hypothesis but that the variances within the samples remain unchanged.

```
. summarize mpg, meanonly
. scalar omean = r(mean)
. summarize mpg if foreign==0, meanonly
. replace mpg = mpg - r(mean) + scalar(omean) if foreign==0
mpg was int now float
(52 real changes made)
. summarize mpg if foreign==1, meanonly
. replace mpg = mpg - r(mean) + scalar(omean) if foreign==1
(22 real changes made)
. sort foreign
. by foreign: summarize mpg
```

```
-> foreign = Domestic
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         mpg |         52     21.2973    4.743297   13.47037   35.47038

-> foreign = Foreign
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         mpg |         22     21.2973    6.611187   10.52457   37.52457
```

Each sample (foreign and domestic) is a stratum, so the bootstrapped samples must have the same number of foreign and domestic cars as the original dataset. This requirement is facilitated by the `strata()` option to `bootstrap`. By typing the following, we bootstrap the test statistic using the modified dataset and save the values in `bsauto2.dta`:

```
. keep mpg foreign
. set seed 1
. bootstrap t=r(t), rep(1000) strata(foreign) saving(bsauto2) nodots: ttest mpg,
> by(foreign) unequal
Warning:  Because ttest is not an estimation command or does not set
          e(sample), bootstrap has no way to determine which observations are
          used in calculating the statistics and so assumes that all
          observations are used.  This means that no observations will be
          excluded from the resampling because of missing values or other
          reasons.

          If the assumption is not true, press Break, save the data, and drop
          the observations that are to be excluded.  Be sure that the dataset
          in memory contains only the relevant data.

Bootstrap results
Number of strata   =         2                  Number of obs      =        74
                                                 Replications       =      1000

      command:  ttest mpg, by(foreign) unequal
            t:  r(t)

------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
           t |   1.75e-07   1.036437     0.00   1.000    -2.031379    2.031379
------------------------------------------------------------------------------
```

We can use the data in `bsauto2.dta` to estimate ASL via the fraction of bootstrap test statistics that are more extreme than `3.1797`.

```
. use bsauto2, clear
(bootstrap: ttest)
. generate indicator = abs(t)>=abs(scalar(tobs))
. summarize indicator, meanonly
. display "ASLboot = " r(mean)
ASLboot = .005
```

The result is $\text{ASL}_{\text{boot}} = 0.005$. Assuming that the mean `mpg` is the same between foreign and domestic cars, we would expect to observe a t statistic more extreme (in absolute value) than `3.1797` in about 0.5% of all possible samples of the type we observed. This finding is still strong evidence to reject the hypothesis that the means are equal.

◁

Bootstrapping a ratio

▷ Example 4

Suppose that we wish to produce a bootstrap estimate of the ratio of two means. Because `summarize` saves results for only one variable, we must call `summarize` twice to compute the means. Actually, we could use `collapse` to compute the means in one call, but calling `summarize` twice is much faster. Thus we will have to write a small program that will return the results we want.

We write the program below and save it to a file called `ratio.ado` (see [U] **17 Ado-files**). Our program takes two variable names as input and saves them in the `local` macros `y` (first variable) and `x` (second variable). It then computes one statistic: the mean of `'y'` divided by the mean of `'x'`. This value is returned as a scalar in `r(ratio)`. `ratio` also returns the ratio of the number of observations used to the mean for each variable.

```
program myratio, rclass
        version 12
        args y x
        confirm var 'y'
        confirm var 'x'
        tempname ymean yn
        summarize 'y', meanonly
        scalar 'ymean' = r(mean)
        return scalar n_'y' = r(N)
        summarize 'x', meanonly
        return scalar n_'x' = r(N)
        return scalar ratio = 'ymean'/r(mean)
end
```

Remember to test any newly written commands before using them with `bootstrap`.

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. summarize price
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       price |         74    6165.257    2949.496       3291      15906
. scalar mean1=r(mean)
. summarize weight
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      weight |         74    3019.459    777.1936       1760       4840
. scalar mean2=r(mean)
. di scalar(mean1)/scalar(mean2)
2.0418412
. myratio price weight
. return list
scalars:
             r(ratio) =  2.041841210168278
          r(n_weight) =  74
           r(n_price) =  74
```

The results of running bootstrap on our program are

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. set seed 1
. bootstrap ratio=r(ratio), reps(1000) nowarn nodots: myratio price weight
Bootstrap results                                 Number of obs      =        74
                                                  Replications       =      1000
      command:  myratio price weight
        ratio:  r(ratio)
------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       ratio |   2.041841   .0942932    21.65   0.000      1.85703    2.226652
------------------------------------------------------------------------------
```

As mentioned previously, we should specify the saving() option if we wish to save the bootstrap dataset.

◁

Warning messages and e(sample)

bootstrap is not meant to be used with weighted calculations. bootstrap determines the presence of weights by parsing the prefixed command with standard syntax. However, commands like stcox and streg require that weights be specified in stset, and some user commands may allow weights to be specified by using an option instead of the standard syntax. Both cases pose a problem for bootstrap because it cannot determine the presence of weights under these circumstances. In these cases, we can only assume that you know what you are doing.

bootstrap does not know which variables of the dataset in memory matter to the calculation at hand. You can speed their execution by dropping unnecessary variables because, otherwise, they are included in each bootstrap sample.

You should thus drop observations with missing values. Leaving in missing values causes no problem in one sense because all Stata commands deal with missing values gracefully. It does, however, cause a statistical problem. Bootstrap sampling is defined as drawing, with replacement, samples of size N from a set of N observations. bootstrap determines N by counting the number of observations in memory, not counting the number of nonmissing values on the relevant variables. The result is that too many observations are resampled; the resulting bootstrap samples, because they are drawn from a population with missing values, are of unequal sizes.

If the number of missing values relative to the sample size is small, this will make little difference. If you have many missing values, however, you should first drop the observations that contain them.

▷ Example 5

To illustrate, we use the previous example but replace some of the values of price with missing values. The number of values of price used to compute the mean for each bootstrap is not constant. This is the purpose of the Warning message.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. replace price = . if inlist(_n,1,3,5,7)
(4 real changes made, 4 to missing)
. set seed 1
```

```
. bootstrap ratio=r(ratio) np=r(n_price) nw=r(n_weight), reps(100) nodots:
> myratio price weight
Warning:  Because myratio is not an estimation command or does not set
          e(sample), bootstrap has no way to determine which observations are
          used in calculating the statistics and so assumes that all
          observations are used.  This means that no observations will be
          excluded from the resampling because of missing values or other
          reasons.

          If the assumption is not true, press Break, save the data, and drop
          the observations that are to be excluded.  Be sure that the dataset
          in memory contains only the relevant data.

Bootstrap results                                 Number of obs      =        74
                                                  Replications       =       100

      command:  myratio price weight
        ratio:  r(ratio)
           np:  r(n_price)
           nw:  r(n_weight)

------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       ratio |   2.063051   .0893669    23.09   0.000     1.887896    2.238207
          np |         70   1.872178    37.39   0.000      66.3306     73.6694
          nw |         74          .        .       .            .           .
------------------------------------------------------------------------------
```

Bootstrapping statistics from data with a complex structure

Here we describe how to bootstrap statistics from data with a complex structure, for example, longitudinal or panel data, or matched data. `bootstrap`, however, is not designed to work with complex survey data. It is important to include all necessary information about the structure of the data in the `bootstrap` syntax to obtain correct bootstrap estimates for standard errors and confidence intervals.

`bootstrap` offers several options identifying the specifics of the data. These options are `strata()`, `cluster()`, `idcluster()`, and `group()`. The usage of `strata()` was described in example 3 above. Below we demonstrate several examples that require specifying the other three options.

▷ Example 6

Suppose that the `auto` data in example 1 above are clustered by `rep78`. We want to obtain bootstrap estimates for the standard errors of the difference between the coefficients on `weight` and `gear_ratio`, taking into account clustering.

We supply the `cluster(rep78)` option to `bootstrap` to request resampling from clusters rather than from observations in the dataset.

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. keep if rep78 < .
(5 observations deleted)
. bootstrap diff=(_b[weight]-_b[gear]), seed(1) cluster(rep78): regress mpg weight
> gear foreign
(running regress on estimation sample)
Bootstrap replications (50)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
Linear regression                               Number of obs      =        69
                                                Replications       =        50
      command:  regress mpg weight gear foreign
         diff:  _b[weight]-_b[gear]
                                    (Replications based on 5 clusters in rep78)
------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        diff |  -1.910396   1.876778    -1.02   0.309    -5.588812    1.768021
------------------------------------------------------------------------------
```

We drop missing values in `rep78` before issuing the command because `bootstrap` does not allow missing values in `cluster()`. See the section above about using `bootstrap` when variables contain missing values.

We can also obtain these same results by using the following syntax:

```
. bootstrap diff=(_b[weight]-_b[gear]), seed(1): regress mpg weight gear foreign,
> vce(cluster rep78)
```

When only clustered information is provided to the command, `bootstrap` can pick up the `vce(cluster` *clustvar*`)` option from the main command and use it to resample from clusters.

◁

▷ Example 7

Suppose now that we have matched data and want to use `bootstrap` to obtain estimates of the standard errors of the exponentiated difference between two coefficients (or, equivalently, the ratio of two odds ratios) estimated by `clogit`. Consider the example of matched case–control data on birthweight of infants described in example 2 of [R] **clogit**.

The infants are paired by being matched on mother's age. All groups, defined by the `pairid` variable, have 1:2 matching. `clogit` requires that the matching information, `pairid`, be supplied to the `group()` (or, equivalently, `strata()`) option to be used in computing the parameter estimates. Because the data are matched, we need to resample from groups rather than from the whole dataset. However, simply supplying the grouping variable `pairid` in `cluster()` is not enough with `bootstrap`, as it is with clustered data.

```
. use http://www.stata-press.com/data/r12/lowbirth2, clear
(Applied Logistic Regression, Hosmer & Lemeshow)
. bootstrap ratio=exp(_b[smoke]-_b[ptd]), seed(1) cluster(pairid): clogit low lwt
> smoke ptd ht ui i.race, group(pairid)
(running clogit on estimation sample)

Bootstrap replications (50)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50

Bootstrap results                               Number of obs      =       112
                                                Replications       =        50

      command:  clogit low lwt smoke ptd ht ui i.race, group(pairid)
        ratio:  exp(_b[smoke]-_b[ptd])

                                 (Replications based on 56 clusters in pairid)
------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       ratio |   .6654095   17.71791     0.04   0.970    -34.06106    35.39187
------------------------------------------------------------------------------
```

For the syntax above, imagine that the first pair was sampled twice during a replication. Then the bootstrap sample has four subjects with `pairid` equal to one, which clearly violates the original 1:2 matching design. As a result, the estimates of the coefficients obtained from this bootstrap sample will be incorrect.

Therefore, in addition to resampling from groups, we need to ensure that resampled groups are uniquely identified in each of the bootstrap samples. The `idcluster(`*newcluster*`)` option is designed for this. It requests that at each replication `bootstrap` create the new variable, *newcluster*, containing unique identifiers for all resampled groups. Thus, to make sure that the correct matching is preserved during each replication, we need to specify the grouping variable in `cluster()`, supply a variable name to `idcluster()`, and use this variable as the grouping variable with `clogit`, as we demonstrate below.

```
. bootstrap ratio=exp(_b[smoke]-_b[ptd]), seed(1) cluster(pairid)
> idcluster(newpairid): clogit low lwt smoke ptd ht ui i.race, group(newpairid)
(running clogit on estimation sample)

Bootstrap replications (50)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50

Bootstrap results                               Number of obs      =       112
                                                Replications       =        50

      command:  clogit low lwt smoke ptd ht ui i.race, group(newpairid)
        ratio:  exp(_b[smoke]-_b[ptd])

                                 (Replications based on 56 clusters in pairid)
------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       ratio |   .6654095   7.919441     0.08   0.933    -14.85641    16.18723
------------------------------------------------------------------------------
```

Note the difference between the estimates of the bootstrap standard error for the two specifications of the `bootstrap` syntax.

◁

❑ Technical note

Similarly, when you have panel (longitudinal) data, all resampled panels must be unique in each of the bootstrap samples to obtain correct bootstrap estimates of statistics. Therefore, both `cluster(`*panelvar*`)` and `idcluster(`*newpanelvar*`)` must be specified with `bootstrap`, and `i(`*newpanelvar*`)` must be used with the main command. Moreover, you must clear the current `xtset` settings by typing `xtset, clear` before calling `bootstrap`.

❑

▷ Example 8

Continuing with our birthweight data, suppose that we have more information about doctors supervising women's pregnancies. We believe that the data on the pairs of infants from the same doctor may be correlated and want to adjust standard errors for possible correlation among the pairs. `clogit` offers the `vce(cluster` *clustvar*`)` option to do this.

Let's add a cluster variable to our dataset. One thing to keep in mind is that to use `vce(cluster` *clustvar*`)`, groups in `group()` must be nested within clusters.

```
. use http://www.stata-press.com/data/r12/lowbirth2, clear
(Applied Logistic Regression, Hosmer & Lemeshow)
. set seed 12345
. by pairid, sort: egen byte doctor = total(int(2*runiform()+1)*(_n == 1))
. clogit low lwt smoke ptd ht ui i.race, group(pairid) vce(cluster doctor)
Iteration 0:   log pseudolikelihood = -26.768693
Iteration 1:   log pseudolikelihood = -25.810476
Iteration 2:   log pseudolikelihood = -25.794296
Iteration 3:   log pseudolikelihood = -25.794271
Iteration 4:   log pseudolikelihood = -25.794271
Conditional (fixed-effects) logistic regression   Number of obs   =        112
                                                  Wald chi2(1)    =          .
                                                  Prob > chi2     =          .
Log pseudolikelihood = -25.794271                 Pseudo R2       =     0.3355
                                (Std. Err. adjusted for 2 clusters in doctor)
------------------------------------------------------------------------------
             |               Robust
         low |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         lwt |  -.0183757   .0217802    -0.84   0.399    -.0610641    .0243128
       smoke |   1.400656   .0085545   163.73   0.000      1.38389    1.417423
         ptd |   1.808009    .938173     1.93   0.054    -.0307765    3.646794
          ht |   2.361152   1.587013     1.49   0.137    -.7493362     5.47164
          ui |   1.401929   .8568119     1.64   0.102    -.2773913     3.08125
             |
        race |
           2 |   .5713643   .0672593     8.49   0.000     .4395385    .7031902
           3 |  -.0253148   .9149785    -0.03   0.978     -1.81864     1.76801
------------------------------------------------------------------------------
```

To obtain correct bootstrap standard errors of the exponentiated difference between the two coefficients in this example, we need to make sure that both resampled clusters and groups within resampled clusters are unique in each of the bootstrap samples. To achieve this, `bootstrap` needs the information about clusters in `cluster()`, the variable name of the new identifier for clusters in `idcluster()`, and the information about groups in `group()`. We demonstrate the corresponding syntax of `bootstrap` below.

```
. bootstrap ratio=exp(_b[smoke]-_b[ptd]), seed(1) cluster(doctor)
> idcluster(uidoctor) group(pairid): clogit low lwt smoke ptd ht ui i.race,
> group(pairid)
(running clogit on estimation sample)

Bootstrap replications (50)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50

Bootstrap results                               Number of obs      =       112
                                                Replications       =        50

      command:  clogit low lwt smoke ptd ht ui i.race, group(pairid)
        ratio:  exp(_b[smoke]-_b[ptd])

                                  (Replications based on 2 clusters in doctor)
------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       ratio |   .6654095   .3156251     2.11   0.035     .0467956    1.284023
------------------------------------------------------------------------------
```

In the above syntax, although we specify `group(pairid)` with `clogit`, it is not the group identifiers of the original `pairid` variable that are used to compute parameter estimates from bootstrap samples. The way `bootstrap` works is that, at each replication, the clusters defined by `doctor` are resampled and the new variable, `uidoctor`, uniquely identifying resampled clusters is created. After that, another new variable uniquely identifying the (`uidoctor`, `group`) combination is created and renamed to have the same name as the grouping variable, `pairid`. This newly defined grouping variable is then used by `clogit` to obtain the parameter estimates from this bootstrap sample of clusters. After all replications are performed, the original values of the grouping variable are restored.

◁

❑ Technical note

The same logic must be used when running `bootstrap` with commands designed for panel (longitudinal) data that allow specifying the `cluster(`*clustervar*`)` option. To ensure that the combination of (*clustervar*, *panelvar*) values are unique in each of the bootstrap samples, `cluster(`*clustervar*`)`, `idcluster(`*newclustervar*`)`, and `group(`*panelvar*`)` must be specified with `bootstrap`, and `i(`*panelvar*`)` must be used with the main command.

❑

Bradley Efron was born in 1938 in Minnesota and studied mathematics and statistics at Caltech and Stanford; he has lived in northern California since 1960. He has worked on empirical Bayes, survival analysis, exponential families, bootstrap and jackknife methods, and confidence intervals, in conjunction with applied work in biostatistics, astronomy, and physics.

Saved results

bootstrap saves the following in e():

Scalars

e(N)	sample size
e(N_reps)	number of complete replications
e(N_misreps)	number of incomplete replications
e(N_strata)	number of strata
e(N_clust)	number of clusters
e(k_eq)	number of equations in e(b)
e(k_exp)	number of standard expressions
e(k_eexp)	number of extended expressions (i.e., _b)
e(k_extra)	number of extra equations beyond the original ones from e(b)
e(level)	confidence level for bootstrap CIs
e(bs_version)	version for bootstrap results
e(rank)	rank of e(V)

Macros

e(cmdname)	command name from *command*
e(cmd)	same as e(cmdname) or bootstrap
e(command)	*command*
e(cmdline)	command as typed
e(prefix)	bootstrap
e(title)	title in estimation output
e(strata)	strata variables
e(cluster)	cluster variables
e(seed)	initial random-number seed
e(size)	from the size(#) option
e(exp#)	expression for the #th statistic
e(mse)	mse, if specified
e(vce)	bootstrap
e(vcetype)	title used to label Std. Err.
e(properties)	b V

Matrices

e(b)	observed statistics
e(b_bs)	bootstrap estimates
e(reps)	number of nonmissing results
e(bias)	estimated biases
e(se)	estimated standard errors
e(z0)	median biases
e(accel)	estimated accelerations
e(ci_normal)	normal-approximation CIs
e(ci_percentile)	percentile CIs
e(ci_bc)	bias-corrected CIs
e(ci_bca)	bias-corrected and accelerated CIs
e(V)	bootstrap variance–covariance matrix
e(V_modelbased)	model-based variance

When *exp_list* is _b, bootstrap will also carry forward most of the results already in e() from *command*.

Methods and formulas

bootstrap is implemented as an ado-file.

Let $\widehat{\theta}$ be the observed value of the statistic, that is, the value of the statistic calculated with the original dataset. Let $i = 1, 2, \ldots, k$ denote the bootstrap samples, and let $\widehat{\theta}_i$ be the value of the statistic from the ith bootstrap sample.

When the `mse` option is specified, the standard error is estimated as

$$\widehat{\text{se}}_{\text{MSE}} = \left\{ \frac{1}{k} \sum_{i=1}^{k} (\widehat{\theta}_i - \widehat{\theta})^2 \right\}^{1/2}$$

Otherwise, the standard error is estimated as

$$\widehat{\text{se}} = \left\{ \frac{1}{k-1} \sum_{i=1}^{k} (\widehat{\theta}_i - \overline{\theta})^2 \right\}^{1/2}$$

where

$$\overline{\theta} = \frac{1}{k} \sum_{i=1}^{k} \widehat{\theta}_i$$

The variance–covariance matrix is similarly computed. The bias is estimated as

$$\widehat{\text{bias}} = \overline{\theta} - \widehat{\theta}$$

Confidence intervals with nominal coverage rates $1 - \alpha$ are calculated according to the following formulas. The normal-approximation method yields the confidence intervals

$$\left[\widehat{\theta} - z_{1-\alpha/2}\, \widehat{\text{se}},\ \widehat{\theta} + z_{1-\alpha/2}\, \widehat{\text{se}} \right]$$

where $z_{1-\alpha/2}$ is the $(1-\alpha/2)$th quantile of the standard normal distribution. If the `mse` option is specified, `bootstrap` will report the normal confidence interval using $\widehat{\text{se}}_{\text{MSE}}$ instead of $\widehat{\text{se}}$. `estat bootstrap` only uses $\widehat{\text{se}}$ in the normal confidence interval.

The percentile method yields the confidence intervals

$$\left[\theta^*_{\alpha/2},\ \theta^*_{1-\alpha/2} \right]$$

where θ^*_p is the pth quantile (the $100p$th percentile) of the bootstrap distribution $(\widehat{\theta}_1, \ldots, \widehat{\theta}_k)$.

Let

$$z_0 = \Phi^{-1}\{\#(\widehat{\theta}_i \leq \widehat{\theta})/k\}$$

where $\#(\widehat{\theta}_i \leq \widehat{\theta})$ is the number of elements of the bootstrap distribution that are less than or equal to the observed statistic and Φ is the standard cumulative normal. z_0 is known as the median bias of $\widehat{\theta}$. Let

$$a = \frac{\sum_{i=1}^{n} (\overline{\theta}_{(\cdot)} - \widehat{\theta}_{(i)})^3}{6\left\{\sum_{i=1}^{n} (\overline{\theta}_{(\cdot)} - \widehat{\theta}_{(i)})^2\right\}^{3/2}}$$

where $\widehat{\theta}_{(i)}$ are the leave-one-out (jackknife) estimates of $\widehat{\theta}$ and $\overline{\theta}_{(\cdot)}$ is their mean. This expression is known as the jackknife estimate of acceleration for $\widehat{\theta}$. Let

$$p_1 = \Phi\left\{ z_0 + \frac{z_0 - z_{1-\alpha/2}}{1 - a(z_0 - z_{1-\alpha/2})} \right\}$$

$$p_2 = \Phi\left\{ z_0 + \frac{z_0 + z_{1-\alpha/2}}{1 - a(z_0 + z_{1-\alpha/2})} \right\}$$

where $z_{1-\alpha/2}$ is the $(1-\alpha/2)$th quantile of the normal distribution. The bias-corrected and accelerated (BC_a) method yields confidence intervals

$$\left[\, \theta^*_{p_1},\, \theta^*_{p_2} \,\right]$$

where θ^*_p is the pth quantile of the bootstrap distribution as defined previously. The bias-corrected (but not accelerated) method is a special case of BC_a with $a = 0$.

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Also see

[R] **bootstrap postestimation** — Postestimation tools for bootstrap

[R] **jackknife** — Jackknife estimation

[R] **permute** — Monte Carlo permutation tests

[R] **simulate** — Monte Carlo simulations

[SVY] **svy bootstrap** — Bootstrap for survey data

[U] **13.5 Accessing coefficients and standard errors**

[U] **13.6 Accessing results from Stata commands**

[U] **20 Estimation and postestimation commands**

Title

bootstrap postestimation — Postestimation tools for bootstrap

Description

The following postestimation command is of special interest after `bootstrap`:

Command	Description
`estat bootstrap`	percentile-based and bias-corrected CI tables

For information about `estat bootstrap`, see below.

The following standard postestimation commands are also available:

Command	Description
*`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
*`hausman`	Hausman's specification test
*`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
*`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
*`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
*`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
*`predict`	predictions, residuals, influence statistics, and other diagnostic measures
*`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
*`pwcompare`	pairwise comparisons of estimates
*`test`	Wald tests of simple and composite linear hypotheses
*`testnl`	Wald tests of nonlinear hypotheses

*This postestimation command is allowed if it may be used after *command*.

See the corresponding entries in the *Stata Base Reference Manual* for details.

Special-interest postestimation command

`estat bootstrap` displays a table of confidence intervals for each statistic from a bootstrap analysis.

Syntax for predict

The syntax of `predict` (and even if `predict` is allowed) following `bootstrap` depends upon the *command* used with `bootstrap`. If `predict` is not allowed, neither is `predictnl`.

Syntax for estat bootstrap

```
estat bootstrap [ , options ]
```

options	Description
bc	bias-corrected CIs; the default
bca	bias-corrected and accelerated (BC_a) CIs
normal	normal-based CIs
percentile	percentile CIs
all	all available CIs
noheader	suppress table header
nolegend	suppress table legend
verbose	display the full table legend

bc, bca, normal, and percentile may be used together.

Menu

Statistics > Postestimation > Reports and statistics

Options for estat bootstrap

bc is the default and displays bias-corrected confidence intervals.

bca displays bias-corrected and accelerated confidence intervals. This option assumes that you also specified the bca option on the bootstrap prefix command.

normal displays normal approximation confidence intervals.

percentile displays percentile confidence intervals.

all displays all available confidence intervals.

noheader suppresses display of the table header. This option implies nolegend.

nolegend suppresses display of the table legend, which identifies the rows of the table with the expressions they represent.

verbose requests that the full table legend be displayed.

Remarks

▷ Example 1

The estat bootstrap postestimation command produces a table containing the observed value of the statistic, an estimate of its bias, the bootstrap standard error, and up to four different confidence intervals.

If we were interested merely in getting bootstrap standard errors for the model coefficients, we could use the bootstrap prefix with our estimation command. If we were interested in performing a thorough bootstrap analysis of the model coefficients, we could use the estat bootstrap postestimation command after fitting the model with the bootstrap prefix.

Using example 1 from [R] **bootstrap**, we need many more replications for the confidence interval types other than the normal based, so let's rerun the estimation command. We will reset the random-number seed—in case we wish to reproduce the results—increase the number of replications, and save the bootstrap distribution as a dataset called `bsauto.dta`.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. set seed 1
. bootstrap _b, reps(1000) saving(bsauto) bca: regress mpg weight gear foreign
  (output omitted)
. estat bootstrap, all
Linear regression                               Number of obs      =        74
                                                Replications       =      1000
```

mpg	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
weight	-.00613903	.0000567	.000628	-.0073699	-.0049082	(N)
				-.0073044	-.0048548	(P)
				-.0074355	-.004928	(BC)
				-.0075282	-.0050258	(BCa)
gear_ratio	1.4571134	.1051696	1.4554785	-1.395572	4.309799	(N)
				-1.262111	4.585372	(P)
				-1.523927	4.174376	(BC)
				-1.492223	4.231356	(BCa)
foreign	-2.2216815	-.0196361	1.2023286	-4.578202	.1348393	(N)
				-4.442199	.2677989	(P)
				-4.155504	.6170642	(BC)
				-4.216531	.5743973	(BCa)
_cons	36.101353	-.502281	5.4089441	25.50002	46.70269	(N)
				24.48569	46.07086	(P)
				25.59799	46.63227	(BC)
				25.85658	47.02108	(BCa)

```
(N)    normal confidence interval
(P)    percentile confidence interval
(BC)   bias-corrected confidence interval
(BCa)  bias-corrected and accelerated confidence interval
```

The estimated standard errors here differ from our previous estimates using only 100 replications by, respectively, 8%, 3%, 11%, and 6%; see example 1 of [R] **bootstrap**. So much for our advice that 50–200 replications are good enough to estimate standard errors. Well, the more replications the better—that advice you should believe.

Which of the methods to compute confidence intervals should we use? If the statistic is unbiased, the percentile (P) and bias-corrected (BC) methods should give similar results. The bias-corrected confidence interval will be the same as the percentile confidence interval when the observed value of the statistic is equal to the median of the bootstrap distribution. Thus, for unbiased statistics, the two methods should give similar results as the number of replications becomes large. For biased statistics, the bias-corrected method should yield confidence intervals with better coverage probability (closer to the nominal value of 95% or whatever was specified) than the percentile method. For statistics with variances that vary as a function of the parameter of interest, the bias-corrected and accelerated method (BC_a) will typically have better coverage probability than the others.

When the bootstrap distribution is approximately normal, all these methods should give similar confidence intervals as the number of replications becomes large. If we examine the normality of these bootstrap distributions using, say, the `pnorm` command (see [R] **diagnostic plots**), we see that they closely follow a normal distribution. Thus here, the normal approximation would also be a valid

choice. The chief advantage of the normal-approximation method is that it (supposedly) requires fewer replications than the other methods. Of course, it should be used only when the bootstrap distribution exhibits normality.

We can load `bsauto.dta` containing the bootstrap distributions for these coefficients:

```
. use bsauto
(bootstrap: regress)
. describe *
              storage  display     value
variable name   type   format      label      variable label
------------------------------------------------------------------------------
_b_weight       float  %9.0g                  _b[weight]
_b_gear_ratio   float  %9.0g                  _b[gear_ratio]
_b_foreign      float  %9.0g                  _b[foreign]
_b_cons         float  %9.0g                  _b[_cons]
```

We can now run other commands, such as `pnorm`, on the bootstrap distributions. As with all standard estimation commands, we can use the `bootstrap` command to replay its output table. The default variable names assigned to the statistics in *exp_list* are `_bs_1`, `_bs_2`, . . . , and each variable is labeled with the associated expression. The naming convention for the extended expressions `_b` and `_se` is to prepend `_b_` and `_se_`, respectively, onto the name of each element of the coefficient vector. Here the first coefficient is `_b[weight]`, so `bootstrap` named it `_b_weight`.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[U] **20 Estimation and postestimation commands**

Title

boxcox — Box–Cox regression models

Syntax

`boxcox` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
`model(lhsonly)`	left-hand-side Box–Cox model; the default
`model(rhsonly)`	right-hand-side Box–Cox model
`model(lambda)`	both sides Box–Cox model with same parameter
`model(theta)`	both sides Box–Cox model with different parameters
`notrans(`*varlist*`)`	nontransformed independent variables
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`lrtest`	perform likelihood-ratio test
Maximization	
`nolog`	suppress full-model iteration log
`nologlr`	suppress restricted-model `lrtest` iteration log
maximize_options	control the maximization process; seldom used

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `xi` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`fweights` and `iweights` are allowed; see [U] **11.1.6 weight**.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Box-Cox regression

Description

`boxcox` finds the maximum likelihood estimates of the parameters of the Box–Cox transform, the coefficients on the independent variables, and the standard deviation of the normally distributed errors for a model in which *depvar* is regressed on *indepvars*. You can fit the following models:

Option	Estimates
`lhsonly`	$y_j^{(\theta)} = \beta_1 x_{1j} + \beta_2 x_{2j} + \cdots + \beta_k x_{kj} + \epsilon_j$
`rhsonly`	$y_j = \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \epsilon_j$
`rhsonly notrans()`	$y_j = \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \gamma_1 z_{1j} + \cdots + \gamma_l z_{lj} + \epsilon_j$
`lambda`	$y_j^{(\lambda)} = \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \epsilon_j$
`lambda notrans()`	$y_j^{(\lambda)} = \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \gamma_1 z_{1j} + \cdots + \gamma_l z_{lj} + \epsilon_j$
`theta`	$y_j^{(\theta)} = \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \epsilon_j$
`theta notrans()`	$y_j^{(\theta)} = \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \gamma_1 z_{1j} + \cdots + \gamma_l z_{lj} + \epsilon_j$

Any variable to be transformed must be strictly positive.

Options

Model

`noconstant`; see [R] **estimation options**.

`model(` `lhsonly` | `rhsonly` | `lambda` | `theta` `)` specifies which of the four models to fit.

`model(lhsonly)` applies the Box–Cox transform to *depvar* only. `model(lhsonly)` is the default.

`model(rhsonly)` applies the transform to the *indepvars* only.

`model(lambda)` applies the transform to both *depvar* and *indepvars*, and they are transformed by the same parameter.

`model(theta)` applies the transform to both *depvar* and *indepvars*, but this time, each side is transformed by a separate parameter.

`notrans(`*varlist*`)` specifies that the variables in *varlist* be included as nontransformed independent variables.

Reporting

`level(#)`; see [R] **estimation options**.

`lrtest` specifies that a likelihood-ratio test of significance be performed and reported for each independent variable.

Maximization

`nolog` suppresses the iteration log when fitting the full model.

`nologlr` suppresses the iteration log when fitting the restricted models required by the `lrtest` option.

maximize_options: `iterate(#)` and `from(`*init_specs*`)`; see [R] **maximize**.

Model	Initial value specification
`lhsonly`	`from(`θ_0`, copy)`
`rhsonly`	`from(`λ_0`, copy)`
`lambda`	`from(`λ_0`, copy)`
`theta`	`from(`λ_0 θ_0`, copy)`

Remarks

Remarks are presented under the following headings:

Introduction
Theta model
Lambda model
Left-hand-side-only model
Right-hand-side-only model

Introduction

The Box–Cox transform

$$y^{(\lambda)} = \frac{y^{\lambda} - 1}{\lambda}$$

has been widely used in applied data analysis. Box and Cox (1964) developed the transformation and argued that the transformation could make the residuals more closely normal and less heteroskedastic. Cook and Weisberg (1982) discuss the transform in this light. Because the transform embeds several popular functional forms, it has received some attention as a method for testing functional forms, in particular,

$$y^{(\lambda)} = \begin{cases} y - 1 & \text{if } \lambda = 1 \\ \ln(y) & \text{if } \lambda = 0 \\ 1 - 1/y & \text{if } \lambda = -1 \end{cases}$$

Davidson and MacKinnon (1993) discuss this use of the transform. Atkinson (1985) also gives a good general treatment.

Theta model

`boxcox` obtains the maximum likelihood estimates of the parameters for four different models. The most general of the models, the `theta` model, is

$$y_j^{(\theta)} = \beta_0 + \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \gamma_1 z_{1j} + \gamma_2 z_{2j} + \cdots + \gamma_l z_{lj} + \epsilon_j$$

where $\epsilon \sim N(0, \sigma^2)$. Here the dependent variable, y, is subject to a Box–Cox transform with parameter θ. Each of the *indepvars*, $x_1, x_2, \ldots, x_k$, is transformed by a Box–Cox transform with parameter λ. The $z_1, z_2, \ldots, z_l$ specified in the `notrans()` option are independent variables that are not transformed.

Box and Cox (1964) argued that this transformation would leave behind residuals that more closely follow a normal distribution than those produced by a simple linear regression model. Bear in mind that the normality of ϵ is assumed and that `boxcox` obtains maximum likelihood estimates of the $k+l+4$ parameters under this assumption. `boxcox` does not choose λ and θ so that the residuals are approximately normally distributed. If you are interested in this type of transformation to normality, see the official Stata commands `lnskew0` and `bcskew0` in [R] **lnskew0**. However, those commands work on a more restrictive model in which none of the independent variables is transformed.

▷ Example 1

Consider an example using the auto data.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. boxcox mpg weight price, notrans(foreign) model(theta) lrtest
Fitting comparison model

Iteration 0:   log likelihood = -234.39434
Iteration 1:   log likelihood = -228.26891
Iteration 2:   log likelihood = -228.26777
Iteration 3:   log likelihood = -228.26777

Fitting full model

Iteration 0:   log likelihood = -194.13727
  (output omitted)
Fitting comparison models for LR tests

Iteration 0:   log likelihood = -179.58214
Iteration 1:   log likelihood = -177.59036
Iteration 2:   log likelihood = -177.58739
Iteration 3:   log likelihood = -177.58739

Iteration 0:   log likelihood = -203.92855
Iteration 1:   log likelihood = -201.30202
Iteration 2:   log likelihood = -201.18257
Iteration 3:   log likelihood = -201.18233
Iteration 4:   log likelihood = -201.18233

Iteration 0:   log likelihood = -178.83799
Iteration 1:   log likelihood = -175.98405
Iteration 2:   log likelihood = -175.97931
Iteration 3:   log likelihood = -175.97931

                                                Number of obs   =         74
                                                LR chi2(4)      =     105.19
Log likelihood = -175.67343                     Prob > chi2     =      0.000
------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     /lambda |   .7601691   .6289991     1.21   0.227    -.4726465    1.992985
      /theta |  -.7189315   .3244439    -2.22   0.027     -1.35483   -.0830332
------------------------------------------------------------------------------
Estimates of scale-variant parameters
------------------------------------------------------------------------------
             |      Coef.  chi2(df)  P>chi2(df)    df of chi2
-------------+----------------------------------------------------------------
Notrans      |
     foreign |  -.0114338     3.828    0.050          1
       _cons |   1.377399
-------------+----------------------------------------------------------------
Trans        |
      weight |   -.000239    51.018   0.000          1
       price |  -6.18e-06     0.612   0.434          1
-------------+----------------------------------------------------------------
      /sigma |   .0143509
------------------------------------------------------------------------------

------------------------------------------------------------------------------
   Test              Restricted
    H0:            log likelihood       chi2       Prob > chi2
-------------------------------------------------------------------------------
theta=lambda = -1     -181.64479        11.94          0.001
theta=lambda =  0      -178.2406         5.13          0.023
theta=lambda =  1     -194.13727        36.93          0.000
------------------------------------------------------------------------------
```

The output is composed of the iteration logs and three distinct tables. The first table contains a standard header for a maximum likelihood estimator and a standard output table for the Box–Cox transform parameters. The second table contains the estimates of the scale-variant parameters. The third table contains the output from likelihood-ratio tests on three standard functional form specifications.

If we were to interpret this output, the right-hand-side transformation would not significantly add to the regression, whereas the left-hand-side transformation would make the 5% but not the 1% cutoff. `price` is certainly not significant, and `foreign` lies right on the 5% cutoff. `weight` is clearly significant. The output also shows that the linear and multiplicative inverse specifications are both strongly rejected. A natural log specification can be rejected at the 5% level but not at the 1% level.

◁

❑ Technical note

Spitzer (1984) showed that the Wald tests of the joint significance of the coefficients of the right-hand-side variables, either transformed or untransformed, are not invariant to changes in the scale of the transformed dependent variable. Davidson and MacKinnon (1993) also discuss this point. This problem demonstrates that Wald statistics can be manipulated in nonlinear models. Lafontaine and White (1986) analyze this problem numerically, and Phillips and Park (1988) analyze it by using Edgeworth expansions. See Drukker (2000b) for a more detailed discussion of this issue. Because the parameter estimates and their Wald tests are not scale invariant, no Wald tests or confidence intervals are reported for these parameters. However, when the `lrtest` option is specified, likelihood-ratio tests are performed and reported. Schlesselman (1971) showed that, if a constant is included in the model, the parameter estimates of the Box–Cox transforms are scale invariant. For this reason, we strongly recommend that you not use the `noconstant` option.

The `lrtest` option does not perform a likelihood-ratio test on the constant, so no value for this statistic is reported. Unless the data are properly scaled, the restricted model does not often converge. For this reason, no likelihood-ratio test on the constant is performed by the `lrtest` option. However, if you have a special interest in performing this test, you can do so by fitting the constrained model separately. If problems with convergence are encountered, rescaling the data by their means may help.

❑

Lambda model

A less general model than the one above is called the `lambda` model. It specifies that the same parameter be used in both the left-hand-side and right-hand-side transformations. Specifically,

$$y_j^{(\lambda)} = \beta_0 + \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \gamma_1 z_{1j} + \gamma_2 z_{2j} + \cdots + \gamma_l z_{lj} + \epsilon_j$$

where $\epsilon \sim N(0, \sigma^2)$. Here the *depvar* variable, y, and each of the *indepvars*, $x_1, x_2, \ldots, x_k$, is transformed by a Box–Cox transform with the common parameter λ. Again the $z_1, z_2, \ldots, z_l$ are independent variables that are not transformed.

Left-hand-side-only model

Even more restrictive than a common transformation parameter is transforming the dependent variable only. Because the dependent variable is on the left-hand side of the equation, this model is known as the `lhsonly` model. Here you are estimating the parameters of the model

$$y_j^{(\theta)} = \beta_0 + \beta_1 x_{1j} + \beta_2 x_{2j} + \cdots + \beta_k x_{kj} + \epsilon_j$$

where $\epsilon \sim N(0, \sigma^2)$. Here only the *depvar*, y, is transformed by a Box–Cox transform with the parameter θ.

▷ Example 2

We again hypothesize `mpg` to be a function of `weight`, `price`, and `foreign` in a Box–Cox model in which only `mpg` is subject to the transform:

```
. boxcox mpg weight price foreign, model(lhs) lrtest nolog nologlr
Fitting comparison model
Fitting full model
Fitting comparison models for LR tests
                                                Number of obs   =         74
                                                LR chi2(3)      =     105.04
Log likelihood = -175.74705                     Prob > chi2     =      0.000
------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      /theta |  -.7826999    .281954    -2.78   0.006    -1.33532   -.2300802
------------------------------------------------------------------------------
Estimates of scale-variant parameters
------------------------------------------------------------------------------
             |      Coef.  chi2(df)  P>chi2(df)    df of chi2
-------------+----------------------------------------------------------------
Notrans      |
      weight |  -.0000294    58.056    0.000          1
       price |  -4.66e-07     0.469    0.493          1
     foreign |  -.0097564     4.644    0.031          1
       _cons |   1.249845
-------------+----------------------------------------------------------------
      /sigma |   .0118454
------------------------------------------------------------------------------

------------------------------------------------------------------------------
   Test         Restricted     LR statistic      P-value
    H0:       log likelihood       chi2       Prob > chi2
------------------------------------------------------------------------------
theta = -1      -176.04312          0.59           0.442
theta =  0      -179.54104          7.59           0.006
theta =  1      -194.13727         36.78           0.000
------------------------------------------------------------------------------
```

This model rejects both linear and log specifications of `mpg` but fails to reject the hypothesis that $1/$`mpg` is linear in the independent variables. These findings are in line with what an engineer would have expected. In engineering terms, gallons per mile represents actual energy consumption, and energy consumption should be approximately linear in weight.

◁

Right-hand-side-only model

The fourth model leaves the *depvar* alone and transforms a subset of the *indepvars* using the parameter λ. This is the `rhsonly` model. In this model, the *depvar*, y, is given by

$$y_j = \beta_0 + \beta_1 x_{1j}^{(\lambda)} + \beta_2 x_{2j}^{(\lambda)} + \cdots + \beta_k x_{kj}^{(\lambda)} + \gamma_1 z_{1j} + \gamma_2 z_{2j} + \cdots + \gamma_l z_{lj} + \epsilon_j$$

where $\epsilon \sim N(0, \sigma^2)$. Here each of the *indepvars*, $x_1, x_2, \ldots, x_k$, is transformed by a Box–Cox transform with the parameter λ. Again the $z_1, z_2, \ldots, z_l$ are independent variables that are not transformed.

▷ Example 3

Here is an example with the `rhsonly` model. `price` and `foreign` are not included in the list of covariates. (You are invited to use the `auto` data and check that they fare no better here than above.)

```
. boxcox mpg weight, model(rhs) lrtest nolog nologlr
Fitting full model
Fitting comparison models for LR tests
Comparison model for LR test on weight is a linear regression.
Lambda is not identified in the restricted model.
                                                Number of obs   =         74
                                                LR chi2(2)      =      82.90
Log likelihood = -192.94368                     Prob > chi2     =      0.000
------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     /lambda |  -.4460916   .6551107    -0.68   0.496    -1.730085    .8379018
------------------------------------------------------------------------------
Estimates of scale-variant parameters
------------------------------------------------------------------------------
             |      Coef.  chi2(df)  P>chi2(df)    df of chi2
-------------+----------------------------------------------------------------
Notrans      |
       _cons |   1359.092
-------------+----------------------------------------------------------------
Trans        |
      weight |  -614.3876    82.901    0.000           1
-------------+----------------------------------------------------------------
      /sigma |   3.281854
------------------------------------------------------------------------------

------------------------------------------------------------------------------
   Test         Restricted     LR statistic      P-value
    H0:       log likelihood       chi2       Prob > chi2
------------------------------------------------------------------------------
lambda = -1      -193.2893          0.69           0.406
lambda =  0      -193.17892         0.47           0.493
lambda =  1      -195.38869         4.89           0.027
------------------------------------------------------------------------------
```

The interpretation of the output is similar to that in all the cases above, with one caveat. As requested, a likelihood-ratio test was performed on the lone independent variable. However, when it is dropped to form the constrained model, the comparison model is not a right-hand-side-only Box–Cox model but rather a simple linear regression on a constant model. When weight is dropped, there are no longer any transformed variables. Hence, λ is not identified, and it must also be dropped. This process leaves a linear regression on a constant as the "comparison model". It also implies that the test statistic has 2 degrees of freedom instead of 1. At the top of the output, a more concise warning informs you of this point.

A similar identification issue can also arise in the `lambda` and `theta` models when only one independent variable is specified. In these cases, warnings also appear on the output.

◁

Saved results

`boxcox` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(ll)`	log likelihood
`e(chi2)`	LR statistic of full vs. comparison
`e(df_m)`	full model degrees of freedom
`e(ll0)`	log likelihood of the restricted model
`e(df_r)`	restricted model degrees of freedom
`e(ll_t1)`	log likelihood of model $\lambda=\theta=1$
`e(chi2_t1)`	LR of $\lambda=\theta=1$ vs. full model
`e(p_t1)`	p-value of $\lambda=\theta=1$ vs. full model
`e(ll_tm1)`	log likelihood of model $\lambda=\theta=-1$
`e(chi2_tm1)`	LR of $\lambda=\theta=-1$ vs. full model
`e(p_tm1)`	p-value of $\lambda=\theta=-1$ vs. full model
`e(ll_t0)`	log likelihood of model $\lambda=\theta=0$
`e(chi2_t0)`	LR of $\lambda=\theta=0$ vs. full model
`e(p_t0)`	p-value of $\lambda=\theta=0$ vs. full model
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code

Macros

`e(cmd)`	`boxcox`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(model)`	`lhsonly`, `rhsonly`, `lambda`, or `theta`
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(ntrans)`	`yes` if nontransformed *indepvars*
`e(chi2type)`	`LR`; type of model χ^2 test
`e(lrtest)`	`lrtest`, if requested
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(marginsnotok)`	predictions disallowed by `margins`

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators (see note below)
`e(pm)`	p-values for LR tests on *indepvars*
`e(df)`	degrees of freedom of LR tests on *indepvars*
`e(chi2m)`	LR statistics for tests on *indepvars*

Functions

`e(sample)`	marks estimation sample

`e(V)` contains all zeros, except for the elements that correspond to the parameters of the Box–Cox transform.

Methods and formulas

`boxcox` is implemented as an ado-file.

In the internal computations,

$$y^{(\lambda)} = \begin{cases} \frac{y^{\lambda}-1}{\lambda} & \text{if } |\lambda| > 10^{-10} \\ \ln(y) & \text{otherwise} \end{cases}$$

The unconcentrated log likelihood for the `theta` model is

$$\ln L = \left(\frac{-N}{2}\right)\left\{\ln(2\pi) + \ln(\sigma^2)\right\} + (\theta-1)\sum_{i=1}^{N}\ln(y_i) - \left(\frac{1}{2\sigma^2}\right)\mathrm{SSR}$$

where

$$\mathrm{SSR} = \sum_{i=1}^{N}(y_i^{(\theta)} - \beta_0 + \beta_1 x_{i1}^{(\lambda)} + \beta_2 x_{i2}^{(\lambda)} + \cdots + \beta_k x_{ik}^{(\lambda)} + \gamma_1 z_{i1} + \gamma_2 z_{i2} + \cdots + \gamma_l z_{il})^2$$

Writing the SSR in matrix form,

$$\mathrm{SSR} = (\mathbf{Y}^{(\theta)} - \mathbf{X}^{(\lambda)}\mathbf{b}' - \mathbf{Z}\mathbf{g}')'(\mathbf{Y}^{(\theta)} - \mathbf{X}^{(\lambda)}\mathbf{b}' - \mathbf{Z}\mathbf{g}')$$

where $\mathbf{Y}^{(\theta)}$ is an $N \times 1$ vector of elementwise transformed data, $\mathbf{X}^{(\lambda)}$ is an $N \times k$ matrix of elementwise transformed data, $\mathbf{Z}$ is an $N \times l$ matrix of untransformed data, $\mathbf{b}$ is a $1 \times k$ vector of coefficients, and $\mathbf{g}$ is a $1 \times l$ vector of coefficients. Letting

$$\mathbf{W}_\lambda = \left(\mathbf{X}^{(\lambda)}\ \mathbf{Z}\right)$$

be the horizontal concatenation of $\mathbf{X}^{(\lambda)}$ and $\mathbf{Z}$ and

$$\mathbf{d}' = \begin{pmatrix} \mathbf{b}' \\ \mathbf{g}' \end{pmatrix}$$

be the vertical concatenation of the coefficients yields

$$\mathrm{SSR} = (\mathbf{Y}^{(\theta)} - \mathbf{W}_\lambda\mathbf{d}')'(\mathbf{Y}^{(\theta)} - \mathbf{W}_\lambda\mathbf{d}')$$

For given values of λ and θ, the solutions for $\mathbf{d}'$ and σ^2 are

$$\widehat{\mathbf{d}}' = (\mathbf{W}_\lambda'\mathbf{W}_\lambda)^{-1}\mathbf{W}_\lambda'\mathbf{Y}^{(\theta)}$$

and

$$\widehat{\sigma}^{\,2} = \frac{1}{N}\left(\mathbf{Y}^{(\theta)} - \mathbf{W}_\lambda\widehat{\mathbf{d}}'\right)'\left(\mathbf{Y}^{(\theta)} - \mathbf{W}_\lambda\widehat{\mathbf{d}}'\right)$$

Substituting these solutions into the log-likelihood function yields the concentrated log-likelihood function

$$\ln L_c = \left(-\frac{N}{2}\right)\left\{\ln(2\pi) + 1 + \ln(\widehat{\sigma}^{\,2})\right\} + (\theta-1)\sum_{i=1}^{N}\ln(y_i)$$

Similar calculations yield the concentrated log-likelihood function for the `lambda` model,

$$\ln L_c = \left(-\frac{N}{2}\right)\left\{\ln(2\pi) + 1 + \ln(\widehat{\sigma}^{\,2})\right\} + (\lambda - 1)\sum_{i=1}^{N}\ln(y_i)$$

the `lhsonly` model,

$$\ln L_c = \left(-\frac{N}{2}\right)\left\{\ln(2\pi) + 1 + \ln(\widehat{\sigma}^{\,2})\right\} + (\theta - 1)\sum_{i=1}^{N}\ln(y_i)$$

and the `rhsonly` model,

$$\ln L_c = \left(-\frac{N}{2}\right)\left\{\ln(2\pi) + 1 + \ln(\widehat{\sigma}^{\,2})\right\}$$

where $\widehat{\sigma}^{\,2}$ is specific to each model and is defined analogously to that in the `theta` model.

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Also see

[R] **boxcox postestimation** — Postestimation tools for boxcox

[R] **regress** — Linear regression

[R] **lnskew0** — Find zero-skewness log or Box–Cox transform

[U] **20 Estimation and postestimation commands**

Title

boxcox postestimation — Postestimation tools for boxcox

Description

The following postestimation commands are available after `boxcox`:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
*`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
*`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
*`test`	Wald tests of simple and composite linear hypotheses
*`testnl`	Wald tests of nonlinear hypotheses

*Inference is valid only for hypotheses concerning λ and θ.

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic*]

statistic	Description
Main	
`xbt`	transformed linear prediction; the default
`yhat`	predicted value of y
`residuals`	residuals

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xbt`, the default, calculates the "linear" prediction. For all the models except `model(lhsonly)`, all the *indepvars* except those specified in the `notrans()` option of `boxcox` are transformed.

`yhat` calculates the predicted value of y.

`residuals` calculates the residuals after the predicted value of y has been subtracted from the actual value.

Remarks

`boxcox` estimates variances only for the λ and θ parameters (see the technical note in [R] **boxcox**), so the extent to which postestimation commands can be used following `boxcox` is limited. Formulas used in `lincom`, `nlcom`, `test`, and `testnl` are dependent on the estimated variances. Therefore, the use of these commands is limited and generally applicable only to inferences on the λ and θ coefficients.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **boxcox** — Box–Cox regression models

[R] **lnskew0** — Find zero-skewness log or Box–Cox transform

[U] **20 Estimation and postestimation commands**

Title

brier — Brier score decomposition

Syntax

`brier` *outcomevar forecastvar* [*if*] [*in*] [`, group(#)`]

`by` is allowed; see [D] **by**.

Menu

Statistics > Epidemiology and related > Other > Brier score decomposition

Description

`brier` computes the Yates, Sanders, and Murphy decompositions of the Brier Mean Probability Score. *outcomevar* contains 0/1 values reflecting the actual outcome of the experiment, and *forecastvar* contains the corresponding probabilities as predicted by, say, logit, probit, or a human forecaster.

Option

Main

`group(#)` specifies the number of groups that will be used to compute the decomposition. `group(10)` is the default.

Remarks

You have a binary (0/1) response and a formula that predicts the corresponding probabilities of having observed a positive outcome (1). If the probabilities were obtained from logistic regression, there are many methods that assess goodness of fit (see, for instance, `estat gof` in [R] **logistic**). However, the probabilities might be computed from a published formula or from a model fit on another sample, both completely unrelated to the data at hand, or perhaps the forecasts are not from a formula at all. In any case, you now have a *test dataset* consisting of the forecast probabilities and observed outcomes. Your test dataset might, for instance, record predictions made by a meteorologist on the probability of rain along with a variable recording whether it actually rained.

The Brier score is an aggregate measure of disagreement between the observed outcome and a prediction—the average squared error difference. The Brier score decomposition is a partition of the Brier score into components that suggest reasons for discrepancy. These reasons fall roughly into three groups: 1) lack of overall calibration between the average predicted probability and the actual probability of the event in your data, 2) misfit of the data in groups defined within your sample, and 3) inability to match actual 0 and 1 responses.

Problem 1 refers to simply overstating or understating the probabilities.

Problem 2 refers to what is standardly called a goodness-of-fit test: the data are grouped, and the predictions for the group are compared with the outcomes.

Problem 3 refers to an individual-level measure of fit. Imagine that the grouped outcomes are predicted on average correctly but that within the group, the outcomes are poorly predicted.

Using logit or probit analysis to fit your data will guarantee that there is no lack of fit due to problem 1, and a good model fitter will be able to avoid problem 2. Problem 3 is inherent in any prediction exercise.

▷ Example 1

We have data on the outcomes of 20 basketball games (`win`) and the probability of victory predicted by a local pundit (`for`).

```
. use http://www.stata-press.com/data/r12/bball
. summarize win for
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
         win |        20         .65    .4893605          0          1
         for |        20       .4785    .2147526        .15         .9
. brier win for, group(5)
Mean probability of outcome   0.6500
                of forecast   0.4785
Correlation                   0.5907
ROC area                      0.8791  p = 0.0030
Brier score                   0.1828
Spiegelhalter's z-statistic  -0.6339  p = 0.7369
Sanders-modified Brier score  0.1861
Sanders resolution            0.1400
Outcome index variance        0.2275
Murphy resolution             0.0875
Reliability-in-the-small      0.0461
Forecast variance             0.0438
Excess forecast variance      0.0285
Minimum forecast variance     0.0153
Reliability-in-the-large      0.0294
2*Forecast-Outcome-Covar      0.1179
```

The mean probabilities of forecast and outcome are simply the mean of the predicted probabilities and the actual outcomes (wins/losses). The correlation is the product-moment correlation between them.

The Brier score measures the total difference between the event (winning) and the forecast probability of that event as an average squared difference. As a benchmark, a perfect forecaster would have a Brier score of 0, a perfect misforecaster (predicts probability of win is 1 when loses and 0 when wins) would have a Brier score of 1, and a fence-sitter (forecasts every game as 50/50) would have a Brier score of 0.25. Our pundit is doing reasonably well.

Spiegelhalter's z statistic is a standard normal test statistic for testing whether an individual Brier score is extreme. The ROC area is the area under the receiver operating curve, and the associated test is a test of whether it is greater than 0.5. The more accurate the forecast probabilities, the larger the ROC area.

The Sanders-modified Brier score measures the difference between a grouped forecast measure and the event, where the data are grouped by sorting the sample on the forecast and dividing it into approximately equally sized groups. The difference between the modified and the unmodified score is typically minimal. For this and the other statistics that require grouping—the Sanders and Murphy resolutions and reliability-in-the-small—to be well-defined, group boundaries are chosen so as not to allocate observations with the same forecast probability to different groups. This task is done by grouping on the forecast using `xtile, n(#)`, with # being the number of groups; see [D] **pctile**.

The Sanders resolution measures error that arises from statistical considerations in evaluating the forecast for a group. A group with all positive or all negative outcomes would have a Sanders resolution of 0; it would most certainly be feasible to predict exactly what happened to each member of the group. If the group had 40% positive responses, on the other hand, a forecast that assigned $p = 0.4$ to each member of the group would be a good one, and yet, there would be "errors" in the squared difference sense. The "error" would be $(1 - 0.4)^2$ or $(0 - 0.4)^2$ for each member. The Sanders resolution is the average across groups of such "expected" errors. The 0.1400 value in our data from an overall Brier score of 0.1828 or 0.1861 suggests that a substantial portion of the "error" in our data is inherent.

Outcome index variance is just the variance of the outcome variable. This is the expected value of the Brier score if all the forecast probabilities were merely the average observed outcome. Remember that a fence-sitter has an expected Brier score of 0.25; a smarter fence sitter (who would guess $p = 0.65$ for these data) would have a Brier score of 0.2275.

The Murphy resolution measures the variation in the average outcomes across groups. If all groups have the same frequency of positive outcomes, little information in any forecast is possible, and the Murphy resolution is 0. If groups differ markedly, the Murphy resolution is as large as 0.25. The 0.0875 means that there is some variation but not a lot, and 0.0875 is probably higher than in most real cases. If you had groups in your data that varied between 40% and 60% positive outcomes, the Murphy resolution would be 0.01; between 30% and 70%, it would be 0.04.

Reliability-in-the-small measures the error that comes from the average forecast within group not measuring the average outcome within group—a classical goodness-of-fit measure, with 0 meaning a perfect fit and 1 meaning a complete lack of fit. The calculated value of 0.0461 shows some amount of lack of fit. Remember, the number is squared, and we are saying that probabilities could be just more than $\sqrt{0.0461} = 0.215$ or 21.5% off.

Forecast variance measures the amount of discrimination being attempted—that is, the variation in the forecasted probabilities. A small number indicates a fence-sitter making constant predictions. If the forecasts were from a logistic regression model, forecast variance would tend to increase with the amount of information available. Our pundit shows considerable forecast variance of 0.0438 (standard deviation $\sqrt{0.0438} = 0.2093$), which is in line with the reliability-in-the-small, suggesting that the forecaster is attempting as much variation as is available in these data.

Excess forecast variance is the amount of actual forecast variance over a theoretical minimum. The theoretical minimum—called the minimum forecast variance—corresponds to forecasts of p_0 for observations ultimately observed to be negative responses and p_1 for observations ultimately observed to be positive outcomes. Moreover, p_0 and p_1 are set to the average forecasts made for the ultimate negative and positive outcomes. These predictions would be just as good as the predictions the forecaster did make, and any variation in the actual forecast probabilities above this is useless. If this number is large, above 1%–2%, then the forecaster may be attempting more than is possible. The 0.0285 in our data suggests this possibility.

Reliability-in-the-large measures the discrepancy between the mean forecast and the observed fraction of positive outcomes. This discrepancy will be 0 for forecasts made by most statistical models—at least when measured on the same sample used for estimation—because they, by design, reproduce sample means. For our human pundit, the 0.0294 says that there is a $\sqrt{0.0294}$, or 17-percentage-point, difference. (This difference can also be found by calculating the difference in the averages of the observed outcomes and forecast probabilities: $0.65 - 0.4785 = 0.17$.) That difference, however, is not significant, as we would see if we typed `ttest win=for`; see [R] **ttest**. If these data were larger and the bias persisted, this difference would be a critical shortcoming of the forecast.

Twice the forecast-outcome covariance is a measure of how accurately the forecast corresponds to the outcome. The concept is similar to that of R-squared in linear regression.

◁

Saved results

`brier` saves the following in `r()`:

Scalars

`r(p_roc)`	significance of ROC area	`r(murphy)`	Murphy resolution
`r(roc_area)`	ROC area	`r(relinsm)`	reliability-in-the-small
`r(z)`	Spiegelhalter's z statistic	`r(Var_f)`	forecast variance
`r(p)`	significance of z statistic	`r(Var_fex)`	excess forecast variance
`r(brier)`	Brier score	`r(Var_fmin)`	minimum forecast variance
`r(brier_s)`	Sanders-modified Brier score	`r(relinla)`	reliability-in-the-large
`r(sanders)`	Sanders resolution	`r(cov_2f)`	2×forecast-outcome-covariance
`r(oiv)`	outcome index variance		

Methods and formulas

`brier` is implemented as an ado-file.

See Wilks (2006, 284–287, 289–292, 298–299) or Schmidt and Griffith (2005) for a discussion of the Brier score.

Let d_j, $j = 1, \ldots, N$, be the observed outcomes with $d_j = 0$ or $d_j = 1$, and let f_j be the corresponding forecasted probabilities that d_j is 1, $0 \leq f_j \leq 1$. Assume that the data are ordered so that $f_{j+1} \geq f_j$ (`brier` sorts the data to obtain this order). Divide the data into K nearly equally sized groups, with group 1 containing observations 1 through $j_2 - 1$, group 2 containing observations j_2 through $j_3 - 1$, and so on.

Define

$$\begin{aligned}
\overline{f}_0 &= \text{average } f_j \text{ among } d_j = 0 \\
\overline{f}_1 &= \text{average } f_j \text{ among } d_j = 1 \\
\overline{f} &= \text{average } f_j \\
\overline{d} &= \text{average } d_j \\
\widetilde{f}_k &= \text{average } f_j \text{ in group } k \\
\widetilde{d}_k &= \text{average } d_j \text{ in group } k \\
\widetilde{n}_k &= \text{number of observations in group } k
\end{aligned}$$

The Brier score is $\sum_j (d_j - f_j)^2/N$.

The Sanders-modified Brier score is $\sum_j (d_j - \widetilde{f}_{k(j)})^2/N$.

Let p_j denote the true but unknown probability that $d_j = 1$. Under the null hypothesis that $p_j = f_j$ for all j, Spiegelhalter (1986) determined that the expectation and variance of the Brier score is given by the following:

$$E(\text{Brier}) = \frac{1}{N}\sum_{j=1}^{N} f_j(1-f_j)$$

$$\text{Var}(\text{Brier}) = \frac{1}{N^2}\sum_{j=1}^{N} f_j(1-f_j)(1-2f_j)^2$$

Denoting the observed value of the Brier score by $O(\text{Brier})$, Spiegelhalter's z statistic is given by

$$Z = \frac{O(\text{Brier}) - E(\text{Brier})}{\sqrt{\text{Var}(\text{Brier})}}$$

The corresponding p-value is given by the upper-tail probability of Z under the standard normal distribution.

The area under the ROC curve is estimated by applying the trapezoidal rule to the empirical ROC curve. This area is Wilcoxon's test statistic, so the corresponding p-value is just that of a one-sided Wilcoxon test of the null hypothesis that the distribution of predictions is constant across the two outcomes.

The Sanders resolution is $\sum_k \widetilde{n}_k\{\widetilde{d}_k(1-\widetilde{d}_k)\}/N$.

The outcome index variance is $\overline{d}(1-\overline{d})$.

The Murphy resolution is $\sum_k \widetilde{n}_k(\widetilde{d}_k - \overline{d})^2/N$.

Reliability-in-the-small is $\sum_k \widetilde{n}_k(\widetilde{d}_k - \widetilde{f}_k)^2/N$.

The forecast variance is $\sum_j (f_j - \overline{f})^2/N$.

The minimum forecast variance is $\{\sum_{j\in F}(f_j - \overline{f}_0)^2 + \sum_{j\in S}(f_j - \overline{f}_1)^2\}/N$, where F is the set of observations for which $d_j = 0$ and S is the complement.

The excess forecast variance is the difference between the forecast variance and the minimum forecast variance.

Reliability-in-the-large is $(\overline{f} - \overline{d})^2$.

Twice the outcome covariance is $2(\overline{f}_1 - \overline{f}_0)\overline{d}(1-\overline{d})$.

Glenn Wilson Brier (1913–1998) was an American meteorological statistician who, after obtaining degrees in physics and statistics, was for many years head of meteorological statistics at the U.S. Weather Bureau in Washington, DC. In the latter part of his career, he was associated with Colorado State University. Brier worked especially on verification and evaluation of predictions and forecasts, statistical decision making, the statistical theory of turbulence, the analysis of weather modification experiments, and the application of permutation techniques.

Acknowledgment

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Also see

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **probit** — Probit regression

Title

bsample — Sampling with replacement

Syntax

`bsample` [*exp*] [*if*] [*in*] [, *options*]

where *exp* is a standard Stata expression; see [U] **13 Functions and expressions**.

options	Description
`strata(`*varlist*`)`	variables identifying strata
`cluster(`*varlist*`)`	variables identifying resampling clusters
`idcluster(`*newvar*`)`	create new cluster ID variable
`weight(`*varname*`)`	replace *varname* with frequency weights

Menu

Statistics > Resampling > Draw bootstrap sample

Description

`bsample` draws bootstrap samples (random samples with replacement) from the data in memory.

exp specifies the size of the sample, which must be less than or equal to the number of sampling units in the data. The observed number of units is the default when *exp* is not specified.

For bootstrap sampling of the observations, *exp* must be less than or equal to `_N` (the number of observations in the data; see [U] **13.4 System variables (_variables)**).

For stratified bootstrap sampling, *exp* must be less than or equal to `_N` within the strata identified by the `strata()` option.

For clustered bootstrap sampling, *exp* must be less than or equal to N_c (the number of clusters identified by the `cluster()` option).

For stratified bootstrap sampling of clusters, *exp* must be less than or equal to N_c within the strata identified by the `strata()` option.

Observations that do not meet the optional `if` and `in` criteria are dropped (not sampled).

Options

`strata(`*varlist*`)` specifies the variables identifying strata. If `strata()` is specified, bootstrap samples are selected within each stratum.

`cluster(`*varlist*`)` specifies the variables identifying resampling clusters. If `cluster()` is specified, the sample drawn during each replication is a bootstrap sample of clusters.

`idcluster(`*newvar*`)` creates a new variable containing a unique identifier for each resampled cluster.

`weight(`*varname*`)` specifies a variable in which the sampling frequencies will be placed. *varname* must be an existing variable, which will be replaced. After `bsample`, *varname* can be used as an `fweight` in any Stata command that accepts `fweight`s, which can speed up resampling for commands like `regress` and `summarize`. This option cannot be combined with `idcluster()`.

By default, `bsample` replaces the data in memory with the sampled observations; however, specifying the `weight()` option causes only the specified *varname* to be changed.

Remarks

Below is a series of examples illustrating how `bsample` is used with various sampling schemes.

▷ Example 1: Bootstrap sampling

We have data on the characteristics of hospital patients and wish to draw a bootstrap sample of 200 patients. We type

```
. use http://www.stata-press.com/data/r12/bsample1
. bsample 200
. count
  200
```

◁

▷ Example 2: Stratified samples with equal sizes

Among the variables in our dataset is `female`, an indicator for the female patients. To get a bootstrap sample of 200 female patients and 200 male patients, we type

```
. use http://www.stata-press.com/data/r12/bsample1, clear
. bsample 200, strata(female)
. tab female
```

female	Freq.	Percent	Cum.
male	200	50.00	50.00
female	200	50.00	100.00
Total	400	100.00	

◁

▷ Example 3: Stratified samples with unequal sizes

To sample 300 females and 200 males, we must generate a variable that is 300 for females and 200 for males and then use this variable in *exp* when we call `bsample`.

```
. use http://www.stata-press.com/data/r12/bsample1, clear
. gen nsamp = cond(female,300,200)
. bsample nsamp, strata(female)
. tab female
```

female	Freq.	Percent	Cum.
male	200	40.00	40.00
female	300	60.00	100.00
Total	500	100.00	

◁

▷ Example 4: Samples satisfying a condition

For a bootstrap sample of 200 female patients, we type

```
. use http://www.stata-press.com/data/r12/bsample1, clear
. bsample 200 if female
. tab female
```

female	Freq.	Percent	Cum.
female	200	100.00	100.00
Total	200	100.00	

◁

▷ Example 5: Generating frequency weights

To identify the sampled observations using frequency weights instead of dropping unsampled observations, we use the `weight()` option (we will need to supply it an existing variable name) and type

```
. use http://www.stata-press.com/data/r12/bsample1, clear
. set seed 1234
. gen fw = .
(5810 missing values generated)
. bsample 200 if female, weight(fw)
. tabulate fw female
```

	female		
fw	male	female	Total
0	2,392	3,221	5,613
1	0	194	194
2	0	3	3
Total	2,392	3,418	5,810

Note that $(194 \times 1) + (3 \times 2) = 200$.

◁

▷ Example 6: Oversampling observations

`bsample` requires the expression in *exp* to evaluate to a number that is less than or equal to the number of observations. To sample twice as many male and female patients as there are already in memory, we must expand the data before using `bsample`. For example,

```
. use http://www.stata-press.com/data/r12/bsample1, clear
. set seed 1234
. expand 2
(5810 observations created)
. bsample, strata(female)
```

```
. tab female
```

female	Freq.	Percent	Cum.
male	4,784	41.17	41.17
female	6,836	58.83	100.00
Total	11,620	100.00	

◁

▷ Example 7: Stratified oversampling with unequal sizes

To sample twice as many female patients as male patients, we must expand the records for the female patients because there are less than twice as many of them as there are male patients, but first put the number of observed male patients in a local macro. After expanding the female records, we generate a variable that contains the number of observations to sample within the two groups.

```
. use http://www.stata-press.com/data/r12/bsample1, clear
. set seed 1234
. count if !female
 2392
. local nmale = r(N)
. expand 2 if female
(3418 observations created)
. gen nsamp = cond(female,2*`nmale',`nmale')
. bsample nsamp, strata(female)
. tab female
```

female	Freq.	Percent	Cum.
male	2,392	33.33	33.33
female	4,784	66.67	100.00
Total	7,176	100.00	

◁

▷ Example 8: Oversampling of clusters

For clustered data, sampling more clusters than are present in the original dataset requires more than just expanding the data. To illustrate, suppose we wanted a bootstrap sample of eight clusters from a dataset consisting of five clusters of observations.

```
. use http://www.stata-press.com/data/r12/bsample2, clear
. tabstat x, stat(n mean) by(group)
Summary for variables: x
     by categories of: group
```

group	N	mean
A	15	-.3073028
B	10	-.00984
C	11	.0810985
D	11	-.1989179
E	29	-.095203
Total	76	-.1153269

`bsample` will complain if we simply expand the dataset.

```
. use http://www.stata-press.com/data/r12/bsample2
. expand 3
(152 observations created)
. bsample 8, cluster(group)
resample size must not be greater than number of clusters
r(498);
```

Expanding the data will only partly solve the problem. We also need a new variable that uniquely identifies the copied clusters. We use the `expandcl` command to accomplish both these tasks; see [D] **expandcl**.

```
. use http://www.stata-press.com/data/r12/bsample2, clear
. set seed 1234
. expandcl 2, generate(expgroup) cluster(group)
(76 observations created)
. tabstat x, stat(n mean) by(expgroup)
Summary for variables: x
     by categories of: expgroup
```

expgroup	N	mean
1	15	-.3073028
2	15	-.3073028
3	10	-.00984
4	10	-.00984
5	11	.0810985
6	11	.0810985
7	11	-.1989179
8	11	-.1989179
9	29	-.095203
10	29	-.095203
Total	152	-.1153269

```
. gen fw = .
(152 missing values generated)
. bsample 8, cluster(expgroup) weight(fw)
. tabulate fw group
```

	group					
fw	A	B	C	D	E	Total
0	15	10	0	0	29	54
1	15	10	22	22	0	69
2	0	0	0	0	29	29
Total	30	20	22	22	58	152

The results from `tabulate` on the generated frequency weight variable versus the original cluster ID (`group`) show us that the bootstrap sample contains one copy of cluster `A`, one copy of cluster `B`, two copies of cluster `C`, two copies of cluster `D`, and two copies of cluster `E` ($1 + 1 + 2 + 2 + 2 = 8$).

◁

▷ Example 9: Stratified oversampling of clusters

Suppose that we have a dataset containing two strata with five clusters in each stratum, but the cluster identifiers are not unique between the strata. To get a stratified bootstrap sample with eight clusters in each stratum, we first use `expandcl` to expand the data and get a new cluster ID variable. We use `cluster(strid group)` in the call to `expandcl`; this action will uniquely identify the $2 * 5 = 10$ clusters across the strata.

```
. use http://www.stata-press.com/data/r12/bsample2, clear
. set seed 1234
. tab group strid
```

group	strid 1	2	Total
A	7	8	15
B	5	5	10
C	5	6	11
D	5	6	11
E	14	15	29
Total	36	40	76

```
. expandcl 2, generate(expgroup) cluster(strid group)
(76 observations created)
```

Now we can use `bsample` with the expanded data, stratum ID variable, and new cluster ID variable.

```
. gen fw = .
(152 missing values generated)
. bsample 8, cluster(expgroup) str(strid) weight(fw)
. by strid, sort: tabulate fw group
```

```
-> strid = 1
```

fw	group A	B	C	D	E	Total
0	0	5	0	5	14	24
1	14	5	10	5	0	34
2	0	0	0	0	14	14
Total	14	10	10	10	28	72

```
-> strid = 2
```

fw	group A	B	C	D	E	Total
0	8	10	0	6	0	24
1	8	0	6	6	15	35
2	0	0	6	0	15	21
Total	16	10	12	12	30	80

The results from `by strid: tabulate` on the generated frequency weight variable versus the original cluster ID (`group`) show us how many times each cluster was sampled for each stratum. For stratum `1`, the bootstrap sample contains two copies of cluster `A`, one copy of cluster `B`, two copies of cluster `C`, one copy of cluster `D`, and two copies of cluster `E` ($2 + 1 + 2 + 1 + 2 = 8$). For stratum `2`, the bootstrap sample contains one copy of cluster `A`, zero copies of cluster `B`, three copies of cluster `C`, one copy of cluster `D`, and three copies of cluster `E` ($1 + 0 + 3 + 1 + 3 = 8$). ◁

Methods and formulas

`bsample` is implemented as an ado-file.

Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **bstat** — Report bootstrap results

[R] **simulate** — Monte Carlo simulations

[D] **sample** — Draw random sample

Title

bstat — Report bootstrap results

Syntax

Bootstrap statistics from variables

`bstat` [*varlist*] [*if*] [*in*] [, *options*]

Bootstrap statistics from file

`bstat` [*namelist*] [`using` *filename*] [*if*] [*in*] [, *options*]

options	Description
Main	
`stat(`*vector*`)`	observed values for each statistic
`accel(`*vector*`)`	acceleration values for each statistic
`mse`	use MSE formula for variance estimation
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`n(#)`	# of observations from which bootstrap samples were taken
`notable`	suppress table of results
`noheader`	suppress table header
`nolegend`	suppress table legend
`verbose`	display the full table legend
`title(`*text*`)`	use *text* as title for bootstrap results
display_options	control column formats and line width

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Resampling > Report bootstrap results

Description

`bstat` is a programmer's command that computes and displays estimation results from bootstrap statistics.

For each variable in *varlist* (the default is all variables), then `bstat` computes a covariance matrix, estimates bias, and constructs several different confidence intervals (CIs). The following CIs are constructed by `bstat`:

1. Normal CIs (using the normal approximation)
2. Percentile CIs
3. Bias-corrected (BC) CIs
4. Bias-corrected and accelerated (BC_a) CIs (optional)

`estat bootstrap` displays a table of one or more of the above confidence intervals; see [R] **bootstrap postestimation**.

If there are bootstrap estimation results in `e()`, `bstat` replays them. If given the `using` modifier, `bstat` uses the data in *filename* to compute the bootstrap statistics while preserving the data currently in memory. Otherwise, `bstat` uses the data in memory to compute the bootstrap statistics.

The following options may be used to replay estimation results from `bstat`:

`level(#) notable noheader nolegend verbose title(`*text*`)`

For all other options and the qualifiers `using`, `if`, and `in`, `bstat` requires a bootstrap dataset.

Options

Main

`stat(`*vector*`)` specifies the observed value of each statistic (that is, the value of the statistic using the original dataset).

`accel(`*vector*`)` specifies the acceleration of each statistic, which is used to construct BC$_a$ CIs.

`mse` specifies that `bstat` compute the variance by using deviations of the replicates from the observed value of the statistics. By default, `bstat` computes the variance by using deviations from the average of the replicates.

Reporting

`level(#)`; see [R] **estimation options**.

`n(#)` specifies the number of observations from which bootstrap samples were taken. This value is used in no calculations but improves the table header when this information is not saved in the bootstrap dataset.

`notable` suppresses the display of the output table.

`noheader` suppresses the display of the table header. This option implies `nolegend`.

`nolegend` suppresses the display of the table legend.

`verbose` specifies that the full table legend be displayed. By default, coefficients and standard errors are not displayed.

`title(`*text*`)` specifies a title to be displayed above the table of bootstrap results; the default title is `Bootstrap results`.

display_options: `cformat(`*%fmt*`)`, `pformat(`*%fmt*`)`, `sformat(`*%fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Bootstrap datasets
Creating a bootstrap dataset

Bootstrap datasets

Although bstat allows you to specify the observed value and acceleration of each bootstrap statistic via the stat() and accel() options, programmers may be interested in what bstat uses when these options are not supplied.

When working from a bootstrap dataset, bstat first checks the data characteristics (see [P] **char**) that it understands:

_dta[bs_version] identifies the version of the bootstrap dataset. This characteristic may be empty (not defined), 2, or 3; otherwise, bstat will quit and display an error message. This version tells bstat which other characteristics to look for in the bootstrap dataset.

bstat uses the following characteristics from version 3 bootstrap datasets:

_dta[N]
_dta[N_strata]
_dta[N_cluster]
_dta[command]
varname[observed]
varname[acceleration]
varname[expression]

bstat uses the following characteristics from version 2 bootstrap datasets:

_dta[N]
_dta[N_strata]
_dta[N_cluster]
varname[observed]
varname[acceleration]

An empty bootstrap dataset version implies that the dataset was created by the bstrap command in a version of Stata earlier than Stata 8. Here bstat expects *varname*[bstrap] to contain the observed value of the statistic identified by *varname* (*varname*[observed] in version 2). All other characteristics are ignored.

_dta[N] is the number of observations in the observed dataset. This characteristic may be overruled by specifying the n() option.

_dta[N_strata] is the number of strata in the observed dataset.

_dta[N_cluster] is the number of clusters in the observed dataset.

_dta[command] is the command used to compute the observed values of the statistics.

varname[observed] is the observed value of the statistic identified by *varname*. To specify a different value, use the stat() option.

varname[acceleration] is the estimate of acceleration for the statistic identified by *varname*. To specify a different value, use the accel() option.

varname[expression] is the expression or label that describes the statistic identified by *varname*.

Creating a bootstrap dataset

Suppose that we are interested in obtaining bootstrap statistics by resampling the residuals from a regression (which is not possible with the bootstrap command). After loading some data, we run a regression, save some results relevant to the bstat command, and save the residuals in a new variable, res.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight length
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =   69.34
       Model |  1616.08062     2  808.040312            Prob > F      =  0.0000
    Residual |  827.378835    71   11.653223            R-squared     =  0.6614
-------------+------------------------------           Adj R-squared =  0.6519
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.4137

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0038515   .001586    -2.43   0.018    -.0070138   -.0006891
      length |  -.0795935   .0553577   -1.44   0.155    -.1899736    .0307867
       _cons |   47.88487   6.08787     7.87   0.000       35.746    60.02374
------------------------------------------------------------------------------
. matrix b = e(b)
. local n = e(N)
. predict res, residuals
```

We can resample the residual values in `res` by generating a random observation ID (`rid`), generate a new response variable (`y`), and run the original regression with the new response variables.

```
. set seed 54321
. gen rid = int(_N*runiform())+1
. matrix score double y = b
. replace y = y + res[rid]
(74 real changes made)
. regress y weight length
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =  103.41
       Model |  1773.23548     2  886.617741            Prob > F      =  0.0000
    Residual |  608.747732    71  8.57391172            R-squared     =  0.7444
-------------+------------------------------           Adj R-squared =  0.7372
       Total |  2381.98321    73   32.629907            Root MSE      =  2.9281

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0059938   .0013604    -4.41   0.000    -.0087064   -.0032813
      length |  -.0127875   .0474837    -0.27   0.788    -.1074673    .0818924
       _cons |   42.23195   5.22194     8.09   0.000       31.8197    52.6442
------------------------------------------------------------------------------
```

Instead of programming this resampling inside a loop, it is much more convenient to write a short program and use the `simulate` command; see [R] **simulate**. In the following, `mysim_r` requires the user to specify a coefficient vector and a residual variable. `mysim_r` then retrieves the list of predictor variables (removing `_cons` from the list), generates a new temporary response variable with the resampled residuals, and regresses the new response variable on the predictors.

```
program mysim_r
        version 12
        syntax name(name=bvector), res(varname)
        tempvar y rid
        local xvars : colnames `bvector'
        local cons _cons
        local xvars : list xvars - cons
        matrix score double `y' = `bvector'
        gen long `rid' = int(_N*runiform()) + 1
        replace `y' = `y' + `res'[`rid']
        regress `y' `xvars'
end
```

We can now give `mysim_r` a test run, but we first set the random-number seed (to reproduce results).

```
. set seed 54321
. mysim_r b, res(res)
(74 real changes made)
```

Source	SS	df	MS		
Model	1773.23548	2	886.617741	Number of obs	= 74
Residual	608.747732	71	8.57391172	F(2, 71)	= 103.41
				Prob > F	= 0.0000
Total	2381.98321	73	32.629907	R-squared	= 0.7444
				Adj R-squared	= 0.7372
				Root MSE	= 2.9281

__000000	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0059938	.0013604	-4.41	0.000	-.0087064	-.0032813
length	-.0127875	.0474837	-0.27	0.788	-.1074673	.0818924
_cons	42.23195	5.22194	8.09	0.000	31.8197	52.6442

Now that we have a program that will compute the results we want, we can use `simulate` to generate a bootstrap dataset and `bstat` to display the results.

```
. set seed 54321
. simulate, reps(200) nodots: mysim_r b, res(res)
      command:  mysim_r b, res(res)
. bstat, stat(b) n(`n')
Bootstrap results                               Number of obs      =        74
                                                Replications       =       200
```

	Observed Coef.	Bootstrap Std. Err.	z	P>|z|	Normal-based [95% Conf.	Interval]
_b_weight	-.0038515	.0015715	-2.45	0.014	-.0069316	-.0007713
_b_length	-.0795935	.0552415	-1.44	0.150	-.1878649	.0286779
_b_cons	47.88487	6.150069	7.79	0.000	35.83096	59.93879

Finally, we see that `simulate` created some of the data characteristics recognized by `bstat`. All we need to do is correctly specify the version of the bootstrap dataset, and `bstat` will automatically use the relevant data characteristics.

```
. char list
_dta[seed]:                 X681014b5c43f462544a474abacbdd93d12a1
_dta[command]:              mysim_r b, res(res)
_b_weight[is_eexp]:         1
_b_weight[colname]:         weight
_b_weight[coleq]:           _
_b_weight[expression]:      _b[weight]
_b_length[is_eexp]:         1
_b_length[colname]:         length
_b_length[coleq]:           _
_b_length[expression]:      _b[length]
_b_cons[is_eexp]:           1
_b_cons[colname]:           _cons
_b_cons[coleq]:             _
_b_cons[expression]:        _b[_cons]
. char _dta[bs_version] 3
. bstat, stat(b) n(‘n’)
Bootstrap results                                 Number of obs      =        74
                                                  Replications       =       200

      command:  mysim_r b, res(res)
```

	Observed Coef.	Bootstrap Std. Err.	z	P>|z|	Normal-based [95% Conf.	Interval]
weight	-.0038515	.0015715	-2.45	0.014	-.0069316	-.0007713
length	-.0795935	.0552415	-1.44	0.150	-.1878649	.0286779
_cons	47.88487	6.150069	7.79	0.000	35.83096	59.93879

See Poi (2004) for another example of residual resampling.

Saved results

bstat saves the following in e():

Scalars

e(N)	sample size
e(N_reps)	number of complete replications
e(N_misreps)	number of incomplete replications
e(N_strata)	number of strata
e(N_clust)	number of clusters
e(k_aux)	number of auxiliary parameters
e(k_eq)	number of equations in e(b)
e(k_exp)	number of standard expressions
e(k_eexp)	number of extended expressions (i.e., _b)
e(k_extra)	number of extra equations beyond the original ones from e(b)
e(level)	confidence level for bootstrap CIs
e(bs_version)	version for bootstrap results
e(rank)	rank of e(V)

Macros

e(cmd)	bstat
e(command)	from _dta[command]
e(cmdline)	command as typed
e(title)	title in estimation output
e(exp#)	expression for the #th statistic
e(prefix)	bootstrap
e(mse)	mse if specified
e(vce)	bootstrap
e(vcetype)	title used to label Std. Err.
e(properties)	b V

Matrices

e(b)	observed statistics
e(b_bs)	bootstrap estimates
e(reps)	number of nonmissing results
e(bias)	estimated biases
e(se)	estimated standard errors
e(z0)	median biases
e(accel)	estimated accelerations
e(ci_normal)	normal-approximation CIs
e(ci_percentile)	percentile CIs
e(ci_bc)	bias-corrected CIs
e(ci_bca)	bias-corrected and accelerated CIs
e(V)	bootstrap variance–covariance matrix

Methods and formulas

bstat is implemented as an ado-file.

Reference

Poi, B. P. 2004. From the help desk: Some bootstrapping techniques. *Stata Journal* 4: 312–328.

Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **bsample** — Sampling with replacement

Title

centile — Report centile and confidence interval

Syntax

`centile` [*varlist*] [*if*] [*in*] [`,` *options*]

options	Description
Main	
`centile(`*numlist*`)`	report specified centiles; default is `centile(50)`
Options	
`cci`	binomial exact; conservative confidence interval
`normal`	normal, based on observed centiles
`meansd`	normal, based on mean and standard deviation
`level(#)`	set confidence level; default is `level(95)`

`by` is allowed; see [D] **by**.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Centiles with CIs

Description

`centile` estimates specified centiles and calculates confidence intervals. If no *varlist* is specified, `centile` calculates centiles for all the variables in the dataset. If `centile()` is not specified, medians (`centile(50)`) are reported.

Options

Main

`centile(`*numlist*`)` specifies the centiles to be reported. The default is to display the 50th centile. Specifying `centile(5)` requests that the fifth centile be reported. Specifying `centile(5 50 95)` requests that the 5th, 50th, and 95th centiles be reported. Specifying `centile(10(10)90)` requests that the 10th, 20th, . . . , 90th centiles be reported; see [U] **11.1.8 numlist**.

Options

`cci` (conservative confidence interval) forces the confidence limits to fall exactly on sample values. Confidence intervals displayed with the `cci` option are slightly wider than those with the default (`nocci`) option.

`normal` causes the confidence interval to be calculated by using a formula for the standard error of a normal-distribution quantile given by Kendall and Stuart (1969, 237). The `normal` option is useful when you want empirical centiles—that is, centiles based on sample order statistics rather than on the mean and standard deviation—and are willing to assume normality.

`meansd` causes the centile and confidence interval to be calculated based on the sample mean and standard deviation, and it assumes normality.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [R] **level**.

Remarks

The qth centile of a continuous random variable, X, is defined as the value of C_q, which fulfills the condition $\Pr(X \leq C_q) = q/100$. The value of q must be in the range $0 < q < 100$, though q is not necessarily an integer. By default, `centile` estimates C_q for the variables in *varlist* and for the values of q given in `centile(`*numlist*`)`. It makes no assumptions about the distribution of X, and, if necessary, uses linear interpolation between neighboring sample values. Extreme centiles (for example, the 99th centile in samples smaller than 100) are fixed at the minimum or maximum sample value. An "exact" confidence interval for C_q is also given, using the binomial-based method described below in *Methods and formulas* and in Conover (1999, 143–148). Again linear interpolation is used to improve the accuracy of the estimated confidence limits, but extremes are fixed at the minimum or maximum sample value.

You can prevent `centile` from interpolating when calculating binomial-based confidence intervals by specifying `cci`. The resulting intervals are generally wider than with the default; that is, the coverage (confidence level) tends to be greater than the nominal value (given as usual by `level(#)`, by default 95%).

If the data are believed to be normally distributed (a common case), there are two alternative methods for estimating centiles. If `normal` is specified, C_q is calculated, as just described, but its confidence interval is based on a formula for the standard error (se) of a normal-distribution quantile given by Kendall and Stuart (1969, 237). If `meansd` is alternatively specified, C_q is estimated as $\overline{x} + z_q \times s$, where $\overline{x}$ and s are the sample mean and standard deviation, and z_q is the qth centile of the standard normal distribution (for example, $z_{95} = 1.645$). The confidence interval is derived from the se of the estimate of C_q.

▷ Example 1

Using `auto.dta`, we estimate the 5th, 50th, and 95th centiles of the `price` variable:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. format price %8.2fc
. centile price, centile(5 50 95)
```

Variable	Obs	Percentile	Centile	— Binom. Interp. — [95% Conf.	Interval]
price	74	5	3,727.75	3,291.23	3,914.16
		50	5,006.50	4,593.57	5,717.90
		95	13,498.00	11,061.53	15,865.30

`summarize` produces somewhat different results from `centile`; see *Methods and formulas*.

```
. summarize price, detail
```

Price

Percentiles		Smallest		
1%	3291	3291		
5%	3748	3299		
10%	3895	3667	Obs	74
25%	4195	3748	Sum of Wgt.	74
50%	5006.5		Mean	6165.257
		Largest	Std. Dev.	2949.496
75%	6342	13466		
90%	11385	13594	Variance	8699526
95%	13466	14500	Skewness	1.653434
99%	15906	15906	Kurtosis	4.819188

The confidence limits produced by using the `cci` option are slightly wider than those produced without this option:

```
. centile price, c(5 50 95) cci
```

Variable	Obs	Percentile	Centile	— Binomial Exact — [95% Conf.	Interval]
price	74	5	3,727.75	3,291.00	3,955.00
		50	5,006.50	4,589.00	5,719.00
		95	13,498.00	10,372.00	15,906.00

If we are willing to assume that `price` is normally distributed, we could include either the `normal` or the `meansd` option:

```
. centile price, c(5 50 95) normal
```

Variable	Obs	Percentile	— Normal, based on observed centiles — Centile	[95% Conf.	Interval]
price	74	5	3,727.75	3,211.19	4,244.31
		50	5,006.50	4,096.68	5,916.32
		95	13,498.00	5,426.81	21,569.19

```
. centile price, c(5 50 95) meansd
```

Variable	Obs	Percentile	— Normal, based on mean and std. dev.— Centile	[95% Conf.	Interval]
price	74	5	1,313.77	278.93	2,348.61
		50	6,165.26	5,493.24	6,837.27
		95	11,016.75	9,981.90	12,051.59

With the `normal` option, the centile estimates are, by definition, the same as before. The confidence intervals for the 5th and 50th centiles are similar to the previous ones, but the interval for the 95th centile is different. The results using the `meansd` option also differ from both previous sets of estimates.

We can use `sktest` (see [R] **sktest**) to check the correctness of the normality assumption:

```
. sktest price
```

Skewness/Kurtosis tests for Normality

Variable	Obs	Pr(Skewness)	Pr(Kurtosis)	joint adj chi2(2)	Prob>chi2
price	74	0.0000	0.0127	21.77	0.0000

sktest reveals that price is definitely not normally distributed, so the normal assumption is not reasonable, and the normal and meansd options are not appropriate for these data. We should rely on the results from the default choice, which does not assume normality. If the data are normally distributed, however, the precision of the estimated centiles and their confidence intervals will be ordered (best) meansd > normal > [default] (worst). The normal option is useful when we really do want empirical centiles (that is, centiles based on sample order statistics rather than on the mean and standard deviation) but are willing to assume normality.

◁

Saved results

centile saves the following in r():

Scalars

r(N)	number of observations
r(n_cent)	number of centiles requested
r(c_#)	value of # centile
r(lb_#)	#-requested centile lower confidence bound
r(ub_#)	#-requested centile upper confidence bound

Macros

r(centiles)	centiles requested

Methods and formulas

centile is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Default case
Normal case
meansd case

Default case

The calculation is based on the method of Mood and Graybill (1963, 408). Let $x_1 \leq x_2 \leq \cdots \leq x_n$ be a sample of size n arranged in ascending order. Denote the estimated qth centile of the x's as c_q. We require that $0 < q < 100$. Let $R = (n+1)q/100$ have integer part r and fractional part f; that is, $r = \text{int}(R)$ and $f = R - r$. (If R is itself an integer, then $r = R$ and $f = 0$.) Note that $0 \leq r \leq n$. For convenience, define $x_0 = x_1$ and $x_{n+1} = x_n$. C_q is estimated by

$$c_q = x_r + f \times (x_{r+1} - x_r)$$

that is, c_q is a weighted average of x_r and x_{r+1}. Loosely speaking, a (conservative) $p\%$ confidence interval for C_q involves finding the observations ranked t and u, which correspond, respectively, to the $\alpha = (100-p)/200$ and $1-\alpha$ quantiles of a binomial distribution with parameters n and $q/100$, that is, $\text{B}(n, q/100)$. More precisely, define the ith value ($i = 0, \ldots, n$) of the cumulative binomial distribution function as $F_i = \Pr(S \leq i)$, where S has distribution $\text{B}(n, q/100)$. For convenience, let $F_{-1} = 0$ and $F_{n+1} = 1$. t is found such that $F_t \leq \alpha$ and $F_{t+1} > \alpha$, and u is found such that $1 - F_u \leq \alpha$ and $1 - F_{u-1} > \alpha$.

With the cci option in force, the (conservative) confidence interval is (x_{t+1}, x_{u+1}), and its actual coverage probability is $F_u - F_t$.

The default case uses linear interpolation on the F_i as follows. Let

$$\begin{aligned} g &= (\alpha - F_t)/(F_{t+1} - F_t) \\ h &= \{\alpha - (1 - F_u)\}/\{(1 - F_{u-1}) - (1 - F_u)\} \\ &= (\alpha - 1 + F_u)/(F_u - F_{u-1}) \end{aligned}$$

The interpolated lower and upper confidence limits (c_{qL}, c_{qU}) for C_q are

$$\begin{aligned} c_{qL} &= x_{t+1} + g \times (x_{t+2} - x_{t+1}) \\ c_{qU} &= x_{u+1} - h \times (x_{u+1} - x_u) \end{aligned}$$

Suppose that we want a 95% confidence interval for the median of a sample of size 13. $n = 13$, $q = 50$, $p = 95$, $\alpha = 0.025$, $R = 14 \times 50/100 = 7$, and $f = 0$. Therefore, the median is the 7th observation. Some example data, x_i, and the values of F_i are as follows:

i	F_i	$1 - F_i$	x_i	i	F_i	$1 - F_i$	x_i
0	0.0001	0.9999	–	7	0.7095	0.2905	33
1	0.0017	0.9983	5	8	0.8666	0.1334	37
2	0.0112	0.9888	7	9	0.9539	0.0461	45
3	0.0461	0.9539	10	10	0.9888	0.0112	59
4	0.1334	0.8666	15	11	0.9983	0.0017	77
5	0.2905	0.7095	23	12	0.9999	0.0001	104
6	0.5000	0.5000	28	13	1.0000	0.0000	211

The median is $x_7 = 33$. Also, $F_2 \leq 0.025$ and $F_3 > 0.025$, so $t = 2$; $1 - F_{10} \leq 0.025$ and $1 - F_9 > 0.025$, so $u = 10$. The conservative confidence interval is therefore

$$(c_{50L}, c_{50U}) = (x_{t+1}, x_{u+1}) = (x_3, x_{11}) = (10, 77)$$

with actual coverage $F_{10} - F_2 = 0.9888 - 0.0112 = 0.9776$ (97.8% confidence). For the interpolation calculation, we have

$$\begin{aligned} g &= (0.025 - 0.0112)/(0.0461 - 0.0112) = 0.395 \\ h &= (0.025 - 1 + 0.9888)/(0.9888 - 0.9539) = 0.395 \end{aligned}$$

So,

$$\begin{aligned} c_{50L} &= x_3 + 0.395 \times (x_4 - x_3) = 10 + 0.395 \times 5 = 11.98 \\ c_{50U} &= x_{11} - 0.395 \times (x_{11} - x_{10}) = 77 - 0.395 \times 18 = 69.89 \end{aligned}$$

Normal case

The value of c_q is as above. Its se is given by the formula

$$s_q = \sqrt{q(100 - q)} \Big/ \Big\{100\sqrt{n} Z(c_q; \overline{x}, s)\Big\}$$

where $\overline{x}$ and s are the mean and standard deviation of the x_i, and

$$Z(Y; \mu, \sigma) = \Big(1/\sqrt{2\pi\sigma^2}\Big) e^{-(Y-\mu)^2/2\sigma^2}$$

is the density function of a normally distributed variable Y with mean μ and standard deviation σ. The confidence interval for C_q is $(c_q - z_{100(1-\alpha)} s_q, c_q + z_{100(1-\alpha)} s_q)$.

meansd case

The value of c_q is $\overline{x} + z_q \times s$. Its se is given by the formula

$$s_q^\star = s\sqrt{1/n + z_q^2/(2n-2)}$$

The confidence interval for C_q is $(c_q - z_{100(1-\alpha)} \times s_q^\star, c_q + z_{100(1-\alpha)} \times s_q^\star)$.

Acknowledgment

`centile` was written by Patrick Royston, MRC Clinical Trials Unit, London.

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Also see

[R] **ci** — Confidence intervals for means, proportions, and counts

[R] **summarize** — Summary statistics

[D] **pctile** — Create variable containing percentiles

Title

ci — Confidence intervals for means, proportions, and counts

Syntax

Syntax for ci

`ci` [*varlist*] [*if*] [*in*] [*weight*] [`,` *options*]

Immediate command for variable distributed as normal

`cii` #$_{\text{obs}}$ #$_{\text{mean}}$ #$_{\text{sd}}$ [`,` *ciin_option*]

Immediate command for variable distributed as binomial

`cii` #$_{\text{obs}}$ #$_{\text{succ}}$ [`,` *ciib_options*]

Immediate command for variable distributed as Poisson

`cii` #$_{\text{exposure}}$ #$_{\text{events}}$ `, poisson` [*ciip_options*]

options	Description
Main	
`binomial`	binomial 0/1 variables; compute exact confidence intervals
`poisson`	Poisson variables; compute exact confidence intervals
`exposure(`*varname*`)`	exposure variable; implies `poisson`
`exact`	calculate exact confidence intervals; the default
`wald`	calculate Wald confidence intervals
`wilson`	calculate Wilson confidence intervals
`agresti`	calculate Agresti–Coull confidence intervals
`jeffreys`	calculate Jeffreys confidence intervals
`total`	add output for all groups combined (for use with `by` only)
`separator(#)`	draw separator line after every # variables; default is `separator(5)`
`level(#)`	set confidence level; default is `level(95)`

`by` is allowed with `ci`; see [D] **by**.

`aweights` and `fweights` are allowed, but `aweights` may not be specified with the `binomial` or `poisson` options; see [U] **11.1.6 weight**.

ciin_option	Description
`level(#)`	set confidence level; default is `level(95)`

ciib_options	Description
level(#)	set confidence level; default is level(95)
exact	calculate exact confidence intervals; the default
wald	calculate Wald confidence intervals
wilson	calculate Wilson confidence intervals
agresti	calculate Agresti–Coull confidence intervals
jeffreys	calculate Jeffreys confidence intervals

ciip_options	Description
*poisson	numbers are Poisson-distributed counts
level(#)	set confidence level; default is level(95)

*poisson is required.

Menu

ci

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Confidence intervals

cii for variable distributed as normal

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Normal CI calculator

cii for variable distributed as binomial

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Binomial CI calculator

cii for variable distributed as Poisson

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Poisson CI calculator

Description

ci computes standard errors and confidence intervals for each of the variables in *varlist*.

cii is the immediate form of ci; see [U] **19 Immediate commands** for a general discussion of immediate commands.

In the binomial and Poisson variants of cii, the second number specified ($\#_{\text{succ}}$ or $\#_{\text{events}}$) must be an integer or between 0 and 1. If the number is between 0 and 1, Stata interprets it as the fraction of successes or events and converts it to an integer number representing the number of successes or events. The computation then proceeds as if two integers had been specified.

Options

Main

binomial tells ci that the variables are 0/1 variables and that binomial confidence intervals will be calculated. (cii produces binomial confidence intervals when only two numbers are specified.)

`poisson` specifies that the variables (or numbers for `cii`) are Poisson-distributed counts; exact Poisson confidence intervals will be calculated.

`exposure(`*varname*`)` is used only with `poisson`. You do not need to specify `poisson` if you specify `exposure()`; `poisson` is assumed. *varname* contains the total exposure (typically a time or an area) during which the number of events recorded in *varlist* were observed.

`exact`, `wald`, `wilson`, `agresti`, and `jeffreys` specify that variables are 0/1 and specify how binomial confidence intervals are to be calculated.

`exact` is the default and specifies exact (also known in the literature as Clopper–Pearson [1934]) binomial confidence intervals.

`wald` specifies calculation of Wald confidence intervals.

`wilson` specifies calculation of Wilson confidence intervals.

`agresti` specifies calculation of Agresti–Coull confidence intervals.

`jeffreys` specifies calculation of Jeffreys confidence intervals.

See Brown, Cai, and DasGupta (2001) for a discussion and comparison of the different binomial confidence intervals.

`total` is for use with the `by` prefix. It requests that, in addition to output for each by-group, output be added for all groups combined.

`separator(#)` specifies how often separation lines should be inserted into the output. The default is `separator(5)`, meaning that a line is drawn after every five variables. `separator(10)` would draw the line after every 10 variables. `separator(0)` suppresses the separation line.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [R] **level**.

Remarks

Remarks are presented under the following headings:

Ordinary confidence intervals
Binomial confidence intervals
Poisson confidence intervals
Immediate form

Ordinary confidence intervals

▷ Example 1

Without the `binomial` or `poisson` options, `ci` produces "ordinary" confidence intervals, meaning those that are correct if the variable is distributed normally, and *asymptotically* correct for all other distributions satisfying the conditions of the central limit theorem.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ci mpg price
    Variable |        Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+--------------------------------------------------------------
         mpg |         74     21.2973    .6725511        19.9569    22.63769
       price |         74    6165.257    342.8719        5481.914      6848.6
```

The standard error of the mean of mpg is 0.67, and the 95% confidence interval is [19.96, 22.64]. We can obtain wider confidence intervals, 99%, by typing

```
. ci mpg price, level(99)
    Variable |        Obs        Mean    Std. Err.       [99% Conf. Interval]
-------------+---------------------------------------------------------------
         mpg |         74     21.2973    .6725511        19.51849    23.07611
       price |         74    6165.257    342.8719        5258.405    7072.108
```

◁

▷ Example 2

by() breaks out the confidence intervals according to by-group; total adds an overall summary. For instance,

```
. ci mpg, by(foreign) total
-------------------------------------------------------------------------------
-> foreign = Domestic
    Variable |        Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+---------------------------------------------------------------
         mpg |         52    19.82692     .657777        18.50638    21.14747
-------------------------------------------------------------------------------
-> foreign = Foreign
    Variable |        Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+---------------------------------------------------------------
         mpg |         22    24.77273     1.40951        21.84149    27.70396
-------------------------------------------------------------------------------
-> Total
    Variable |        Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+---------------------------------------------------------------
         mpg |         74     21.2973    .6725511         19.9569    22.63769
```

◁

❑ Technical note

You can control the formatting of the numbers in the output by specifying a display format for the variable; see [U] **12.5 Formats: Controlling how data are displayed**. For instance,

```
. format mpg %9.2f
. ci mpg
    Variable |        Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+---------------------------------------------------------------
         mpg |         74       21.30        0.67           19.96       22.64
```

❑

Binomial confidence intervals

▷ Example 3

We have data on employees, including a variable marking whether the employee was promoted last year.

```
. use http://www.stata-press.com/data/r12/promo
. ci promoted, binomial
```

Variable	Obs	Mean	Std. Err.	— Binomial Exact — [95% Conf.	Interval]
promoted	20	.1	.067082	.0123485	.3169827

The above interval is the default for binomial data, known equivalently as both the exact binomial and the Clopper–Pearson interval.

Nominally, the interpretation of a 95% confidence interval is that under repeated samples or experiments, 95% of the resultant intervals would contain the unknown parameter in question. However, for binomial data, the actual coverage probability, regardless of method, usually differs from that interpretation. This result occurs because of the discreteness of the binomial distribution, which produces only a finite set of outcomes, meaning that coverage probabilities are subject to discrete jumps and the exact nominal level cannot always be achieved. Therefore, the term *exact confidence interval* refers to its being derived from the binomial distribution, the distribution exactly generating the data, rather than resulting in exactly the nominal coverage.

For the Clopper–Pearson interval, the actual coverage probability is guaranteed to be greater than or equal to the nominal confidence level, here 95%. Because of the way it is calculated—see *Methods and formulas*—it may also be interpreted as follows: If the true probability of being promoted were 0.012, the chances of observing a result as extreme or more extreme than the result observed ($20 \times 0.1 = 2$ or more promotions) would be 2.5%. If the true probability of being promoted were 0.317, the chances of observing a result as extreme or more extreme than the result observed (two or fewer promotions) would be 2.5%.

◁

▷ Example 4

The Clopper–Pearson interval is desirable because it guarantees nominal coverage; however, by dropping this restriction, you may obtain accurate intervals that are not as conservative. In this vein, you might opt for the Wilson (1927) interval,

```
. ci promoted, binomial wilson
```

Variable	Obs	Mean	Std. Err.	——— Wilson ——— [95% Conf.	Interval]
promoted	20	.1	.067082	.0278665	.3010336

the Agresti–Coull (1998) interval,

```
. ci promoted, binomial agresti
```

Variable	Obs	Mean	Std. Err.	— Agresti-Coull — [95% Conf.	Interval]
promoted	20	.1	.067082	.0156562	.3132439

or the Bayesian-derived Jeffreys interval (Brown, Cai, and DasGupta 2001),

```
. ci promoted, binomial jeffreys
```

Variable	Obs	Mean	Std. Err.	——— Jeffreys ——— [95% Conf.	Interval]
promoted	20	.1	.067082	.0213725	.2838533

Picking the best interval is a matter of balancing accuracy (coverage) against precision (average interval length) and depends on sample size and success probability. Brown, Cai, and DasGupta (2001) recommend the Wilson or Jeffreys interval for small sample sizes ($\leq$40) yet favor the Agresti–Coull interval for its simplicity, decent performance for sample sizes less than or equal to 40, and performance comparable to Wilson/Jeffreys for sample sizes greater than 40. They also deem the Clopper–Pearson interval to be "wastefully conservative and [. . .] not a good choice for practical use", unless of course one requires, at a minimum, the nominal coverage level.

◁

Finally, the binomial Wald confidence interval is obtained by specifying the `binomial` and `wald` options. The Wald interval is the one taught in most introductory statistics courses and for the above is simply, for level $1-\alpha$, `Mean`$\pm z_\alpha$(`Std. Err.`), where z_α is the $1-\alpha/2$ quantile of the standard normal. Because its overall poor performance makes it impractical, the Wald interval is available mainly for pedagogical purposes. The binomial Wald interval is also similar to the interval produced by treating binary data as normal data and using `ci` without the `binomial` option, with two exceptions. First, when `binomial` is specified, the calculation of the standard error uses denominator n rather than $n-1$, used for normal data. Second, confidence intervals for normal data are based on the t distribution rather than the standard normal. Of course, both discrepancies vanish as sample size increases.

❑ Technical note

Let's repeat example 3, but this time with data in which there are no promotions over the observed period:

```
. use http://www.stata-press.com/data/r12/promonone
. ci promoted, binomial
                                                      — Binomial Exact —
    Variable |       Obs        Mean    Std. Err.     [95% Conf. Interval]
-------------+--------------------------------------------------------------
    promoted |        20           0           0                0    .1684335*
(*) one-sided, 97.5% confidence interval
```

The confidence interval is $[0, 0.168]$, and this is the confidence interval that most books publish. It is not, however, a true 95% confidence interval because the lower tail has vanished. As Stata notes, it is a one-sided, 97.5% confidence interval. If you wanted to put 5% in the right tail, you could type `ci promoted, binomial level(90)`.

❑

❑ Technical note

`ci` with the `binomial` option ignores any variables that do not take on the values 0 and 1 exclusively. For instance, with our automobile dataset,

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ci mpg foreign, binomial
                                                      — Binomial Exact —
    Variable |       Obs        Mean    Std. Err.     [95% Conf. Interval]
-------------+--------------------------------------------------------------
     foreign |        74    .2972973    .0531331      .196584    .4148353
```

We also requested the confidence interval for `mpg`, but Stata ignored us. It does that so you can type `ci, binomial` and obtain correct confidence intervals for all the variables that are 0/1 in your data.

❑

Poisson confidence intervals

▷ Example 5

We have data on the number of bacterial colonies on a Petri dish. The dish has been divided into 36 small squares, and the number of colonies in each square has been counted. Each observation in our dataset represents a square on the dish. The variable `count` records the number of colonies in each square counted, which varies from 0 to 5.

```
. use http://www.stata-press.com/data/r12/petri
. ci count, poisson
```

Variable	Exposure	Mean	Std. Err.	— Poisson Exact — [95% Conf.	Interval]
count	36	2.333333	.2545875	1.861158	2.888825

`ci` reports that the average number of colonies per square is 2.33. If the expected number of colonies per square were as low as 1.86, the probability of observing 2.33 or more colonies per square would be 2.5%. If the expected number were as large as 2.89, the probability of observing 2.33 or fewer colonies per square would be 2.5%.

◁

❑ Technical note

The number of "observations"—how finely the Petri dish is divided—makes no difference. The Poisson distribution is a function only of the count. In example 4, we observed a total of $2.33 \times 36 = 84$ colonies and a confidence interval of $[\,1.86 \times 36, 2.89 \times 36\,] = [\,67, 104\,]$. We would obtain the same $[\,67, 104\,]$ confidence interval if our dish were divided into, say, 49 squares, rather than 36.

For the counts, it is not even important that all the squares be of the same size. For *rate*s, however, such differences do matter, but in an easy-to-calculate way. Rates are obtained from counts by dividing by exposure, which is typically a number multiplied by either time or an area. For our Petri dishes, we divide by an area to obtain a rate, but if our example were cast in terms of being infected by a disease, we might divide by person-years to obtain the rate. Rates are convenient because they are easier to compare: we might have 2.3 colonies per square inch or 0.0005 infections per person-year.

So, let's assume that we wish to obtain the number of colonies per square inch, and, moreover, that not all the "squares" on our dish are of equal size. We have a variable called `area` that records the area of each "square":

```
. ci count, exposure(area)
```

Variable	Exposure	Mean	Std. Err.	— Poisson Exact — [95% Conf.	Interval]
count	3	28	3.055051	22.3339	34.66591

The rates are now in more familiar terms. In our sample, there are 28 colonies per square inch and the 95% confidence interval is $[\,22.3, 34.7\,]$. When we did not specify `exposure()`, `ci` assumed that each observation contributed 1 to exposure.

❑

❑ Technical note

As with the binomial option, if there were no colonies on our dish, ci would calculate a one-sided confidence interval:

```
. use http://www.stata-press.com/data/r12/petrinone
. ci count, poisson
```

Variable	Exposure	Mean	Std. Err.	— Poisson Exact — [95% Conf.	Interval]
count	36	0	0	0	.1024689*

(*) one-sided, 97.5% confidence interval

❑

Immediate form

▷ Example 6

We are reading a soon-to-be-published paper by a colleague. In it is a table showing the number of observations, mean, and standard deviation of 1980 median family income for the Northeast and West. We correctly think that the paper would be much improved if it included the confidence intervals. The paper claims that for 166 cities in the Northeast, the average of median family income is $19,509 with a standard deviation of $4,379:

For the Northeast:

```
. cii 166 19509 4379
```

Variable	Obs	Mean	Std. Err.	[95% Conf.	Interval]
	166	19509	339.8763	18837.93	20180.07

For the West:

```
. cii 256 22557 5003
```

Variable	Obs	Mean	Std. Err.	[95% Conf.	Interval]
	256	22557	312.6875	21941.22	23172.78

◁

▷ Example 7

We flip a coin 10 times, and it comes up heads only once. We are shocked and decide to obtain a 99% confidence interval for this coin:

```
. cii 10 1, level(99)
```

Variable	Obs	Mean	Std. Err.	— Binomial Exact — [99% Conf.	Interval]
	10	.1	.0948683	.0005011	.5442871

◁

▷ Example 8

The number of reported traffic accidents in Santa Monica over a 24-hour period is 27. We need know nothing else:

```
. cii 1 27, poisson
```

Variable	Exposure	Mean	Std. Err.	— Poisson Exact — [95% Conf. Interval]	
	1	27	5.196152	17.79317	39.28358

◁

Saved results

`ci` and `cii` saves the following in `r()`:

Scalars

`r(N)`	number of observations or exposure	`r(lb)`	lower bound of confidence interval
`r(mean)`	mean	`r(ub)`	upper bound of confidence interval
`r(se)`	estimate of standard error		

Methods and formulas

`ci` and `cii` are implemented as ado-files.

Methods and formulas are presented under the following headings:

Ordinary
Binomial
Poisson

Ordinary

Define n, $\overline{x}$, and s^2 as, respectively, the number of observations, (weighted) average, and (unbiased) estimated variance of the variable in question; see [R] **summarize**.

The standard error of the mean, s_μ, is defined as $\sqrt{s^2/n}$.

Let α be $1 - l/100$, where l is the significance level specified by the user. Define t_α as the two-sided t statistic corresponding to a significance level of α with $n-1$ degrees of freedom; t_α is obtained from Stata as `invttail(`n`-1,0.5*`α`)`. The lower and upper confidence bounds are, respectively, $\overline{x} - s_\mu t_\alpha$ and $\overline{x} + s_\mu t_\alpha$.

Binomial

Given k successes of n trials, the estimated probability is $\widehat{p} = k/n$ with standard error $\sqrt{\widehat{p}(1-\widehat{p})/n}$. `ci` calculates the exact (Clopper–Pearson) confidence interval $[\,p_1, p_2\,]$ such that

$$\Pr(K \geq k | p = p_1) = \alpha/2$$

and

$$\Pr(K \leq k | p = p_2) = \alpha/2$$

where K is distributed as binomial(n, p). The endpoints may be obtained directly by using Stata's `invbinomial()` function. If $k = 0$ or $k = n$, the calculation of the appropriate tail is skipped.

The Wald interval is $\widehat{p} \pm z_\alpha \sqrt{\widehat{p}(1-\widehat{p})/n}$, where z_α is the $1 - \alpha/2$ quantile of the standard normal. The interval is obtained by inverting the acceptance region of the large-sample Wald test of $H_0 : p = p_0$ versus the two-sided alternative. That is, the confidence interval is the set of all p_0 such that

$$\left| \frac{\widehat{p} - p_0}{\sqrt{n^{-1}\widehat{p}(1-\widehat{p})}} \right| \leq z_\alpha$$

The Wilson interval is a variation on the Wald interval, using the null standard error $\sqrt{n^{-1}p_0(1-p_0)}$ in place of the estimated standard error $\sqrt{n^{-1}\widehat{p}(1-\widehat{p})}$ in the above expression. Inverting this acceptance region is more complicated yet results in the closed form

$$\frac{k + z_\alpha^2/2}{n + z_\alpha^2} \pm \frac{z_\alpha n^{1/2}}{n + z_\alpha^2/2} \left\{ \widehat{p}(1-\widehat{p}) + \frac{z_\alpha^2}{4n} \right\}^{1/2}$$

The Agresti–Coull interval is basically a Wald interval that borrows its center from the Wilson interval. Defining $\widetilde{k} = k + z_\alpha^2/2$, $\widetilde{n} = n + z_\alpha^2$, and (hence) $\widetilde{p} = \widetilde{k}/\widetilde{n}$, the Agresti–Coull interval is

$$\widetilde{p} \pm z_\alpha \sqrt{\widetilde{p}(1-\widetilde{p})/\widetilde{n}}$$

When $\alpha = 0.05$, z_α is near enough to 2 that $\widetilde{p}$ can be thought of as a typical estimate of proportion where two successes and two failures have been added to the sample (Agresti and Coull 1998). This typical estimate of proportion makes the Agresti–Coull interval an easy-to-present alternative for introductory statistics students.

The Jeffreys interval is a Bayesian interval and is based on the Jeffreys prior, which is the Beta$(1/2, 1/2)$ distribution. Assigning this prior to p results in a posterior distribution for p that is Beta with parameters $k+1/2$ and $n-k+1/2$. The Jeffreys interval is then taken to be the $1-\alpha$ central posterior probability interval, namely, the $\alpha/2$ and $1-\alpha/2$ quantiles of the Beta$(k+1/2, n-k+1/2)$ distribution. These quantiles may be obtained directly by using Stata's `invibeta()` function.

Poisson

Given the total cases, k, the estimate of the expected count λ is k, and its standard error is $\sqrt{k}$. `ci` calculates the exact confidence interval $[\lambda_1, \lambda_2]$ such that

$$\Pr(K \geq k | \lambda = \lambda_1) = \alpha/2$$

and

$$\Pr(K \leq k | \lambda = \lambda_2) = \alpha/2$$

where K is Poisson with mean λ. Solution is by Newton's method. If $k = 0$, the calculation of λ_1 is skipped. All values are then reported as rates, which are the above numbers divided by the total exposure.

Harold Jeffreys (1891–1989) was born near Durham, England, and spent more than 75 years studying and working at the University of Cambridge, principally on theoretical and observational problems in geophysics, astronomy, mathematics, and statistics. He developed a systematic Bayesian approach to inference in his monograph *Theory of Probability*.

Edwin Bidwell (E. B.) Wilson (1879–1964) majored in mathematics at Harvard and studied and taught at Yale and MIT before returning to Harvard in 1922. He worked in mathematics, physics, and statistics. His method for binomial intervals can be considered a precursor, for a particular problem, of Neyman's concept of confidence intervals.

Jerzy Neyman (1894–1981) was born in Bendery, Russia, now Moldavia. He studied and then taught at Kharkov University, moving from physics to mathematics. In 1921, Neyman moved to Poland, where he worked in statistics at Bydgoszcz and then Warsaw. Neyman received a Rockefeller Fellowship to work with Karl Pearson at University College London. There, he collaborated with Egon Pearson, Karl's son, on the theory of hypothesis testing. Life in Poland became progressively more difficult, and Neyman returned to UCL to work there from 1934 to 1938. At this time, he published on the theory of confidence intervals. He then was offered a post in California at Berkeley, where he settled. Neyman established an outstanding statistics department and remained highly active in research, including applications in astronomy, meteorology, and medicine. He was one of the great statisticians of the 20th century.

Acknowledgment

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Also see

[R] **bitest** — Binomial probability test

[R] **prtest** — One- and two-sample tests of proportions

[R] **ttest** — Mean-comparison tests

[R] **ameans** — Arithmetic, geometric, and harmonic means

[R] **centile** — Report centile and confidence interval

[R] **summarize** — Summary statistics

[D] **pctile** — Create variable containing percentiles

Title

clogit — Conditional (fixed-effects) logistic regression

Syntax

`clogit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] , `group(`*varname*`)` [*options*]

options	Description
Model	
* `group(`*varname*`)`	matched group variable
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
`nonest`	do not check that panels are nested within clusters
Reporting	
`level(`#`)`	set confidence level; default is `level(95)`
`or`	report odds ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

*`group(`*varname*`)` is required.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()`, `nonest`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed (see [U] **11.1.6 weight**), but they are interpreted to apply to groups as a whole, not to individual observations. See *Use of weights* below.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Categorical outcomes > Conditional logistic regression

Description

`clogit` fits what biostatisticians and epidemiologists call conditional logistic regression for matched case–control groups (see, for example, Hosmer and Lemeshow [2000, chap. 7]) and what economists and other social scientists call fixed-effects logit for panel data (see, for example, Chamberlain [1980]). Computationally, these models are the same. *depvar* equal to nonzero and nonmissing (typically *depvar* equal to one) indicates a positive outcome, whereas *depvar* equal to zero indicates a negative outcome.

See [R] **asclogit** if you want to fit McFadden's choice model (McFadden 1974). Also see [R] **logistic** for a list of related estimation commands.

Options

Model

`group(`*varname*`)` is required; it specifies an identifier variable (numeric or string) for the matched groups. `strata(`*varname*`)` is a synonym for `group()`.

`offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`nonest`, available only with `vce(cluster` *clustvar*`)`, prevents checking that matched groups are nested within clusters. It is the user's responsibility to verify that the standard errors are theoretically correct.

Reporting

`level(#)`; see [R] **estimation options**.

`or` reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. `or` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `clogit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Matched case–control data
Use of weights
Fixed-effects logit

Introduction

`clogit` fits maximum likelihood models with a dichotomous dependent variable coded as 0/1 (more precisely, `clogit` interprets 0 and not 0 to indicate the dichotomy). Conditional logistic analysis differs from regular logistic regression in that the data are grouped and the likelihood is calculated relative to each group; that is, a conditional likelihood is used. See *Methods and formulas* at the end of this entry.

Biostatisticians and epidemiologists fit these models when analyzing matched case–control studies with $1:1$ matching, $1:k_{2i}$ matching, or $k_{1i}:k_{2i}$ matching, where i denotes the ith matched group for $i = 1, 2, \ldots, n$, where n is the total number of groups. `clogit` fits a model appropriate for all these matching schemes or for any mix of the schemes because the matching $k_{1i}:k_{2i}$ can vary from group to group. `clogit` always uses the true conditional likelihood, not an approximation. Biostatisticians and epidemiologists sometimes refer to the matched groups as "strata", but we will stick to the more generic term "group".

Economists and other social scientists fitting fixed-effects logit models have data that look exactly like the data biostatisticians and epidemiologists call $k_{1i}:k_{2i}$ matched case–control data. In terms of how the data are arranged, $k_{1i}:k_{2i}$ matching means that in the ith group, the dependent variable is 1 a total of k_{1i} times and 0 a total of k_{2i} times. There are a total of $T_i = k_{1i} + k_{2i}$ observations for the ith group. This data arrangement is what economists and other social scientists call "panel data", "longitudinal data", or "cross-sectional time-series data".

So no matter what terminology you use, the computation and the use of the `clogit` command is the same. The following example shows how your data should be arranged to use `clogit`.

▷ Example 1

Suppose that we have grouped data with the variable `id` containing a unique identifier for each group. Our outcome variable, `y`, contains 0s and 1s. If we were biostatisticians, `y` = 1 would indicate a case, `y` = 0 would be a control, and `id` would be an identifier variable that indicates the groups of matched case–control subjects.

If we were economists, `y` = 1 might indicate that a person was unemployed at any time during a year and `y` = 0, that a person was employed all year, and `id` would be an identifier variable for persons.

If we list the first few observations of this dataset, it looks like

```
. use http://www.stata-press.com/data/r12/clogitid
. list y x1 x2 id in 1/11
```

	y	x1	x2	id
1.	0	0	4	1014
2.	0	1	4	1014
3.	0	1	6	1014
4.	1	1	8	1014
5.	0	0	1	1017
6.	0	0	7	1017
7.	1	1	10	1017
8.	0	0	1	1019
9.	0	1	7	1019
10.	1	1	7	1019
11.	1	1	9	1019

Pretending that we are biostatisticians, we describe our data as follows. The first group (`id` $= 1014$) consists of four matched persons: 1 case (`y` $= 1$) and three controls (`y` $= 0$), that is, $1:3$ matching. The second group has $1:2$ matching, and the third $2:2$.

Pretending that we are economists, we describe our data as follows. The first group consists of 4 observations (one per year) for person 1014. This person had a period of unemployment during 1 year of 4. The second person had a period of unemployment during 1 year of 3, and the third had a period of 2 years of 4.

Our independent variables are `x1` and `x2`. To fit the conditional (fixed-effects) logistic model, we type

```
. clogit y x1 x2, group(id)
note: multiple positive outcomes within groups encountered.
Iteration 0:   log likelihood = -123.42828
Iteration 1:   log likelihood = -123.41386
Iteration 2:   log likelihood = -123.41386
Conditional (fixed-effects) logistic regression   Number of obs   =        369
                                                  LR chi2(2)      =       9.07
                                                  Prob > chi2     =     0.0107
Log likelihood = -123.41386                       Pseudo R2       =     0.0355
------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          x1 |    .653363   .2875215     2.27   0.023     .0898312    1.216895
          x2 |   .0659169   .0449555     1.47   0.143    -.0221943    .1540281
------------------------------------------------------------------------------
```

◁

❑ Technical note

The message "note: multiple positive outcomes within groups encountered" at the top of the `clogit` output for the previous example merely informs us that we have $k_{1i} : k_{2i}$ matching with $k_{1i} > 1$ for at least one group. If your data should be $1 : k_{2i}$ matched, this message tells you that there is an error in the data somewhere.

We can see the distribution of k_{1i} and $T_i = k_{1i} + k_{2i}$ for the data of the previous example by using the following steps:

```
. by id, sort: gen k1 = sum(y)
. by id: replace k1 = . if _n < _N
(303 real changes made, 303 to missing)
. by id: gen T = sum(y < .)
. by id: replace T = . if _n < _N
(303 real changes made, 303 to missing)
. tab k1
```

k1	Freq.	Percent	Cum.
1	48	72.73	72.73
2	12	18.18	90.91
3	4	6.06	96.97
4	2	3.03	100.00
Total	66	100.00	

```
. tab T
```

T	Freq.	Percent	Cum.
2	5	7.58	7.58
3	5	7.58	15.15
4	12	18.18	33.33
5	11	16.67	50.00
6	13	19.70	69.70
7	8	12.12	81.82
8	3	4.55	86.36
9	7	10.61	96.97
10	2	3.03	100.00
Total	66	100.00	

We see that k_{1i} ranges from 1 to 4 and T_i ranges from 2 to 10 for these data.

❑

❑ Technical note

For $k_{1i} : k_{2i}$ matching (and hence in the general case of fixed-effects logit), `clogit` uses a recursive algorithm to compute the likelihood, which means that there are no limits on the size of T_i. However, computation time is proportional to $\sum T_i \min(k_{1i}, k_{2i})$, so `clogit` will take roughly 10 times longer to fit a model with 10 : 10 matching than one with 1 : 10 matching. But `clogit` is fast, so computation time becomes an issue only when $\min(k_{1i}, k_{2i})$ is around 100 or more. See *Methods and formulas* for details.

❑

Matched case–control data

Here we give a more detailed example of matched case−control data.

▷ Example 2

Hosmer and Lemeshow (2000, 25) present data on matched pairs of infants, each pair having one with low birthweight and another with regular birthweight. The data are matched on age of the mother. Several possible maternal exposures are considered: race (three categories), smoking status, presence of hypertension, presence of uterine irritability, previous preterm delivery, and weight at the last menstrual period.

```
. use http://www.stata-press.com/data/r12/lowbirth2, clear
(Applied Logistic Regression, Hosmer & Lemeshow)
. describe
Contains data from http://www.stata-press.com/data/r12/lowbirth2.dta
  obs:           112                          Applied Logistic Regression,
                                                Hosmer & Lemeshow
 vars:             9                          26 Apr 2011 09:33
 size:         1,456
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
pairid          byte   %8.0g                  Case-control pair ID
low             byte   %8.0g                  Baby has low birthweight
age             byte   %8.0g                  Age of mother
lwt             int    %8.0g                  Mother's last menstrual weight
smoke           byte   %8.0g                  Mother smoked during pregnancy
ptd             byte   %8.0g                  Mother had previous preterm baby
ht              byte   %8.0g                  Mother has hypertension
ui              byte   %8.0g                  Uterine irritability
race            float  %9.0g                  race of mother: 1=white, 2=black,
                                                3=other
-------------------------------------------------------------------------------
Sorted by:
```

We list the case–control indicator variable, `low`; the match identifier variable, `pairid`; and two of the covariates, `lwt` and `smoke`, for the first 10 observations.

```
. list low lwt smoke pairid in 1/10
```

	low	lwt	smoke	pairid
1.	0	135	0	1
2.	1	101	1	1
3.	0	98	0	2
4.	1	115	0	2
5.	0	95	0	3
6.	1	130	0	3
7.	0	103	0	4
8.	1	130	1	4
9.	0	122	1	5
10.	1	110	1	5

We fit a conditional logistic model of low birthweight on mother's weight, race, smoking behavior, and history.

```
. clogit low lwt smoke ptd ht ui i.race, group(pairid) nolog
Conditional (fixed-effects) logistic regression   Number of obs   =        112
                                                  LR chi2(7)      =      26.04
                                                  Prob > chi2     =     0.0005
Log likelihood = -25.794271                       Pseudo R2       =     0.3355

------------------------------------------------------------------------------
         low |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         lwt |  -.0183757   .0100806    -1.82   0.068    -.0381333    .0013819
       smoke |   1.400656   .6278396     2.23   0.026     .1701131    2.631199
         ptd |   1.808009   .7886502     2.29   0.022     .2622828    3.353735
          ht |   2.361152   1.086128     2.17   0.030     .2323796    4.489924
          ui |   1.401929   .6961585     2.01   0.044     .0374836    2.766375
             |
        race |
           2 |   .5713643    .689645     0.83   0.407    -.7803149    1.923044
           3 |  -.0253148   .6992044    -0.04   0.971     -1.39573    1.345101
------------------------------------------------------------------------------
```

We might prefer to see results presented as odds ratios. We could have specified the `or` option when we first fit the model, or we can now redisplay results and specify `or`:

```
. clogit, or
Conditional (fixed-effects) logistic regression   Number of obs   =        112
                                                  LR chi2(7)      =      26.04
                                                  Prob > chi2     =     0.0005
Log likelihood = -25.794271                       Pseudo R2       =     0.3355

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         lwt |   .9817921    .009897    -1.82   0.068     .9625847    1.001383
       smoke |   4.057862   2.547686     2.23   0.026     1.185439    13.89042
         ptd |   6.098293    4.80942     2.29   0.022     1.299894    28.60938
          ht |   10.60316   11.51639     2.17   0.030     1.261599    89.11467
          ui |    4.06303   2.828513     2.01   0.044     1.038195    15.90088
             |
        race |
           2 |   1.770681   1.221141     0.83   0.407     .4582617     6.84175
           3 |    .975003   .6817263    -0.04   0.971     .2476522    3.838573
------------------------------------------------------------------------------
```

Smoking, previous preterm delivery, hypertension, uterine irritability, and possibly the mother's weight all contribute to low birthweight. `2.race` (mother black) and `3.race` (mother other) are statistically insignificant when compared with the `1.race` (mother white) omitted group, although the `2.race` effect is large. We can test the joint statistical significance of `2.race` and `3.race` by using `test`:

```
. test 2.race 3.race
 ( 1)  [low]2.race = 0
 ( 2)  [low]3.race = 0

           chi2(  2) =    0.88
         Prob > chi2 =    0.6436
```

For a more complete description of `test`, see [R] **test**. `test` presents results in coefficients rather than odds ratios. Jointly testing that the coefficients on `2.race` and `3.race` are 0 is equivalent to jointly testing that the odds ratios are 1.

Here one case was matched to one control, that is, 1:1 matching. From `clogit`'s point of view, that was not important—k_1 cases could have been matched to k_2 controls ($k_1 : k_2$ matching), and we would have fit the model in the same way. Furthermore, the matching can change from group to group, which we have denoted as $k_{1i} : k_{2i}$ matching, where i denotes the group. `clogit` does not care. To fit the conditional logistic regression model, we specified the `group(`*varname*`)` option, `group(pairid)`. The case and control are stored in separate observations. `clogit` knew that they were linked (in the same group) because the related observations share the same value of `pairid`.

◁

❑ Technical note

`clogit` provides a way to extend McNemar's test to multiple controls per case ($1 : k_{2i}$ matching) and to multiple controls matched with multiple cases ($k_{1i} : k_{2i}$ matching).

In Stata, McNemar's test is calculated by the `mcc` command; see [ST] **epitab**. The `mcc` command, however, requires that the matched case and control appear in one observation, so the data will need to be manipulated from 1 to 2 observations per stratum before using `clogit`. Alternatively, if you begin with `clogit`'s 2-observations-per-group organization, you will have to change it to 1 observation per group if you wish to use `mcc`. In either case, `reshape` provides an easy way to change the organization of the data. We will demonstrate its use below, but we direct you to [D] **reshape** for a more thorough discussion.

In the example above, we used `clogit` to analyze the relationship between low birthweight and various characteristics of the mother. Assume that we now want to assess the relationship between low birthweight and smoking, ignoring the mother's other characteristics. Using `clogit`, we obtain the following results:

```
. clogit low smoke, group(pairid) or
Iteration 0:   log likelihood = -35.425931
Iteration 1:   log likelihood = -35.419283
Iteration 2:   log likelihood = -35.419282
Conditional (fixed-effects) logistic regression   Number of obs   =        112
                                                  LR chi2(1)      =       6.79
                                                  Prob > chi2     =     0.0091
Log likelihood = -35.419282                       Pseudo R2       =     0.0875
------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       smoke |        2.75   1.135369     2.45   0.014     1.224347    6.176763
------------------------------------------------------------------------------
```

Let's compare our estimated odds ratio and 95% confidence interval with that produced by `mcc`. We begin by reshaping the data:

```
. keep low smoke pairid
. reshape wide smoke, i(pairid) j(low 0 1)
Data                               long   ->   wide
-----------------------------------------------------------------------------
Number of obs.                      112   ->     56
Number of variables                   3   ->      3
j variable (2 values)               low   ->   (dropped)
xij variables:
                                  smoke   ->   smoke0 smoke1
-----------------------------------------------------------------------------
```

We now have the variables `smoke0` (formed from `smoke` and `low` = 0), recording 1 if the control mother smoked and 0 otherwise; and `smoke1` (formed from `smoke` and `low` = 1), recording 1 if the case mother smoked and 0 otherwise. We can now use `mcc`:

```
. mcc smoke1 smoke0
```

Cases	Controls Exposed	Unexposed	Total
Exposed	8	22	30
Unexposed	8	18	26
Total	16	40	56

```
McNemar's chi2(1) =      6.53    Prob > chi2 = 0.0106
Exact McNemar significance probability       = 0.0161

Proportion with factor
        Cases       .5357143
        Controls    .2857143     [95% Conf. Interval]
        ---------   ---------    --------------------
        difference        .25      .0519726   .4480274
        ratio            1.875     1.148685   3.060565
        rel. diff.         .35      .1336258   .5663742
        odds ratio        2.75      1.179154   7.143667   (exact)
```

Both methods estimated the same odds ratio, and the 95% confidence intervals are similar. `clogit` produced a confidence interval of $[1.22, 6.18]$, whereas `mcc` produced a confidence interval of $[1.18, 7.14]$.

❑

Use of weights

With `clogit`, weights apply to groups as a whole, not to individual observations. For example, if there is a group in your dataset with a frequency weight of 3, there are a total of three groups in your sample with the same values of the dependent and independent variables as this one group. Weights must have the same value for all observations belonging to the same group; otherwise, an error message will be displayed.

▷ Example 3

We use the example from the above discussion of the `mcc` command. Here we have a total of 56 matched case–control groups, each with one case matched to one control. We had 8 matched pairs in which both the case and the control are exposed, 22 pairs in which the case is exposed and the control is unexposed, 8 pairs in which the case is unexposed and the control is exposed, and 18 pairs in which they are both unexposed.

With weights, it is easy to enter these data into Stata and run `clogit`.

```
. clear
. input id case exposed weight
           id       case    exposed     weight
  1. 1 1 1 8
  2. 1 0 1 8
  3. 2 1 1 22
  4. 2 0 0 22
  5. 3 1 0 8
  6. 3 0 1 8
  7. 4 1 0 18
  8. 4 0 0 18
  9. end
. clogit case exposed [w=weight], group(id) or
(frequency weights assumed)
Iteration 0:   log likelihood = -35.425931
Iteration 1:   log likelihood = -35.419283
Iteration 2:   log likelihood = -35.419282
Conditional (fixed-effects) logistic regression   Number of obs   =        112
                                                  LR chi2(1)      =       6.79
                                                  Prob > chi2     =     0.0091
Log likelihood = -35.419282                       Pseudo R2       =     0.0875
```

case	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
exposed	2.75	1.135369	2.45	0.014	1.224347	6.176763

Fixed-effects logit

The fixed-effects logit model can be written as

$$\Pr(y_{it} = 1 \mid \mathbf{x}_{it}) = F(\alpha_i + \mathbf{x}_{it}\boldsymbol{\beta})$$

where F is the cumulative logistic distribution

$$F(z) = \frac{\exp(z)}{1 + \exp(z)}$$

$i = 1, 2, \ldots, n$ denotes the independent units (called "groups" by `clogit`), and $t = 1, 2, \ldots, T_i$ denotes the observations for the ith unit (group).

Fitting this model by using a full maximum-likelihood approach leads to difficulties, however. When T_i is fixed, the maximum likelihood estimates for α_i and $\boldsymbol{\beta}$ are inconsistent (Andersen 1970; Chamberlain 1980). This difficulty can be circumvented by looking at the probability of $\mathbf{y}_i = (y_{i1}, \ldots, y_{iT_i})$ conditional on $\sum_{t=1}^{T_i} y_{it}$. This conditional probability does not involve the α_i, so they are never estimated when the resulting conditional likelihood is used. See Hamerle and Ronning (1995) for a succinct and lucid development. See *Methods and formulas* for the estimation equation.

▷ Example 4

We are studying unionization of women in the United States by using the `union` dataset; see [XT] **xt**. We fit the fixed-effects logit model:

```
. use http://www.stata-press.com/data/r12/union, clear
(NLS Women 14-24 in 1968)
. clogit union age grade not_smsa south black, group(idcode)
note: multiple positive outcomes within groups encountered.
note: 2744 groups (14165 obs) dropped because of all positive or
      all negative outcomes.
note: black omitted because of no within-group variance.
Iteration 0:   log likelihood = -4521.3385
Iteration 1:   log likelihood = -4516.1404
Iteration 2:   log likelihood = -4516.1385
Iteration 3:   log likelihood = -4516.1385
Conditional (fixed-effects) logistic regression   Number of obs   =      12035
                                                  LR chi2(4)      =      68.09
                                                  Prob > chi2     =     0.0000
Log likelihood = -4516.1385                       Pseudo R2       =     0.0075
```

union	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.0170301	.004146	4.11	0.000	.0089042	.0251561
grade	.0853572	.0418781	2.04	0.042	.0032777	.1674368
not_smsa	.0083678	.1127963	0.07	0.941	-.2127088	.2294445
south	-.748023	.1251752	-5.98	0.000	-.9933619	-.5026842
black	0	(omitted)				

We received three messages at the top of the output. The first one, "multiple positive outcomes within groups encountered", we expected. Our data do indeed have multiple positive outcomes (`union` = 1) in many groups. (Here a group consists of all the observations for a particular individual.)

The second message tells us that 2,744 groups were "dropped" by `clogit`. When either `union` = 0 or `union` = 1 for all observations for an individual, this individual's contribution to the log-likelihood is zero. Although these are perfectly valid observations in every sense, they have no effect on the estimation, so they are not included in the total "Number of obs". Hence, the reported "Number of obs" gives the effective sample size of the estimation. Here it is 12,035 observations—only 46% of the total 26,200.

We can easily check that there are indeed 2,744 groups with `union` either all 0 or all 1. We will generate a variable that contains the fraction of observations for each individual who has `union` = 1.

```
. by idcode, sort: generate fraction = sum(union)/sum(union < .)
. by idcode: replace fraction = . if _n < _N
(21766 real changes made, 21766 to missing)
. tabulate fraction
```

fraction	Freq.	Percent	Cum.
0	2,481	55.95	55.95
.0833333	30	0.68	56.63
.0909091	33	0.74	57.37
.1	53	1.20	58.57
(*output omitted*)			
.9	10	0.23	93.59
.9090909	11	0.25	93.84
.9166667	10	0.23	94.07
1	263	5.93	100.00
Total	4,434	100.00	

Because $2481 + 263 = 2744$, we confirm what `clogit` did.

The third warning message from `clogit` said "black omitted because of no within-group variance". Obviously, race stays constant for an individual across time. Any such variables are collinear with the α_i (that is, the fixed effects), and just as the α_i drop out of the conditional likelihood, so do all variables that are unchanging within groups. Thus they cannot be estimated with the conditional fixed-effects model.

There are several other estimators implemented in Stata that we could use with these data:

```
cloglog ... ,  vce(cluster idcode)
logit ... ,  vce(cluster idcode)
probit ... ,  vce(cluster idcode)
scobit ... ,  vce(cluster idcode)
xtcloglog ...
xtgee ... , family(binomial) link(logit) corr(exchangeable)
xtlogit ...
xtprobit ...
```

See [R] **cloglog**, [R] **logit**, [R] **probit**, [R] **scobit**, [XT] **xtcloglog**, [XT] **xtgee**, [XT] **xtlogit**, and [XT] **xtprobit** for details.

◁

Saved results

clogit saves the following in e():

Scalars

e(N)	number of observations
e(N_drop)	number of observations dropped because of all positive or all negative outcomes
e(N_group_drop)	number of groups dropped because of all positive or all negative outcomes
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	clogit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(group)	name of group() variable
e(multiple)	multiple if multiple positive outcomes within group
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance
e(gradient)	gradient vector

Functions

e(sample)	marks estimation sample

Methods and formulas

clogit is implemented as an ado-file.

Breslow and Day (1980, 247–279), Collett (2003, 251–267), and Hosmer and Lemeshow (2000, 223–259) provide a biostatistical point of view on conditional logistic regression. Hamerle and Ronning (1995) give a succinct and lucid review of fixed-effects logit; Chamberlain (1980) is a standard reference for this model. Greene (2012, chap. 17) provides a straightforward textbook description of conditional logistic regression from an economist's point of view, as well as a brief description of choice models.

Let $i = 1, 2, \ldots, n$ denote the groups and let $t = 1, 2, \ldots, T_i$ denote the observations for the ith group. Let y_{it} be the dependent variable taking on values 0 or 1. Let $\mathbf{y}_i = (y_{i1}, \ldots, y_{iT_i})$ be the outcomes for the ith group as a whole. Let $\mathbf{x}_{it}$ be a row vector of covariates. Let

$$k_{1i} = \sum_{t=1}^{T_i} y_{it}$$

be the observed number of ones for the dependent variable in the ith group. Biostatisticians would say that there are k_{1i} cases matched to $k_{2i} = T_i - k_{1i}$ controls in the ith group.

We consider the probability of a possible value of $\mathbf{y}_i$ conditional on $\sum_{t=1}^{T_i} y_{it} = k_{1i}$ (Hamerle and Ronning 1995, eq. 8.33; Hosmer and Lemeshow 2000, eq. 7.4),

$$\Pr\left(\mathbf{y}_i \mid \textstyle\sum_{t=1}^{T_i} y_{it} = k_{1i}\right) = \frac{\exp\left(\sum_{t=1}^{T_i} y_{it}\mathbf{x}_{it}\boldsymbol{\beta}\right)}{\sum_{\mathbf{d}_i \in S_i} \exp\left(\sum_{t=1}^{T_i} d_{it}\mathbf{x}_{it}\boldsymbol{\beta}\right)}$$

where d_{it} is equal to 0 or 1 with $\sum_{t=1}^{T_i} d_{it} = k_{1i}$, and S_i is the set of all possible combinations of k_{1i} ones and k_{2i} zeros. Clearly, there are $\binom{T_i}{k_{1i}}$ such combinations, but we need not count all these combinations to compute the denominator of the above equation. It can be computed recursively.

Denote the denominator by

$$f_i(T_i, k_{1i}) = \sum_{\mathbf{d}_i \in S_i} \exp\left(\sum_{t=1}^{T_i} d_{it}\mathbf{x}_{it}\boldsymbol{\beta}\right)$$

Consider, computationally, how f_i changes as we go from a total of 1 observation in the group to 2 observations to 3, etc. Doing this, we derive the recursive formula

$$f_i(T, k) = f_i(T-1, k) + f_i(T-1, k-1)\, \exp(\mathbf{x}_{iT}\boldsymbol{\beta})$$

where we define $f_i(T, k) = 0$ if $T < k$ and $f_i(T, 0) = 1$.

The conditional log-likelihood is

$$\ln L = \sum_{i=1}^{n} \left\{ \sum_{t=1}^{T_i} y_{it}\mathbf{x}_{it}\boldsymbol{\beta} - \log f_i(T_i, k_{1i}) \right\}$$

The derivatives of the conditional log-likelihood can also be computed recursively by taking derivatives of the recursive formula for f_i.

Computation time is roughly proportional to

$$p^2 \sum_{i=1}^{n} T_i \, \min(k_{1i}, k_{2i})$$

where p is the number of independent variables in the model. If $\min(k_{1i}, k_{2i})$ is small, computation time is not an issue. But if it is large—say, 100 or more—patience may be required.

If T_i is large for all groups, the bias of the unconditional fixed-effects estimator is not a concern, and we can confidently use `logit` with an indicator variable for each group (provided, of course, that the number of groups does not exceed `matsize`; see [R] **matsize**).

This command supports the clustered version of the Huber/White/sandwich estimator of the variance using `vce(robust)` and `vce(cluster` *clustvar*`)`. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. Specifying `vce(robust)` is equivalent to specifying `vce(cluster` *groupvar*`)`, where *groupvar* is the variable for the matched groups.

`clogit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **clogit postestimation** — Postestimation tools for clogit

[R] **asclogit** — Alternative-specific conditional logit (McFadden's choice) model

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **nlogit** — Nested logit regression

[R] **ologit** — Ordered logistic regression

[R] **scobit** — Skewed logistic regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtgee** — Fit population-averaged panel-data models by using GEE

[XT] **xtlogit** — Fixed-effects, random-effects, and population-averaged logit models

[U] **20 Estimation and postestimation commands**

Title

clogit postestimation — Postestimation tools for clogit

Description

The following standard postestimation commands are available after `clogit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`[2]	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

[2] The default prediction statistic `pc1` cannot be correctly handled by `margins`; however, `margins` can be used after `clogit` with options `predict(pu0)` and `predict(xb)`.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]
```

statistic	Description
Main	
pc1	probability of a positive outcome; the default
pu0	probability of a positive outcome, assuming fixed effect is zero
xb	linear prediction
stdp	standard error of the linear prediction
* dbeta	Delta-β influence statistic
* dx2	Delta-χ^2 lack-of-fit statistic
* gdbeta	Delta-β influence statistic for each group
* gdx2	Delta-χ^2 lack-of-fit statistic for each group
* hat	Hosmer and Lemeshow leverage
* residuals	Pearson residuals
* rstandard	standardized Pearson residuals
score	first derivative of the log likelihood with respect to $\mathbf{x}_j\beta$

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

Starred statistics are available for multiple controls per case-matching design only. They are not available if `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweights` were specified with `clogit`.

`dbeta`, `dx2`, `gdbeta`, `gdx2`, `hat`, and `rstandard` are not available if `constraints()` was specified with `clogit`.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pc1`, the default, calculates the probability of a positive outcome conditional on one positive outcome within group.

`pu0` calculates the probability of a positive outcome, assuming that the fixed effect is zero.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`dbeta` calculates the Delta-β influence statistic, a standardized measure of the difference in the coefficient vector that is due to deletion of the observation.

`dx2` calculates the Delta-χ^2 influence statistic, reflecting the decrease in the Pearson chi-squared that is due to deletion of the observation.

`gdbeta` calculates the approximation to the Pregibon stratum-specific Delta-β influence statistic, a standardized measure of the difference in the coefficient vector that is due to deletion of the entire stratum.

`gdx2` calculates the approximation to the Pregibon stratum-specific Delta-χ^2 influence statistic, reflecting the decrease in the Pearson chi-squared that is due to deletion of the entire stratum.

`hat` calculates the Hosmer and Lemeshow leverage or the diagonal element of the hat matrix.

`residuals` calculates the Pearson residuals.

`rstandard` calculates the standardized Pearson residuals.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_{it}\boldsymbol{\beta})$.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `clogit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$. This option cannot be specified with `dbeta`, `dx2`, `gdbeta`, `gdx2`, `hat`, and `rstandard`.

Remarks

`predict` may be used after `clogit` to obtain predicted values of the index $\mathbf{x}_{it}\boldsymbol{\beta}$. Predicted probabilities for conditional logistic regression must be interpreted carefully. Probabilities are estimated for each group as a whole, not for individual observations. Furthermore, the probabilities are conditional on the number of positive outcomes in the group (that is, the number of cases and the number of controls), or it is assumed that the fixed effect is zero. `predict` may also be used to obtain influence and lack of fit statistics for an individual observation and for the whole group, to compute Pearson, standardized Pearson residuals, and leverage values.

`predict` may be used for both within-sample and out-of-sample predictions.

▷ Example 1

Suppose that we have $1:k_{2i}$ matched data and that we have previously fit the following model:

```
. use http://www.stata-press.com/data/r12/clogitid
. clogit y x1 x2, group(id)
  (output omitted)
```

To obtain the predicted values of the index, we could type `predict idx, xb` to create a new variable called `idx`. From `idx`, we could then calculate the predicted probabilities. Easier, however, would be to type

```
. predict phat
(option pc1 assumed; probability of success given one success within group)
```

`phat` would then contain the predicted probabilities.

As noted previously, the predicted probabilities are really predicted probabilities for the group as a whole (that is, they are the predicted probability of observing $y_{it} = 1$ *and* $y_{it'} = 0$ for all $t' \neq t$). Thus, if we want to obtain the predicted probabilities for the estimation sample, it is important that, when we make the calculation, predictions be restricted to the same sample on which we estimated the data. We cannot predict the probabilities and then just keep the relevant ones because the entire sample determines each probability. Thus, assuming that we are not attempting to make out-of-sample predictions, we type

```
. predict phat2 if e(sample)
(option pc1 assumed; probability of success given one success within group)
```

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Recall that $i = 1, \ldots, n$ denote the groups and $t = 1, \ldots, T_i$ denote the observations for the ith group.

`predict` produces probabilities of a positive outcome within group conditional on there being one positive outcome (`pc1`),

$$\Pr\left(y_{it} = 1 \;\middle|\; \sum_{t=1}^{T_i} y_{it} = 1\right) = \frac{\exp(\mathbf{x}_{it}\boldsymbol{\beta})}{\sum_{t=1}^{T_i} \exp(\mathbf{x}_{it}\boldsymbol{\beta})}$$

or `predict` calculates the unconditional `pu0`:

$$\Pr(y_{it} = 1) = \frac{\exp(\mathbf{x}_{it}\boldsymbol{\beta})}{1 + \exp(\mathbf{x}_{it}\boldsymbol{\beta})}$$

Let $N = \sum_{j=1}^{n} T_j$ denote the total number of observations, p denote the number of covariates, and $\widehat{\theta}_{it}$ denote the conditional predicted probabilities of a positive outcome (`pc1`).

For the multiple control per case ($1 : k_{2i}$) matching, Hosmer and Lemeshow (2000, 248–251) propose the following diagnostics:

The Pearson residual is

$$r_{it} = \frac{(y_{it} - \widehat{\theta}_{it})}{\sqrt{\widehat{\theta}_{it}}}$$

The leverage (hat) value is defined as

$$h_{it} = \widehat{\theta}_{it}\widetilde{\mathbf{x}}_{it}^{T}(\widetilde{\mathbf{X}}^{T}\mathbf{U}\widetilde{\mathbf{X}})^{-1}\widetilde{\mathbf{x}}_{it}$$

where $\widetilde{\mathbf{x}}_{it} = \mathbf{x}_{it} - \sum_{j=1}^{T_i} \mathbf{x}_{ij}\widehat{\theta}_{ij}$ is the $1 \times p$ row vector of centered by a weighted stratum-specific mean covariate values, $\mathbf{U}_N = \text{diag}\{\widehat{\theta}_{it}\}$, and the rows of $\widetilde{\mathbf{X}}_{N\times p}$ are composed of $\widetilde{\mathbf{x}}_{it}$ values.

The standardized Pearson residual is

$$r_{sit} = \frac{r_{it}}{\sqrt{1 - h_{it}}}$$

The lack of fit and influence diagnostics for an individual observation are (respectively) computed as

$$\Delta\chi_{it}^{2} = r_{sit}^{2}$$

and

$$\Delta\widehat{\beta}_{it} = \Delta\chi_{it}^{2}\frac{h_{it}}{1 - h_{it}}$$

The lack of fit and influence diagnostics for the groups are the group-specific totals of the respective individual diagnostics shown above.

Reference

Hosmer, D. W., Jr., and S. Lemeshow. 2000. *Applied Logistic Regression*. 2nd ed. New York: Wiley.

Also see

[R] **clogit** — Conditional (fixed-effects) logistic regression

[U] **20 Estimation and postestimation commands**

Title

cloglog — Complementary log-log regression

Syntax

```
cloglog depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
eform	report exponentiated coefficients
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, jackknife, mi estimate, nestreg, rolling, statsby, stepwise, and svy are allowed; see [U] **11.1.10 Prefix commands**.

vce(bootstrap) and vce(jackknife) are not allowed with the mi estimate prefix; see [MI] **mi estimate**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

vce() and weights are not allowed with the svy prefix; see [SVY] **svy**.

fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

coeflegend does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Binary outcomes > Complementary log-log regression

Description

`cloglog` fits maximum-likelihood complementary log-log models.

See [R] **logistic** for a list of related estimation commands.

Options

Model

`noconstant`, `offset(`*varname*`)`; see [R] **estimation options**.

`asis` forces retention of perfect predictor variables and their associated perfectly predicted observations and may produce instabilities in maximization; see [R] **probit**.

`constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`eform` displays the exponentiated coefficients and corresponding standard errors and confidence intervals.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `cloglog` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction to complementary log-log regression
Robust standard errors

Introduction to complementary log-log regression

`cloglog` fits maximum likelihood models with dichotomous dependent variables coded as 0/1 (or, more precisely, coded as 0 and not 0).

▷ Example 1

We have data on the make, weight, and mileage rating of 22 foreign and 52 domestic automobiles. We wish to fit a model explaining whether a car is foreign based on its weight and mileage. Here is an overview of our data:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. keep make mpg weight foreign
. describe
Contains data from http://www.stata-press.com/data/r12/auto.dta
  obs:            74                          1978 Automobile Data
 vars:             4                          13 Apr 2011 17:45
 size:         1,702                          (_dta has notes)
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
make            str18  %-18s                  Make and Model
mpg             int    %8.0g                  Mileage (mpg)
weight          int    %8.0gc                 Weight (lbs.)
foreign         byte   %8.0g       origin     Car type
-------------------------------------------------------------------------------
Sorted by:  foreign
     Note:  dataset has changed since last saved

. inspect foreign
foreign:  Car type                              Number of Observations
-----------------------                    ------------------------------
                                                Total   Integers   Nonintegers
|   #                          Negative           -          -          -
|   #                          Zero              52         52          -
|   #                          Positive          22         22          -
|   #                                         ------     ------     ------
|   #   #                      Total             74         74          -
|   #   #                      Missing            -
+-----------------------     ------
0                       1                       74
   (2 unique values)
      foreign is labeled and all values are documented in the label.
```

The variable `foreign` takes on two unique values, 0 and 1. The value 0 denotes a domestic car, and 1 denotes a foreign car.

The model that we wish to fit is

$$\Pr(\texttt{foreign} = 1) = F(\beta_0 + \beta_1\texttt{weight} + \beta_2\texttt{mpg})$$

where $F(z) = 1 - \exp\{-\exp(z)\}$.

To fit this model, we type

```
. cloglog foreign weight mpg
Iteration 0:   log likelihood = -34.054593
Iteration 1:   log likelihood = -27.869915
Iteration 2:   log likelihood = -27.742997
Iteration 3:   log likelihood = -27.742769
Iteration 4:   log likelihood = -27.742769
Complementary log-log regression                Number of obs     =         74
                                                Zero outcomes     =         52
                                                Nonzero outcomes  =         22
                                                LR chi2(2)        =      34.58
Log likelihood = -27.742769                     Prob > chi2       =     0.0000
------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0029153   .0006974    -4.18   0.000    -.0042823   -.0015483
         mpg |  -.1422911    .076387    -1.86   0.062    -.2920069    .0074247
       _cons |   10.09694   3.351841     3.01   0.003     3.527448    16.66642
------------------------------------------------------------------------------
```

We find that heavier cars are less likely to be foreign and that cars yielding better gas mileage are also less likely to be foreign, at least when holding the weight of the car constant.

See [R] **maximize** for an explanation of the output.

◁

❑ Technical note

Stata interprets a value of 0 as a negative outcome (failure) and treats all other values (except missing) as positive outcomes (successes). Thus, if your dependent variable takes on the values 0 and 1, 0 is interpreted as failure and 1 as success. If your dependent variable takes on the values 0, 1, and 2, 0 is still interpreted as failure, but both 1 and 2 are treated as successes.

If you prefer a more formal mathematical statement, when you type `cloglog` y x, Stata fits the model

$$\Pr(y_j \neq 0 \mid \mathbf{x}_j) = 1 - \exp\Big\{-\exp(\mathbf{x}_j\boldsymbol{\beta})\Big\}$$

❑

Robust standard errors

If you specify the `vce(robust)` option, `cloglog` reports robust standard errors, as described in [U] **20.20 Obtaining robust variance estimates**. For the model of `foreign` on `weight` and `mpg`, the robust calculation increases the standard error of the coefficient on `mpg` by 44%:

```
. cloglog foreign weight mpg, vce(robust)

Iteration 0:   log pseudolikelihood = -34.054593
Iteration 1:   log pseudolikelihood = -27.869915
Iteration 2:   log pseudolikelihood = -27.742997
Iteration 3:   log pseudolikelihood = -27.742769
Iteration 4:   log pseudolikelihood = -27.742769

Complementary log-log regression                Number of obs     =         74
                                                Zero outcomes     =         52
                                                Nonzero outcomes  =         22

                                                Wald chi2(2)      =      29.74
Log pseudolikelihood = -27.742769               Prob > chi2       =     0.0000

------------------------------------------------------------------------------
             |               Robust
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0029153   .0007484    -3.90   0.000    -.0043822   -.0014484
         mpg |  -.1422911   .1102466    -1.29   0.197    -.3583704    .0737882
       _cons |   10.09694   4.317305     2.34   0.019     1.635174    18.5587
------------------------------------------------------------------------------
```

Without `vce(robust)`, the standard error for the coefficient on `mpg` was reported to be 0.076, with a resulting confidence interval of $[-0.29, 0.01]$.

The `vce(cluster` *clustvar*`)` option can relax the independence assumption required by the complementary log-log estimator to being just independence between clusters. To demonstrate this ability, we will switch to a different dataset.

We are studying unionization of women in the United States by using the `union` dataset; see [XT] **xt**. We fit the following model, ignoring that women are observed an average of 5.9 times each in this dataset:

```
. use http://www.stata-press.com/data/r12/union, clear
(NLS Women 14-24 in 1968)

. cloglog union age grade not_smsa south##c.year

Iteration 0:   log likelihood = -13606.373
Iteration 1:   log likelihood = -13540.726
Iteration 2:   log likelihood = -13540.607
Iteration 3:   log likelihood = -13540.607

Complementary log-log regression                Number of obs     =      26200
                                                Zero outcomes     =      20389
                                                Nonzero outcomes  =       5811

                                                LR chi2(6)        =     647.24
Log likelihood = -13540.607                     Prob > chi2       =     0.0000

------------------------------------------------------------------------------
       union |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0185346   .0043616     4.25   0.000      .009986    .0270833
       grade |   .0452772   .0057125     7.93   0.000     .0340809    .0564736
    not_smsa |  -.1886592   .0317801    -5.94   0.000    -.2509471   -.1263712
     1.south |  -1.422292   .3949381    -3.60   0.000    -2.196356    -.648227
        year |  -.0133007   .0049576    -2.68   0.007    -.0230174   -.0035839

south#c.year |
          1  |   .0105659   .0049234     2.15   0.032     .0009161    .0202157

       _cons |  -1.219801   .2952374    -4.13   0.000    -1.798455   -.6411462
------------------------------------------------------------------------------
```

The reported standard errors in this model are probably meaningless. Women are observed repeatedly, and so the observations are not independent. Looking at the coefficients, we find a large southern effect against unionization and a different time trend for the south. The `vce(cluster` *clustvar*`)` option provides a way to fit this model and obtains correct standard errors:

```
. cloglog union age grade not_smsa south##c.year, vce(cluster id) nolog
Complementary log-log regression                Number of obs     =      26200
                                                Zero outcomes     =      20389
                                                Nonzero outcomes  =       5811
                                                Wald chi2(6)      =     160.76
Log pseudolikelihood = -13540.607               Prob > chi2       =     0.0000
                              (Std. Err. adjusted for 4434 clusters in idcode)
------------------------------------------------------------------------------
             |               Robust
       union |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0185346   .0084873     2.18   0.029     .0018999    .0351694
       grade |   .0452772   .0125776     3.60   0.000     .0206255     .069929
    not_smsa |  -.1886592   .0642068    -2.94   0.003    -.3145021   -.0628162
   1.south   |  -1.422292    .506517    -2.81   0.005    -2.415047   -.4295365
        year |  -.0133007   .0090628    -1.47   0.142    -.0310633     .004462
             |
south#c.year |
          1  |   .0105659   .0063175     1.67   0.094    -.0018162     .022948
             |
       _cons |  -1.219801   .5175129    -2.36   0.018    -2.234107   -.2054942
------------------------------------------------------------------------------
```

These standard errors are larger than those reported by the inappropriate conventional calculation. By comparison, another way we could fit this model is with an equal-correlation population-averaged complementary log-log model:

```
. xtcloglog union age grade not_smsa south##c.year, pa nolog
GEE population-averaged model                   Number of obs      =      26200
Group variable:                       idcode    Number of groups   =       4434
Link:                                 cloglog   Obs per group: min =          1
Family:                              binomial                 avg =        5.9
Correlation:                    exchangeable                 max =         12
                                                Wald chi2(6)       =     234.66
Scale parameter:                             1  Prob > chi2        =     0.0000
------------------------------------------------------------------------------
       union |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0153737   .0081156     1.89   0.058    -.0005326      .03128
       grade |   .0549518   .0095093     5.78   0.000     .0363139    .0735897
    not_smsa |  -.1045232   .0431082    -2.42   0.015    -.1890138   -.0200326
   1.south   |  -1.714868   .3384558    -5.07   0.000    -2.378229   -1.051507
        year |  -.0115881   .0084125    -1.38   0.168    -.0280763    .0049001
             |
south#c.year |
          1  |   .0149796   .0041687     3.59   0.000     .0068091    .0231501
             |
       _cons |  -1.488278   .4468005    -3.33   0.001    -2.363991   -.6125652
------------------------------------------------------------------------------
```

The coefficient estimates are similar, but these standard errors are smaller than those produced by `cloglog, vce(cluster` *clustvar*`)`. This finding is as we would expect. If the within-panel correlation assumptions are valid, the population-averaged estimator should be more efficient.

In addition to this estimator, we may use the `xtgee` command to fit a panel estimator (with complementary log-log link) and any number of assumptions on the within-idcode correlation.

`cloglog, vce(cluster` *clustvar*`)` is robust to assumptions about within-cluster correlation. That is, it inefficiently sums within cluster for the standard-error calculation rather than attempting to exploit what might be assumed about the within-cluster correlation (as do the `xtgee` population-averaged models).

Saved results

`cloglog` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(N_f)`	number of zero outcomes
`e(N_s)`	number of nonzero outcomes
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

`e(cmd)`	`cloglog`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(clustvar)`	name of cluster variable
`e(offset)`	linear offset variable
`e(chi2type)`	`Wald` or `LR`; type of model χ^2 test
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(opt)`	type of optimization
`e(which)`	`max` or `min`; whether optimizer is to perform maximization or minimization
`e(ml_method)`	type of `ml` method
`e(user)`	name of likelihood-evaluator program
`e(technique)`	maximization technique
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(Cns)`	constraints matrix
`e(ilog)`	iteration log (up to 20 iterations)
`e(gradient)`	gradient vector
`e(V)`	variance–covariance matrix of the estimators
`e(V_modelbased)`	model-based variance

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`cloglog` is implemented as an ado-file.

Complementary log-log analysis (related to the gompit model, so named because of its relationship to the Gompertz distribution) is an alternative to logit and probit analysis, but it is unlike these other estimators in that the transformation is not symmetric. Typically, this model is used when the positive (or negative) outcome is rare.

The log-likelihood function for complementary log-log is

$$\ln L = \sum_{j \in S} w_j \ln F(\mathbf{x}_j\mathbf{b}) + \sum_{j \notin S} w_j \ln\Big\{1 - F(\mathbf{x}_j\mathbf{b})\Big\}$$

where S is the set of all observations j such that $y_j \neq 0$, $F(z) = 1 - \exp\big\{-\exp(z)\big\}$, and w_j denotes the optional weights. $\ln L$ is maximized as described in [R] **maximize**.

We can fit a gompit model by reversing the success–failure sense of the dependent variable and using `cloglog`.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. The scores are calculated as $\mathbf{u}_j = [\exp(\mathbf{x}_j\mathbf{b})\exp\big\{-\exp(\mathbf{x}_j\mathbf{b})\big\}/F(\mathbf{x}_j\mathbf{b})]\mathbf{x}_j$ for the positive outcomes and $\{-\exp(\mathbf{x}_j\mathbf{b})\}\mathbf{x}_j$ for the negative outcomes.

`cloglog` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

Acknowledgment

We thank Joseph Hilbe of Arizona State University for providing the inspiration for the `cloglog` command (Hilbe 1996, 1998).

References

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Long, J. S. 1997. *Regression Models for Categorical and Limited Dependent Variables*. Thousand Oaks, CA: Sage.

Long, J. S., and J. Freese. 2006. *Regression Models for Categorical Dependent Variables Using Stata*. 2nd ed. College Station, TX: Stata Press.

Xu, J., and J. S. Long. 2005. Confidence intervals for predicted outcomes in regression models for categorical outcomes. *Stata Journal* 5: 537–559.

Also see

[R] **cloglog postestimation** — Postestimation tools for cloglog

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **glm** — Generalized linear models

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **scobit** — Skewed logistic regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtcloglog** — Random-effects and population-averaged cloglog models

[U] **20 Estimation and postestimation commands**

Title

cloglog postestimation — Postestimation tools for cloglog

Description

The following postestimation commands are available after `cloglog`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic* `nooffset`]

statistic	Description
Main	
`pr`	probability of a positive outcome; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction
`score`	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of a positive outcome.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `cloglog`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

Remarks

Once you have fit a model, you can obtain the predicted probabilities by using the `predict` command for both the estimation sample and other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**. Here we will make only a few comments.

`predict` without arguments calculates the predicted probability of a positive outcome. With the `xb` option, it calculates the linear combination $\mathbf{x}_j\mathbf{b}$, where $\mathbf{x}_j$ are the independent variables in the jth observation and $\mathbf{b}$ is the estimated parameter vector.

With the `stdp` option, `predict` calculates the standard error of the linear prediction, which is not adjusted for replicated covariate patterns in the data.

▷ Example 1

In example 1 in [R] **cloglog**, we fit the complementary log-log model `cloglog foreign weight mpg`. To obtain predicted probabilities,

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. cloglog foreign weight mpg
  (output omitted)
. predict p
(option pr assumed; Pr(foreign))
. summarize foreign p
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
     foreign |        74    .2972973    .4601885          0          1
           p |        74    .2928348      .29732   .0032726   .9446067
```

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **cloglog** — Complementary log-log regression

[U] **20 Estimation and postestimation commands**

Title

cnsreg — Constrained linear regression

Syntax

`cnsreg` *depvar indepvars* [*if*] [*in*] [*weight*] , `constraints(`*constraints*`)` [*options*]

options	Description
Model	
* `constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
`noconstant`	suppress constant term
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `ols`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`mse1`	force MSE to be 1
`coeflegend`	display legend instead of statistics

*`constraints(`*constraints*`)` is required.
indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`bootstrap`, `by`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.
`vce()`, `mse1`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`aweights`, `fweights`, `pweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.
`mse1` and `coeflegend` do not appear in the dialog.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Constrained linear regression

Description

`cnsreg` fits constrained linear regression models.

Options

Model

`constraints(`*constraints*`)`, `collinear`, `noconstant`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(ols)`, the default, uses the standard variance estimator for ordinary least-squares regression.

Reporting

`level(#)`; see [R] **estimation options**.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following options are available with `cnsreg` but are not shown in the dialog box:

`mse1` is used only in programs and ado-files that use `cnsreg` to fit models other than constrained linear regression. `mse1` sets the mean squared error to 1, thus forcing the variance–covariance matrix of the estimators to be $(\mathbf{X}'\mathbf{D}\mathbf{X})^{-1}$ (see *Methods and formulas* in [R] **regress**) and affecting calculated standard errors. Degrees of freedom for t statistics are calculated as n rather than $n-p+c$, where p is the total number of parameters (prior to restrictions and including the constant) and c is the number of constraints.

`mse1` is not allowed with the `svy` prefix.

`coeflegend`; see [R] **estimation options**.

Remarks

For a discussion of constrained linear regression, see Greene (2012, 121–122); Hill, Griffiths, and Lim (2011, 231–233); or Davidson and MacKinnon (1993, 17).

▷ Example 1

In principle, we can obtain constrained linear regression estimates by modifying the list of independent variables. For instance, if we wanted to fit the model

$$\texttt{mpg} = \beta_0 + \beta_1\,\texttt{price} + \beta_2\,\texttt{weight} + u$$

and constrain $\beta_1 = \beta_2$, we could write

$$\texttt{mpg} = \beta_0 + \beta_1(\texttt{price} + \texttt{weight}) + u$$

and run a regression of `mpg` on `price` + `weight`. The estimated coefficient on the sum would be the constrained estimate of β_1 and β_2. Using `cnsreg`, however, is easier:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. constraint 1 price = weight
. cnsreg mpg price weight, constraint(1)
Constrained linear regression                   Number of obs =      74
                                                F(  1,    72) =   37.59
                                                Prob > F      =  0.0000
                                                Root MSE      =   4.722
 ( 1)  price - weight = 0
------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       price |  -.0009875   .0001611    -6.13   0.000    -.0013086   -.0006664
      weight |  -.0009875   .0001611    -6.13   0.000    -.0013086   -.0006664
       _cons |   30.36718   1.577958    19.24   0.000     27.22158    33.51278
------------------------------------------------------------------------------
```

We define constraints by using the `constraint` command; see [R] **constraint**. We fit the model with `cnsreg` and specify the constraint number or numbers in the `constraints()` option.

Just to show that the results above are correct, here is the result of applying the constraint by hand:

```
. generate x = price + weight
. regress mpg x
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =   37.59
       Model |  838.065767     1  838.065767            Prob > F      =  0.0000
    Residual |  1605.39369    72  22.2971346            R-squared     =  0.3430
-------------+------------------------------           Adj R-squared =  0.3339
       Total |  2443.45946    73  33.4720474            Root MSE      =   4.722
------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
           x |  -.0009875   .0001611    -6.13   0.000    -.0013086   -.0006664
       _cons |   30.36718   1.577958    19.24   0.000     27.22158    33.51278
------------------------------------------------------------------------------
```

◁

▷ Example 2

Models can be fit subject to multiple simultaneous constraints. We simply define the constraints and then include the constraint numbers in the `constraints()` option. For instance, say that we wish to fit the model

$$\texttt{mpg} = \beta_0 + \beta_1\,\texttt{price} + \beta_2\,\texttt{weight} + \beta_3\,\texttt{displ} + \beta_4\,\texttt{gear\_ratio} + \beta_5\,\texttt{foreign} + \beta_6\,\texttt{length} + u$$

subject to the constraints

$$\beta_1 = \beta_2 = \beta_3 = \beta_6$$
$$\beta_4 = -\beta_5 = \beta_0/20$$

(This model, like the one in example 1, is admittedly senseless.) We fit the model by typing

```
. constraint 1 price=weight
. constraint 2 displ=weight
. constraint 3 length=weight
```

```
. constraint 5 gear_ratio = -foreign
. constraint 6 gear_ratio = _cons/20
. cnsreg mpg price weight displ gear_ratio foreign length, c(1-3,5-6)
Constrained linear regression                   Number of obs =      74
                                                F(  2,    72) =  785.20
                                                Prob > F      =  0.0000
                                                Root MSE      =  4.6823

 ( 1)  price - weight = 0
 ( 2) - weight + displacement = 0
 ( 3) - weight + length = 0
 ( 4)  gear_ratio + foreign = 0
 ( 5)  gear_ratio - .05 _cons = 0
```

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
price	-.000923	.0001534	-6.02	0.000	-.0012288	-.0006172
weight	-.000923	.0001534	-6.02	0.000	-.0012288	-.0006172
displacement	-.000923	.0001534	-6.02	0.000	-.0012288	-.0006172
gear_ratio	1.326114	.0687589	19.29	0.000	1.189046	1.463183
foreign	-1.326114	.0687589	-19.29	0.000	-1.463183	-1.189046
length	-.000923	.0001534	-6.02	0.000	-.0012288	-.0006172
_cons	26.52229	1.375178	19.29	0.000	23.78092	29.26365

There are many ways we could have specified the `constraints()` option (which we abbreviated `c()` above). We typed `c(1-3,5-6)`, meaning that we want constraints 1 through 3 and 5 and 6; those numbers correspond to the constraints we defined. The only reason we did not use the number 4 was to emphasize that constraints do not have to be consecutively numbered. We typed `c(1-3,5-6)`, but we could have typed `c(1,2,3,5,6)` or `c(1-3,5,6)` or `c(1-2,3,5,6)` or even `c(1-6)`, which would have worked as long as constraint 4 was not defined. If we had previously defined a constraint 4, then `c(1-6)` would have included it.

◁

Saved results

cnsreg saves the following in e():

Scalars

e(N)	number of observations
e(df_m)	model degrees of freedom
e(df_r)	residual degrees of freedom
e(F)	F statistic
e(rmse)	root mean squared error
e(ll)	log likelihood
e(N_clust)	number of clusters
e(rank)	rank of e(V)

Macros

e(cmd)	cnsreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

cnsreg is implemented as an ado-file.

Let n be the number of observations, p be the total number of parameters (prior to restrictions and including the constant), and c be the number of constraints. The coefficients are calculated as $\mathbf{b}' = \mathbf{T}\{(\mathbf{T}'\mathbf{X}'\mathbf{W}\mathbf{X}\mathbf{T})^{-1}(\mathbf{T}'\mathbf{X}'\mathbf{W}\mathbf{y} - \mathbf{T}'\mathbf{X}'\mathbf{W}\mathbf{X}\mathbf{a}')\} + \mathbf{a}'$, where $\mathbf{T}$ and $\mathbf{a}$ are as defined in [P] **makecns**. $\mathbf{W} = \mathbf{I}$ if no weights are specified. If weights are specified, let $\mathbf{v}$: $1 \times n$ be the specified weights. If fweight frequency weights are specified, $\mathbf{W} = \mathrm{diag}(\mathbf{v})$. If aweight analytic weights are specified, then $\mathbf{W} = \mathrm{diag}[\mathbf{v}/(\mathbf{1}'\mathbf{v})(\mathbf{1}'\mathbf{1})]$, meaning that the weights are normalized to sum to the number of observations.

The mean squared error is $s^2 = (\mathbf{y}'\mathbf{W}\mathbf{y} - 2\mathbf{b}'\mathbf{X}'\mathbf{W}\mathbf{y} + \mathbf{b}'\mathbf{X}'\mathbf{W}\mathbf{X}\mathbf{b})/(n-p+c)$. The variance–covariance matrix is $s^2\mathbf{T}(\mathbf{T}'\mathbf{X}'\mathbf{W}\mathbf{X}\mathbf{T})^{-1}\mathbf{T}'$.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using vce(robust) and vce(cluster *clustvar*), respectively. See [P] **_robust**, particularly *Introduction* and *Methods and formulas*.

cnsreg also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

Davidson, R., and J. G. MacKinnon. 1993. *Estimation and Inference in Econometrics*. New York: Oxford University Press.

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

Hill, R. C., W. E. Griffiths, and G. C. Lim. 2011. *Principles of Econometrics*. 4th ed. Hoboken, NJ: Wiley.

Also see

[R] **cnsreg postestimation** — Postestimation tools for cnsreg

[R] **regress** — Linear regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

cnsreg postestimation — Postestimation tools for cnsreg

Description

The following postestimation commands are available after `cnsreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat (svy)`.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [, *statistic*]

statistic	Description
Main	
`xb`	linear prediction; the default
`residuals`	residuals
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`pr(`*a*`,`*b*`)`	$\Pr(a < y_j < b)$
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$
`score`	equivalent to `residuals`

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

where a and b may be numbers or variables; a missing ($a \geq .$) means $-\infty$, and b missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`residuals` calculates the residuals, that is, $y_j - \mathbf{x}_j\mathbf{b}$.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \,|\, a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated. *a* and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`score` is equivalent to `residuals` for linear regression models.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **cnsreg** — Constrained linear regression

[U] **20 Estimation and postestimation commands**

Title

constraint — Define and list constraints

Syntax

Define constraints

```
constraint [define] # [exp=exp | coeflist]
```

List constraints

```
constraint dir [numlist | _all]

constraint list [numlist | _all]
```

Drop constraints

```
constraint drop {numlist | _all}
```

Programmer's commands

```
constraint get #

constraint free
```

where *coeflist* is as defined in [R] **test** and # is restricted to the range 1–1,999, inclusive.

Menu

Statistics > Other > Manage constraints

Description

`constraint` defines, lists, and drops linear constraints. Constraints are for use by models that allow constrained estimation.

Constraints are defined by the `constraint` command. The currently defined constraints can be listed by either `constraint list` or `constraint dir`; both do the same thing. Existing constraints can be eliminated by `constraint drop`.

`constraint get` and `constraint free` are programmer's commands. `constraint get` returns the contents of the specified constraint in macro `r(contents)` and returns in scalar `r(defined)` 0 or 1—1 being returned if the constraint was defined. `constraint free` returns the number of a free (unused) constraint in macro `r(free)`.

Remarks

Using constraints is discussed in [R] **cnsreg**, [R] **mlogit**, and [R] **reg3**; this entry is concerned only with practical aspects of defining and manipulating constraints.

▷ Example 1

Constraints are numbered from 1 to 1,999, and we assign the number when we define the constraint:

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. constraint 2 [Indemnity]2.site = 0
```

The currently defined constraints can be listed by `constraint list`:

```
. constraint list
     2:  [indemnity]2.site = 0
```

`constraint drop` drops constraints:

```
. constraint drop 2
. constraint list
```

The empty list after `constraint list` indicates that no constraints are defined. Below we demonstrate the various syntaxes allowed by `constraint`:

```
. constraint 1 [Indemnity]
. constraint 10 [Indemnity]: 1.site 2.site
. constraint 11 [Indemnity]: 3.site
. constraint 21 [Prepaid=Uninsure]: nonwhite
. constraint 30 [Prepaid]
. constraint 31 [Insure]
. constraint list
     1:  [Indemnity]
    10:  [Indemnity]: 1.site 2.site
    11:  [Indemnity]: 3.site
    21:  [Prepaid=Uninsure]: nonwhite
    30:  [Prepaid]
    31:  [Insure]
. constraint drop 21-25, 31
. constraint list
     1:  [Indemnity]
    10:  [Indemnity]: 1.site 2.site
    11:  [Indemnity]: 3.site
    30:  [Prepaid]
. constraint drop _all
. constraint list
```

◁

❑ Technical note

The `constraint` command does not check the syntax of the constraint itself because a constraint can be interpreted only in the context of a model. Thus `constraint` is willing to define constraints that later will not make sense. Any errors in the constraints will be detected and mentioned at the time of estimation.

❑

Reference

Weesie, J. 1999. sg100: Two-stage linear constrained estimation. *Stata Technical Bulletin* 47: 24–30. Reprinted in *Stata Technical Bulletin Reprints*, vol. 8, pp. 217–225. College Station, TX: Stata Press.

Also see

[R] **cnsreg** — Constrained linear regression

Title

contrast — Contrasts and linear hypothesis tests after estimation

Syntax

```
contrast termlist [ , options ]
```

where *termlist* is a list of factor variables or interactions that appear in the current estimation results. The variables may be typed with or without contrast operators, and you may use any factor-variable syntax:

```
. contrast sex group sex#group
. contrast r.sex
```

See the *operators (op.)* table below for the list of contrast operators.

options	Description
Main	
`overall`	add a joint hypothesis test for all specified contrasts
`asobserved`	treat all factor variables as observed
`lincom`	treat user-defined contrasts as linear combinations
Equations	
`equation(`*eqspec*`)`	perform contrasts in *termlist* for equation *eqspec*
`atequations`	perform contrasts in *termlist* within each equation
Advanced	
`emptycells(`*empspec*`)`	treatment of empty cells for balanced factors
`noestimcheck`	suppress estimability checks
Reporting	
`level(#)`	confidence level; default is `level(95)`
`mcompare(`*method*`)`	adjust for multiple comparisons; default is `mcompare(noadjust)`
`noeffects`	suppress table of individual contrasts
`cieffects`	show effects table with confidence intervals
`pveffects`	show effects table with p-values
`effects`	show effects table with confidence intervals and p-values
`nowald`	suppress table of Wald tests
`noatlevels`	report only the overall Wald test for terms that use the within `@` or nested `|` operator
`nosvyadjust`	compute unadjusted Wald tests for survey results
`sort`	sort the individual contrast values in each term
`post`	post contrasts and their VCEs as estimation results
display_options	control column formats, row spacing, and line width
eform_option	report exponentiated contrasts

Term	Description
Main effects	
`A`	joint test of the main effects of `A`
r`.A`	individual contrasts that decompose `A` using *r*.
Interaction effects	
`A#B`	joint test of the two-way interaction effects of `A` and `B`
`A#B#C`	joint test of the three-way interaction effects of `A`, `B`, and `C`
r`.A#`*g*`.B`	individual contrasts for each interaction of `A` and `B` defined by *r*. and *g*.
Partial interaction effects	
r`.A#B`	joint tests of interactions of `A` and `B` within each contrast defined by *r*`.A`
`A#`*r*`.B`	joint tests of interactions of `A` and `B` within each contrast defined by *r*`.B`
Simple effects	
`A@B`	joint tests of the effects of `A` within each level of `B`
`A@B#C`	joint tests of the effects of `A` within each combination of the levels of `B` and `C`
r`.A@B`	individual contrasts of `A` that decompose `A@B` using *r*.
r`.A@B#C`	individual contrasts of `A` that decompose `A@B#C` using *r*.
Other conditional effects	
`A#B@C`	joint tests of the interaction effects of `A` and `B` within each level of `C`
`A#B@C#D`	joint tests of the interaction effects of `A` and `B` within each combination of the levels of `C` and `D`
r`.A#`*g*`.B@C`	individual contrasts for each interaction of `A` and `B` that decompose `A#B@C` using *r*. and *g*.
Nested effects	
`A|B`	joint tests of the effects of `A` nested in each level of `B`
`A|B#C`	joint tests of the effects of `A` nested in each combination of the levels of `B` and `C`
`A#B|C`	joint tests of the interaction effects of `A` and `B` nested in each level of `C`
`A#B|C#D`	joint tests of the interaction effects of `A` and `B` nested in each combination of the levels of `C` and `D`
r`.A|B`	individual contrasts of `A` that decompose `A|B` using *r*.
r`.A|B#C`	individual contrasts of `A` that decompose `A|B#C` using *r*.
r`.A#`*g*`.B|C`	individual contrasts for each interaction of `A` and `B` defined by *r*. and *g*. nested in each level of `C`
Slope effects	
`A#c.x`	joint test of the effects of `A` on the slopes of `x`
`A#c.x#c.y`	joint test of the effects of `A` on the slopes of the product (interaction) of `x` and `y`
`A#B#c.x`	joint test of the interaction effects of `A` and `B` on the slopes of `x`
`A#B#c.x#c.y`	joint test of the interaction effects of `A` and `B` on the slopes of the product (interaction) of `x` and `y`
r`.A#c.x`	individual contrasts of `A`'s effects on the slopes of `x` using *r*.
Denominators	
`... /` *term2*	use *term2* as the denominator in the F tests of the preceding terms
`... /`	use the residual as the denominator in the F tests of the preceding terms (the default if no other `/`s are specified)

A, B, C, and D represent any factor variable in the current estimation results.

x and y represent any continuous variable in the current estimation results.

r. and *g.* represent any contrast operator. See the table below.

c. specifies that a variable be treated as continuous; see [U] **11.4.3 Factor variables**.

Operators are allowed on any factor variable that does not appear to the right of @ or |. Operators decompose the effects of the associated factor variable into one-degree-of-freedom effects (contrasts).

Higher-level interactions are allowed anywhere an interaction operator (#) appears in the table.

Time-series operators are allowed if they were used in the estimation.

_eqns designates the equations in manova, mlogit, mprobit, and mvreg and can be specified anywhere a factor variable appears.

/ is allowed only after anova, cnsreg, manova, mvreg, or regress.

operators (op.)	Description
r.	differences from a reference (base) level; the default
a.	differences from the next level (adjacent contrasts)
ar.	differences from the previous level (reverse adjacent contrasts)
As-balanced operators	
g.	differences from the balanced grand mean
h.	differences from the balanced mean of subsequent levels (Helmert contrasts)
j.	differences from the balanced mean of previous levels (reverse Helmert contrasts)
p.	orthogonal polynomial in the level values
q.	orthogonal polynomial in the level sequence
As-observed operators	
gw.	differences from the observation-weighted grand mean
hw.	differences from the observation-weighted mean of subsequent levels
jw.	differences from the observation-weighted mean of previous levels
pw.	observation-weighted orthogonal polynomial in the level values
qw.	observation-weighted orthogonal polynomial in the level sequence

One or more individual contrasts may be selected by using the *op#.* or *op*(*numlist*). syntax. For example, a3.A selects the adjacent contrast for level 3 of A, and p(1/2).B selects the linear and quadratic effects of B. Also see *Orthogonal polynomial contrasts* and *Beyond linear models*.

Custom contrasts	Description
{A *numlist*}	user-defined contrast on the levels of factor A
{A#B *numlist*}	user-defined contrast on the levels of the interaction between A and B

Custom contrasts may be part of a term, such as {A *numlist*}#B, {A *numlist*}@B, {A *numlist*}|B, {A#B *numlist*}, and {A *numlist*}#{B *numlist*}. The same is true of higher-order custom contrasts, such as {A#B *numlist*}@C, {A#B *numlist*}#*r.*C, and {A#B *numlist*}#c.x.

Higher-order interactions with at most eight factor variables are allowed with custom contrasts.

method	Description
noadjust	do not adjust for multiple comparisons; the default
bonferroni [adjustall]	Bonferroni's method; adjust across all terms
sidak [adjustall]	Šidák's method; adjust across all terms
scheffe	Scheffé's method

Menu

Statistics > Postestimation > Contrasts

Description

`contrast` tests linear hypotheses and forms contrasts involving factor variables and their interactions from the most recently fit model. The tests include ANOVA-style tests of main effects, simple effects, interactions, and nested effects. `contrast` can use named contrasts to decompose these effects into comparisons against reference categories, comparisons of adjacent levels, comparisons against the grand mean, orthogonal polynomials, and such. Custom contrasts may also be specified.

`contrast` can be used with `svy` estimation results; see [SVY] **svy postestimation**.

Contrasts can also be computed for margins of linear and nonlinear responses; see [R] **margins, contrast**.

Options

Main

`overall` specifies that a joint hypothesis test over all terms be performed.

`asobserved` specifies that factor covariates be evaluated using the cell frequencies observed in the estimation sample. The default is to treat all factor covariates as though there were an equal number of observations in each level.

`lincom` specifies that user-defined contrasts be treated as linear combinations. The default is to require that all user-defined contrasts sum to zero. (Summing to zero is part of the definition of a contrast.)

Equations

`equation(`*eqspec*`)` specifies the equation from which contrasts are to be computed. The default is to compute contrasts from the first equation.

`atequations` specifies that the contrasts be computed within each equation.

Advanced

`emptycells(`*empspec*`)` specifies how empty cells are handled in interactions involving factor variables that are being treated as balanced.

`emptycells(strict)` is the default; it specifies that contrasts involving empty cells be treated as not estimable.

`emptycells(reweight)` specifies that the effects of the observed cells be increased to accommodate any missing cells. This makes the contrast estimable but changes its interpretation.

`noestimcheck` specifies that `contrast` not check for estimability. By default, the requested contrasts are checked and those found not estimable are reported as such. Nonestimability is usually caused by empty cells. If `noestimcheck` is specified, estimates are computed in the usual way and reported even though the resulting estimates are manipulable, which is to say they can differ across equivalent models having different parameterizations.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`mcompare(`*method*`)` specifies the method for computing p-values and confidence intervals that account for multiple comparisons within a factor-variable term.

Most methods adjust the comparisonwise error rate, α_c, to achieve a prespecified experimentwise error rate, α_e.

`mcompare(noadjust)` is the default; it specifies no adjustment.

$$\alpha_c = \alpha_e$$

`mcompare(bonferroni)` adjusts the comparisonwise error rate based on the upper limit of the Bonferroni inequality

$$\alpha_e \leq m\alpha_c$$

where *m* is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = \alpha_e/m$$

`mcompare(sidak)` adjusts the comparisonwise error rate based on the upper limit of the probability inequality

$$\alpha_e \leq 1 - (1 - \alpha_c)^m$$

where *m* is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = 1 - (1 - \alpha_e)^{1/m}$$

This adjustment is exact when the *m* comparisons are independent.

`mcompare(scheffe)` controls the experimentwise error rate using the F or χ^2 distribution with degrees of freedom equal to the rank of the term.

`mcompare(`*method* `adjustall)` specifies that the multiple-comparison adjustments count all comparisons across all terms rather than performing multiple comparisons term by term. This leads to more conservative adjustments when multiple variables or terms are specified in *marginslist*. This option is compatible only with the `bonferroni` and `sidak` methods.

`noeffects` suppresses the table of individual contrasts with confidence intervals. This table is produced by default when the `mcompare()` option is specified or when a term in *termlist* implies all individual contrasts.

`cieffects` specifies that a table containing a confidence interval for each individual contrast be reported.

`pveffects` specifies that a table containing a p-value for each individual contrast be reported.

`effects` specifies that a single table containing a confidence interval and p-value for each individual contrast be reported.

`nowald` suppresses the table of Wald tests.

`noatlevels` indicates that only the overall Wald test be reported for each term containing within or nested (`@` or `|`) operators.

`nosvyadjust` is for use with `svy` estimation commands. It specifies that the Wald test be carried out without the default adjustment for the design degrees of freedom. That is to say the test is carried out as $W/k \sim F(k,d)$ rather than as $(d-k+1)W/(kd) \sim F(k,d-k+1)$, where k is the dimension of the test and d is the total number of sampled PSUs minus the total number of strata.

`sort` specifies that the table of individual contrasts be sorted by the contrast values within each term.

`post` causes `contrast` to behave like a Stata estimation (e-class) command. `contrast` posts the vector of estimated contrasts along with the estimated variance–covariance matrix to `e()`, so you can treat the estimated contrasts just as you would results from any other estimation command. For example, you could use `test` to perform simultaneous tests of hypotheses on the contrasts, or you could use `lincom` to create linear combinations.

display_options: `vsquish`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`.

`vsquish` specifies that the blank space separating factor-variable terms or time-series–operated variables from other variables in the model be suppressed.

`cformat(%`*fmt*`)` specifies how to format contrasts, standard errors, and confidence limits in the table of estimated contrasts.

`pformat(%`*fmt*`)` specifies how to format p-values in the table of estimated contrasts.

`sformat(%`*fmt*`)` specifies how to format test statistics in the table of estimated contrasts.

`nolstretch` specifies that the width of the table of estimated contrasts not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the table of estimated contrasts up to the width of the Results window. To change the default, use `set lstretch off`. `nolstretch` is not shown in the dialog box.

eform_option specifies that the contrasts table be displayed in exponentiated form. e^{contrast} is displayed rather than contrast. Standard errors and confidence intervals are also transformed. See [R] ***eform_option*** for the list of available options.

Remarks

Remarks are presented under the following headings:

Introduction
One-way models
  Estimated cell means
  Testing equality of cell means
  Reference category contrasts
  Reverse adjacent contrasts
  Orthogonal polynomial contrasts
Two-way models
  Estimated interaction cell means
  Simple effects
  Interaction effects
  Main effects
  Partial interaction effects
Three-way and higher-order models
Contrast operators
  Differences from a reference level (r.)
  Differences from the next level (a.)
  Differences from the previous level (ar.)
  Differences from the grand mean (g.)
  Differences from the mean of subsequent levels (h.)
  Differences from the mean of previous levels (j.)
  Orthogonal polynomials (p. and q.)
User-defined contrasts
Empty cells
Empty cells, ANOVA style
Nested effects
Multiple comparisons
Unbalanced data
  Using observed cell frequencies
  Weighted contrast operators
Testing factor effects on slopes
Chow tests
Beyond linear models
Multiple equations

Introduction

`contrast` performs ANOVA-style tests of main effects, interactions, simple effects, and nested effects. It can easily decompose these tests into constituent contrasts using either named contrasts (codings) or user-specified contrasts. Comparing levels of factor variables—whether as main effects, interactions, or simple effects—is as easy as adding a contrast operator to the variable. The operators can compare each level with the previous level, each level with a reference level, each level with the mean of previous levels, and more.

`contrast` tests and estimates contrasts. A contrast of the parameters $\mu_1, \mu_2, \ldots, \mu_p$ is a linear combination $\sum_i c_i\mu_i$ whose c_i sum to zero. A difference of population means that $\mu_1 - \mu_2$ is a contrast, as are most other comparisons of population or model quantities (Coster 2005). Some contrasts may be estimated with `lincom`, but `contrast` is much more powerful. `contrast` can handle multiple contrasts simultaneously, and the command's contrast operators make it easy to specify complicated linear combinations.

Both the contrast operation and the creation of the margins for comparison can be performed as though the data were balanced (typical for experimental designs) or using the observed frequencies in the estimation sample (typical for observational studies). `contrast` can perform these analyses on the results of almost all of Stata's estimators, not just the linear-models estimators.

Most of contrast's computations can be considered comparisons of estimated cell means from a model fit. Tests of interactions are tests of whether the cell means for the interaction are all equal. Tests of main effects are tests of whether the marginal cell means for the factor are all equal. More focused comparisons of cell means (for example, is level 2 equal to level 1) are specified using contrast operators. More formally, all of contrast's computations are comparisons of conditional expectations; cell means are one type of conditional expectation.

All contrasts can also easily be graphed; see [R] **marginsplot**.

For a discussion of contrasts and testing for linear models, see Searle (1971) and Searle (1997). For discussions specifically related to experimental design, see Kuehl (2000), Winer, Brown, and Michels (1991), and Milliken and Johnson (2009). Rosenthal, Rosnow, and Rubin (2000) focus on contrasts with applications in behavioral sciences.

contrast is a flexible tool for understanding the effects of categorical covariates. If your model contains categorical covariates, and especially if it contains interactions, you will want to use contrast.

One-way models

Suppose we have collected data on cholesterol levels for individuals from five age groups. To study the effect of age group on cholesterol, we can begin by fitting a one-way model using regress:

```
. use http://www.stata-press.com/data/r12/cholesterol
(Artificial cholesterol data)
. label list ages
ages:
           1 10-19
           2 20-29
           3 30-39
           4 40-59
           5 60-79
. regress chol i.agegrp
      Source |       SS       df       MS              Number of obs =      75
-------------+------------------------------           F(  4,    70) =   35.02
       Model |  14943.3997     4  3735.84993            Prob > F      =  0.0000
    Residual |  7468.21971    70  106.688853            R-squared     =  0.6668
-------------+------------------------------           Adj R-squared =  0.6477
       Total |  22411.6194    74  302.859722            Root MSE      =  10.329

------------------------------------------------------------------------------
        chol |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      agegrp |
          2  |   8.203575   3.771628     2.18   0.033     .6812991    15.72585
          3  |   21.54105   3.771628     5.71   0.000     14.01878    29.06333
          4  |   30.15067   3.771628     7.99   0.000      22.6284    37.67295
          5  |   38.76221   3.771628    10.28   0.000     31.23993    46.28448
             |
       _cons |   180.5198   2.666944    67.69   0.000     175.2007    185.8388
------------------------------------------------------------------------------
```

Estimated cell means

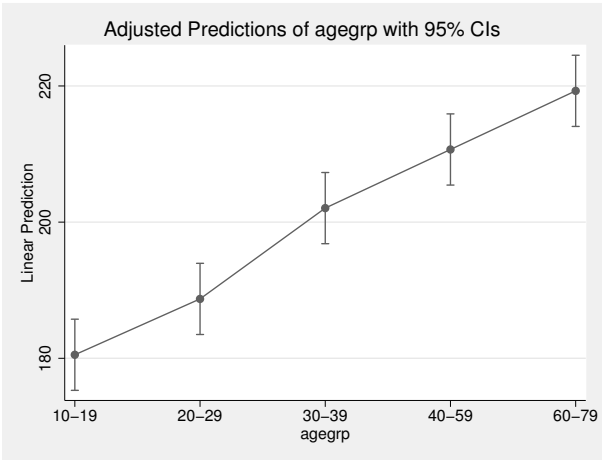
`margins` will show us the estimated cell means for each age group based on our fitted model:

```
. margins agegrp
Adjusted predictions                              Number of obs   =         75
Model VCE    : OLS
Expression   : Linear prediction, predict()
```

	Delta-method					
	Margin	Std. Err.	z	P>|z|	[95% Conf.	Interval]
agegrp						
1	180.5198	2.666944	67.69	0.000	175.2926	185.7469
2	188.7233	2.666944	70.76	0.000	183.4962	193.9504
3	202.0608	2.666944	75.76	0.000	196.8337	207.2879
4	210.6704	2.666944	78.99	0.000	205.4433	215.8975
5	219.282	2.666944	82.22	0.000	214.0548	224.5091

We can graph those means with `marginsplot`:

```
. marginsplot
  Variables that uniquely identify margins: agegrp
```



Testing equality of cell means

Are all the means equal? That is to say is there an effect of age group on cholesterol level? We can answer that by asking `contrast` to test whether the means of the age groups are identical.

```
. contrast agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp	4	35.02	0.0000
Residual	70		

The means are clearly different. We could have obtained this same test directly had we fit our model using `anova` rather than `regress`.

```
. anova chol agegrp
                    Number of obs =      75     R-squared     =  0.6668
                    Root MSE      =  10.329     Adj R-squared =  0.6477
```

Source	Partial SS	df	MS	F	Prob > F
Model	14943.3997	4	3735.84993	35.02	0.0000
agegrp	14943.3997	4	3735.84993	35.02	0.0000
Residual	7468.21971	70	106.688853		
Total	22411.6194	74	302.859722		

Achieving a more direct test result is why we recommend using `anova` instead of `regress` for models where our focus is on the categorical covariates. The models fit by `anova` and `regress` are identical; they merely parameterize the effects differently. The results of `contrast` will be identical regardless of which command is used to fit the model. If, however, we were fitting models whose responses are nonlinear functions of the covariates, such as logistic regression, then there would be no analogue to `anova`, and we would appreciate `contrast`'s ability to quickly test main effects and interactions.

Reference category contrasts

Now that we know that the overall effect of age group is statistically significant, we can explore the effects of each age group. One way to do that is to use the reference category operator, `r.`:

```
. contrast r.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(2 vs 1)	1	4.73	0.0330
(3 vs 1)	1	32.62	0.0000
(4 vs 1)	1	63.91	0.0000
(5 vs 1)	1	105.62	0.0000
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(2 vs 1)	8.203575	3.771628	.6812991	15.72585
(3 vs 1)	21.54105	3.771628	14.01878	29.06333
(4 vs 1)	30.15067	3.771628	22.6284	37.67295
(5 vs 1)	38.76221	3.771628	31.23993	46.28448

The cell mean of each age group is compared against the base age group (group 1, ages 10–19). The first table shows that each difference is significant. The second table gives an estimate and confidence interval for each contrast. These are the comparisons that linear regression gives with a factor covariate and no interactions. The contrasts are identical to the coefficients from our linear regression.

Reverse adjacent contrasts

We have far more flexibility with `contrast`. Age group is ordinal, so it is interesting to compare each age group with the preceding age group (rather than against one reference group). We specify that analysis by using the reverse adjacent operator, `ar.`:

```
. contrast ar.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(2 vs 1)	1	4.73	0.0330
(3 vs 2)	1	12.51	0.0007
(4 vs 3)	1	5.21	0.0255
(5 vs 4)	1	5.21	0.0255
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(2 vs 1)	8.203575	3.771628	.6812991	15.72585
(3 vs 2)	13.33748	3.771628	5.815204	20.85976
(4 vs 3)	8.60962	3.771628	1.087345	16.1319
(5 vs 4)	8.611533	3.771628	1.089257	16.13381

Age group 2's cholesterol level is 8.2 points higher than age group 1's; age group 3's is 13.3 points higher than age group 2's; and so on. Each age group is statistically different from the preceding age group at the 5% level.

Orthogonal polynomial contrasts

The relationship between age group and cholesterol level looked almost linear in our graph. We can examine that relationship further by using the orthogonal polynomial operator, `p.`:

```
. contrast p.agegrp, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Residual	70		

Only the linear effect is statistically significant.

We can even perform the joint test that all effects beyond linear are zero. We do that by selecting all polynomial contrasts above linear—that is, polynomial contrasts 2, 3, and 4.

```
. contrast p(2 3 4).agegrp, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	3	0.32	0.8129
Residual	70		

The joint test has three degrees of freedom and is clearly insignificant. A linear effect of age group seems adequate for this model.

Two-way models

Suppose we are investigating the effects of different dosages of a blood pressure medication and believe that the effects may be different for men and women. We can fit the following ANOVA model for `bpchange`, the change in diastolic blood pressure. Change is defined as the after measurement minus the before measurement, so that negative values of `bpchange` correspond to decreases in blood pressure.

```
. use http://www.stata-press.com/data/r12/bpchange
(Artificial blood pressure data)
. label list gender
gender:
           1 male
           2 female
. anova bpchange dose##gender
```

Number of obs =	30	R-squared	=	0.9647	
Root MSE =	1.4677	Adj R-squared	=	0.9573	

Source	Partial SS	df	MS	F	Prob > F
Model	1411.9087	5	282.381741	131.09	0.0000
dose	963.481795	2	481.740897	223.64	0.0000
gender	355.118817	1	355.118817	164.85	0.0000
dose#gender	93.3080926	2	46.6540463	21.66	0.0000
Residual	51.699253	24	2.15413554		
Total	1463.60796	29	50.4692399		

Estimated interaction cell means

Everything is significant, including the interaction. So increasing dosage is effective and differs by gender. Let's explore the effects. First, let's look at the estimated cell mean of blood pressure change for each combination of gender and dosage.

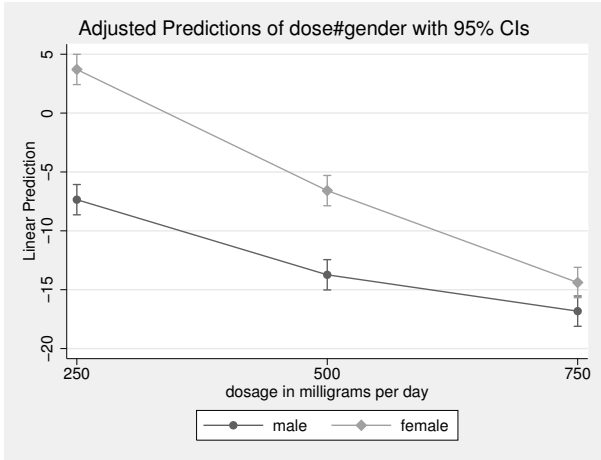
```
. margins dose#gender
Adjusted predictions                              Number of obs   =         30
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
dose#gender						
250 1	-7.35384	.6563742	-11.20	0.000	-8.64031	-6.06737
250 2	3.706567	.6563742	5.65	0.000	2.420097	4.993037
500 1	-13.73386	.6563742	-20.92	0.000	-15.02033	-12.44739
500 2	-6.584167	.6563742	-10.03	0.000	-7.870637	-5.297697
750 1	-16.82108	.6563742	-25.63	0.000	-18.10754	-15.53461
750 2	-14.38795	.6563742	-21.92	0.000	-15.67442	-13.10148

Our data are balanced, so these results will not be affected by the many different ways that `margins` can compute cell means. Moreover, because our model consists of only `dose` and `gender`, these are also the point estimates for each combination.

We can graph the results:

```
. marginsplot
  Variables that uniquely identify margins: dose gender
```



The lines are not parallel, which we expected because the interaction term is significant. Males experience a greater decline in blood pressure at every dosage level, but the effect of increasing dosage is greater for females. In fact, it is not clear if we can tell the difference between male and female response at the maximum dosage.

Simple effects

We can contrast the male and female responses within dosage to see the simple effects of `gender`. Because there are only two levels in `gender`, the choice of contrast operator is largely irrelevant. Aside from orthogonal polynomials, all operators produce the same estimates, although the effects can change signs.

```
. contrast r.gender@dose
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
gender@dose			
(2 vs 1) 250	1	141.97	0.0000
(2 vs 1) 500	1	59.33	0.0000
(2 vs 1) 750	1	6.87	0.0150
Joint	3	69.39	0.0000
Residual	24		

	Contrast	Std. Err.	[95% Conf.	Interval]
gender@dose				
(2 vs 1) 250	11.06041	.9282533	9.144586	12.97623
(2 vs 1) 500	7.149691	.9282533	5.23387	9.065512
(2 vs 1) 750	2.433124	.9282533	.5173031	4.348944

The effect for males is about 11 points higher than for females at a dosage of 250, and that shrinks to 2.4 points higher at the maximum dosage of 750.

We can form the simple effects the other way by contrasting the effect of `dose` at each level of `gender`:

```
. contrast ar.dose@gender
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
dose@gender			
(500 vs 250) 1	1	47.24	0.0000
(500 vs 250) 2	1	122.90	0.0000
(750 vs 500) 1	1	11.06	0.0028
(750 vs 500) 2	1	70.68	0.0000
Joint	4	122.65	0.0000
Residual	24		

	Contrast	Std. Err.	[95% Conf.	Interval]
dose@gender				
(500 vs 250) 1	-6.380018	.9282533	-8.295839	-4.464198
(500 vs 250) 2	-10.29073	.9282533	-12.20655	-8.374914
(750 vs 500) 1	-3.087217	.9282533	-5.003038	-1.171396
(750 vs 500) 2	-7.803784	.9282533	-9.719605	-5.887963

Here we use the `ar.` reverse adjacent contrast operator so that first we are comparing a dosage of 500 with a dosage of 250, and then we are comparing 750 with 500. We see that increasing the dosage has a larger effect on females—10.3 points when going from 250 to 500 compared with 6.4 points for males, and 7.8 points when going from 500 to 750 versus 3.1 points for males.

Interaction effects

By specifying contrast operators on both factors, we can decompose the interaction effect into separate interaction contrasts.

```
. contrast ar.dose#r.gender
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
dose#gender			
(500 vs 250) (2 vs 1)	1	8.87	0.0065
(750 vs 500) (2 vs 1)	1	12.91	0.0015
Joint	2	21.66	0.0000
Residual	24		

	Contrast	Std. Err.	[95% Conf.	Interval]
dose#gender				
(500 vs 250) (2 vs 1)	-3.910716	1.312748	-6.620095	-1.201336
(750 vs 500) (2 vs 1)	-4.716567	1.312748	-7.425947	-2.007187

Look for departures from zero to indicate an interaction effect between `dose` and `gender`. Both contrasts are significantly different from zero. Of course, we already knew the overall interaction was significant from our ANOVA results. The effect of increasing `dose` from 250 to 500 is 3.9 points greater in females than in males, and the effect of increasing `dose` from 500 to 750 is 4.7 points greater in females than in males. The confidence intervals for both estimates easily exclude zero, meaning that there is an interaction effect.

The joint test of these two interaction effects reproduces the test of interaction effects in the `anova` output. We can see that the F statistic of 21.66 matches the statistic from our original ANOVA results.

Main effects

We can perform tests of the main effects by listing each variable individually in `contrast`.

```
. contrast dose gender
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
dose	2	223.64	0.0000
gender	1	164.85	0.0000
Residual	24		

The F tests are equivalent to the tests of main effects in the `anova` output. This is true only for linear models. `contrast` provides an easy way to obtain main effects and other ANOVA-style tests for models whose responses are not linear in the parameters—`logistic`, `probit`, `glm`, etc.

If we include contrast operators on the variables, we can also decompose the main effects into individual contrasts:

```
. contrast ar.dose r.gender
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
dose			
(500 vs 250)	1	161.27	0.0000
(750 vs 500)	1	68.83	0.0000
Joint	2	223.64	0.0000
gender	1	164.85	0.0000
Residual	24		

	Contrast	Std. Err.	[95% Conf.	Interval]
dose				
(500 vs 250)	-8.335376	.6563742	-9.690066	-6.980687
(750 vs 500)	-5.4455	.6563742	-6.80019	-4.090811
gender				
(2 vs 1)	6.881074	.5359273	5.774974	7.987173

By specifying the `ar.` operator on `dose`, we decompose the main effect for dose into two one-degree-of-freedom contrasts, comparing the marginal mean of blood pressure change for each dosage level with that of the previous level. Because `gender` has only two levels, we cannot decompose this main effect any further. However, specifying a contrast operator on `gender` allowed us to calculate the difference in the marginal means for women and men.

Partial interaction effects

At this point, we have looked at the total interaction effects and at the main effects of each variable. The partial interaction effects are a midpoint between these two types of effects where we collect the individual interaction effects along the levels of one of the variables and perform a joint test of those interactions. If we think of the interaction effects as forming a table, with the levels of one factor variable forming the rows and the levels of the other forming the columns, partial interaction effects are joint tests of the interactions in a row or a column. To perform these tests, we specify a contrast operator on only one of the variables in our interaction. For this particular model, these are not very interesting because our variables have only two and three levels. Therefore, the tests of the partial interaction effects reproduce the tests that we obtained for the total interaction effects. We specify a contrast operator only on `dose` to decompose the overall test for interaction effects into joint tests for each `ar.dose` contrast:

```
. contrast ar.dose#gender
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
dose#gender			
(500 vs 250) (joint)	1	8.87	0.0065
(750 vs 500) (joint)	1	12.91	0.0015
Joint	2	21.66	0.0000
Residual	24		

The first row is a joint test of all the interaction effects involving the `(500 vs 250)` comparison of dosages. The second row is a joint test of all the interaction effects involving the `(750 vs 500)` comparison. If we look back at our output in *Interaction effects*, we can see that there was only one of each of these interaction effects. Therefore, each test labeled `(joint)` has only one degree-of-freedom.

We could have instead included a contrast operator on `gender` to compute the partial interaction effects along the other dimension:

```
. contrast dose#r.gender
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
dose#gender	2	21.66	0.0000
Residual	24		

Here we obtain a joint test of all the interaction effects involving the `(2 vs 1)` comparison for `gender`. Because `gender` has only two levels, the `(2 vs 1)` contrast is the only reference category contrast possible. Therefore, we obtain a single joint test of all the interaction effects.

Clearly, the partial interaction effects are not interesting for this particular model. However, if our factors had more levels, the partial interaction effects would produce tests that are not available in the total interaction effects. For example, if our model included factors for four dosage levels and three races, then typing

```
. contrast ar.dose#race
```

would produce three joint tests, one for each of the reverse adjacent contrasts for dosage. Each of these tests would be a two-degree-of-freedom test because race has three levels.

Three-way and higher-order models

All the contrasts and tests that we reviewed above for two-way models can be used with models that have more terms. For instance, we could fit a three-way full factorial model by using the `anova` command:

```
. use http://www.stata-press.com/data/r12/cont3way
. anova y race##sex##group
```

We could then test the simple effects of `race` within each level of the interaction between `sex` and `group`:

```
. contrast race@sex#group
```

To see the reference category contrasts that decompose these simple effects, type

```
. contrast r.race@sex#group
```

We could test the three-way interaction effects by typing

```
. contrast race#sex#group
```

or the interaction effects for the interaction of `race` and `sex` by typing

```
. contrast race#sex
```

To see the individual reference category contrasts that decompose this interaction effect, type

```
. contrast r.race#r.sex
```

We could even obtain joint tests for the interaction of `race` and `sex` within each level of `group` by typing

```
. contrast race#sex@group
```

For tests of the main effects of each factor, we can type

```
. contrast race sex group
```

We can calculate the individual reference category contrasts that decompose these main effects:

```
. contrast r.race r.sex r.group
```

For the partial interaction effects, we could type

```
. contrast r.race#group
```

to obtain a joint test of the two-way interaction effects of `race` and `group` for each of the individual `r.race` contrasts.

We could type

```
. contrast r.race#sex#group
```

to obtain a joint test of all the three-way interaction terms for each of the individual `r.race` contrasts.

Contrast operators

`contrast` recognizes a set of contrast operators that are used to specify commonly used contrasts. When these operators are used, `contrast` will report a test for each individual contrast in addition to the joint test for the term. We have already seen a few of these, like `r.` and `ar.`, in the previous examples. Here we will take a closer look at each of the unweighted operators.

Here we use the cholesterol dataset and the one-way ANOVA model from the example in *One-way models*:

```
. use http://www.stata-press.com/data/r12/cholesterol
(Artificial cholesterol data)
. anova chol agegrp
  (output omitted)
```

The `margins` command reports the estimated cell means, $\widehat{\mu}_1$, ..., $\widehat{\mu}_5$, for each of the five age groups.

```
. margins agegrp
Adjusted predictions                            Number of obs   =         75
Expression   : Linear prediction, predict()
```

	Delta-method					
	Margin	Std. Err.	z	P>|z|	[95% Conf.	Interval]
agegrp						
1	180.5198	2.666944	67.69	0.000	175.2926	185.7469
2	188.7233	2.666944	70.76	0.000	183.4962	193.9504
3	202.0608	2.666944	75.76	0.000	196.8337	207.2879
4	210.6704	2.666944	78.99	0.000	205.4433	215.8975
5	219.282	2.666944	82.22	0.000	214.0548	224.5091

Contrast operators provide an easy way to make certain types of comparisons of these cell means. We use the ordinal factor `agegrp` to demonstrate these operators because some types of contrasts are only meaningful when the levels of the factor have a natural ordering. We demonstrate these contrast operators using a one-way model; however, they are equally applicable to main effects, simple effects, and interactions for more complicated models.

Differences from a reference level (r.)

The `r.` operator specifies that each level of the attached factor variable be compared with a reference level. These are referred to as reference-level or reference-category contrasts (or effects), and `r.` is the reference-level operator.

In the following, we use the `r.` operator to test the effect of each category of age group when that category is compared with a reference category.

```
. contrast r.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(2 vs 1)	1	4.73	0.0330
(3 vs 1)	1	32.62	0.0000
(4 vs 1)	1	63.91	0.0000
(5 vs 1)	1	105.62	0.0000
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(2 vs 1)	8.203575	3.771628	.6812991	15.72585
(3 vs 1)	21.54105	3.771628	14.01878	29.06333
(4 vs 1)	30.15067	3.771628	22.6284	37.67295
(5 vs 1)	38.76221	3.771628	31.23993	46.28448

In the first table, the row labeled `(2 vs 1)` is a test of $\mu_2 = \mu_1$, a test that the mean cholesterol levels for the 10–19 age group (`agegrp` $= 1$) and the 20–29 age group (`agegrp` $= 2$) are equal. The tests in the next three rows are defined similarly. The row labeled `Joint` provides the joint test for these four hypotheses, which is just the test of the main effects of age group.

The second table provides the contrasts of each category with the reference category along with confidence intervals. The contrast in the row labeled `(2 vs 1)` is the difference in the cell means of the second age group and the first age group, $\widehat{\mu}_2 - \widehat{\mu}_1$.

The first level of a factor is the default reference level, but we can specify a different reference level by using the `b.` operator; see [U] **11.4.3.2 Base levels**. Here we use the last age group, `agegrp` $= 5$, instead of the first as the reference category. We also include the `nowald` option so that only the table of contrasts and their confidence intervals is produced.

```
. contrast rb5.agegrp, nowald
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(1 vs 5)	-38.76221	3.771628	-46.28448	-31.23993
(2 vs 5)	-30.55863	3.771628	-38.08091	-23.03636
(3 vs 5)	-17.22115	3.771628	-24.74343	-9.698877
(4 vs 5)	-8.611533	3.771628	-16.13381	-1.089257

Now the first row is labeled `(1 vs 5)` and is the difference in the cell means of the first and fifth age groups.

Differences from the next level (a.)

The `a.` operator specifies that each level of the attached factor variable be compared with the next level. These are referred to as adjacent contrasts (or effects), and `a.` is the adjacent operator. This operator is only meaningful with factor variables that have a natural ordering in the levels.

We can use the `a.` operator to perform tests that each level of age group differs from the next adjacent level.

```
. contrast a.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(1 vs 2)	1	4.73	0.0330
(2 vs 3)	1	12.51	0.0007
(3 vs 4)	1	5.21	0.0255
(4 vs 5)	1	5.21	0.0255
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(1 vs 2)	-8.203575	3.771628	-15.72585	-.6812991
(2 vs 3)	-13.33748	3.771628	-20.85976	-5.815204
(3 vs 4)	-8.60962	3.771628	-16.1319	-1.087345
(4 vs 5)	-8.611533	3.771628	-16.13381	-1.089257

In the first table, the row labeled `(1 vs 2)` tests the effect of belonging to the 10–19 age group instead of the 20–29 age group. Likewise, the rows labeled `(2 vs 3)`, `(3 vs 4)`, and `(4 vs 5)` are tests for the effects of being in the younger of the two age groups instead of the older one.

In the second table, the contrast in the row labeled `(1 vs 2)` is the difference in the cell means of the first and second age groups, $\widehat{\mu}_1 - \widehat{\mu}_2$. The contrasts in the other rows are defined similarly.

Differences from the previous level (ar.)

The ar. operator specifies that each level of the attached factor variable be compared with the previous level. These are referred to as reverse adjacent contrasts (or effects), and ar. is the reverse adjacent operator. As with the a. operator, this operator is only meaningful with factor variables that have a natural ordering in the levels.

In the following, we use the ar. operator to report tests for the individual reverse adjacent effects of agegrp.

```
. contrast ar.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(2 vs 1)	1	4.73	0.0330
(3 vs 2)	1	12.51	0.0007
(4 vs 3)	1	5.21	0.0255
(5 vs 4)	1	5.21	0.0255
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(2 vs 1)	8.203575	3.771628	.6812991	15.72585
(3 vs 2)	13.33748	3.771628	5.815204	20.85976
(4 vs 3)	8.60962	3.771628	1.087345	16.1319
(5 vs 4)	8.611533	3.771628	1.089257	16.13381

Here the Wald tests in the first table for the individual reverse adjacent effects are equivalent to the tests for the adjacent effects in the previous example. However, if we compare values of the contrasts in the bottom tables, we see the difference between the r. and the ar. operators. This time, the contrast in the first row is labeled (2 vs 1) and is the difference in the cell means of the second and first age groups, $\widehat{\mu}_2 - \widehat{\mu}_1$. This is the estimated effect of belonging to the 20–29 age group instead of the 10–19 age group. The remaining rows make similar comparisons to the previous level.

Differences from the grand mean (g.)

The g. operator specifies that each level of a factor variable be compared with the grand mean of all levels. For this operator, the grand mean is computed using a simple average of the cell means.

Here are the grand mean effects of agegrp:

```
. contrast g.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(1 vs mean)	1	68.42	0.0000
(2 vs mean)	1	23.36	0.0000
(3 vs mean)	1	0.58	0.4506
(4 vs mean)	1	19.08	0.0000
(5 vs mean)	1	63.65	0.0000
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(1 vs mean)	-19.7315	2.385387	-24.48901	-14.974
(2 vs mean)	-11.52793	2.385387	-16.28543	-6.770423
(3 vs mean)	1.809552	2.385387	-2.947953	6.567057
(4 vs mean)	10.41917	2.385387	5.661668	15.17668
(5 vs mean)	19.0307	2.385387	14.2732	23.78821

There are five age groups in our estimation sample. Thus the row labeled (1 vs mean) tests $\mu_1 = (\mu_1+\mu_2+\mu_3+\mu_4+\mu_5)/5$. The row labeled (2 vs mean) tests $\mu_2 = (\mu_1+\mu_2+\mu_3+\mu_4+\mu_5)/5$. The remaining rows perform similar tests for the third, fourth, and fifth age groups. In our example, the means for all age groups except group 3 (30–39 age group) are statistically different from the grand mean.

Differences from the mean of subsequent levels (h.)

The h. operator specifies that each level of the attached factor variable be compared with the mean of subsequent levels. These are referred to as Helmert contrasts (or effects), and h. is the Helmert operator. For this operator, the mean is computed using a simple average of the cell means. This operator is only meaningful with factor variables that have a natural ordering in the levels.

Here are the Helmert contrasts for agegrp:

```
. contrast h.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(1 vs >1)	1	68.42	0.0000
(2 vs >2)	1	50.79	0.0000
(3 vs >3)	1	15.63	0.0002
(4 vs 5)	1	5.21	0.0255
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(1 vs >1)	-24.66438	2.981734	-30.61126	-18.7175
(2 vs >2)	-21.94774	3.079522	-28.08965	-15.80583
(3 vs >3)	-12.91539	3.266326	-19.42987	-6.400905
(4 vs 5)	-8.611533	3.771628	-16.13381	-1.089257

The row labeled `(1 vs >1)` tests $\mu_1 = (\mu_2 + \mu_3 + \mu_4 + \mu_5)/4$, that is, that the cell mean for the youngest age group is equal to the average of the cell means for the older age groups. The row labeled `(2 vs >2)` tests $\mu_2 = (\mu_3 + \mu_4 + \mu_5)/3$. The tests in the other rows are defined similarly.

Differences from the mean of previous levels (j.)

The `j.` operator specifies that each level of the attached factor variable be compared with the mean of the previous levels. These are referred to as reverse Helmert contrasts (or effects), and `j.` is the reverse Helmert operator. For this operator, the mean is computed using a simple average of the cell means. This operator is only meaningful with factor variables that have a natural ordering in the levels.

Here are the reverse Helmert contrasts of `agegrp`:

```
. contrast j.agegrp
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(2 vs 1)	1	4.73	0.0330
(3 vs <3)	1	28.51	0.0000
(4 vs <4)	1	43.18	0.0000
(5 vs <5)	1	63.65	0.0000
Joint	4	35.02	0.0000
Residual	70		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp				
(2 vs 1)	8.203575	3.771628	.6812991	15.72585
(3 vs <3)	17.43927	3.266326	10.92479	23.95375
(4 vs <4)	20.2358	3.079522	14.09389	26.37771
(5 vs <5)	23.78838	2.981734	17.8415	29.73526

The row labeled `(2 vs 1)` tests $\mu_2 = \mu_1$, that is, that the cell means for the 20–29 and the 10–19 age groups are equal. The row labeled `(3 vs <3)` tests $\mu_3 = (\mu_1 + \mu_2)/2$, that is, that the cell mean for the 30–39 age group is equal to the average of the cell means for the 10–19 and 20–29 age groups. The tests in the remaining rows are defined similarly.

Orthogonal polynomials (p. and q.)

The p. and q. operators specify that orthogonal polynomials be applied to the attached factor variable. Orthogonal polynomial contrasts allow us to partition the effects of a factor variable into linear, quadratic, cubic, and higher-order polynomial components. The p. operator applies orthogonal polynomials using the values of the factor variable. The q. operator applies orthogonal polynomials using the level indices. If the level values of the factor variable are equally spaced, as with our agegrp variable, then the p. and q. operators yield the same result. These operators are only meaningful with factor variables that have a natural ordering in the levels.

Because agegrp has five levels, contrast can test the linear, quadratic, cubic, and quartic effects of agegrp.

```
. contrast p.agegrp, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Residual	70		

The row labeled (linear) tests the linear effect of agegrp, the only effect that appears to be significant in this case.

The labels for our agegrp variable show the age ranges that correspond to each level.

```
. label list ages
ages:
           1 10-19
           2 20-29
           3 30-39
           4 40-59
           5 60-79
```

Notice that these groups do not have equal widths. Now let's refit our model using the agemidpt variable. The values of agemidpt indicate the midpoint of each age group that was defined by the agegrp variable and are, therefore, not equally spaced.

```
. anova chol agemidpt
                          Number of obs =      75     R-squared     =  0.6668
                          Root MSE      =  10.329     Adj R-squared =  0.6477
```

Source	Partial SS	df	MS	F	Prob > F
Model	14943.3997	4	3735.84993	35.02	0.0000
agemidpt	14943.3997	4	3735.84993	35.02	0.0000
Residual	7468.21971	70	106.688853		
Total	22411.6194	74	302.859722		

Now if we use the `q.` operator, we will obtain the same results as above because the level indices of `agemidpt` are equivalent to the values of `agegrp`.

```
. contrast q.agemidpt, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agemidpt			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Residual	70		

However, if we use the `p.` operator, we will instead fit an orthogonal polynomial to the midpoint values.

```
. contrast p.agemidpt, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agemidpt			
(linear)	1	133.45	0.0000
(quadratic)	1	5.40	0.0230
(cubic)	1	0.05	0.8198
(quartic)	1	1.16	0.2850
Joint	4	35.02	0.0000
Residual	70		

Using the values of the midpoints, the quadratic effect is also significant at the 5% level.

❑ Technical note

We used the `noeffects` option when working with orthogonal polynomial contrasts. Apart from perhaps the sign of the contrast, the values of the individual contrasts are not meaningful for orthogonal polynomial contrasts. In addition, many textbooks provide tables with contrast coefficients that can be used to compute orthogonal polynomial contrasts where the levels of a factor are equally spaced. If we use these coefficients and calculate the contrasts manually with user-defined contrasts, as described below, the Wald tests for the polynomial terms will be equivalent, but the values of the individual contrasts will not necessarily match those that we obtain when using the polynomial contrast operator. When we use one of these contrast operators, an algorithm is used to calculate the coefficients of the polynomial contrast that will allow for unequal spacing in the levels of the factor as well as in the weights for the cell frequencies (when using `pw.` or `qw.`), as described in *Methods and formulas*.

❑

User-defined contrasts

In the previous examples, we performed tests using contrast operators. When there is not a contrast operator available to calculate the contrast in which we are interested, we can specify custom contrasts.

Here we fit a one-way model for cholesterol on the factor `race`, which has three levels:

```
. label list race
race:
           1 black
           2 white
           3 other
. anova chol race
                          Number of obs =      75     R-squared     =  0.0299
                          Root MSE      = 17.3775     Adj R-squared =  0.0029
```

Source	Partial SS	df	MS	F	Prob > F
Model	669.278235	2	334.639117	1.11	0.3357
race	669.278235	2	334.639117	1.11	0.3357
Residual	21742.3412	72	301.976961		
Total	22411.6194	74	302.859722		

`margins` calculates the estimated cell mean cholesterol level for each race:

```
. margins race
Adjusted predictions                                  Number of obs   =         75
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
race						
1	204.4279	3.475497	58.82	0.000	197.6161	211.2398
2	197.6132	3.475497	56.86	0.000	190.8014	204.425
3	198.7127	3.475497	57.18	0.000	191.9008	205.5245

Suppose we want to test the following linear combination:

$$\sum_{i=1}^{3} c_i \mu_i$$

where μ_i is the cell mean of `chol` when `race` is equal to its ith level (the means estimated using `margins` above). Assuming the c_i elements sum to zero, this linear combination is a contrast. We can specify this type of custom contrast by using the following syntax:

$$\{\texttt{race}\ c_1\ c_2\ c_3\}$$

The null hypothesis for the test of the main effects of `race` is

$$H_{0_{\text{race}}}\colon \mu_1 = \mu_2 = \mu_3$$

Although $H_{0_{\text{race}}}$ can be tested using any of several different contrasts on the cell means, we will test it by comparing the second and third cell means with the first. To test that the cell means for blacks and whites are equal, $\mu_1 = \mu_2$, we can specify the contrast

```
{race -1 1 0}
```

To test that the cell means for blacks and other races are equal, $\mu_1 = \mu_3$, we can specify the contrast

```
{race -1 0 1}
```

We can use both in a single call to `contrast`.

```
. contrast {race -1 1 0} {race -1 0 1}
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race			
(1)	1	1.92	0.1699
(2)	1	1.35	0.2488
Joint	2	1.11	0.3357
Residual	72		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(1)	-6.814717	4.915095	-16.61278	2.983345
(2)	-5.715261	4.915095	-15.51332	4.082801

The row labeled `(1)` is the test for $\mu_1 = \mu_2$, the first specified contrast. The row labeled `(2)` is the test for $\mu_1 = \mu_3$, the second specified contrast. The row labeled `Joint` is the overall test for the main effects of `race`.

Now let's fit a model with two factors, race and age group:

```
. anova chol race##agegrp
```

Number of obs = 75 R-squared = 0.7524
Root MSE = 9.61785 Adj R-squared = 0.6946

Source	Partial SS	df	MS	F	Prob > F
Model	16861.438	14	1204.38843	13.02	0.0000
race	669.278235	2	334.639117	3.62	0.0329
agegrp	14943.3997	4	3735.84993	40.39	0.0000
race#agegrp	1248.76005	8	156.095006	1.69	0.1201
Residual	5550.18143	60	92.5030238		
Total	22411.6194	74	302.859722		

The null hypothesis for the test of the main effects of `race` is now

$$H_{0_{\text{race}}}\colon \mu_{1\cdot} = \mu_{2\cdot} = \mu_{3\cdot}$$

where $\mu_{i\cdot}$ is the marginal mean of `chol` when `race` is equal to its ith level.

We can use the same syntax as above to perform this test by specifying contrasts on the marginal means of `race`:

```
. contrast {race -1 1 0} {race -1 0 1}
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race			
(1)	1	6.28	0.0150
(2)	1	4.41	0.0399
Joint	2	3.62	0.0329
Residual	60		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(1)	-6.814717	2.720339	-12.2562	-1.37323
(2)	-5.715261	2.720339	-11.15675	-.2737739

Custom contrasts may be specified on the cell means of interactions, too. Here we use `margins` to calculate the mean of `chol` for each cell in the interaction of `race` and `agegrp`:

```
. margins race#agegrp
Adjusted predictions                              Number of obs   =         75
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
race#agegrp						
1 1	179.2309	4.301233	41.67	0.000	170.8006	187.6611
1 2	196.4777	4.301233	45.68	0.000	188.0474	204.908
1 3	210.6694	4.301233	48.98	0.000	202.2391	219.0996
1 4	214.097	4.301233	49.78	0.000	205.6668	222.5273
1 5	221.6646	4.301233	51.54	0.000	213.2344	230.0949
2 1	186.0727	4.301233	43.26	0.000	177.6425	194.503
2 2	184.6714	4.301233	42.93	0.000	176.2411	193.1017
2 3	196.2633	4.301233	45.63	0.000	187.833	204.6936
2 4	209.9953	4.301233	48.82	0.000	201.5651	218.4256
2 5	211.0633	4.301233	49.07	0.000	202.633	219.4935
3 1	176.2556	4.301233	40.98	0.000	167.8254	184.6859
3 2	185.0209	4.301233	43.02	0.000	176.5906	193.4512
3 3	199.2498	4.301233	46.32	0.000	190.8195	207.68
3 4	207.9189	4.301233	48.34	0.000	199.4887	216.3492
3 5	225.118	4.301233	52.34	0.000	216.6877	233.5483

Now we are interested in testing the following linear combination of these cell means:

$$\sum_{i=1}^{3}\sum_{j=1}^{5} c_{ij}\mu_{ij}$$

We can specify this type of custom contrast using the following syntax:

{race#agegrp c_{11} c_{12} ... c_{15} c_{21} c_{22} ... c_{25} c_{31} c_{32} ... c_{35}}

Because the marginal means of chol for each level of race are linear combinations of the cell means, we can compose the test for the main effects of race in terms of the cell means directly. The constraint that the marginal means for blacks and whites are equal, $\mu_{1\cdot} = \mu_{2\cdot}$, translates to the following constraint on the cell means:

$$\frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15}) = \frac{1}{5}(\mu_{21} + \mu_{22} + \mu_{23} + \mu_{24} + \mu_{25})$$

Ignoring the common factor, we can specify this contrast as

```
{race#agegrp -1 -1 -1 -1 -1 1 1 1 1 1 0 0 0 0 0}
```

contrast will fill in the trailing zeros for us if we neglect to specify them, so

```
{race#agegrp -1 -1 -1 -1 -1 1 1 1 1 1}
```

is also allowed. The other constraint, $\mu_{1\cdot} = \mu_{3\cdot}$, translates to

$$\frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15}) = \frac{1}{5}(\mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35})$$

This can be specified to contrast as

```
{race#agegrp -1 -1 -1 -1 -1 0 0 0 0 0 1 1 1 1 1}
```

The following call to contrast yields the same test results as above.

```
. contrast {race#agegrp -1 -1 -1 -1 -1 1 1 1 1 1}
>          {race#agegrp -1 -1 -1 -1 -1 0 0 0 0 0 1 1 1 1 1}, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race#agegrp			
(1) (1)	1	6.28	0.0150
(2) (2)	1	4.41	0.0399
Joint	2	3.62	0.0329
Residual	60		

The row labeled (1) (1) is the test for

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{21} + \mu_{22} + \mu_{23} + \mu_{24} + \mu_{25}$$

It was the first specified contrast. The row labeled (2) (2) is the test for

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35}$$

It was the second specified contrast. The row labeled Joint tests (1) (1) and (2) (2) simultaneously.

We used the `noeffects` option above to suppress the table of contrasts. We can omit the $1/5$ from the equations for $\mu_{1\cdot} = \mu_{2\cdot}$ and $\mu_{1\cdot} = \mu_{3\cdot}$ and still obtain the appropriate tests. However, if we want to calculate the differences in the marginal means, we must include the $1/5 = 0.2$ on each of the contrast coefficients as follows:

```
. contrast {race#agegrp -0.2 -0.2 -0.2 -0.2 -0.2
                         0.2  0.2  0.2  0.2  0.2}
           {race#agegrp -0.2 -0.2 -0.2 -0.2 -0.2
                           0    0    0    0    0
                         0.2  0.2  0.2  0.2  0.2}
```

So far, we have reproduced the reference category contrasts by specifying user-defined contrasts on the marginal means and then on the cell means. For this test, it would have been easier to use the `r.` contrast operator:

```
. contrast r.race, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race			
(2 vs 1)	1	6.28	0.0150
(3 vs 1)	1	4.41	0.0399
Joint	2	3.62	0.0329
Residual	60		

In most cases, we can use contrast operators to perform tests. However, if we want to compare, for instance, the second and third age groups with the fourth and fifth age groups with the test

$$\frac{1}{2}(\mu_{\cdot 2} + \mu_{\cdot 3}) = \frac{1}{2}(\mu_{\cdot 4} + \mu_{\cdot 5})$$

there is not a contrast operator that corresponds to this particular contrast. A custom contrast is necessary.

```
. contrast {agegrp 0 -0.5 -0.5 0.5 0.5}
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp	1	62.19	0.0000
Residual	60		

	Contrast	Std. Err.	[95% Conf.	Interval]
agegrp (1)	19.58413	2.483318	14.61675	24.5515

Empty cells

An empty cell is a combination of the levels of factor variables that is not observed in the estimation sample. In the previous examples, we have seen data with three levels of `race`, five levels of `agegrp`, and all level combinations of `race` and `agegrp` present. Suppose there are no observations for white individuals in the second age group (ages 20–29).

```
. use http://www.stata-press.com/data/r12/cholesterol2
(Artificial cholesterol data, empty cells)
. label list
race:
           1 black
           2 white
           3 other
ages:
           1 10-19
           2 20-29
           3 30-39
           4 40-59
           5 60-79
. regress chol race##agegrp
note: 2.race#2.agegrp identifies no observations in the sample
```

Source	SS	df	MS		
Model	15751.6113	13	1211.66241	Number of obs =	70
Residual	5022.71559	56	89.6913498	F(13, 56) =	13.51
				Prob > F =	0.0000
				R-squared =	0.7582
				Adj R-squared =	0.7021
Total	20774.3269	69	301.077201	Root MSE =	9.4706

chol	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
race						
2	12.84185	5.989703	2.14	0.036	.8430383	24.84067
3	-.167627	5.989703	-0.03	0.978	-12.16644	11.83119
agegrp						
2	17.24681	5.989703	2.88	0.006	5.247991	29.24562
3	31.43847	5.989703	5.25	0.000	19.43966	43.43729
4	34.86613	5.989703	5.82	0.000	22.86732	46.86495
5	44.43374	5.989703	7.42	0.000	32.43492	56.43256
race#agegrp						
2 2	0	(empty)				
2 3	-22.83983	8.470719	-2.70	0.009	-39.80872	-5.870939
2 4	-14.67558	8.470719	-1.73	0.089	-31.64447	2.293306
2 5	-10.51115	8.470719	-1.24	0.220	-27.48004	6.457735
3 2	-6.054425	8.470719	-0.71	0.478	-23.02331	10.91446
3 3	-11.48083	8.470719	-1.36	0.181	-28.44971	5.488063
3 4	-.6796112	8.470719	-0.08	0.936	-17.6485	16.28928
3 5	-1.578052	8.470719	-0.19	0.853	-18.54694	15.39084
_cons	175.2309	4.235359	41.37	0.000	166.7464	183.7153

Now let's use `contrast` to test the main effects of `race`:

```
. contrast race
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race	(not testable)		
Residual	56		

By "not testable", `contrast` means that it cannot form a test for the main effects of `race` based on estimable functions of the model coefficients. `agegrp` has five levels, so `contrast` constructs an estimate of the ith margin for `race` as

$$\widehat{\mu}_{i\cdot} = \frac{1}{5}\sum_{j=1}^{5}\widehat{\mu}_{ij} = \widehat{\mu}_0 + \widehat{\alpha}_i + \frac{1}{5}\sum_{j=1}^{5}\left\{\widehat{\beta}_j + \widehat{(\alpha\beta)}_{ij}\right\}$$

but $\widehat{(\alpha\beta)}_{22}$ was constrained to zero because of the empty cell, so $\widehat{\mu}_{2\cdot}$ is not an estimable function of the model coefficients.

See *Estimable functions* in *Methods and formulas* of [R] **margins** for a technical description of estimable functions. The `emptycells(reweight)` option causes `contrast` to estimate $\mu_{2\cdot}$ by

$$\widehat{\mu}_{2\cdot} = \frac{\widehat{\mu}_{21} + \widehat{\mu}_{23} + \widehat{\mu}_{24} + \widehat{\mu}_{25}}{4}$$

which is an estimable function of the model coefficients.

```
. contrast race, emptycells(reweight)
Contrasts of marginal linear predictions
Margins      : asbalanced
Empty cells  : reweight
```

	df	F	P>F
race	2	3.17	0.0498
Residual	56		

We can reconstruct the effect of the `emptycells(reweight)` option by using custom contrasts.

```
. contrast {race#agegrp -4 -4 -4 -4 -4 5 0 5 5 5}
>          {race#agegrp -1 -1 -1 -1 -1 0 0 0 0 0 1 1 1 1 1}, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race#agegrp			
(1) (1)	1	1.06	0.3080
(2) (2)	1	2.37	0.1291
Joint	2	3.17	0.0498
Residual	56		

The row labeled `(1) (1)` is the test for

$$\frac{1}{5}(\mu_{11}+\mu_{12}+\mu_{13}+\mu_{14}+\mu_{15}) = \frac{1}{4}(\mu_{21}+\mu_{23}+\mu_{24}+\mu_{25})$$

It was the first specified contrast. The row labeled `(2) (2)` is the test for

$$\mu_{11}+\mu_{12}+\mu_{13}+\mu_{14}+\mu_{15} = \mu_{31}+\mu_{32}+\mu_{33}+\mu_{34}+\mu_{35}$$

It was the second specified contrast. The row labeled `Joint` is the overall test of the main effects of `race`.

Empty cells, ANOVA style

Let's refit the linear model from the previous example with `anova` to compare with `contrast`'s test for the main effects of `race`.

```
. anova chol race##agegrp
```

```
                  Number of obs =      70     R-squared     =  0.7582
                  Root MSE      = 9.47055     Adj R-squared =  0.7021
```

Source	Partial SS	df	MS	F	Prob > F
Model	15751.6113	13	1211.66241	13.51	0.0000
race	305.49046	2	152.74523	1.70	0.1914
agegrp	14387.8559	4	3596.96397	40.10	0.0000
race#agegrp	795.807574	7	113.686796	1.27	0.2831
Residual	5022.71559	56	89.6913498		
Total	20774.3269	69	301.077201		

`contrast` and `anova` handled the empty cell differently; the F statistic reported by `contrast` was 3.17, but `anova` reported 1.70. To see how they differ, consider the following table of the cell means and margins for our situation.

		agegrp					
		1	2	3	4	5	
race	1	μ_{11}	μ_{12}	μ_{13}	μ_{14}	μ_{15}	$\mu_{1\cdot}$
	2	μ_{21}		μ_{23}	μ_{24}	μ_{25}	
	3	μ_{31}	μ_{32}	μ_{33}	μ_{34}	μ_{35}	$\mu_{3\cdot}$
		$\mu_{\cdot 1}$		$\mu_{\cdot 3}$	$\mu_{\cdot 4}$	$\mu_{\cdot 5}$	

For testing the main effects of `race`, we know that we will be testing the equality of the marginal means for rows 1 and 3, that is, $\mu_{1\cdot} = \mu_{3\cdot}$. This translates into the following constraint:

$$\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15} = \mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35}$$

Because row 2 contains an empty cell in column 2, `anova` dropped column 2 and tested the equality of the marginal mean for row 2 with the average of the marginal means from rows 1 and 3, using only the remaining cell means. This translates into the following constraint:

$$2(\mu_{21} + \mu_{23} + \mu_{24} + \mu_{25}) = \mu_{11} + \mu_{13} + \mu_{14} + \mu_{15} + \mu_{31} + \mu_{33} + \mu_{34} + \mu_{35} \qquad (1)$$

Now that we know the constraints that `anova` used to test for the main effects of `race`, we can use custom contrasts to reproduce the `anova` test result.

```
. contrast {race#agegrp -1 -1 -1 -1 -1  0 0  0  0  0 1 1 1 1 1}
>          {race#agegrp  1  0  1  1  1 -2 0 -2 -2 -2 1 0 1 1 1}, noeffects
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race#agegrp			
(1) (1)	1	2.37	0.1291
(2) (2)	1	1.03	0.3138
Joint	2	1.70	0.1914
Residual	56		

The row labeled `(1) (1)` is the test for $\mu_{1\cdot} = \mu_{3\cdot}$; it was the first specified contrast. The row labeled `(2) (2)` is the test for the constraint in (1); it was the second specified contrast. The row labeled `Joint` is an overall test for the main effects of `race`.

Nested effects

`contrast` has the `|` operator for computing simple effects when the levels of one factor are nested within the levels of another. Here is a fictional example where we are interested in the effect of five methods of teaching algebra on students' scores for the math portion of the SAT. Suppose three algebra classes are randomly sampled from classes using each of the five methods so that `class` is nested in `method` as demonstrated in the following tabulation.

```
. use http://www.stata-press.com/data/r12/SAT
(Artificial SAT data)
. tabulate class method
```

class	method 1	2	3	4	5	Total
1	5	0	0	0	0	5
2	5	0	0	0	0	5
3	5	0	0	0	0	5
4	0	5	0	0	0	5
5	0	5	0	0	0	5
6	0	5	0	0	0	5
7	0	0	5	0	0	5
8	0	0	5	0	0	5
9	0	0	5	0	0	5
10	0	0	0	5	0	5
11	0	0	0	5	0	5
12	0	0	0	5	0	5
13	0	0	0	0	5	5
14	0	0	0	0	5	5
15	0	0	0	0	5	5
Total	15	15	15	15	15	75

We will consider `method` as fixed and `class` nested in `method` as random. To use `class` nested in `method` as the error term for `method`, we can specify the following `anova` model:

```
. anova score method / class|method /
```

```
                   Number of obs =      75     R-squared     =  0.7599
                   Root MSE      = 71.8517     Adj R-squared =  0.7039
```

Source	Partial SS	df	MS	F	Prob > F
Model	980312	14	70022.2857	13.56	0.0000
method	905872	4	226468	30.42	0.0000
class|method	74440	10	7444		
class|method	74440	10	7444	1.44	0.1845
Residual	309760	60	5162.66667		
Total	1290072	74	17433.4054		

Like `anova`, `contrast` allows the `|` operator, which specifies that one variable is nested in the levels of another. We can use `contrast` to test the main effects of `method` and the simple effects of `class` within `method`.

```
. contrast method class|method
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
method	(not testable)		
class|method			
1	2	2.80	0.0687
2	2	0.91	0.4089
3	2	1.10	0.3390
4	2	0.22	0.8025
5	2	2.18	0.1221
Joint	10	1.44	0.1845
Residual	60		

Although `contrast` was able to perform the individual tests for the simple effects of `class` within `method`, empty cells in the interaction between `method` and `class` prevented `contrast` from testing for a main effect of `method`. Here we add the `emptycells(reweight)` option so that `contrast` can take the empty cells into account when computing the marginal means for `method`.

```
. contrast method class|method, emptycells(reweight)
Contrasts of marginal linear predictions
Margins      : asbalanced
Empty cells  : reweight
```

	df	F	P>F
method	4	43.87	0.0000
class|method			
1	2	2.80	0.0687
2	2	0.91	0.4089
3	2	1.10	0.3390
4	2	0.22	0.8025
5	2	2.18	0.1221
Joint	10	1.44	0.1845
Residual	60		

Now `contrast` does report a test for the main effects of `method`. However, if we compare this with the `anova` results, we will see that the results are different. They are different because `contrast` uses the residual error term to compute the F test by default. Using notation similar to `anova`, we can use the `/` operator to specify a different error term for the test. Therefore, we can reproduce the test of main effects from our `anova` command by typing

```
. contrast method / class|method /, emptycells(reweight)
Contrasts of marginal linear predictions
Margins      : asbalanced
Empty cells  : reweight
```

	df	F	P>F
method	4	30.42	0.0000
class|method	10	(denominator)	
class|method			
1	2	2.80	0.0687
2	2	0.91	0.4089
3	2	1.10	0.3390
4	2	0.22	0.8025
5	2	2.18	0.1221
Joint	10	1.44	0.1845
Residual	60		

Multiple comparisons

We have seen that `contrast` can report the individual linear combinations that make up the requested effects. Depending upon the specified option, `contrast` will report confidence intervals, p-values, or both in the effects table. By default, the reported confidence intervals and p-values are not adjusted for multiple comparisons. Use the `mcompare()` option to adjust the confidence intervals and p-values for multiple comparisons of the individual effects.

Let's compute the grand mean effects of `race` using the `g.` operator. We also specify the `mcompare(bonferroni)` option to compute p-values and confidence intervals using Bonferroni's adjustment.

```
. use http://www.stata-press.com/data/r12/cholesterol
(Artificial cholesterol data)
. anova chol race##agegrp
  (output omitted )
. contrast g.race, mcompare(bonferroni)
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F	Bonferroni P>F
race				
(1 vs mean)	1	7.07	0.0100	0.0301
(2 vs mean)	1	2.82	0.0982	0.2947
(3 vs mean)	1	0.96	0.3312	0.9936
Joint	2	3.62	0.0329	
Residual	60			

```
Note: Bonferroni-adjusted p-values are reported for tests
      on individual contrasts only.
```

	Number of Comparisons
race	3

	Contrast	Std. Err.	Bonferroni [95% Conf.	Interval]
race				
(1 vs mean)	4.17666	1.570588	.3083743	8.044945
(2 vs mean)	-2.638058	1.570588	-6.506343	1.230227
(3 vs mean)	-1.538602	1.570588	-5.406887	2.329684

The last table reports a Bonferroni-adjusted confidence interval for each individual contrast. (Use the `effects` option to add p-values to the last table.) The first table includes a Bonferroni-adjusted p-value for each test that is not a joint test.

Joint tests are never adjusted for multiple comparisons. For example,

```
. contrast race@agegrp, mcompare(bonferroni)
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race@agegrp			
1	2	1.37	0.2620
2	2	2.44	0.0958
3	2	3.12	0.0512
4	2	0.53	0.5889
5	2	2.90	0.0628
Joint	10	2.07	0.0409
Residual	60		

```
Note: Bonferroni-adjusted p-values are reported
      for tests on individual contrasts only.
```

	Number of Comparisons
race@agegrp	10

	Contrast	Std. Err.	Bonferroni [95% Conf.	Interval]
race@agegrp				
(2 vs base) 1	6.841855	6.082862	-10.88697	24.57068
(2 vs base) 2	-11.80631	6.082862	-29.53513	5.922513
(2 vs base) 3	-14.40607	6.082862	-32.13489	3.322751
(2 vs base) 4	-4.101691	6.082862	-21.83051	13.62713
(2 vs base) 5	-10.60137	6.082862	-28.33019	7.127448
(3 vs base) 1	-2.975244	6.082862	-20.70407	14.75358
(3 vs base) 2	-11.45679	6.082862	-29.18561	6.272031
(3 vs base) 3	-11.41958	6.082862	-29.1484	6.309244
(3 vs base) 4	-6.17807	6.082862	-23.90689	11.55075
(3 vs base) 5	3.453375	6.082862	-14.27545	21.1822

Here we have five tests of simple effects with two degrees of freedom each. No Bonferroni-adjusted p-values are available for these tests, but the confidence intervals for the individual contrasts are adjusted.

Unbalanced data

By default, `contrast` treats all factors as balanced when computing marginal means. By balanced, we mean that `contrast` assumes an equal number of observations in each level of each factor and an equal number of observations in each cell of each interaction. If our data are balanced, there is no issue. If, however, our data are not balanced, we might prefer that `contrast` use the actual cell frequencies from our data in computing marginal means. We instruct `contrast` to use observed frequencies by adding the `asobserved` option.

Even if our data are unbalanced, we might still want `contrast` to compute balanced marginal means. It depends on what we want to test and what our data represent. If we have data from a designed experiment that started with an equal number of males and females but the data became unbalanced because the data from a few males were unusable, we might still want our margins computed as though the data were balanced. If, however, we have a representative sample of individuals from Los Angeles with 40% of European descent, 34% African-American, 25% Hispanic, and 1% Australian, we probably want our margins computed using these representative frequencies. We do not want Australians receiving the same weight as Europeans.

The following examples will use an unbalanced version of our dataset.

```
. use http://www.stata-press.com/data/r12/cholesterol3
(Artificial cholesterol data, unbalanced)
. tab race agegrp
```

	agegrp					
race	10-19	20-29	30-39	40-59	60-79	Total
black	1	5	5	4	3	18
white	4	5	7	4	4	24
other	3	7	6	5	4	25
Total	8	17	18	13	11	67

The row labeled `Total` gives observed cell frequencies for age group. These can be obtained by summing frequencies from the cells in the corresponding column. In this respect, we can also refer to them as marginal frequencies. We use the terms marginal frequencies and cell frequencies interchangeably below.

We begin by fitting the two-factor model with an interaction.

```
. anova chol race##agegrp
```

Number of obs =	67		R-squared =		0.8179
Root MSE =	8.37496		Adj R-squared =		0.7689
Source	Partial SS	df	MS	F	Prob > F
Model	16379.9926	14	1169.99947	16.68	0.0000
race	230.754396	2	115.377198	1.64	0.2029
agegrp	13857.9877	4	3464.49693	49.39	0.0000
race#agegrp	857.815209	8	107.226901	1.53	0.1701
Residual	3647.2774	52	70.13995		
Total	20027.27	66	303.443485		

Using observed cell frequencies

Recall that the marginal means are computed from the cell means. Treating the factors as balanced yields the following marginal means for `race`:

$$\eta_{1\cdot} = \frac{1}{5}(\mu_{11} + \mu_{12} + \mu_{13} + \mu_{14} + \mu_{15})$$

$$\eta_{2\cdot} = \frac{1}{5}(\mu_{21} + \mu_{22} + \mu_{23} + \mu_{24} + \mu_{25})$$

$$\eta_{3\cdot} = \frac{1}{5}(\mu_{31} + \mu_{32} + \mu_{33} + \mu_{34} + \mu_{35})$$

If we have a fixed population and unbalanced cells, then the $\eta_{i\cdot}$ do not represent population means. If, however, our data are representative of the population, we can use the frequencies from our estimation sample to estimate the population marginal means, denoted $\mu_{i\cdot}$.

Here are the results of testing for a main effect of `race`, treating all the factors as balanced.

```
. contrast r.race
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race			
(2 vs 1)	1	3.28	0.0757
(3 vs 1)	1	1.50	0.2263
Joint	2	1.64	0.2029
Residual	52		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(2 vs 1)	-5.324254	2.93778	-11.21934	.5708338
(3 vs 1)	-3.596867	2.93778	-9.491955	2.298221

The row labeled `(2 vs 1)` is the test for $\eta_{2\cdot} = \eta_{1\cdot}$. The row labeled `(3 vs 1)` is the test for $\eta_{3\cdot} = \eta_{1\cdot}$.

If the observed marginal frequencies are representative of the distribution of the levels of `agegrp`, we can use them to form the marginal means of `chol` for each of the levels of `race` from the cell means.

$$\mu_{1\cdot} = \frac{1}{67}(8\mu_{11} + 17\mu_{12} + 18\mu_{13} + 13\mu_{14} + 11\mu_{15})$$

$$\mu_{2\cdot} = \frac{1}{67}(8\mu_{21} + 17\mu_{22} + 18\mu_{23} + 13\mu_{24} + 11\mu_{25})$$

$$\mu_{3\cdot} = \frac{1}{67}(8\mu_{31} + 17\mu_{32} + 18\mu_{33} + 13\mu_{34} + 11\mu_{35})$$

Here are the results of testing for the main effects of `race`, using the observed marginal frequencies:

```
. contrast r.race, asobserved
Contrasts of marginal linear predictions
Margins      : asobserved
```

	df	F	P>F
race			
(2 vs 1)	1	7.25	0.0095
(3 vs 1)	1	3.89	0.0538
Joint	2	3.74	0.0304
Residual	52		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(2 vs 1)	-7.232433	2.686089	-12.62246	-1.842402
(3 vs 1)	-5.231198	2.651203	-10.55123	.0888295

The row labeled `(2 vs 1)` is the test for $\mu_{2\cdot} = \mu_{1\cdot}$. The row labeled `(3 vs 1)` is the test for $\mu_{3\cdot} = \mu_{1\cdot}$. Both tests were insignificant when we tested the cell means resulting from balanced frequencies; however, when we tested the cell means from observed frequencies, the first test is significant beyond the 5% level (and the second test is nearly so).

Here we reproduce the results of the `asobserved` option with custom contrasts. Because we are modifying the way that the marginal means are constructed from the cell means, we will specify the contrasts on the predicted cell means. We use macro expansion, `=`*exp*, to evaluate the fractions instead of approximating them with decimals. Macro expansion guarantees that the contrast coefficients sum to zero. For more information, see *Macro expansion operators and function* in [P] **macro**.

```
. contrast {race#agegrp -‘=8/67’ -‘=17/67’ -‘=18/67’ -‘=13/67’ -‘=11/67’
>                        ‘=8/67’  ‘=17/67’  ‘=18/67’  ‘=13/67’  ‘=11/67’}
>          {race#agegrp -‘=8/67’ -‘=17/67’ -‘=18/67’ -‘=13/67’ -‘=11/67’
>                         0         0         0         0         0
>                        ‘=8/67’  ‘=17/67’  ‘=18/67’  ‘=13/67’  ‘=11/67’}
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race#agegrp			
(1) (1)	1	7.25	0.0095
(2) (2)	1	3.89	0.0538
Joint	2	3.74	0.0304
Residual	52		

	Contrast	Std. Err.	[95% Conf.	Interval]
race#agegrp				
(1) (1)	-7.232433	2.686089	-12.62246	-1.842402
(2) (2)	-5.231198	2.651203	-10.55123	.0888295

Weighted contrast operators

`contrast` provides observation-weighted versions of five of the contrast operators—`gw.`, `hw.`, `jw.`, `pw.`, and `qw.`. The first three of these operators perform comparisons of means across cells, and like the marginal means just discussed, these means can be computed in two ways: 1) as though the cell frequencies were equal or 2) using the observed cell frequencies from the estimation sample. The weighted operators provide versions of the standard (as balanced) operators that weight these means by their cell frequencies. The two orthogonal polynomial operators involve similar adjustments for weighting.

Let’s examine what this means by using the `gw.` operator. The `gw.` operator is a weighted version of the `g.` operator. The `gw.` operator computes the grand mean using the cell frequencies for `race` obtained from the model fit.

Here we test the effects of `race`, comparing each level with the weighted grand mean but otherwise treating the factors as balanced in the marginal mean calculations.

```
. contrast gw.race
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race			
(1 vs mean)	1	2.78	0.1014
(2 vs mean)	1	2.06	0.1573
(3 vs mean)	1	0.06	0.8068
Joint	2	1.64	0.2029
Residual	52		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(1 vs mean)	3.24931	1.948468	-.6605779	7.159198
(2 vs mean)	-2.074944	1.44618	-4.976915	.8270276
(3 vs mean)	-.347557	1.414182	-3.18532	2.490206

The observed marginal frequencies of `race` are 18, 24, and 25. Thus the row labeled `(1 vs mean)` tests $\eta_{1\cdot} = (18\eta_{1\cdot}+24\eta_{2\cdot}+25\eta_{3\cdot})/67$; the row labeled `(2 vs mean)` tests $\eta_{2\cdot} = (18\eta_{1\cdot}+24\eta_{2\cdot}+25\eta_{3\cdot})/67$; and the row labeled `(3 vs mean)` tests $\eta_{3\cdot} = (18\eta_{1\cdot} + 24\eta_{2\cdot} + 25\eta_{3\cdot})/67$.

Now we reproduce the above results using custom contrasts. We are weighting the calculation of the grand mean from the marginal means for each of the races, but we are not weighting the calculation of the marginal means themselves. Therefore, we can specify the custom contrast on the marginal means for `race` instead of on the cell means.

```
. contrast {race  `=49/67' -`=24/67' -`=25/67'}
>          {race -`=18/67'  `=43/67' -`=25/67'}
>          {race -`=18/67' -`=24/67'  `=42/67'}
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
race			
(1)	1	2.78	0.1014
(2)	1	2.06	0.1573
(3)	1	0.06	0.8068
Joint	2	1.64	0.2029
Residual	52		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(1)	3.24931	1.948468	-.6605779	7.159198
(2)	-2.074944	1.44618	-4.976915	.8270276
(3)	-.347557	1.414182	-3.18532	2.490206

Now we will test for each `race` the difference between the marginal mean and the weighted grand mean, treating the factors as observed in the marginal mean calculations.

```
. contrast gw.race, asobserved wald ci
Contrasts of marginal linear predictions
Margins      : asobserved
```

	df	F	P>F
race			
(1 vs mean)	1	6.81	0.0118
(2 vs mean)	1	3.74	0.0587
(3 vs mean)	1	0.26	0.6099
Joint	2	3.74	0.0304
Residual	52		

	Contrast	Std. Err.	[95% Conf.	Interval]
race				
(1 vs mean)	4.542662	1.740331	1.050432	8.034891
(2 vs mean)	-2.689771	1.39142	-5.481859	.1023172
(3 vs mean)	-.6885363	1.341261	-3.379973	2.002901

The row labeled `(1 vs mean)` tests $\mu_{1.} = (18\mu_{1.} + 24\mu_{2.} + 25\mu_{3.})/67$; the row labeled `(2 vs mean)` tests $\mu_{2.} = (18\mu_{1.} + 24\mu_{2.} + 25\mu_{3.})/67$; and the row labeled `(3 vs mean)` tests $\mu_{3.} = (18\mu_{1.} + 24\mu_{2.} + 25\mu_{3.})/67$.

Here we use a custom contrast to reproduce the above result testing $\mu_{1.} = (18\mu_{1.} + 24\mu_{2.} + 25\mu_{3.})/67$. Because both the calculation of the marginal means and the calculation of the grand mean are adjusted, we specify the custom contrast on the cell means.

```
. contrast {race#agegrp  `=49/67*8/67'  `=49/67*17/67'  `=49/67*18/67'
>                        `=49/67*13/67'  `=49/67*11/67'
>                       -`=24/67*8/67' -`=24/67*17/67' -`=24/67*18/67'
>                       -`=24/67*13/67' -`=24/67*11/67'
>                       -`=25/67*8/67' -`=25/67*17/67' -`=25/67*18/67'
>                       -`=25/67*13/67' -`=25/67*11/67'}, nowald
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	[95% Conf.	Interval]
race#agegrp				
(1) (1)	4.542662	1.740331	1.050432	8.034891

The Helmert and reverse Helmert contrasts also involve calculating averages of the marginal means; therefore, weighted versions of these parameters are available as well. The `hw.` operator is a weighted version of the `h.` operator that computes the mean of the subsequent levels using the cell frequencies obtained from the model fit. The `jw.` operator is a weighted version of the `j.` operator that computes the mean of the previous levels using the cell frequencies obtained from the model fit.

For orthogonal polynomials, we can use the `pw.` and `qw.` operators, which are the weighted versions of the `p.` and `q.` operators. In this case, the cell frequencies from the model fit are used in the calculation of the orthogonal polynomial contrast coefficients.

Testing factor effects on slopes

For linear models where the independent variables are all factor variables, the linear prediction at fixed levels of the factor variables turns out to be a cell mean. With these models, `contrast` computes and tests the effects of the factor variables on the expected mean of the dependent variable. When factor variables are interacted with continuous variables, `contrast` distinguishes factor effects on the intercept from factor effects on the slope.

Here we have 1980 census data including information on the birth rate (`brate`), the median age (`medage`), and the region of the country (`region`) for each of the 50 states. We can fit an ANCOVA model for `brate` using main effects of the factor variable `region` and the continuous variable `medage`.

```
. use http://www.stata-press.com/data/r12/census3
(1980 Census data by state)
. label list cenreg
cenreg:
           1 NE
           2 N Cntrl
           3 South
           4 West
. anova brate i.region c.medage
```

	Number of obs = 50	R-squared = 0.8264
	Root MSE = 12.7575	Adj R-squared = 0.8110

Source	Partial SS	df	MS	F	Prob > F
Model	34872.8589	4	8718.21473	53.57	0.0000
region	2197.75453	3	732.584844	4.50	0.0076
medage	15327.423	1	15327.423	94.18	0.0000
Residual	7323.96108	45	162.754691		
Total	42196.82	49	861.159592		

For those more comfortable with linear regression, this is equivalent to the regression model

```
. regress brate i.region c.medage
```

You may use either.

We can use `contrast` to compute reference category effects for `region`. These contrasts compare the adjusted means of regions 2, 3, and 4 with the adjusted mean of region 1.

```
. contrast r.region
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
region			
(2 vs 1)	1	2.24	0.1417
(3 vs 1)	1	0.78	0.3805
(4 vs 1)	1	10.33	0.0024
Joint	3	4.50	0.0076
Residual	45		

	Contrast	Std. Err.	[95% Conf.	Interval]
region				
(2 vs 1)	9.061063	6.057484	-3.139337	21.26146
(3 vs 1)	5.06991	5.72396	-6.458738	16.59856
(4 vs 1)	21.71328	6.755616	8.106774	35.31979

Let's add the interaction between `region` and `medage` to the model.

```
. anova brate region##c.medage
```

Number of obs = 50 R-squared = 0.9000
Root MSE = 10.0244 Adj R-squared = 0.8833

Source	Partial SS	df	MS	F	Prob > F
Model	37976.3149	7	5425.18784	53.99	0.0000
region	3405.07044	3	1135.02348	11.30	0.0000
medage	5279.71448	1	5279.71448	52.54	0.0000
region#medage	3103.45597	3	1034.48532	10.29	0.0000
Residual	4220.5051	42	100.488217		
Total	42196.82	49	861.159592		

The parameterization for the expected value of `brate` as a function of `region` and `medage` is given by

$$E(\texttt{brate}|\texttt{region} = i, \texttt{medage}) = \alpha_0 + \alpha_i + \beta_0\texttt{medage} + \beta_i\texttt{medage}$$

where α_0 is the intercept and β_0 is the slope of `medage`. We are modeling the effects of `region` in two different ways. The α_i parameters measure the effect of `region` on the intercept, and the β_i parameters measure the effect of `region` on the slope of `medage`.

`contrast` computes and tests effects on slopes separately from effects on intercepts. First, we will compute the reference category effects of `region` on the intercept:

```
. contrast r.region
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
region			
(2 vs 1)	1	0.09	0.7691
(3 vs 1)	1	0.01	0.9389
(4 vs 1)	1	8.50	0.0057
Joint	3	11.30	0.0000
Residual	42		

	Contrast	Std. Err.	[95% Conf.	Interval]
region				
(2 vs 1)	-49.38396	167.1281	-386.6622	287.8942
(3 vs 1)	-9.058983	117.424	-246.0302	227.9123
(4 vs 1)	343.0024	117.6547	105.5656	580.4393

Now we will compute the reference category effects of `region` on the slope of `medage`:

```
. contrast r.region#c.medage
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
region#c.medage			
(2 vs 1)	1	0.16	0.6917
(3 vs 1)	1	0.03	0.8558
(4 vs 1)	1	8.18	0.0066
Joint	3	10.29	0.0000
Residual	42		

	Contrast	Std. Err.	[95% Conf.	Interval]
region#c.medage				
(2 vs 1)	2.208539	5.530981	-8.953432	13.37051
(3 vs 1)	.6928008	3.788735	-6.953175	8.338777
(4 vs 1)	-10.94649	3.827357	-18.67041	-3.22257

At the 5% level, the slope of `medage` for the fourth region differs from that of the first region, but at that level of significance, we cannot say that the slope for the second or third region differs from that of the first.

This model is simple enough that the reference category contrasts reproduce the coefficients for `region` and for the interactions in an equivalent model fit by `regress`.

```
. regress brate region##c.medage
```

Source	SS	df	MS		
Model	37976.3149	7	5425.18784	Number of obs	= 50
Residual	4220.5051	42	100.488217	F(7, 42)	= 53.99
Total	42196.82	49	861.159592	Prob > F	= 0.0000
				R-squared	= 0.9000
				Adj R-squared	= 0.8833
				Root MSE	= 10.024

brate	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
region						
2	-49.38396	167.1281	-0.30	0.769	-386.6622	287.8942
3	-9.058983	117.424	-0.08	0.939	-246.0302	227.9123
4	343.0024	117.6547	2.92	0.006	105.5656	580.4393
medage	-8.802707	3.462865	-2.54	0.015	-15.79105	-1.814362
region# c.medage						
2	2.208539	5.530981	0.40	0.692	-8.953432	13.37051
3	.6928008	3.788735	0.18	0.856	-6.953175	8.338777
4	-10.94649	3.827357	-2.86	0.007	-18.67041	-3.22257
_cons	411.8268	108.2084	3.81	0.000	193.4533	630.2002

This will not be the case for models that are more complicated.

Chow tests

Now let's suppose we are fitting a model for birth rates on median age and marriage rate. We are also interested in whether the regression coefficients differ for states in the east versus states in the west. We use census divisions to create a new variable, `west`, that indicates which states are in the western half of the United States.

```
. generate west = inlist(division, 4, 7, 8, 9)
```

We fit a model that includes a separate intercept for `west` as well as an interaction between `west` and each of the other variables in our model.

```
. regress brate i.west##c.medage i.west##c.mrgrate
```

Source	SS	df	MS		
Model	38516.2172	5	7703.24344	Number of obs	= 50
Residual	3680.60281	44	83.6500639	F(5, 44)	= 92.09
				Prob > F	= 0.0000
				R-squared	= 0.9128
				Adj R-squared	= 0.9029
Total	42196.82	49	861.159592	Root MSE	= 9.146

brate	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
1.west	327.8733	58.71793	5.58	0.000	209.5351	446.2115
medage	-7.532304	1.387624	-5.43	0.000	-10.32888	-4.735731
west# c.medage 1	-10.11443	1.849103	-5.47	0.000	-13.84105	-6.387808
mrgrate	828.6813	643.3443	1.29	0.204	-467.8939	2125.257
west# c.mrgrate 1	-800.8036	645.488	-1.24	0.221	-2101.699	500.092
_cons	366.5325	47.08904	7.78	0.000	271.6308	461.4343

We can test the effects of `west` on the intercept and on the slopes of `medage` and `mrgrate`. We will specify all these effects in a single `contrast` command and include the `overall` option to obtain a joint test of effects, that is, a test that the coefficients for eastern states and for western states are equal.

```
. contrast west west#c.medage west#c.mrgrate, overall
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
west	1	31.18	0.0000
west#c.medage	1	29.92	0.0000
west#c.mrgrate	1	1.54	0.2213
Overall	3	22.82	0.0000
Residual	44		

This overall test is referred to as a Chow test in econometrics (Chow 1960).

Beyond linear models

`contrast` may be used after almost any estimation command, with the added benefit that `contrast` provides direct support for testing main and interaction effects that is not available in most estimation commands. To illustrate, we will use `contrast` with results from a logistic regression. Stata's `logit` command fits logistic regression models, reporting the fitted regression coefficients. The `logistic` command fits the same models but reports odds ratios. Although `contrast` can report odds ratios for the computed effects, the tests are all computed from linear combinations of the model coefficients regardless of which estimation command we used.

Suppose we have data on patient satisfaction for three hospitals in a city. Let's begin by fitting a model for `satisfied`, whether the patient was satisfied with his or her treatment, using the main effects of `hospital`:

```
. use http://www.stata-press.com/data/r12/hospital, clear
(Artificial hospital satisfaction data)
. logit satisfied i.hospital
Iteration 0:   log likelihood = -393.72216
Iteration 1:   log likelihood = -387.55736
Iteration 2:   log likelihood =  -387.4768
Iteration 3:   log likelihood = -387.47679
Logistic regression                               Number of obs   =        802
                                                  LR chi2(2)      =      12.49
                                                  Prob > chi2     =     0.0019
Log likelihood = -387.47679                       Pseudo R2       =     0.0159
```

satisfied	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
hospital						
2	.5348129	.2136021	2.50	0.012	.1161604	.9534654
3	.7354519	.2221929	3.31	0.001	.2999618	1.170942
_cons	1.034708	.1391469	7.44	0.000	.7619855	1.307431

Because there are no other independent variables in this model, the reference category effects of `hospital` computed by `contrast` will match the fitted model coefficients, assuming a common reference level.

```
. contrast r.hospital
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	chi2	P>chi2
hospital			
(2 vs 1)	1	6.27	0.0123
(3 vs 1)	1	10.96	0.0009
Joint	2	12.55	0.0019

	Contrast	Std. Err.	[95% Conf.	Interval]
hospital				
(2 vs 1)	.5348129	.2136021	.1161604	.9534654
(3 vs 1)	.7354519	.2221929	.2999618	1.170942

We see that the reference category effects are equal to the fitted coefficients. They also have the same interpretation, the difference in log odds from the reference category. The top table also provides a joint test of these effects, a test of the main effects of `hospital`.

We also have information on the condition for which each patient is being treated in the variable `illness`. Here we fit a logistic regression using a two-way crossed model of `hospital` and `illness`.

```
. label list illness
illness:
           1 heart attack
           2 stroke
           3 pneumonia
           4 lung disease
           5 kidney failure
. logistic satisfied hospital##illness
Logistic regression                               Number of obs   =        802
                                                  LR chi2(14)     =      38.51
                                                  Prob > chi2     =     0.0004
Log likelihood = -374.46865                       Pseudo R2       =     0.0489
```

satisfied	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
hospital						
2	1.226496	.5492177	0.46	0.648	.509921	2.950049
3	1.711111	.8061016	1.14	0.254	.6796395	4.308021
illness						
2	1.328704	.6044214	0.62	0.532	.544779	3.240678
3	.7993827	.3408305	-0.53	0.599	.3466015	1.843653
4	1.231481	.5627958	0.46	0.649	.5028318	3.016012
5	1.25	.5489438	0.51	0.611	.5285676	2.956102
hospital# illness						
2 2	2.434061	1.768427	1.22	0.221	.5860099	10.11016
2 3	4.045805	2.868559	1.97	0.049	1.008058	16.23769
2 4	.54713	.3469342	-0.95	0.342	.1578866	1.89599
2 5	1.594425	1.081104	0.69	0.491	.4221288	6.022312
3 2	.5416535	.3590089	-0.93	0.355	.1477555	1.985635
3 3	1.579502	1.042504	0.69	0.489	.4332209	5.758783
3 4	3.137388	2.595748	1.38	0.167	.6198955	15.87881
3 5	1.672727	1.226149	0.70	0.483	.3976256	7.036812
_cons	2.571429	.8099239	3.00	0.003	1.386983	4.767358

Using `contrast`, we can obtain an ANOVA-style table of tests for the main effects and interaction effects of `hospital` and `illness`.

```
. contrast hospital##illness
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	chi2	P>chi2
hospital	2	14.92	0.0006
illness	4	4.09	0.3937
hospital#illness	8	20.45	0.0088

Our interaction effect is significant, so we decide to evaluate the simple reference category effects of `hospital` within `illness`. We are particularly interested in patient satisfaction when being treated for a heart attack or stroke, so we will use the `i.` operator to limit our output to simple effects within the first two illnesses.

```
. contrast r.hospital@i(1 2).illness, nowald
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	[95% Conf.	Interval]
hospital@illness				
(2 vs 1) 1	.2041611	.4477942	-.6734995	1.081822
(2 vs 1) 2	1.093722	.5721288	-.0276296	2.215074
(3 vs 1) 1	.5371429	.4710983	-.3861928	1.460479
(3 vs 1) 2	-.0759859	.4662325	-.9897847	.8378129

The row labeled `(2 vs 1) 1` estimates simple effects on the log odds when comparing hospital 2 with hospital 1 for patients having heart attacks. These effects are differences in the cell means of the linear predictions.

We can add the `or` option to report an odds ratio for each of these simple effects:

```
. contrast r.hospital@i(1 2).illness, nowald or
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	Odds Ratio	Std. Err.	[95% Conf.	Interval]
hospital@illness				
(2 vs 1) 1	1.226496	.5492177	.509921	2.950049
(2 vs 1) 2	2.985366	1.708014	.9727486	9.162089
(3 vs 1) 1	1.711111	.8061016	.6796395	4.308021
(3 vs 1) 2	.9268293	.4321179	.3716567	2.311306

These odds ratios are just the exponentiated version of the contrasts in the previous table.

For contrasts of the margins of nonlinear predictions, such as predicted probabilities, see [R] **margins, contrast**.

Multiple equations

contrast works with models containing multiple equations. Commands such as intreg and gnbreg allow their ancillary parameters to be modeled as functions of independent variables, and contrast can compute and test effects within these equations. In addition, contrast allows a special pseudofactor for equation—called _eqns—when working with results from manova, mvreg, mlogit, and mprobit.

In example 4 of [MV] **manova**, we fit a two-way MANOVA model using data from Woodard (1931). Here we will fit this model using mvreg. The data represent patients with jaw fractures. y1 is the patient's age, y2 is blood lymphocytes, and y3 is blood polymorphonuclears. Two factor variables, gender and fracture, are used as independent variables.

```
. use http://www.stata-press.com/data/r12/jaw
(Table 4.6 Two-Way Unbalanced Data for Fractures of the Jaw -- Rencher (1998))
. mvreg y1 y2 y3 = gender##fracture, vsquish
```

Equation	Obs	Parms	RMSE	"R-sq"	F	P
y1	27	6	10.21777	0.4086	2.902124	0.0382
y2	27	6	5.268768	0.4743	3.78967	0.0133
y3	27	6	4.993647	0.4518	3.460938	0.0195

	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
y1						
2.gender	-17.5	11.03645	-1.59	0.128	-40.45156	5.451555
fracture						
2	-12.625	5.518225	-2.29	0.033	-24.10078	-1.149222
3	5.666667	5.899231	0.96	0.348	-6.601456	17.93479
gender#						
fracture						
2 2	21.375	12.68678	1.68	0.107	-5.008595	47.75859
2 3	8.833333	13.83492	0.64	0.530	-19.93796	37.60463
_cons	39.5	4.171386	9.47	0.000	30.82513	48.17487
y2						
2.gender	20.5	5.69092	3.60	0.002	8.665083	32.33492
fracture						
2	-3.125	2.84546	-1.10	0.285	-9.042458	2.792458
3	.6666667	3.041925	0.22	0.829	-5.659362	6.992696
gender#						
fracture						
2 2	-19.625	6.541907	-3.00	0.007	-33.22964	-6.02036
2 3	-23.66667	7.133946	-3.32	0.003	-38.50252	-8.830813
_cons	35.5	2.150966	16.50	0.000	31.02682	39.97318
y3						
2.gender	-18.16667	5.393755	-3.37	0.003	-29.38359	-6.949739
fracture						
2	1.083333	2.696877	0.40	0.692	-4.52513	6.691797
3	-3	2.883083	-1.04	0.310	-8.9957	2.9957
gender#						
fracture						
2 2	19.91667	6.200305	3.21	0.004	7.022426	32.81091
2 3	23.5	6.76143	3.48	0.002	9.438837	37.56116
_cons	61.16667	2.038648	30.00	0.000	56.92707	65.40627

contrast computes Wald tests using the coefficients from the first equation by default.

```
. contrast gender##fracture
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
y1			
gender	1	2.16	0.1569
fracture	2	2.74	0.0880
gender#fracture	2	1.69	0.2085
Residual	21		

Here we use the `equation()` option to compute the Wald tests in the `y2` equation:

```
. contrast gender##fracture, equation(y2)
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
y2			
gender	1	5.41	0.0301
fracture	2	7.97	0.0027
gender#fracture	2	5.97	0.0088
Residual	21		

Here we use the equation index to compute the Wald tests in the third equation:

```
. contrast gender##fracture, equation(#3)
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
y3			
gender	1	2.23	0.1502
fracture	2	6.36	0.0069
gender#fracture	2	6.66	0.0058
Residual	21		

Here we use the `atequations` option to compute Wald tests for each equation in the model. We also use the `vsquish` option to suppress the extra blank lines between terms.

```
. contrast gender##fracture, atequations vsquish
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
y1			
gender	1	2.16	0.1569
fracture	2	2.74	0.0880
gender#fracture	2	1.69	0.2085
y2			
gender	1	5.41	0.0301
fracture	2	7.97	0.0027
gender#fracture	2	5.97	0.0088
y3			
gender	1	2.23	0.1502
fracture	2	6.36	0.0069
gender#fracture	2	6.66	0.0058
Residual	21		

Because we are investigating the results from `mvreg`, we can use the special `_eqns` factor to test for a marginal effect on the means among the dependent variables:

```
. contrast _eqns
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
_eqns	2	49.19	0.0000
Residual	21		

Here we test whether the main effects of `gender` differ among the dependent variables:

```
. contrast gender#_eqns
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
gender#_eqns	2	3.61	0.0448
Residual	21		

Although it is not terribly interesting in this case, we can even calculate contrasts across equations:

```
. contrast gender#r._eqns
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
gender#_eqns			
(joint) (2 vs 1)	1	5.82	0.0251
(joint) (3 vs 1)	1	0.40	0.5352
Joint	2	3.61	0.0448
Residual	21		

Saved results

`contrast` saves the following in `r()`:

Scalars

`r(df_r)`	variance degrees of freedom, from original estimation results
`r(k_terms)`	number of terms in *termlist*
`r(level)`	confidence level of confidence intervals

Macros

`r(cmd)`	`contrast`
`r(cmdline)`	command as typed
`r(est_cmd)`	`e(cmd)` from original estimation results
`r(est_cmdline)`	`e(cmdline)` from original estimation results
`r(title)`	title in output
`r(overall)`	`overall` or empty
`r(emptycells)`	*empspec* from `emptycells()`
`r(mcmethod)`	*method* from `mcompare()`
`r(mctitle)`	title for *method* from `mcompare()`
`r(mcadjustall)`	`adjustall` or empty
`r(margin_method)`	`asbalanced` or `asobserved`

Matrices

`r(b)`	contrast estimates
`r(V)`	variance–covariance matrix of the contrast estimates
`r(error)`	contrast estimability codes; `0` means estimable, `8` means not estimable
`r(L)`	matrix of contrasts applied to the model coefficients
`r(table)`	matrix containing the contrasts with their standard errors, test statistics, p-values, and confidence intervals
`r(F)`	vector of F statistics; `r(df_r)` present
`r(chi2)`	vector of χ^2 statistics; `r(df_r)` not present
`r(p)`	vector of p-values corresponding to `r(F)` or `r(chi2)`
`r(df)`	vector of degrees of freedom corresponding to `r(p)`
`r(df2)`	vector of denominator degrees of freedom corresponding to `r(F)`

contrast with the post option saves the following in e():

Scalars

e(df_r)	variance degrees of freedom, from original estimation results
e(k_terms)	number of terms in *termlist*

Macros

e(cmd)	contrast
e(cmdline)	command as typed
e(est_cmd)	e(cmd) from original estimation results
e(est_cmdline)	e(cmdline) from original estimation results
e(title)	title in output
e(overall)	overall or empty
e(emptycells)	*empspec* from emptycells()
e(margin_method)	asbalanced or asobserved
e(properties)	b V

Matrices

e(b)	contrast estimates
e(V)	variance–covariance matrix of the contrast estimates
e(error)	contrast estimability codes; 0 means estimable, 8 means not estimable
e(L)	matrix of contrasts applied to the model coefficients
e(F)	vector of F statistics; e(df_r) present
e(chi2)	vector of χ^2 statistics; e(df_r) not present
e(p)	vector of p-values corresponding to e(F) or e(chi2)
e(df)	vector of degrees of freedom corresponding to e(p)
e(df2)	vector of denominator degrees of freedom corresponding to e(F)

Methods and formulas

contrast is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Marginal linear predictions
Contrast operators
Reference level contrasts
Adjacent contrasts
Grand mean contrasts
Helmert contrasts
Reverse Helmert contrasts
Orthogonal polynomial contrasts
Contrasts within interactions
Multiple comparisons

Marginal linear predictions

contrast treats intercept effects separately from slope effects. To illustrate, consider the following parameterization for a quadratic regression of y on x that also models the effects of two factor variables A and B, where the levels of A are indexed by $i = 1, \ldots, k_a$ and the levels of B are indexed by $j = 1, \ldots, k_b$.

$$E(y|A = i, B = j, x) = \eta_{0ij} + \eta_{1ij}x + \eta_{2ij}x^2$$

$$\eta_{0ij} = \eta_0 + \alpha_{0i} + \beta_{0j} + (\alpha\beta)_{0ij}$$

$$\eta_{1ij} = \eta_1 + \alpha_{1i} + \beta_{1j} + (\alpha\beta)_{1ij}$$

$$\eta_{2ij} = \eta_2 + \alpha_{2i} + \beta_{2j} + (\alpha\beta)_{2ij}$$

We have partitioned the coefficients into three groups of parameters: η_{0ij} is a cell prediction for the intercept, η_{1ij} is a cell prediction for the slope on x, and η_{2ij} is a cell prediction for the slope on x^2. For the intercept parameters, η_0 is the intercept, α_{0i} represents a main effect for factor A at its ith level, β_{0j} represents a main effect for factor B at its jth level, and $(\alpha\beta)_{0ij}$ represents an effect for the interaction of A and B at the ijth level. The individual coefficients in η_{1ij} and η_{2ij} have similar interpretations, but the effects are on the slopes of x and x^2, respectively.

The marginal intercepts for A are given by

$$\eta_{0i.} = \sum_{j=1}^{k_b} f_{ij}\eta_{0ij}$$

where f_{ij} is a marginal relative frequency of the jth level of B and is controlled by the `asobserved` and `emptycells(reweight)` options according to

$$f_{ij} = \begin{cases} 1/k_b, & \text{default} \\ w_{.j}/w_{..}, & \texttt{asobserved} \\ 1/(k_b - e_{i.}), & \texttt{emptycells(reweight)} \\ w_{ij}/w_{i.}, & \texttt{emptycells(reweight)} \text{ and } \texttt{asobserved} \end{cases}$$

Above, w_{ij} is the number of individuals with A at its ith level and B at its jth,

$$w_{i.} = \sum_{j=1}^{k_b} w_{ij}$$

$$w_{.j} = \sum_{i=1}^{k_a} w_{ij}$$

$$w_{..} = \sum_{i=1}^{k_a}\sum_{j=1}^{k_b} w_{ij}$$

and $e_{i.}$ is the number of empty cells where A is at its ith level. The marginal intercepts for B and marginal slopes on x and x^2 are similarly defined.

Estimates for the cell intercepts and slopes are computed using the corresponding linear combination of the coefficients from the fitted model. For example, the estimated cell intercepts are computed using

$$\widehat{\eta}_{0ij} = \widehat{\eta}_0 + \widehat{\alpha}_{0i} + \widehat{\beta}_{0j} + \widehat{(\alpha\beta)}_{0ij}$$

and the estimated marginal intercepts for A are computed as

$$\widehat{\eta}_{0i.} = \sum_{j=1}^{k_b} f_{ij}\widehat{\eta}_{0ij}$$

Contrast operators

`contrast` performs Wald tests using linear combinations of marginal linear predictions. For example, the following linear combination can be used to test for a specific effect of factor A on the marginal intercepts.

$$\sum_{i=1}^{k_a} c_i \eta_{0i.}$$

If the c_i elements sum to zero, the linear combination is called a contrast. If the factor A is represented by a variable named `A`, then we specify this contrast using the following syntax:

`{A` c_1 c_2 `...` c_{k_a}`}`

Similarly, the following linear combination can be used to test for a specific interaction effect of factors A and B on the marginal slope of x.

$$\sum_{i=1}^{k_a}\sum_{j=1}^{k_b} c_{ij}\eta_{1ij}$$

If the factor B is represented by a variable named `B`, then we specify this contrast using the following syntax:

`{A#B` c_{11} c_{12} `...` c_{1k_b} c_{21} `...` $c_{k_ak_b}$`}`

`contrast` has variable operators for several commonly used contrasts. Each contrast operator specifies a matrix of linear combinations that yield the requested set of contrasts to be applied to the marginal linear predictions associated with the attached factor variable.

Reference level contrasts

The `r.` operator compares each level with a reference level. Let $\mathbf{R}$ be the corresponding contrast matrix for factor A, and then $\mathbf{R}$ is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{R}_{ij} = \begin{cases} -1, & \text{if } j \text{ is the reference level} \\ 1, & \text{if } i = j \text{ and } j \text{ is less than the reference level} \\ 1, & \text{if } i + 1 = j \text{ and } j \text{ is greater than the reference level} \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$ and the reference level is the third level of A (specified as `rb(#3).A`), then

$$\mathbf{R} = \begin{pmatrix} 1 & 0 & -1 & 0 & 0 \\ 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & -1 & 1 & 0 \\ 0 & 0 & -1 & 0 & 1 \end{pmatrix}$$

Adjacent contrasts

The `a.` operator compares each level with the next level. Let $\mathbf{A}$ be the corresponding contrast matrix for factor A, and then $\mathbf{A}$ is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{A}_{ij} = \begin{cases} 1, & \text{if } i = j \\ -1, & \text{if } i + 1 = j \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$, then

$$\mathbf{A} = \begin{pmatrix} 1 & -1 & 0 & 0 & 0 \\ 0 & 1 & -1 & 0 & 0 \\ 0 & 0 & 1 & -1 & 0 \\ 0 & 0 & 0 & 1 & -1 \end{pmatrix}$$

The `ar.` operator compares each level with the previous level. If $\mathbf{A}$ is the contrast matrix for the `a.` operator, then $-\mathbf{A}$ is the corresponding contrast matrix for the `ar.` operator.

Grand mean contrasts

The `g.` operator compares each level with the mean of all the levels. Let $\mathbf{G}$ be the corresponding contrast matrix for factor A, and then $\mathbf{G}$ is a $k_a \times k_a$ matrix with elements

$$\mathbf{G}_{ij} = \begin{cases} 1 - 1/k_a, & \text{if } i = j \\ -1/k_a, & \text{if } i \neq j \end{cases}$$

If $k_a = 5$, then

$$\mathbf{G} = \begin{pmatrix} 4/5 & -1/5 & -1/5 & -1/5 & -1/5 \\ -1/5 & 4/5 & -1/5 & -1/5 & -1/5 \\ -1/5 & -1/5 & 4/5 & -1/5 & -1/5 \\ -1/5 & -1/5 & -1/5 & 4/5 & -1/5 \\ -1/5 & -1/5 & -1/5 & -1/5 & 4/5 \end{pmatrix}$$

The `gw.` operator compares each level with the weighted mean of all the levels. The weights are taken from the observed weighted cell frequencies in the estimation sample of the fitted model. Let $\mathbf{G}_w$ be the corresponding contrast matrix for factor A, and then $\mathbf{G}_w$ is a $k_a \times k_a$ matrix with elements

$$\mathbf{G}_{ij} = \begin{cases} 1 - w_i/w., & \text{if } i = j \\ \quad - w_j/w., & \text{if } i \neq j \end{cases}$$

where w_i is a marginal weight representing the number of individuals with A at its ith level and $w. = \sum_i w_i$.

Helmert contrasts

The `h.` operator compares each level with the mean of the subsequent levels. Let $\mathbf{H}$ be the corresponding contrast matrix for factor A, and then $\mathbf{H}$ is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{H}_{ij} = \begin{cases} 1, & \text{if } i = j \\ -1/(k_a - i), & \text{if } i < j \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$, then

$$\mathbf{H} = \begin{pmatrix} 1 & -1/4 & -1/4 & -1/4 & -1/4 \\ 0 & 1 & -1/3 & -1/3 & -1/3 \\ 0 & 0 & 1 & -1/2 & -1/2 \\ 0 & 0 & 0 & 1 & -1 \end{pmatrix}$$

The `hw.` operator compares each level with the weighted mean of the subsequent levels. Let $\mathbf{H}_w$ be the corresponding contrast matrix for factor A, and then $\mathbf{H}_w$ is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{H}_{wij} = \begin{cases} 1, & \text{if } i = j \\ -w_j / \sum_{l=j}^{k_a} w_l, & \text{if } i < j \\ 0, & \text{otherwise} \end{cases}$$

Reverse Helmert contrasts

The `j.` operator compares each level with the mean of the previous levels. Let $\mathbf{J}$ be the corresponding contrast matrix for factor A, and then $\mathbf{J}$ is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{J}_{ij} = \begin{cases} 1, & \text{if } i + 1 = j \\ -1/i, & \text{if } j \leq i \\ 0, & \text{otherwise} \end{cases}$$

If $k_a = 5$, then

$$\mathbf{H} = \begin{pmatrix} -1 & 1 & 0 & 0 & 0 \\ -1/2 & -1/2 & 1 & 0 & 0 \\ -1/3 & -1/3 & -1/3 & 1 & 0 \\ -1/4 & -1/4 & -1/4 & -1/4 & 1 \end{pmatrix}$$

The `jw.` operator compares each level with the weighted mean of the previous levels. Let $\mathbf{J}_w$ be the corresponding contrast matrix for factor A, and then $\mathbf{J}_w$ is a $(k_a - 1) \times k_a$ matrix with elements

$$\mathbf{J}_{wij} = \begin{cases} 1, & \text{if } i+1 = j \\ -w_j / \sum_{l=1}^{i} w_l, & \text{if } i \leq j \\ 0, & \text{otherwise} \end{cases}$$

Orthogonal polynomial contrasts

The `p.` operator applies orthogonal polynomial contrasts using the level values of the attached factor variable. The `q.` operator applies orthogonal polynomial contrasts using the level indices of the attached factor variable. These two operators are equivalent when the level values of the attached factor are equally spaced. The `pw.` and `qw.` operators are weighted versions of `p.` and `q.`, where the weights are taken from the observed weighted cell frequencies in the estimation sample of the fitted model. `contrast` uses the Christoffel–Darboux recurrence formula for computing orthogonal polynomial contrasts (Abramowitz and Stegun 1972). The elements of the contrasts are normalized such that

$$\mathbf{Q}'\mathbf{W}\mathbf{Q} = \frac{1}{w_.}\mathbf{I}$$

where $\mathbf{W}$ is a diagonal matrix of the marginal cell weights $w_1, w_2, \ldots, w_k$ of the attached factor variable (all 1 for `p.` and `q.`), and $w_.$ is the sum of the weights (the number of levels k for `p.` and `q.`).

Contrasts within interactions

Contrast operators are allowed to be specified on factor variables participating in interactions. In such cases, `contrast` applies the proper matrix product of the contrast matrices to the cell margins of the interacted factor variables.

For example, consider the contrasts implied by specifying `r.A#h.B`. Let $\mathbf{M}$ be the matrix of estimated cell margins for the levels of A and B, where the rows of $\mathbf{M}$ are indexed by the levels of A and the columns are indexed by the levels of B. `contrast` puts the estimated cell margins in the following vector form:

$$\mathbf{v} = \text{vec}(\mathbf{M}') = \begin{pmatrix} \mathbf{M}_{11} \\ \mathbf{M}_{12} \\ \vdots \\ \mathbf{M}_{1k_b} \\ \mathbf{M}_{21} \\ \mathbf{M}_{22} \\ \vdots \\ \mathbf{M}_{2k_b} \\ \vdots \\ \mathbf{M}_{k_a k_b} \end{pmatrix}$$

The individual contrasts are then given by the elements of

$$(\mathbf{R} \otimes \mathbf{H})\mathbf{v}$$

where $\otimes$ denotes the Kronecker direct product.

Multiple comparisons

See [R] **pwcompare** for details on the methods and formulas used to adjust p-values and confidence intervals for multiple comparisons. The formulas for Bonferroni's method and Šidák's method are presented with $m = k(k-1)/2$, the number of pairwise comparisons for a factor term with k levels. For contrasts, m is instead the number of contrasts being performed on the factor term; often, $m = k - 1$ for a term with k levels.

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Also see

[R] **contrast postestimation** — Postestimation tools for contrast

[R] **lincom** — Linear combinations of estimators

[R] **margins** — Marginal means, predictive margins, and marginal effects

[R] **margins, contrast** — Contrasts of margins

[R] **pwcompare** — Pairwise comparisons

[R] **test** — Test linear hypotheses after estimation

[U] **20 Estimation and postestimation commands**

Title

contrast postestimation — Postestimation tools for contrast

Description

The following postestimation commands are available after `contrast, post`:

Command	Description
`estat`	VCE; `estat vce` only
`estat` (svy)	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Remarks

In *Orthogonal polynomial contrasts* in [R] **contrast**, we used the `p.` operator to test the orthogonal polynomial effects of age group.

```
. contrast p.agegrp, noeffects
```

We then used a second `contrast` command,

```
. contrast p(2 3 4).agegrp, noeffects
```

selecting levels to test whether the quadratic, cubic, and quartic contrasts were jointly significant.

We can perform the same joint test by using the `test` command after specifying the `post` option with our first `contrast` command.

```
. use http://www.stata-press.com/data/r12/cholesterol
(Artificial cholesterol data)
. anova chol agegrp
  (output omitted)
. contrast p.agegrp, noeffects post
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
agegrp			
(linear)	1	139.11	0.0000
(quadratic)	1	0.15	0.6962
(cubic)	1	0.37	0.5448
(quartic)	1	0.43	0.5153
Joint	4	35.02	0.0000
Residual	70		

```
. test p2.agegrp p3.agegrp p4.agegrp
 ( 1)  p2.agegrp = 0
 ( 2)  p3.agegrp = 0
 ( 3)  p4.agegrp = 0
       F(  3,    70) =    0.32
            Prob > F =    0.8129
```

Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[U] **20 Estimation and postestimation commands**

Title

copyright — Display copyright information

Syntax

```
copyright
```

Description

`copyright` presents copyright notifications concerning tools, libraries, etc., used in the construction of Stata.

Remarks

The correct form for a copyright notice is

Copyright *dates* by *author/owner*

The word "Copyright" is spelled out. You can use the © symbol, but "(C)" has never been given legal recognition. The phrase "All Rights Reserved" was historically required but is no longer needed.

Currently, most works are copyrighted from the moment they are written, and no copyright notice is required. Copyright concerns the protection of the expression and structure of facts and ideas, not the facts and ideas themselves. Copyright concerns the ownership of the expression and not the name given to the expression, which is covered under trademark law.

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There are significant differences in the understanding of copyright in the English- and non–English-speaking world. The Napoleonic or Civil Code, the dominant legal system in the non–English-speaking world, splits the rights into two classes: the author's economic rights and the author's moral rights. Moral rights are available only to "natural persons". Legal persons (corporations) have economic rights but not moral rights.

Also see

Copyright page of this book

Title

copyright boost — Boost copyright notification

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Also see

[R] **copyright** — Display copyright information

Title

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Title

correlate — Correlations (covariances) of variables or coefficients

Syntax

Display correlation matrix or covariance matrix

`correlate` [*varlist*] [*if*] [*in*] [*weight*] [, *correlate_options*]

Display all pairwise correlation coefficients

`pwcorr` [*varlist*] [*if*] [*in*] [*weight*] [, *pwcorr_options*]

correlate_options	Description
Options	
`means`	display means, standard deviations, minimums, and maximums with matrix
`noformat`	ignore display format associated with variables
`covariance`	display covariances
`wrap`	allow wide matrices to wrap

pwcorr_options	Description
Main	
`obs`	print number of observations for each entry
`sig`	print significance level for each entry
`listwise`	use listwise deletion to handle missing values
`casewise`	synonym for `listwise`
`print(#)`	significance level for displaying coefficients
`star(#)`	significance level for displaying with a star
`bonferroni`	use Bonferroni-adjusted significance level
`sidak`	use Šidák-adjusted significance level

varlist may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`by` is allowed with `correlate` and `pwcorr`; see [D] **by**.
`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

correlate

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Correlations and covariances

pwcorr

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Pairwise correlations

Description

The `correlate` command displays the correlation matrix or covariance matrix for a group of variables. If *varlist* is not specified, the matrix is displayed for all variables in the dataset. Also see the `estat vce` command in [R] **estat**.

`pwcorr` displays all the pairwise correlation coefficients between the variables in *varlist* or, if *varlist* is not specified, all the variables in the dataset.

Options for correlate

Options

`means` displays summary statistics (means, standard deviations, minimums, and maximums) with the matrix.

`noformat` displays the summary statistics requested by the `means` option in `g` format, regardless of the display formats associated with the variables.

`covariance` displays the covariances rather than the correlation coefficients.

`wrap` requests that no action be taken on wide correlation matrices to make them readable. It prevents Stata from breaking wide matrices into pieces to enhance readability. You might want to specify this option if you are displaying results in a window wider than 80 characters. Then you may need to `set linesize` to however many characters you can display across a line; see [R] **log**.

Options for pwcorr

Main

`obs` adds a line to each row of the matrix reporting the number of observations used to calculate the correlation coefficient.

`sig` adds a line to each row of the matrix reporting the significance level of each correlation coefficient.

`listwise` handles missing values through listwise deletion, meaning that the entire observation is omitted from the estimation sample if any of the variables in *varlist* is missing for that observation. By default, `pwcorr` handles missing values by pairwise deletion; all available observations are used to calculate each pairwise correlation without regard to whether variables outside that pair are missing.

`correlate` uses listwise deletion. Thus `listwise` allows users of `pwcorr` to mimic `correlate`'s treatment of missing values while retaining access to `pwcorr`'s features.

`casewise` is a synonym for `listwise`.

`print(#)` specifies the significance level of correlation coefficients to be printed. Correlation coefficients with larger significance levels are left blank in the matrix. Typing `pwcorr, print(.10)` would list only correlation coefficients significant at the 10% level or better.

`star(#)` specifies the significance level of correlation coefficients to be starred. Typing `pwcorr, star(.05)` would star all correlation coefficients significant at the 5% level or better.

`bonferroni` makes the Bonferroni adjustment to calculated significance levels. This option affects printed significance levels and the `print()` and `star()` options. Thus `pwcorr, print(.05) bonferroni` prints coefficients with Bonferroni-adjusted significance levels of 0.05 or less.

`sidak` makes the Šidák adjustment to calculated significance levels. This option affects printed significance levels and the `print()` and `star()` options. Thus `pwcorr, print(.05) sidak` prints coefficients with Šidák-adjusted significance levels of 0.05 or less.

Remarks

Remarks are presented under the following headings:

correlate
pwcorr

correlate

Typing `correlate` by itself produces a correlation matrix for all variables in the dataset. If you specify the *varlist*, a correlation matrix for just those variables is displayed.

▷ Example 1

We have state data on demographic characteristics of the population. To obtain a correlation matrix, we type

```
. use http://www.stata-press.com/data/r12/census13
(1980 Census data by state)
. correlate
(obs=50)
```

	state	brate	pop	medage	division	region	mrgrate
state	1.0000						
brate	0.0208	1.0000					
pop	-0.0540	-0.2830	1.0000				
medage	-0.0624	-0.8800	0.3294	1.0000			
division	-0.1345	0.6356	-0.1081	-0.5207	1.0000		
region	-0.1339	0.6086	-0.1515	-0.5292	0.9688	1.0000	
mrgrate	0.0509	0.0677	-0.1502	-0.0177	0.2280	0.2490	1.0000
dvcrate	-0.0655	0.3508	-0.2064	-0.2229	0.5522	0.5682	0.7700
medagesq	-0.0621	-0.8609	0.3324	0.9984	-0.5162	-0.5239	-0.0202

	dvcrate	medagesq
dvcrate	1.0000	
medagesq	-0.2192	1.0000

Because we did not specify the `wrap` option, Stata did its best to make the result readable by breaking the table into two parts.

To obtain the correlations between mrgrate, dvcrate, and medage, we type

```
. correlate mrgrate dvcrate medage
(obs=50)
             | mrgrate  dvcrate   medage
-------------+---------------------------
    mrgrate  |  1.0000
    dvcrate  |  0.7700   1.0000
     medage  | -0.0177  -0.2229   1.0000
```

◁

▷ Example 2

The pop variable in our previous example represents the total population of the state. Thus, to obtain population-weighted correlations among mrgrate, dvcrate, and medage, we type

```
. correlate mrgrate dvcrate medage [w=pop]
(analytic weights assumed)
(sum of wgt is   2.2591e+08)
(obs=50)
             | mrgrate  dvcrate   medage
-------------+---------------------------
    mrgrate  |  1.0000
    dvcrate  |  0.5854   1.0000
     medage  | -0.1316  -0.2833   1.0000
```

◁

With the covariance option, correlate can be used to obtain covariance matrices, as well as correlation matrices, for both weighted and unweighted data.

▷ Example 3

To obtain the matrix of covariances between mrgrate, dvcrate, and medage, we type correlate mrgrate dvcrate medage, covariance:

```
. correlate mrgrate dvcrate medage, covariance
(obs=50)
             | mrgrate  dvcrate   medage
-------------+---------------------------
    mrgrate  |  .000662
    dvcrate  |  .000063  1.0e-05
     medage  | -.000769 -.001191  2.86775
```

We could have obtained the pop-weighted covariance matrix by typing correlate mrgrate dvcrate medage [w=pop], covariance.

◁

pwcorr

correlate calculates correlation coefficients by using casewise deletion; when you request correlations of variables x_1, x_2, ..., x_k, any observation for which any of x_1, x_2, ..., x_k is missing is not used. Thus if x_3 and x_4 have no missing values, but x_2 is missing for half the data, the correlation between x_3 and x_4 is calculated using only the half of the data for which x_2 is not missing. Of course, you can obtain the correlation between x_3 and x_4 by using all the data by typing correlate x_3 x_4.

pwcorr makes obtaining such pairwise correlation coefficients easier.

▷ Example 4

Using `auto.dta`, we investigate the correlation between several of the variables.

```
. use http://www.stata-press.com/data/r12/auto1
(Automobile Models)
. pwcorr mpg price rep78 foreign, obs sig
```

	mpg	price	rep78	foreign
mpg	1.0000			
	74			
price	-0.4594	1.0000		
	0.0000			
	74	74		
rep78	0.3739	0.0066	1.0000	
	0.0016	0.9574		
	69	69	69	
foreign	0.3613	0.0487	0.5922	1.0000
	0.0016	0.6802	0.0000	
	74	74	69	74

```
. pwcorr mpg price headroom rear_seat trunk rep78 foreign, print(.05) star(.01)
```

	mpg	price	headroom	rear_s~t	trunk	rep78	foreign
mpg	1.0000						
price	-0.4594*	1.0000					
headroom	-0.4220*		1.0000				
rear_seat	-0.5213*	0.4194*	0.5238*	1.0000			
trunk	-0.5703*	0.3143*	0.6620*	0.6480*	1.0000		
rep78	0.3739*					1.0000	
foreign	0.3613*		-0.2939	-0.2409	-0.3594*	0.5922*	1.0000

```
. pwcorr mpg price headroom rear_seat trunk rep78 foreign, print(.05) bon
```

	mpg	price	headroom	rear_s~t	trunk	rep78	foreign
mpg	1.0000						
price	-0.4594	1.0000					
headroom	-0.4220		1.0000				
rear_seat	-0.5213	0.4194	0.5238	1.0000			
trunk	-0.5703		0.6620	0.6480	1.0000		
rep78	0.3739					1.0000	
foreign	0.3613				-0.3594	0.5922	1.0000

◁

❑ Technical note

The `correlate` command will report the correlation matrix of the data, but there are occasions when you need the matrix stored as a Stata matrix so that you can further manipulate it. You can obtain the matrix by typing

```
. matrix accum R = varlist, nocons dev
. matrix R = corr(R)
```

The first line places the cross-product matrix of the data in matrix `R`. The second line converts that to a correlation matrix. Also see [P] **matrix define** and [P] **matrix accum**.

❑

Saved results

correlate saves the following in r():

Scalars

r(N)	number of observations
r(rho)	ρ (first and second variables)
r(cov_12)	covariance (covariance only)
r(Var_1)	variance of first variable (covariance only)
r(Var_2)	variance of second variable (covariance only)

Matrices

r(C)	correlation or covariance matrix

pwcorr will leave in its wake only the results of the last call that it makes internally to correlate for the correlation between the last variable and itself. Only rarely is this feature useful.

Methods and formulas

pwcorr is implemented as an ado-file.

For a discussion of correlation, see, for instance, Snedecor and Cochran (1989, 177–195); for an introductory explanation using Stata examples, see Acock (2010, 186–192).

According to Snedecor and Cochran (1989, 180), the term "co-relation" was first proposed by Galton (1888). The product-moment correlation coefficient is often called the Pearson product-moment correlation coefficient because Pearson (1896) and Pearson and Filon (1898) were partially responsible for popularizing its use. See Stigler (1986) for information on the history of correlation.

The estimate of the product-moment correlation coefficient, ρ, is

$$\widehat{\rho} = \frac{\sum_{i=1}^{n} w_i(x_i - \overline{x})(y_i - \overline{y})}{\sqrt{\sum_{i=1}^{n} w_i(x_i - \overline{x})^2}\sqrt{\sum_{i=1}^{n} w_i(y_i - \overline{y})^2}}$$

where w_i are the weights, if specified, or $w_i = 1$ if weights are not specified. $\overline{x} = (\sum w_i x_i)/(\sum w_i)$ is the mean of x, and $\overline{y}$ is similarly defined.

The unadjusted significance level is calculated by pwcorr as

$$p = 2 * \texttt{ttail}(n-2, |\widehat{\rho}|\sqrt{n-2}/\sqrt{1-\widehat{\rho}^2})$$

Let v be the number of variables specified so that $k = v(v-1)/2$ correlation coefficients are to be estimated. If bonferroni is specified, the adjusted significance level is $p' = \min(1, kp)$. If sidak is specified, $p' = \min\{1, 1-(1-p)^k\}$. In both cases, see *Methods and formulas* in [R] **oneway** for a more complete description of the logic behind these adjustments.

Carlo Emilio Bonferroni (1892–1960) studied in Turin and taught there and in Bari and Florence. He published on actuarial mathematics, probability, statistics, analysis, geometry, and mechanics. His work on probability inequalities has been applied to simultaneous statistical inference, although the method known as Bonferroni adjustment usually relies only on an inequality established earlier by Boole.

Karl Pearson (1857–1936) studied mathematics at Cambridge. He was professor of applied mathematics (1884–1911) and eugenics (1911–1933) at University College London. His publications include literary, historical, philosophical, and religious topics. Statistics became his main interest in the early 1890s after he learned about its application to biological problems. His work centered on distribution theory, the method of moments, correlation, and regression. Pearson introduced the chi-squared test and the terms coefficient of variation, contingency table, heteroskedastic, histogram, homoskedastic, kurtosis, mode, random sampling, random walk, skewness, standard deviation, and truncation. Despite many strong qualities, he also fell into prolonged disagreements with others, most notably, William Bateson and R. A. Fisher.

Zbyněk Šidák (1933–1999) was a notable Czech statistician and probabilist. He worked on Markov chains, rank tests, multivariate distribution theory and multiple-comparison methods, and he served as the chief editor of *Applications of Mathematics*.

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Also see

[R] **pcorr** — Partial and semipartial correlation coefficients

[R] **spearman** — Spearman's and Kendall's correlations

[R] **summarize** — Summary statistics

[R] **tetrachoric** — Tetrachoric correlations for binary variables

Title

cumul — Cumulative distribution

Syntax

`cumul` *varname* [*if*] [*in*] [*weight*] , `generate(`*newvar*`)` [*options*]

options	Description
Main	
* `generate(`*newvar*`)`	create variable *newvar*
`freq`	use frequency units for cumulative
`equal`	generate equal cumulatives for tied values

* `generate(`*newvar*`)` is required.

`by` is allowed; see [D] **by**.

`fweights` and `aweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Distributional plots and tests > Generate cumulative distribution

Description

`cumul` creates *newvar*, defined as the empirical cumulative distribution function of *varname*.

Options

Main

`generate(`*newvar*`)` is required. It specifies the name of the new variable to be created.

`freq` specifies that the cumulative be in frequency units; otherwise, it is normalized so that *newvar* is 1 for the largest value of *varname*.

`equal` requests that observations with equal values in *varname* get the same cumulative value in *newvar*.

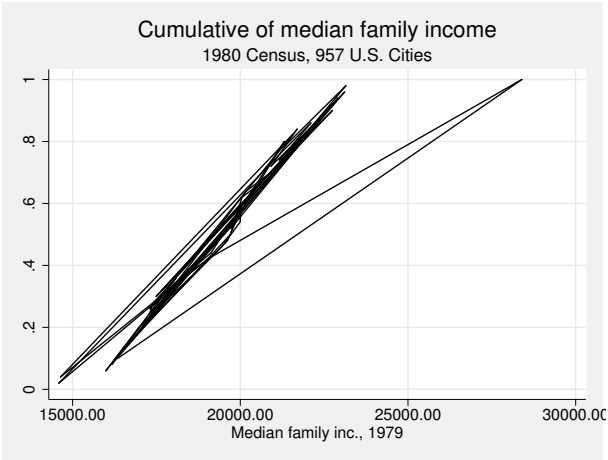
Jean Baptiste Joseph Fourier (1768–1830) was born in Auxerre in France. As a young man, Fourier became entangled in the complications of the French Revolution. As a result, he was arrested and put into prison, where he feared he might meet his end at the guillotine. When he was not in prison, he was studying, researching, and teaching mathematics. Later, he served Napolean's army in Egypt as a scientific adviser. Upon his return to France in 1801, he was appointed Prefect of the Department of Isère. While prefect, Fourier worked on the mathematical basis of the theory of heat, which is based on what are now called Fourier series. This work was published in 1822, despite the skepticism of Lagrange, Laplace, Legendre, and others—who found the work lacking in generality and even rigor—and disagreements of both priority and substance with Biot and Poisson.

Remarks

Example 1

`cumul` is most often used with `graph` to graph the empirical cumulative distribution. For instance, we have data on the median family income of 957 U.S. cities:

```
. use http://www.stata-press.com/data/r12/hsng
(1980 Census housing data)
. cumul faminc, gen(cum)
. sort cum
. line cum faminc, ylab(, grid) ytitle("") xlab(, grid)
> title("Cumulative of median family income")
> subtitle("1980 Census, 957 U.S. Cities")
```



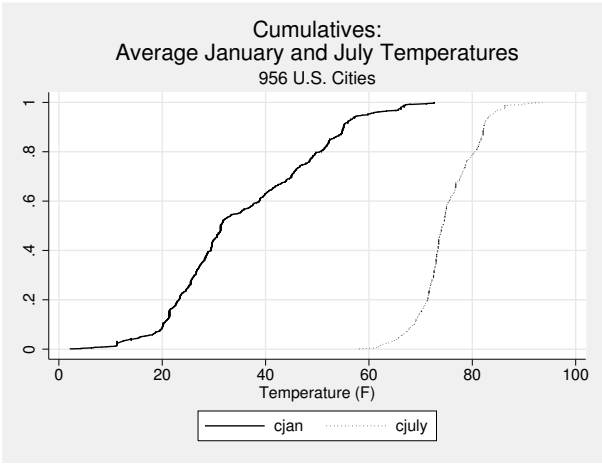
It would have been enough to type `line cum faminc`, but we wanted to make the graph look better; see [G-2] **graph twoway line**.

If we had wanted a weighted cumulative, we would have typed `cumul faminc [w=pop]` at the first step. ◁

Example 2

To graph two (or more) cumulatives on the same graph, use `cumul` and `stack`; see [D] **stack**. For instance, we have data on the average January and July temperatures of 956 U.S. cities:

```
. use http://www.stata-press.com/data/r12/citytemp, clear
(City Temperature Data)
. cumul tempjan, gen(cjan)
. cumul tempjuly, gen(cjuly)
. stack  cjan tempjan  cjuly tempjuly, into(c temp) wide clear
. line cjan cjuly temp, sort ylab(, grid) ytitle("") xlab(, grid)
> xtitle("Temperature (F)")
> title("Cumulatives:" "Average January and July Temperatures")
> subtitle("956 U.S. Cities") clstyle(. dot)
```



As before, it would have been enough to type `line cjan cjuly temp, sort`. See [D] **stack** for an explanation of how the `stack` command works.

◁

❑ Technical note

According to Beniger and Robyn (1978), Fourier (1821) published the first graph of a cumulative frequency distribution, which was later given the name "ogive" by Galton (1875).

❑

Methods and formulas

`cumul` is implemented as an ado-file.

Acknowledgment

The `equal` option was added by Nicholas J. Cox, Durham University, Durham, UK.

References

Beniger, J. R., and D. L. Robyn. 1978. Quantitative graphics in statistics: A brief history. *American Statistician* 32: 1–11.

Clayton, D. G., and M. Hills. 1999. gr37: Cumulative distribution function plots. *Stata Technical Bulletin* 49: 10–12. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 96–98. College Station, TX: Stata Press.

Cox, N. J. 1999. gr41: Distribution function plots. *Stata Technical Bulletin* 51: 12–16. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 108–112. College Station, TX: Stata Press.

Fourier, J. B. J. 1821. Notions générales, sur la population. *Recherches Statistiques sur la Ville de Paris et le Département de la Seine* 1: 1–70.

Galton, F. 1875. Statistics by intercomparison, with remarks on the law of frequency of error. *Philosophical Magazine* 49: 33–46.

Wilk, M. B., and R. Gnanadesikan. 1968. Probability plotting methods for the analysis of data. *Biometrika* 55: 1–17.

Also see

[D] **stack** — Stack data

[R] **diagnostic plots** — Distributional diagnostic plots

[R] **kdensity** — Univariate kernel density estimation

Title

cusum — Graph cumulative spectral distribution

Syntax

`cusum` *yvar xvar* [*if*] [*in*] [, *options*]

options	Description
Main	
`generate(`*newvar*`)`	save cumulative sum in *newvar*
`yfit(`*fitvar*`)`	calculate cumulative sum against *fitvar*
`nograph`	suppress the plot
`nocalc`	suppress cusum test statistics
Cusum plot	
connect_options	affect the rendition of the plotted line
Add plots	
`addplot(`*plot*`)`	add plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Other > Quality control > Cusum plots and tests for binary variables

Description

`cusum` graphs the cumulative sum (cusum) of a binary (0/1) variable, *yvar*, against a (usually) continuous variable, *xvar*.

Options

Main

`generate(`*newvar*`)` saves the cusum in *newvar*.

`yfit(`*fitvar*`)` calculates a cusum against *fitvar*, that is, the running sums of the "residuals" *fitvar* minus *yvar*. Typically, *fitvar* is the predicted probability of a positive outcome obtained from a logistic regression analysis.

`nograph` suppresses the plot.

`nocalc` suppresses calculation of the cusum test statistics.

Cusum plot

connect_options affect the rendition of the plotted line; see [G-3] ***connect_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

The cusum is the running sum of the proportion of ones in the sample, a constant number, minus *yvar*,

$$c_j = \sum_{k=1}^{j} f - yvar_{(k)}, \qquad 1 \le j \le N$$

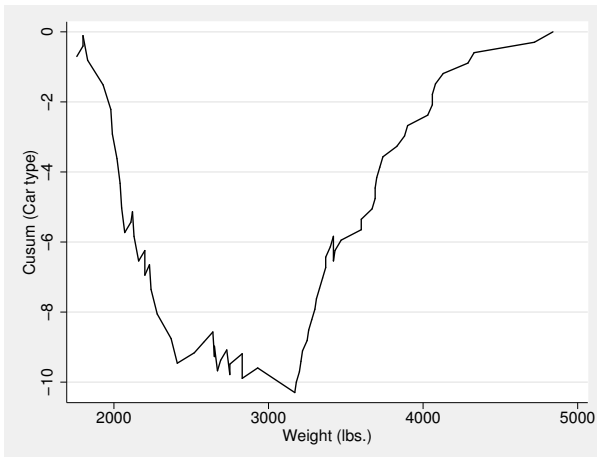
where $f = (\sum yvar)/N$ and $yvar_{(k)}$ refers to the corresponding value of *yvar* when *xvar* is placed in ascending order: $xvar_{(k+1)} \ge xvar_{(k)}$. Tied values of *xvar* are broken at random. If you want them broken the same way in two runs, you must set the random-number seed to the same value before giving the `cusum` command; see [R] **set seed**.

A U-shaped or inverted U-shaped cusum indicates, respectively, a negative or a positive trend of *yvar* with *xvar*. A sinusoidal shape is evidence of a nonmonotonic (for example, quadratic) trend. `cusum` displays the maximum absolute cusum for monotonic and nonmonotonic trends of *yvar* on *xvar*. These are nonparametric tests of departure from randomness of *yvar* with respect to *xvar*. Approximate values for the tests are given.

▷ Example 1

For the automobile dataset, `auto.dta`, we wish to investigate the relationship between `foreign` (0 = domestic, 1 = foreign) and car weight as follows:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. cusum foreign weight
```

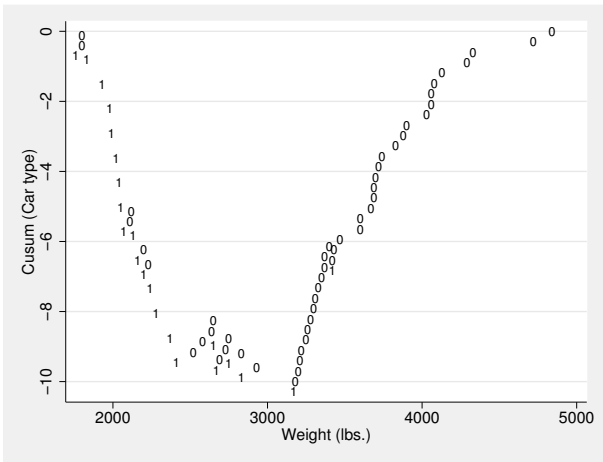


Variable	Obs	Pr(1)	CusumL	zL	Pr>zL	CusumQ	zQ	Pr>zQ
foreign	74	0.2973	10.30	3.963	0.000	3.32	0.469	0.320

The resulting plot, which is U-shaped, suggests a negative monotonic relationship. The trend is confirmed by a highly significant linear cusum statistic, labeled `CusumL` in the output above.

Some 29.73% of the cars are foreign (coded 1). The proportion of foreign cars diminishes with increasing weight. The domestic cars are crudely heavier than the foreign ones. We could have discovered that by typing `table foreign, stats(mean weight)`, but such an approach does not give the full picture of the relationship. The quadratic cusum (`CusumQ`) is not significant, so we do not suspect any tendency for the very heavy cars to be foreign rather than domestic. A slightly enhanced version of the plot shows the preponderance of domestic (coded 0) cars at the heavy end of the weight axis:

```
. label values foreign
. cusum foreign weight, s(none) recast(scatter) mlabel(foreign) mlabp(0)
```



Variable	Obs	Pr(1)	CusumL	zL	Pr>zL	CusumQ	zQ	Pr>zQ
foreign	74	0.2973	10.30	3.963	0.000	2.92	0.064	0.475

The example is, of course, artificial, because we would not really try to model the probability of a car being foreign given its weight.

◁

Saved results

`cusum` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(P_zl)`	p-value for test (linear)
`r(prop1)`	proportion of positive outcomes	`r(cusumq)`	quadratic cusum
`r(cusuml)`	cusum	`r(zq)`	test (quadratic)
`r(zl)`	test (linear)	`r(P_zq)`	p-value for test (quadratic)

Methods and formulas

`cusum` is implemented as an ado-file.

Acknowledgment

`cusum` was written by Patrick Royston, MRC Clinical Trials Unit, London.

References

Royston, P. 1992. The use of cusums and other techniques in modelling continuous covariates in logistic regression. *Statistics in Medicine* 11: 1115–1129.

——. 1993. sqv7: Cusum plots and tests for binary variables. *Stata Technical Bulletin* 12: 16–17. Reprinted in *Stata Technical Bulletin Reprints*, vol. 2, pp. 175–177. College Station, TX: Stata Press.

Also see

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **probit** — Probit regression

Title

db — Launch dialog

Syntax

Syntax for db

`db` *commandname*

For programmers

`db` *commandname* [`, message(`*string*`) debug dryrun`]

Set system parameter

`set maxdb #` [`, permanently`]

where # must be between 5 and 1,000.

Description

`db` is the command-line way to launch a dialog for a Stata command.

The second syntax (which is the same but includes options) is for use by programmers.

If you wish to allow the launching of dialogs from a help file, see [P] **smcl** for information on the `dialog` SMCL directive.

`set maxdb` sets the maximum number of dialog boxes whose contents are remembered from one invocation to the next during a session. The default value of `maxdb` is 50.

Options

`message(`*string*`)` specifies that *string* be passed to the dialog box, where it can be referred to from the `__MESSAGE STRING` property.

`debug` specifies that the underlying dialog box be loaded with debug messaging turned on.

`dryrun` specifies that, rather than launching the dialog, `db` show the commands it would issue to launch the dialog.

`permanently` specifies that, in addition to making the change right now, the `maxdb` setting be remembered and become the default setting when you invoke Stata.

Remarks

The usual way to launch a dialog is to open the **Data**, **Graphics**, or **Statistics** menu and to make your selection from there. When you know the name of the command that you want to run, however, `db` provides a way to invoke the dialog from the command line.

`db` follows the same abbreviation rules that Stata's command-line interface follows. So, to launch the dialog for `regress`, you can type

```
. db regress
```

or

```
. db reg
```

Say that you use the dialog box for `regress`, either by selecting

Statistics > Linear models and related > Linear regression

or by typing

```
. db regress
```

You fit a regression.

Much later during the session, you return to the `regress` dialog box. It will have the contents as you left them if 1) you have not typed `clear all` between the first and second invocations; 2) you have not typed `discard` between the two invocations; and 3) you have not used more than 50 different dialog boxes—regardless of how many times you have used each—between the first and second invocations of `regress`. If you use 51 or more, the contents of the `regress` dialog box will be forgotten.

`set maxdb` determines how many different dialog boxes are remembered. A dialog box takes, on average, about 20 KB of memory, so the 50 default corresponds to allowing dialog boxes to consume about 1 MB of memory.

Methods and formulas

`db` is implemented as an ado-file.

Also see

[R] **query** — Display system parameters

Title

diagnostic plots — Distributional diagnostic plots

Syntax

Symmetry plot

`symplot` *varname* [*if*] [*in*] [, *options*$_1$]

Ordered values of varname against quantiles of uniform distribution

`quantile` *varname* [*if*] [*in*] [, *options*$_1$]

Quantiles of varname$_1$ *against quantiles of varname*$_2$

`qqplot` *varname*$_1$ *varname*$_2$ [*if*] [*in*] [, *options*$_1$]

Quantiles of varname against quantiles of normal distribution

`qnorm` *varname* [*if*] [*in*] [, *options*$_2$]

Standardized normal probability plot

`pnorm` *varname* [*if*] [*in*] [, *options*$_2$]

Quantiles of varname against quantiles of χ^2 *distribution*

`qchi` *varname* [*if*] [*in*] [, *options*$_3$]

χ^2 *probability plot*

`pchi` *varname* [*if*] [*in*] [, *options*$_3$]

options$_1$	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

options$_2$	Description
Main	
`grid`	add grid lines
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

options$_3$	Description
Main	
`grid`	add grid lines
`df(#)`	degrees of freedom of χ^2 distribution; default is `df(1)`
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

symplot

Statistics > Summaries, tables, and tests > Distributional plots and tests > Symmetry plot

quantile

Statistics > Summaries, tables, and tests > Distributional plots and tests > Quantiles plot

qqplot

Statistics > Summaries, tables, and tests > Distributional plots and tests > Quantile-quantile plot

qnorm

Statistics > Summaries, tables, and tests > Distributional plots and tests > Normal quantile plot

pnorm

Statistics > Summaries, tables, and tests > Distributional plots and tests > Normal probability plot, standardized

qchi

Statistics > Summaries, tables, and tests > Distributional plots and tests > Chi-squared quantile plot

pchi

Statistics > Summaries, tables, and tests > Distributional plots and tests > Chi-squared probability plot

Description

`symplot` graphs a symmetry plot of *varname*.

`quantile` plots the ordered values of *varname* against the quantiles of a uniform distribution.

`qqplot` plots the quantiles of $varname_1$ against the quantiles of $varname_2$ (Q−Q plot).

`qnorm` plots the quantiles of *varname* against the quantiles of the normal distribution (Q−Q plot).

`pnorm` graphs a standardized normal probability plot (P−P plot).

`qchi` plots the quantiles of *varname* against the quantiles of a χ^2 distribution (Q−Q plot).

`pchi` graphs a χ^2 probability plot (P−P plot).

See [R] **regress postestimation** for regression diagnostic plots and [R] **logistic postestimation** for logistic regression diagnostic plots.

Options for symplot, quantile, and qqplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affect the rendition of the reference line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Options for qnorm and pnorm

Main

`grid` adds grid lines at the 0.05, 0.10, 0.25, 0.50, 0.75, 0.90, and 0.95 quantiles when specified with `qnorm`. With `pnorm`, `grid` is equivalent to `yline(.25,.5,.75) xline(.25,.5,.75)`.

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affect the rendition of the reference line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Options for qchi and pchi

Main

`grid` adds grid lines at the 0.05, 0.10, 0.25, 0.50, 0.75, 0.90, and .95 quantiles when specified with `qchi`. With `pchi`, `grid` is equivalent to `yline(.25,.5,.75) xline(.25,.5,.75)`.

`df(#)` specifies the degrees of freedom of the χ^2 distribution. The default is `df(1)`.

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affect the rendition of the reference line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Remarks are presented under the following headings:

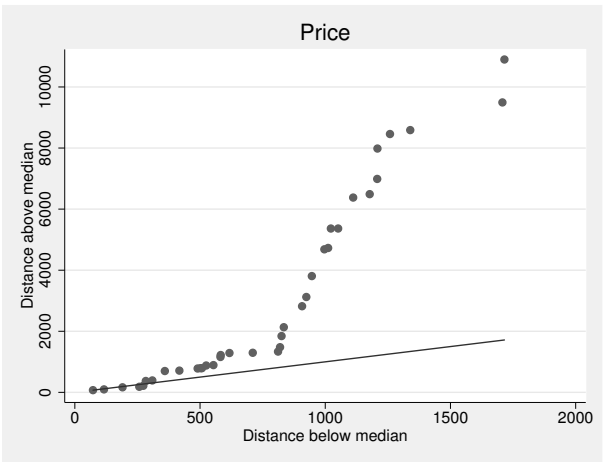
symplot
quantile
qqplot
qnorm
pnorm
qchi
pchi

symplot

▷ Example 1

We have data on 74 automobiles. To make a symmetry plot of the variable `price`, we type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. symplot price
```



All points would lie along the reference line (defined as $y = x$) if car prices were symmetrically distributed. The points in this plot lie above the reference line, indicating that the distribution of car prices is skewed to the right—the most expensive cars are far more expensive than the least expensive cars are inexpensive.

The logic works as follows: a variable, z, is distributed symmetrically if

$$\text{median} - z_{(i)} = z_{(N+1-i)} - \text{median}$$

where $z_{(i)}$ indicates the ith-order statistic of z. `symplot` graphs $y_i = \text{median} - z_{(i)}$ versus $x_i = z_{(N+1-i)} - \text{median}$.

For instance, consider the largest and smallest values of `price` in the example above. The most expensive car costs \$15,906 and the least expensive, \$3,291. Let's compare these two cars with the typical car in the data and see how much more it costs to buy the most expensive car, and compare that with how much less it costs to buy the least expensive car. If the automobile price distribution is symmetric, the price differences would be the same.

Before we can make this comparison, we must agree on a definition for the word "typical". Let's agree that "typical" means median. The price of the median car is \$5,006.50, so the most expensive car costs \$10,899.50 more than the median car, and the least expensive car costs \$1,715.50 less than the median car. We now have one piece of evidence that the car price distribution is not symmetric. We can repeat the experiment for the second-most-expensive car and the second-least-expensive car. We find that the second-most-expensive car costs \$9,494.50 more than the median car, and the second-least-expensive car costs \$1,707.50 less than the median car. We now have more evidence. We can continue doing this with the third most expensive and the third least expensive, and so on.

Once we have all these numbers, we want to compare each pair and ask how similar, on average, they are. The easiest way to do that is to plot all the pairs.

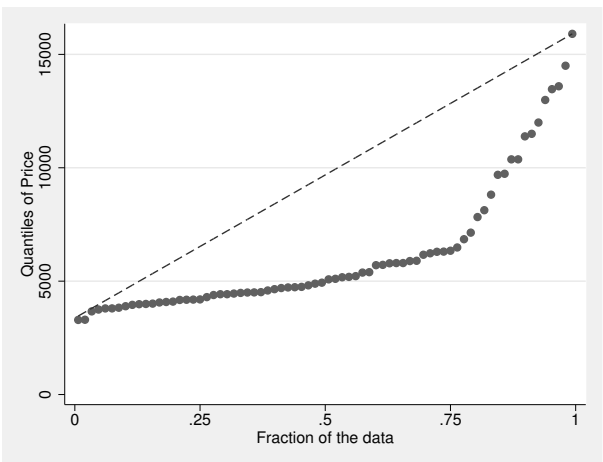
◁

quantile

▷ Example 2

We have data on the prices of 74 automobiles. To make a quantile plot of `price`, we type

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. quantile price, rlopts(clpattern(dash))
```



We changed the pattern of the reference line by specifying `rlopts(clpattern(dash))`.

In a quantile plot, each value of the variable is plotted against the fraction of the data that have values less than that fraction. The diagonal line is a reference line. If automobile prices were rectangularly distributed, all the data would be plotted along the line. Because all the points are below the reference line, we know that the price distribution is skewed right.

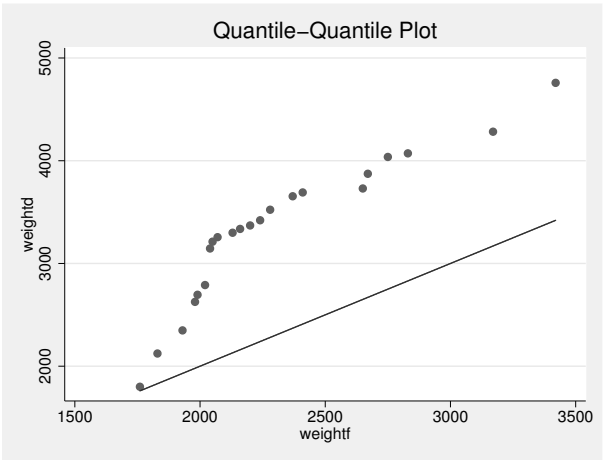
◁

qqplot

▷ Example 3

We have data on the weight and country of manufacture of 74 automobiles. We wish to compare the distributions of weights for domestic and foreign automobiles:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. generate weightd=weight if !foreign
(22 missing values generated)
. generate weightf=weight if foreign
(52 missing values generated)
. qqplot weightd weightf
```



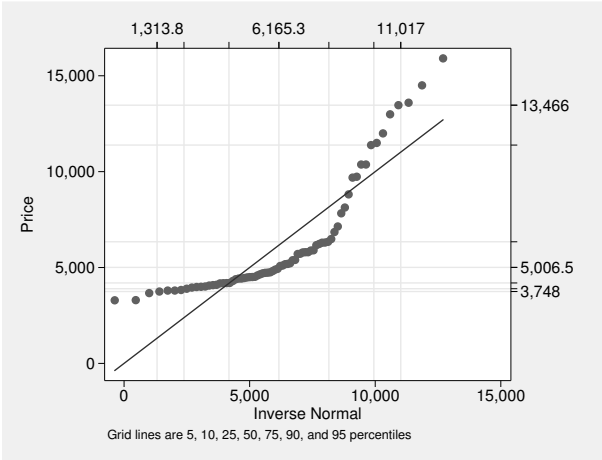
◁

qnorm

▷ Example 4

Continuing with our price data on 74 automobiles, we now wish to compare the distribution of `price` with the normal distribution:

```
. qnorm price, grid ylabel(, angle(horizontal) axis(1))
> ylabel(, angle(horizontal) axis(2))
```



The result shows that the distributions are different.

◁

❑ Technical note

The idea behind `qnorm` is recommended strongly by Miller (1997): he calls it probit plotting. His recommendations from much practical experience should interest many users. "My recommendation for detecting nonnormality is *probit plotting*" (Miller 1997, 10). "If a deviation from normality cannot be spotted by eye on probit paper, it is not worth worrying about. I never use the Kolmogorov–Smirnov test (or one of its cousins) or the χ^2 test as a preliminary test of normality. They do not tell you how the sample is differing from normality, and I have a feeling they are more likely to detect irregularities in the middle of the distribution than in the tails" (Miller 1997, 13–14).

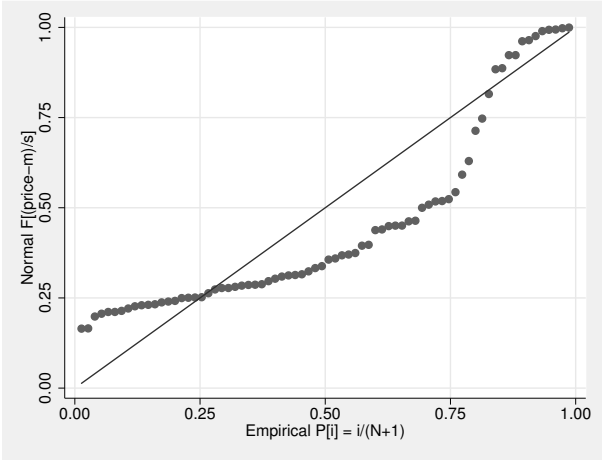
❑

pnorm

▷ Example 5

Quantile–normal plots emphasize the tails of the distribution. Normal probability plots put the focus on the center of the distribution:

```
. pnorm price, grid
```

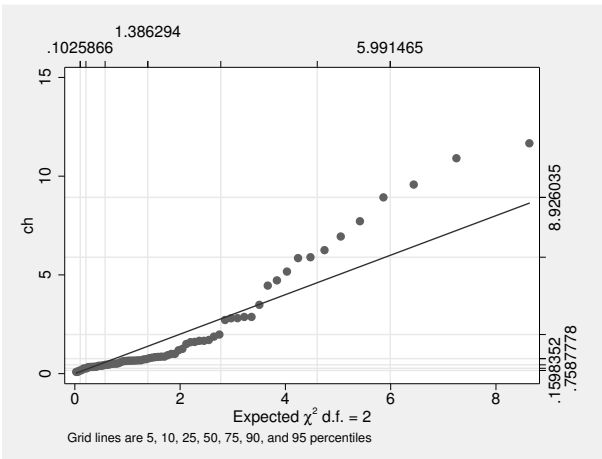


qchi

▷ Example 6

Suppose that we want to examine the distribution of the sum of squares of `price` and `mpg`, standardized for their variances.

```
. egen c1 = std(price)
. egen c2 = std(mpg)
. generate ch = c1^2 + c2^2
. qchi ch, df(2) grid ylabel(, alt axis(2)) xlabel(, alt axis(2))
```



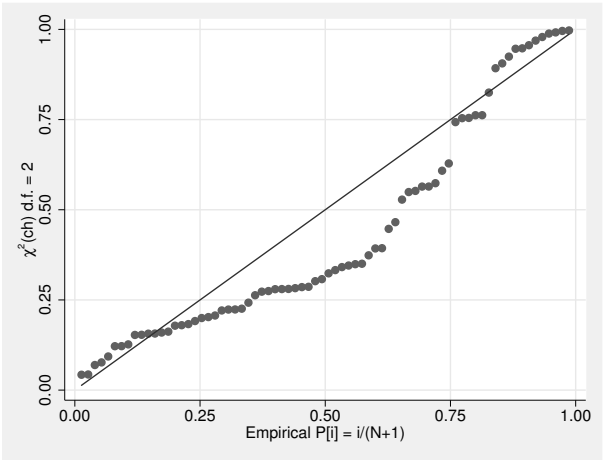
The quadratic form is clearly not χ^2 with 2 degrees of freedom.

pchi

▷ Example 7

We can focus on the center of the distribution by doing a probability plot:

```
. pchi ch, df(2) grid
```



◁

Methods and formulas

`symplot`, `quantile`, `qqplot`, `qnorm`, `pnorm`, `qchi`, and `pchi` are implemented as ado-files. Let $x_{(1)}$, $x_{(2)}$, ..., $x_{(N)}$ be the data sorted in ascending order.

If a continuous variable, x, has a cumulative distribution function $F(x) = P(X \leq x) = p$, the quantiles x_{p_i} are such that $F(x_{p_i}) = p_i$. For example, if $p_i = 0.5$, then $x_{0.5}$ is the median. When we plot data, the probabilities, p_i, are often referred to as plotting positions. There are many different conventions for choice of plotting positions, given $x_{(1)} \leq \cdots \leq x_{(N)}$. Most belong to the family $(i-a)/(N-2a+1)$. $a = 0.5$ (suggested by Hazen) and $a = 0$ (suggested by Weibull) are popular choices.

For a wider discussion of the calculation of plotting positions, see Cox (2002).

`symplot` plots median $- x_{(i)}$ versus $x_{(N+1-i)} -$ median.

`quantile` plots $x_{(i)}$ versus $(i - 0.5)/N$ (the Hazen position).

`qnorm` plots $x_{(i)}$ against q_i, where $q_i = \Phi^{-1}(p_i)$, Φ is the cumulative normal distribution, and $p_i = i/(N+1)$ (the Weibull position).

`pnorm` plots $\Phi\{(x_i - \widehat{\mu})/\widehat{\sigma}\}$ versus $p_i = i/(N+1)$, where $\widehat{\mu}$ is the mean of the data and $\widehat{\sigma}$ is the standard deviation.

`qchi` and `pchi` are similar to `qnorm` and `pnorm`; the cumulative χ^2 distribution is used in place of the cumulative normal distribution.

`qqplot` is just a two-way scatterplot of one variable against the other after both variables have been sorted into ascending order, and both variables have the same number of nonmissing observations. If the variables have unequal numbers of nonmissing observations, interpolated values of the variable with more data are plotted against the variable with fewer data.

Ramanathan Gnanadesikan (1932–) was born in Madras. He obtained degrees from the Universities of Madras and North Carolina. He worked in industry at Procter & Gamble, Bell Labs, and Bellcore, as well as in universities, retiring from Rutgers in 1998. Among many contributions to statistics he is especially well known for work on probability plotting, robustness, outlier detection, clustering, classification, and pattern recognition.

Martin Bradbury Wilk (1922–) was born in Montreal. He obtained degrees in chemical engineering and statistics from McGill and Iowa State Universities. After holding several statistics-related posts in industry and at universities (including periods at Princeton, Bell Labs, and Rutgers), Wilk was appointed Chief Statistician at Statistics Canada (1980–1986). He is especially well known for his work with Gnanadesikan on probability plotting and with Shapiro on tests for normality.

Acknowledgments

We thank Peter A. Lachenbruch of the Department of Public Health, Oregon State University, for writing the original version of `qchi` and `pchi`. Patrick Royston of the MRC Clinical Trials Unit, London, also published a similar command in the *Stata Technical Bulletin* (Royston 1996).

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Also see

[R] **cumul** — Cumulative distribution

[R] **kdensity** — Univariate kernel density estimation

[R] **logistic postestimation** — Postestimation tools for logistic

[R] **lv** — Letter-value displays

[R] **regress postestimation** — Postestimation tools for regress

Title

display — Substitute for a hand calculator

Syntax

`display` *exp*

Description

`display` displays strings and values of scalar expressions.

`display` really has many more features and a more complex syntax diagram, but the diagram shown above is adequate for interactive use. For a full discussion of `display`'s capabilities, see [P] **display**.

Remarks

`display` can be used as a substitute for a hand calculator.

▷ Example 1

`display 2+2` produces the output `4`. Stata variables may also appear in the expression, such as in `display myvar/2`. Because `display` works only with scalars, the resulting calculation is performed only for the first observation. You could type `display myvar[10]/2` to display the calculation for the 10th observation. Here are more examples:

```
. display sqrt(2)/2
.70710678
. display normal(-1.1)
.13566606
. di (57.2-3)/(12-2)
5.42
. display myvar/10
7
. display myvar[10]/2
3.5
```

◁

Also see

[P] **display** — Display strings and values of scalar expressions

[U] **13 Functions and expressions**

Title

do — Execute commands from a file

Syntax

{do | run} *filename* [*arguments*] [, nostop]

Menu

File > Do...

Description

do and run cause Stata to execute the commands stored in *filename* just as if they were entered from the keyboard. do echoes the commands as it executes them, whereas run is silent. If *filename* is specified without an extension, .do is assumed.

Option

nostop allows the do-file to continue executing even if an error occurs. Normally, Stata stops executing the do-file when it detects an error (nonzero return code).

Remarks

You can create *filename* (called a *do-file*) using Stata's Do-file Editor; see [R] **doedit**. This file will be a standard ASCII (text) file. A complete discussion of do-files can be found in [U] **16 Do-files**.

You can also create *filename* by using a non-Stata text editor; see [D] **shell** for a way to invoke your favorite editor from inside Stata. Make sure that you save the file in ASCII format.

If the path or *filename* contains spaces, it should be enclosed in double quotes.

Reference

Jenkins, S. P. 2006. Stata tip 32: Do not stop. *Stata Journal* 6: 281.

Also see

[R] **doedit** — Edit do-files and other text files

[P] **include** — Include commands from file

[GSM] **13 Using the Do-file Editor—automating Stata**

[GSU] **13 Using the Do-file Editor—automating Stata**

[GSW] **13 Using the Do-file Editor—automating Stata**

[U] **15 Saving and printing output—log files**

[U] **16 Do-files**

Title

doedit — Edit do-files and other text files

Syntax

`doedit` [*filename*]

Menu

Window > Do-file Editor

Description

`doedit` opens a text editor that lets you edit do-files and other text files.

The Do-file Editor lets you submit several commands to Stata at once.

Remarks

Clicking on the **Do-file Editor** button is equivalent to typing `doedit`.

`doedit`, typed by itself, invokes the Editor with an empty document. If you specify *filename*, that file is displayed in the Editor.

You may have more than one Do-file Editor open at once. Each time you submit the `doedit` command, a new window will be opened.

A tutorial discussion of `doedit` can be found in the *Getting Started with Stata* manual. Read [U] **16 Do-files** for an explanation of do-files, and then read [GSW] **13 Using the Do-file Editor—automating Stata** to learn how to use the Do-file Editor to create and execute do-files.

Also see

[GSM] **13 Using the Do-file Editor—automating Stata**

[GSU] **13 Using the Do-file Editor—automating Stata**

[GSW] **13 Using the Do-file Editor—automating Stata**

[U] **16 Do-files**

Title

dotplot — Comparative scatterplots

Syntax

Dotplot of varname, with one column per value of groupvar

```
dotplot varname [if] [in] [, options]
```

Dotplot for each variable in varlist, with one column per variable

```
dotplot varlist [if] [in] [, options]
```

options	Description
Options	
`over(`*groupvar*`)`	display one columnar dotplot for each value of *groupvar*
`nx(#)`	horizontal dot density; default is `nx(0)`
`ny(#)`	vertical dot density; default is `ny(35)`
`incr(#)`	label every # group; default is `incr(1)`
`mean` | `median`	plot a horizontal line of pluses at the mean or median
`bounded`	use minimum and maximum as boundaries
`bar`	plot horizontal dashed lines at shoulders of each group
`nogroup`	use the actual values of *yvar*
`center`	center the dot for each column
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Graphics > Distributional graphs > Distribution dotplot

Description

A dotplot is a scatterplot with values grouped together vertically ("binning", as in a histogram) and with plotted points separated horizontally. The aim is to display all the data for several variables or groups in one compact graphic.

In the first syntax, `dotplot` produces a columnar dotplot of *varname*, with one column per value of *groupvar*. In the second syntax, `dotplot` produces a columnar dotplot for each variable in *varlist*, with one column per variable; `over(`*groupvar*`)` is not allowed. In each case, the "dots" are plotted as small circles to increase readability.

Options

Options

`over(`*groupvar*`)` identifies the variable for which `dotplot` will display one columnar dotplot for each value of *groupvar*.

`nx(#)` sets the horizontal dot density. A larger value of # will increase the dot density, reducing the horizontal separation between dots. This option will increase the separation between columns if two or more groups or variables are used.

`ny(#)` sets the vertical dot density (number of "bins" on the y axis). A larger value of # will result in more bins and a plot that is less spread out horizontally. # should be determined in conjunction with `nx()` to give the most pleasing appearance.

`incr(#)` specifies how the x axis is to be labeled. `incr(1)`, the default, labels all groups. `incr(2)` labels every second group.

[`mean` | `median`] plots a horizontal line of pluses at the mean or median of each group.

`bounded` forces the minimum and maximum of the variable to be used as boundaries of the smallest and largest bins. It should be used with one variable whose support is not the whole of the real line and whose density does not tend to zero at the ends of its support, for example, a uniform random variable or an exponential random variable.

`bar` plots horizontal dashed lines at the "shoulders" of each group. The shoulders are taken to be the upper and lower quartiles unless `mean` has been specified; here they will be the mean plus or minus the standard deviation.

`nogroup` uses the actual values of *yvar* rather than grouping them (the default). This option may be useful if *yvar* takes on only a few values.

`center` centers the dots for each column on a hidden vertical line.

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

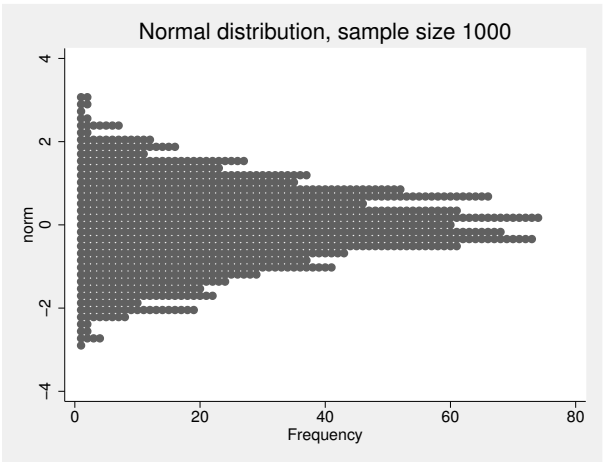
Remarks

`dotplot` produces a figure that has elements of a boxplot, a histogram, and a scatterplot. Like a boxplot, it is most useful for comparing the distributions of several variables or the distribution of 1 variable in several groups. Like a histogram, the figure provides a crude estimate of the density, and, as with a scatterplot, each symbol (dot) represents 1 observation.

Example 1

`dotplot` may be used as an alternative to Stata's histogram graph for displaying the distribution of one variable.

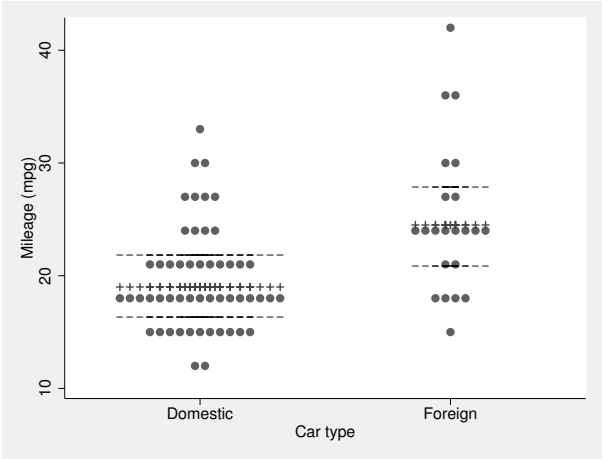
```
. set seed 123456789
. set obs 1000
. generate norm = rnormal()
. dotplot norm, title("Normal distribution, sample size 1000")
```



Example 2

The `over()` option lets us use `dotplot` to compare the distribution of one variable within different levels of a grouping variable. The `center`, `median`, and `bar` options create a graph that may be compared with Stata's boxplot; see [G-2] **graph box**. The next graph illustrates this option with Stata's automobile dataset.

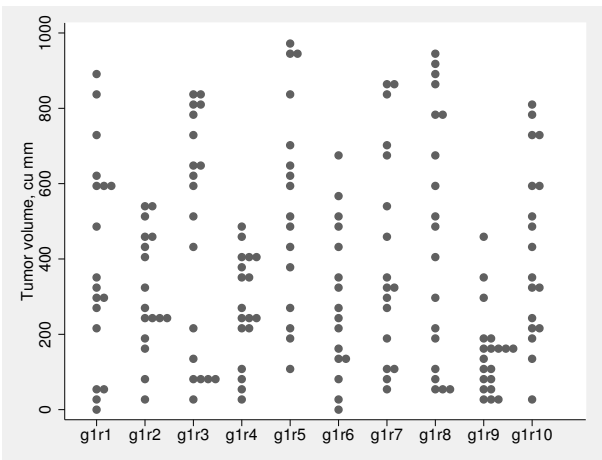
```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. dotplot mpg, over(foreign) nx(25) ny(10) center median bar
```



Example 3

The second version of `dotplot` lets us compare the distribution of several variables. In the next graph, all 10 variables contain measurements on tumor volume.

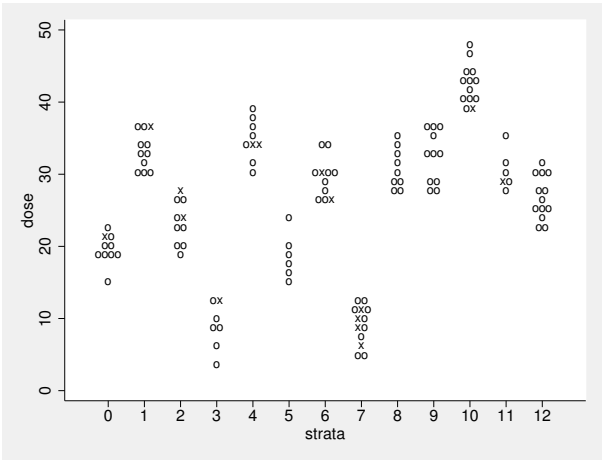
```
. use http://www.stata-press.com/data/r12/dotgr
. dotplot g1r1-g1r10, ytitle("Tumor volume, cu mm")
```



Example 4

When using the first form with the `over()` option, we can encode a third dimension in a dotplot by using a different plotting symbol for different groups. The third dimension cannot be encoded with a varlist. The example is of a hypothetical matched case–control study. The next graph shows the exposure of each individual in each matched stratum. Cases are marked by the letter 'x', and controls are marked by the letter 'o'.

```
. use http://www.stata-press.com/data/r12/dotdose
. label define symbol 0 "o" 1 "x"
. label values case symbol
. dotplot dose, over(strata) m(none) mlabel(case) mlabp(0) center
```

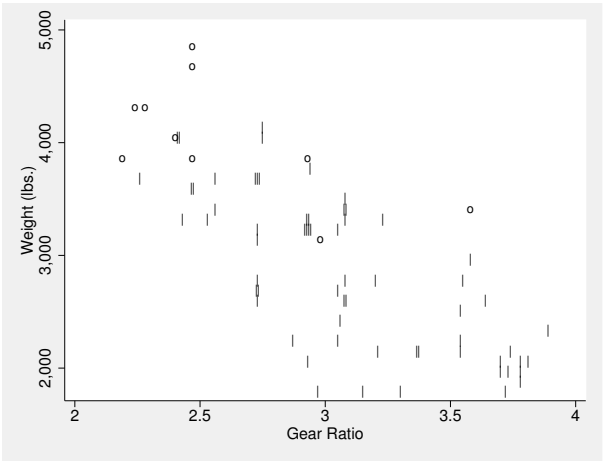


Example 5

`dotplot` can also be used with two virtually continuous variables as an alternative to jittering the data to distinguish ties. We must use the `xlabel()` option, because otherwise `dotplot` will attempt to label too many points on the x axis. It is often useful in such instances to use a value of `nx` that is smaller than the default. That was not necessary in this example, partly because of our choice of symbols.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. generate byte hi_price = (price>10000) if price < .
. label define symbol 0 "|" 1 "o"
. label values hi_price symbol
```

```
. dotplot weight, over(gear_ratio) m(none) mlabel(hi_price) mlabp(0) center
> xlabel(#5)
```

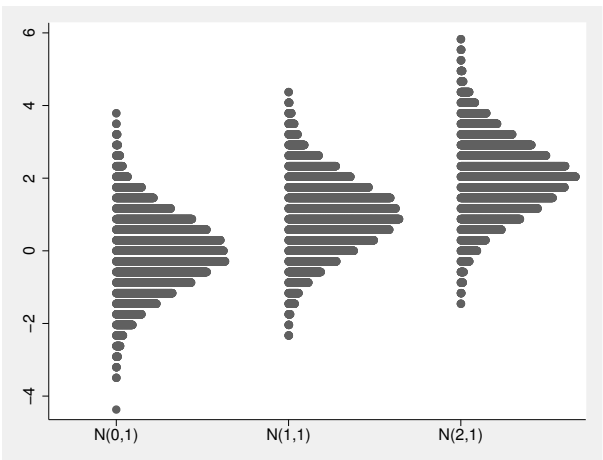


◁

▷ Example 6

The following figure is included mostly for aesthetic reasons. It also demonstrates `dotplot`'s ability to cope with even very large datasets. The sample size for each variable is 10,000, so it may take a long time to print.

```
. clear all
. set seed 123456789
. set obs 10000
. gen norm0 = rnormal()
. gen norm1 = rnormal() + 1
. gen norm2 = rnormal() + 2
. label variable norm0 "N(0,1)"
. label variable norm1 "N(1,1)"
. label variable norm2 "N(2,1)"
. dotplot norm0 norm1 norm2
```



◁

Saved results

dotplot saves the following in r():

Scalars

r(nx)	horizontal dot density
r(ny)	vertical dot density

Methods and formulas

dotplot is implemented as an ado-file.

Acknowledgments

dotplot was written by Peter Sasieni of the Wolfson Institute of Preventive Medicine, London, and Patrick Royston of the MRC Clinical Trials Unit, London.

References

Sasieni, P., and P. Royston. 1994. gr14: dotplot: Comparative scatterplots. *Stata Technical Bulletin* 19: 8–10. Reprinted in *Stata Technical Bulletin Reprints*, vol. 4, pp. 50–54. College Station, TX: Stata Press.

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Title

dstdize — Direct and indirect standardization

Syntax

Direct standardization

```
dstdize charvar popvar stratavars [if] [in] , by(groupvars) [dstdize_options]
```

Indirect standardization

```
istdize casevar_s popvar_s stratavars [if] [in] using filename,
    { popvars(casevar_p popvar_p) | rate(ratevar_p {# | crudevar_p}) }
    [istdize_options]
```

dstdize_options	Description
Main	
* `by(`*groupvars*`)`	study populations
`using(`*filename*`)`	use standard population from Stata dataset
`base(`*# | string*`)`	use standard population from a value of grouping variable
`level(#)`	set confidence level; default is `level(95)`
Options	
`saving(`*filename*`)`	save computed standard population distribution as a Stata dataset
`format(%`*fmt*`)`	final summary table display format; default is `%10.0g`
`print`	include table summary of standard population in output
`nores`	suppress saving results in `r()`

*`by(`*groupvars*`)` is required.

istdize_options	Description
Main	
* `popvars(`*casevar*$_p$ *popvar*$_p$`)`	for standard population, *casevar*$_p$ is number of cases and *popvar*$_p$ is number of individuals
* `rate(`*ratevar*$_p$ {*# | crudevar*$_p$}`)`	*ratevar*$_p$ is stratum-specific rates and # or *crudevar*$_p$ is the crude case rate value or variable
`level(#)`	set confidence level; default is `level(95)`
Options	
`by(`*groupvars*`)`	variables identifying study populations
`format(%`*fmt*`)`	final summary table display format; default is `%10.0g`
`print`	include table summary of standard population in output

*Either `popvars(`*casevar*$_p$ *popvar*$_p$`)` or `rate(`*ratevar*$_p$ {*# \| crudevar*$_p$}`)` must be specified.

Menu

dstdize

Statistics > Epidemiology and related > Other > Direct standardization

istdize

Statistics > Epidemiology and related > Other > Indirect standardization

Description

`dstdize` produces standardized rates for *charvar*, which are defined as a weighted average of the stratum-specific rates. These rates can be used to compare the characteristic *charvar* across different populations identified by *groupvars*. Weights used in the standardization are given by *popvar*; the strata across which the weights are to be averaged are defined by *stratavars*.

`istdize` produces indirectly standardized rates for a study population based on a standard population. This standardization method is appropriate when the stratum-specific rates for the population being studied are either unavailable or based on small samples and thus are unreliable. The standardization uses the stratum-specific rates of a standard population to calculate the expected number of cases in the study population(s), sums them, and then compares them with the actual number of cases observed. The standard population is in another Stata data file specified by `using` *filename*, and it must contain *popvar* and *stratavars*.

In addition to calculating rates, the indirect standardization command produces point estimates and exact confidence intervals of the study population's standardized mortality ratio (SMR), if death is the event of interest, or the standardized incidence ratio (SIR) for studies of incidence. Here we refer to both ratios as SMR.

$casevar_s$ is the variable name for the study population's number of cases (usually deaths). It must contain integers, and for each group, defined by *groupvar*, each subpopulation identified by *stratavars* must have the same values or missing.

$popvar_s$ identifies the number of subjects represented by each observation in the study population.

stratavars define the strata.

Options for dstdize

Main

`by(`*groupvars*`)` is required for the `dstdize` command; it specifies the variables identifying the study populations. If `base()` is also specified, there must be only one variable in the `by()` group. If you do not have a variable for this option, you can generate one by using something like `gen newvar=1` and then use `newvar` as the argument to this option.

`using(`*filename*`)` or `base(`*#* | *string*`)` may be used to specify the standard population. You may not specify both options. `using(`*filename*`)` supplies the name of a `.dta` file containing the standard population. The standard population must contain the *popvar* and the *stratavars*. If `using()` is not specified, the standard population distribution will be obtained from the data. `base(`*#* | *string*`)` lets you specify one of the values of *groupvar*—either a numeric value or a string—to be used as the standard population. If neither `base()` nor `using()` is specified, the entire dataset is used to determine an estimate of the standard population.

`level(#)` specifies the confidence level, as a percentage, for a confidence interval of the adjusted rate. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

Options

`saving(`*filename*`)` saves the computed standard population distribution as a Stata dataset that can be used in further analyses.

`format(%`*fmt*`)` specifies the format in which to display the final summary table. The default is `%10.0g`.

`print` includes a table summary of the standard population before displaying the study population results.

`nores` suppresses saving results in `r()`. This option is seldom specified. Some saved results are stored in matrices. If there are more groups than `matsize`, `dstdize` will report "matsize too small". Then you can either increase `matsize` or specify `nores`. The `nores` option does not change how results are calculated but specifies that results need not be left behind for use by other programs.

Options for istdize

Main

`popvars(`$casevar_p$ $popvar_p$`)` or `rate(`$ratevar_p$ `#` | $ratevar_p$ $crudevar_p$`)` must be specified with `istdize`. Only one of these two options is allowed. These options are used to describe the standard population's data.

With `popvars(`$casevar_p$ $popvar_p$`)`, $casevar_p$ records the number of cases (deaths) for each stratum in the standard population, and $popvar_p$ records the total number of individuals in each stratum (individuals at risk).

With `rate(`$ratevar_p$ {`#` | $crudevar_p$}`)`, $ratevar_p$ contains the stratum-specific rates. `#` | $crudevar_p$ specifies the crude case rate either by a variable name or by the crude case rate value. If a crude rate variable is used, it must be the same for all observations, although it could be missing for some.

`level(#)` specifies the confidence level, as a percentage, for a confidence interval of the adjusted rate. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

Options

`by(`*groupvars*`)` specifies variables identifying study populations when more than one exists in the data. If this option is not specified, the entire study population is treated as one group.

`format(%`*fmt*`)` specifies the format in which to display the final summary table. The default is `%10.0g`.

`print` outputs a table summary of the standard population before displaying the study population results.

Remarks

Remarks are presented under the following headings:

Direct standardization
Indirect standardization

In epidemiology and other fields, you will often need to compare rates for some characteristic across different populations. These populations often differ on factors associated with the characteristic under study; thus directly comparing overall rates may be misleading.

See van Belle et al. (2004, 642–684), Fleiss, Levin, and Paik (2003, chap. 19), or Kirkwood and Sterne (2003, chap. 25) for a discussion of direct and indirect standardization.

Direct standardization

The direct method of adjusting for differences among populations involves computing the overall rates that would result if, instead of having different distributions, all populations had the same standard distribution. The standardized rate is defined as a weighted average of the stratum-specific rates, with the weights taken from the standard distribution. Direct standardization may be applied only when the specific rates for a given population are available.

`dstdize` generates adjusted summary measures of occurrence, which can be used to compare prevalence, incidence, or mortality rates between populations that may differ on certain characteristics (for example, age, gender, race). These underlying differences may affect the crude prevalence, mortality, or incidence rates.

▷ Example 1

We have data (Rothman 1986, 42) on mortality rates for Sweden and Panama for 1962, and we wish to compare mortality in these two countries:

```
. use http://www.stata-press.com/data/r12/mortality
(1962 Mortality, Sweden & Panama)
. describe
Contains data from http://www.stata-press.com/data/r12/mortality.dta
  obs:             6                          1962 Mortality, Sweden & Panama
 vars:             4                          14 Apr 2011 16:18
 size:            90
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
nation          str6   %9s                    Nation
age_category    byte   %9.0g       age_lbl    Age Category
population      float  %10.0gc                Population in Age Category
deaths          float  %9.0gc                 Deaths in Age Category
-------------------------------------------------------------------------------
Sorted by:
```

```
. list, sepby(nation) abbrev(12) divider
```

	nation	age_category	population	deaths
1.	Sweden	0 - 29	3145000	3,523
2.	Sweden	30 - 59	3057000	10,928
3.	Sweden	60+	1294000	59,104
4.	Panama	0 - 29	741,000	3,904
5.	Panama	30 - 59	275,000	1,421
6.	Panama	60+	59,000	2,456

We divide the total number of cases in the population by the population to obtain the *crude rate*:

```
. collapse (sum) pop deaths, by(nation)
. list, abbrev(10) divider
```

	nation	population	deaths
1.	Panama	1075000	7,781
2.	Sweden	7496000	73,555

```
. generate crude = deaths/pop
. list, abbrev(10) divider
```

	nation	population	deaths	crude
1.	Panama	1075000	7,781	.0072381
2.	Sweden	7496000	73,555	.0098126

If we examine the total number of deaths in the two nations, the total crude mortality rate in Sweden is higher than that in Panama. From the original data, we see one possible explanation: Swedes are older than Panamanians, making direct comparison of the mortality rates difficult.

Direct standardization lets us remove the distortion caused by the different age distributions. The adjusted rate is defined as the weighted sum of the crude rates, where the weights are given by the standard distribution. Suppose that we wish to standardize these mortality rates to the following age distribution:

```
. use http://www.stata-press.com/data/r12/1962, clear
(Standard Population Distribution)
. list, abbrev(12) divider
```

	age_category	population
1.	0 - 29	.35
2.	30 - 59	.35
3.	60+	.3

```
. sort age_cat
. save 1962, replace
file 1962.dta saved
```

If we multiply the above weights for the age strata by the crude rate for the corresponding age category, the sum gives us the standardized rate.

```
. use http://www.stata-press.com/data/r12/mortality
(1962 Mortality, Sweden & Panama)
. generate crude=deaths/pop
. drop pop
. sort age_cat
. merge m:1 age_cat using 1962
age_category was byte now float
    Result                           # of obs.
    -----------------------------------------
    not matched                             0
    matched                                 6  (_merge==3)
    -----------------------------------------
. list, sepby(age_category) abbrev(12)
```

	nation	age_category	deaths	crude	population	_merge
1.	Sweden	0 - 29	3,523	.0011202	.35	matched (3)
2.	Panama	0 - 29	3,904	.0052686	.35	matched (3)
3.	Sweden	30 - 59	10,928	.0035747	.35	matched (3)
4.	Panama	30 - 59	1,421	.0051673	.35	matched (3)
5.	Panama	60+	2,456	.0416271	.3	matched (3)
6.	Sweden	60+	59,104	.0456754	.3	matched (3)

```
. generate product = crude*pop
. by nation, sort: egen adj_rate = sum(product)
. drop _merge
. list, sepby(nation)
```

	nation	age_ca~y	deaths	crude	popula~n	product	adj_rate
1.	Panama	30 - 59	1,421	.0051673	.35	.0018085	.0161407
2.	Panama	0 - 29	3,904	.0052686	.35	.001844	.0161407
3.	Panama	60+	2,456	.0416271	.3	.0124881	.0161407
4.	Sweden	0 - 29	3,523	.0011202	.35	.0003921	.0153459
5.	Sweden	60+	59,104	.0456754	.3	.0137026	.0153459
6.	Sweden	30 - 59	10,928	.0035747	.35	.0012512	.0153459

Comparing the standardized rates indicates that the Swedes have a slightly lower mortality rate.

To perform the above analysis with `dstdize`, type

```
. use http://www.stata-press.com/data/r12/mortality, clear
(1962 Mortality, Sweden & Panama)
. dstdize deaths pop age_cat, by(nation) using(1962)
```

```
-> nation= Panama
                          ------Unadjusted------  Std.
                                Pop.  Stratum  Pop.
  Stratum       Pop.      Cases  Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------
   0 - 29     741000       3904  0.689 0.0053  0.350 0.0018
  30 - 59     275000       1421  0.256 0.0052  0.350 0.0018
      60+      59000       2456  0.055 0.0416  0.300 0.0125
------------------------------------------------------------
Totals:      1075000       7781    Adjusted Cases:  17351.2
                                        Crude Rate:   0.0072
                                     Adjusted Rate:   0.0161
                          95% Conf. Interval: [0.0156, 0.0166]
------------------------------------------------------------
-> nation= Sweden
                          ------Unadjusted------  Std.
                                Pop.  Stratum  Pop.
  Stratum       Pop.      Cases  Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------
   0 - 29    3145000       3523  0.420 0.0011  0.350 0.0004
  30 - 59    3057000      10928  0.408 0.0036  0.350 0.0013
      60+    1294000      59104  0.173 0.0457  0.300 0.0137
------------------------------------------------------------
Totals:      7496000      73555    Adjusted Cases: 115032.5
                                        Crude Rate:   0.0098
                                     Adjusted Rate:   0.0153
                          95% Conf. Interval: [0.0152, 0.0155]
Summary of Study Populations:
   nation             N      Crude     Adj_Rate       Confidence Interval
  ------------------------------------------------------------------------
   Panama       1075000   0.007238     0.016141    [  0.015645,    0.016637]
   Sweden       7496000   0.009813     0.015346    [  0.015235,    0.015457]
```

The summary table above lets us make a quick inspection of the results within the study populations, and the detail tables give the behavior among the strata within the study populations.

◁

▷ Example 2

We have individual-level data on persons in four cities over several years. Included in the data is a variable indicating whether the person has high blood pressure, together with information on the person's age, sex, and race. We wish to obtain standardized high blood pressure rates for each city for 1990 and 1992, using, as the standard, the age, sex, and race distribution of the four cities and two years combined.

Our dataset contains

```
. use http://www.stata-press.com/data/r12/hbp
. describe
Contains data from http://www.stata-press.com/data/r12/hbp.dta
  obs:         1,130
 vars:             7                          21 Feb 2011 06:42
 size:        19,210
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
id              str10  %10s                   Record identification number
city            byte   %8.0g
year            int    %8.0g
sex             byte   %8.0g       sexfmt
age_group       byte   %8.0g       agefmt
race            byte   %8.0g       racefmt
hbp             byte   %8.0g       yn         high blood pressure
-------------------------------------------------------------------------------
Sorted by:
```

The `dstdize` command is designed to work with aggregate data but will work with individual-level data only if we create a variable recording the population represented by each observation. For individual-level data, this is one:

```
. gen pop = 1
```

On the next page, we specify `print` to obtain a listing of the standard population and `level(90)` to request 90% rather than 95% confidence intervals. Typing `if year==1990 | year==1992` restricts the data to the two years for both summary tables and the standard population.

```
. dstdize hbp pop age race sex if year==1990 | year==1992, by(city year) print
> level(90)
```

Standard Population

Stratum			Pop.	Dist.
15 - 19	Black	Female	35	0.077
15 - 19	Black	Male	44	0.097
15 - 19	Hispanic	Female	5	0.011
15 - 19	Hispanic	Male	10	0.022
15 - 19	White	Female	7	0.015
15 - 19	White	Male	5	0.011
20 - 24	Black	Female	43	0.095
20 - 24	Black	Male	67	0.147
20 - 24	Hispanic	Female	14	0.031
20 - 24	Hispanic	Male	13	0.029
20 - 24	White	Female	4	0.009
20 - 24	White	Male	21	0.046
25 - 29	Black	Female	17	0.037
25 - 29	Black	Male	44	0.097
25 - 29	Hispanic	Female	7	0.015
25 - 29	Hispanic	Male	13	0.029
25 - 29	White	Female	9	0.020
25 - 29	White	Male	16	0.035
30 - 34	Black	Female	16	0.035
30 - 34	Black	Male	32	0.070
30 - 34	Hispanic	Female	2	0.004
30 - 34	Hispanic	Male	3	0.007
30 - 34	White	Female	5	0.011
30 - 34	White	Male	23	0.051
Total:			455	

(6 observations excluded because of missing values)

-> city year= 1 1990

				Unadjusted		Std.	
				Pop.	Stratum	Pop.	
Stratum			Pop.	Cases	Dist.	Rate[s]	Dst[P]	s*P
15 - 19	Black	Female	6	2	0.128	0.3333	0.077	0.0256
15 - 19	Black	Male	6	0	0.128	0.0000	0.097	0.0000
15 - 19	Hispanic	Male	1	0	0.021	0.0000	0.022	0.0000
20 - 24	Black	Female	3	0	0.064	0.0000	0.095	0.0000
20 - 24	Black	Male	11	0	0.234	0.0000	0.147	0.0000
25 - 29	Black	Female	4	0	0.085	0.0000	0.037	0.0000
25 - 29	Black	Male	6	1	0.128	0.1667	0.097	0.0161
25 - 29	Hispanic	Female	2	0	0.043	0.0000	0.015	0.0000
25 - 29	White	Female	1	0	0.021	0.0000	0.020	0.0000
30 - 34	Black	Female	1	0	0.021	0.0000	0.035	0.0000
30 - 34	Black	Male	6	0	0.128	0.0000	0.070	0.0000
Totals:			47	3		Adjusted Cases:		2.0
						Crude Rate:		0.0638
						Adjusted Rate:		0.0418
					90% Conf. Interval:			[0.0074, 0.0761]

```
-> city year= 1 1992
                                                  ------Unadjusted------  Std.
                                                        Pop.  Stratum  Pop.
                    Stratum       Pop.      Cases     Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------------------------
  15 - 19     Black   Female          3          0   0.054  0.0000  0.077 0.0000
  15 - 19     Black     Male          9          0   0.161  0.0000  0.097 0.0000
  15 - 19 Hispanic      Male          1          0   0.018  0.0000  0.022 0.0000
  20 - 24     Black   Female          7          0   0.125  0.0000  0.095 0.0000
  20 - 24     Black     Male          9          0   0.161  0.0000  0.147 0.0000
  20 - 24 Hispanic    Female          1          0   0.018  0.0000  0.031 0.0000
  25 - 29     Black   Female          2          0   0.036  0.0000  0.037 0.0000
  25 - 29     Black     Male         11          1   0.196  0.0909  0.097 0.0088
  25 - 29 Hispanic      Male          1          0   0.018  0.0000  0.029 0.0000
  30 - 34     Black   Female          7          0   0.125  0.0000  0.035 0.0000
  30 - 34     Black     Male          4          0   0.071  0.0000  0.070 0.0000
  30 - 34     White   Female          1          0   0.018  0.0000  0.011 0.0000
------------------------------------------------------------------------------
Totals:                              56          1    Adjusted Cases:      0.5
                                                        Crude Rate:   0.0179
                                                     Adjusted Rate:   0.0088
                                    90% Conf. Interval: [0.0000, 0.0226]

------------------------------------------------------------------------------
-> city year= 2 1990
                                                  ------Unadjusted------  Std.
                                                        Pop.  Stratum  Pop.
                    Stratum       Pop.      Cases     Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------------------------
  15 - 19     Black   Female          5          0   0.078  0.0000  0.077 0.0000
  15 - 19     Black     Male          7          1   0.109  0.1429  0.097 0.0138
  15 - 19 Hispanic      Male          1          0   0.016  0.0000  0.022 0.0000
  20 - 24     Black   Female          7          1   0.109  0.1429  0.095 0.0135
  20 - 24     Black     Male          8          0   0.125  0.0000  0.147 0.0000
  20 - 24 Hispanic    Female          5          0   0.078  0.0000  0.031 0.0000
  20 - 24 Hispanic      Male          2          0   0.031  0.0000  0.029 0.0000
  20 - 24     White     Male          2          0   0.031  0.0000  0.046 0.0000
  25 - 29     Black   Female          3          0   0.047  0.0000  0.037 0.0000
  25 - 29     Black     Male          9          0   0.141  0.0000  0.097 0.0000
  25 - 29 Hispanic    Female          2          0   0.031  0.0000  0.015 0.0000
  25 - 29     White   Female          1          0   0.016  0.0000  0.020 0.0000
  25 - 29     White     Male          2          1   0.031  0.5000  0.035 0.0176
  30 - 34     Black   Female          1          0   0.016  0.0000  0.035 0.0000
  30 - 34     Black     Male          5          0   0.078  0.0000  0.070 0.0000
  30 - 34 Hispanic    Female          2          0   0.031  0.0000  0.004 0.0000
  30 - 34     White   Female          1          0   0.016  0.0000  0.011 0.0000
  30 - 34     White     Male          1          0   0.016  0.0000  0.051 0.0000
------------------------------------------------------------------------------
Totals:                              64          3    Adjusted Cases:      2.9
                                                        Crude Rate:   0.0469
                                                     Adjusted Rate:   0.0449
                                    90% Conf. Interval: [0.0091, 0.0807]
```

-> city year= 2 1992

Stratum	Pop.	Cases	Unadjusted Pop. Dist.	Unadjusted Stratum Rate[s]	Std. Pop. Dst[P]	s*P
15 - 19 Black Female	1	0	0.015	0.0000	0.077	0.0000
15 - 19 Black Male	5	0	0.075	0.0000	0.097	0.0000
15 - 19 Hispanic Female	3	0	0.045	0.0000	0.011	0.0000
15 - 19 Hispanic Male	1	0	0.015	0.0000	0.022	0.0000
15 - 19 White Male	1	0	0.015	0.0000	0.011	0.0000
20 - 24 Black Female	8	0	0.119	0.0000	0.095	0.0000
20 - 24 Black Male	11	0	0.164	0.0000	0.147	0.0000
20 - 24 Hispanic Female	6	0	0.090	0.0000	0.031	0.0000
20 - 24 Hispanic Male	4	2	0.060	0.5000	0.029	0.0143
20 - 24 White Female	1	0	0.015	0.0000	0.009	0.0000
20 - 24 White Male	2	0	0.030	0.0000	0.046	0.0000
25 - 29 Black Female	2	0	0.030	0.0000	0.037	0.0000
25 - 29 Black Male	3	0	0.045	0.0000	0.097	0.0000
25 - 29 Hispanic Female	2	0	0.030	0.0000	0.015	0.0000
25 - 29 Hispanic Male	4	0	0.060	0.0000	0.029	0.0000
25 - 29 White Female	4	0	0.060	0.0000	0.020	0.0000
25 - 29 White Male	2	0	0.030	0.0000	0.035	0.0000
30 - 34 Black Female	1	0	0.015	0.0000	0.035	0.0000
30 - 34 Black Male	2	0	0.030	0.0000	0.070	0.0000
30 - 34 Hispanic Male	1	0	0.015	0.0000	0.007	0.0000
30 - 34 White Female	2	0	0.030	0.0000	0.011	0.0000
30 - 34 White Male	1	0	0.015	0.0000	0.051	0.0000
Totals:	67	2	Adjusted Cases:			1.0
			Crude Rate:			0.0299
			Adjusted Rate:			0.0143
			90% Conf. Interval:			[0.0025, 0.0260]

-> city year= 3 1990

Stratum	Pop.	Cases	Unadjusted Pop. Dist.	Unadjusted Stratum Rate[s]	Std. Pop. Dst[P]	s*P
15 - 19 Black Female	3	0	0.043	0.0000	0.077	0.0000
15 - 19 Black Male	1	0	0.014	0.0000	0.097	0.0000
15 - 19 Hispanic Female	1	0	0.014	0.0000	0.011	0.0000
15 - 19 White Female	3	0	0.043	0.0000	0.015	0.0000
15 - 19 White Male	1	0	0.014	0.0000	0.011	0.0000
20 - 24 Black Female	1	0	0.014	0.0000	0.095	0.0000
20 - 24 Black Male	9	0	0.130	0.0000	0.147	0.0000
20 - 24 Hispanic Male	3	0	0.043	0.0000	0.029	0.0000
20 - 24 White Female	2	0	0.029	0.0000	0.009	0.0000
20 - 24 White Male	8	1	0.116	0.1250	0.046	0.0058
25 - 29 Black Female	1	0	0.014	0.0000	0.037	0.0000
25 - 29 Black Male	8	3	0.116	0.3750	0.097	0.0363
25 - 29 Hispanic Male	4	0	0.058	0.0000	0.029	0.0000
25 - 29 White Female	1	0	0.014	0.0000	0.020	0.0000
25 - 29 White Male	6	0	0.087	0.0000	0.035	0.0000
30 - 34 Black Male	6	2	0.087	0.3333	0.070	0.0234
30 - 34 White Male	11	5	0.159	0.4545	0.051	0.0230
Totals:	69	11	Adjusted Cases:			6.1
			Crude Rate:			0.1594
			Adjusted Rate:			0.0885
			90% Conf. Interval:			[0.0501, 0.1268]

```
-> city year= 3 1992
                                                  ------Unadjusted------  Std.
                                                        Pop.  Stratum  Pop.
                    Stratum       Pop.      Cases     Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------------------------
  15 - 19    Black   Female          2          0    0.054 0.0000  0.077 0.0000
  15 - 19 Hispanic     Male          3          0    0.081 0.0000  0.022 0.0000
  15 - 19    White   Female          2          0    0.054 0.0000  0.015 0.0000
  15 - 19    White     Male          1          0    0.027 0.0000  0.011 0.0000
  20 - 24    Black     Male          3          0    0.081 0.0000  0.147 0.0000
  20 - 24 Hispanic   Female          1          0    0.027 0.0000  0.031 0.0000
  20 - 24 Hispanic     Male          3          0    0.081 0.0000  0.029 0.0000
  20 - 24    White   Female          1          0    0.027 0.0000  0.009 0.0000
  20 - 24    White     Male          6          1    0.162 0.1667  0.046 0.0077
  25 - 29 Hispanic     Male          1          0    0.027 0.0000  0.029 0.0000
  25 - 29    White     Male          5          1    0.135 0.2000  0.035 0.0070
  30 - 34    Black     Male          1          0    0.027 0.0000  0.070 0.0000
  30 - 34    White     Male          8          5    0.216 0.6250  0.051 0.0316
------------------------------------------------------------------------------
Totals:                             37          7    Adjusted Cases:      1.7
                                                        Crude Rate:    0.1892
                                                     Adjusted Rate:    0.0463
                                    90% Conf. Interval: [0.0253, 0.0674]

------------------------------------------------------------------------------
-> city year= 5 1990
                                                  ------Unadjusted------  Std.
                                                        Pop.  Stratum  Pop.
                    Stratum       Pop.      Cases     Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------------------------
  15 - 19    Black   Female          9          0    0.196 0.0000  0.077 0.0000
  15 - 19    Black     Male          7          0    0.152 0.0000  0.097 0.0000
  15 - 19 Hispanic     Male          1          0    0.022 0.0000  0.022 0.0000
  15 - 19    White     Male          1          0    0.022 0.0000  0.011 0.0000
  20 - 24    Black   Female          4          0    0.087 0.0000  0.095 0.0000
  20 - 24    Black     Male          6          0    0.130 0.0000  0.147 0.0000
  20 - 24 Hispanic   Female          1          0    0.022 0.0000  0.031 0.0000
  25 - 29    Black   Female          3          1    0.065 0.3333  0.037 0.0125
  25 - 29    Black     Male          5          0    0.109 0.0000  0.097 0.0000
  25 - 29 Hispanic   Female          1          0    0.022 0.0000  0.015 0.0000
  25 - 29    White   Female          2          1    0.043 0.5000  0.020 0.0099
  30 - 34    Black   Female          2          0    0.043 0.0000  0.035 0.0000
  30 - 34    Black     Male          3          0    0.065 0.0000  0.070 0.0000
  30 - 34    White     Male          1          0    0.022 0.0000  0.051 0.0000
------------------------------------------------------------------------------
Totals:                             46          2    Adjusted Cases:      1.0
                                                        Crude Rate:    0.0435
                                                     Adjusted Rate:    0.0223
                                    90% Conf. Interval: [0.0020, 0.0426]
```

```
-> city year= 5 1992
                                                  ------Unadjusted------  Std.
                                                        Pop.  Stratum  Pop.
                    Stratum       Pop.      Cases     Dist. Rate[s] Dst[P]  s*P
------------------------------------------------------------------------------
  15 - 19    Black   Female          6          0    0.087 0.0000  0.077 0.0000
  15 - 19    Black     Male          9          0    0.130 0.0000  0.097 0.0000
  15 - 19 Hispanic   Female          1          0    0.014 0.0000  0.011 0.0000
  15 - 19 Hispanic     Male          2          0    0.029 0.0000  0.022 0.0000
  15 - 19    White   Female          2          0    0.029 0.0000  0.015 0.0000
  15 - 19    White     Male          1          0    0.014 0.0000  0.011 0.0000
  20 - 24    Black   Female         13          0    0.188 0.0000  0.095 0.0000
  20 - 24    Black     Male         10          0    0.145 0.0000  0.147 0.0000
  20 - 24 Hispanic     Male          1          0    0.014 0.0000  0.029 0.0000
  20 - 24    White     Male          3          0    0.043 0.0000  0.046 0.0000
  25 - 29    Black   Female          2          0    0.029 0.0000  0.037 0.0000
  25 - 29    Black     Male          2          0    0.029 0.0000  0.097 0.0000
  25 - 29 Hispanic     Male          3          0    0.043 0.0000  0.029 0.0000
  25 - 29    White     Male          1          0    0.014 0.0000  0.035 0.0000
  30 - 34    Black   Female          4          0    0.058 0.0000  0.035 0.0000
  30 - 34    Black     Male          5          0    0.072 0.0000  0.070 0.0000
  30 - 34 Hispanic     Male          2          0    0.029 0.0000  0.007 0.0000
  30 - 34    White   Female          1          0    0.014 0.0000  0.011 0.0000
  30 - 34    White     Male          1          1    0.014 1.0000  0.051 0.0505
------------------------------------------------------------------------------
Totals:                            69          1    Adjusted Cases:      3.5
                                                       Crude Rate:   0.0145
                                                    Adjusted Rate:   0.0505
                                      90% Conf. Interval: [0.0505, 0.0505]


Summary of Study Populations:
     city
     year              N      Crude     Adj_Rate       Confidence Interval
-------------------------------------------------------------------------
        1
     1990            47   0.063830     0.041758    [  0.007427,    0.076089]
        1
     1992            56   0.017857     0.008791    [  0.000000,    0.022579]
        2
     1990            64   0.046875     0.044898    [  0.009072,    0.080724]
        2
     1992            67   0.029851     0.014286    [  0.002537,    0.026035]
        3
     1990            69   0.159420     0.088453    [  0.050093,    0.126813]
        3
     1992            37   0.189189     0.046319    [  0.025271,    0.067366]
        5
     1990            46   0.043478     0.022344    [  0.002044,    0.042644]
        5
     1992            69   0.014493     0.050549    [  0.050549,    0.050549]
```

Indirect standardization

Standardization of rates can be performed via the indirect method whenever the stratum-specific rates are either unknown or unreliable. If the stratum-specific rates are known, the direct standardization method is preferred.

To apply the indirect method, you must have the following information:

- The observed number of cases in each population to be standardized, O. For example, if death rates in two states are being standardized using the U.S. death rate for the same period, you must know the total number of deaths in each state.
- The distribution across the various strata for the population being studied, $n_1, \ldots, n_k$. If you are standardizing the death rate in the two states, adjusting for age, you must know the number of individuals in each of the k age groups.
- The stratum-specific rates for the standard population, $p_1, \ldots, p_k$. For example, you must have the U.S. death rate for each stratum (age group).
- The crude rate of the standard population, C. For example, you must have the U.S. mortality rate for the year.

The indirect adjusted rate is then

$$R_{\text{indirect}} = C\frac{O}{E}$$

where E is the expected number of cases (deaths) in each population. See *Methods and formulas* for a more detailed description of calculations.

▷ Example 3

This example is borrowed from Kahn and Sempos (1989, 95–105). We want to compare 1970 mortality rates in California and Maine, adjusting for age. Although we have age-specific population counts for the two states, we lack age-specific death rates. Direct standardization is not feasible here. We can use the U.S. population census data for the same year to produce indirectly standardized rates for these two states.

From the U.S. census, the standard population for this example was entered into Stata and saved in `popkahn.dta`.

```
. use http://www.stata-press.com/data/r12/popkahn, clear
. list age pop deaths rate, sep(4)
```

	age	population	deaths	rate
1.	<15	57,900,000	103,062	.00178
2.	15-24	35,441,000	45,261	.00128
3.	25-34	24,907,000	39,193	.00157
4.	35-44	23,088,000	72,617	.00315
5.	45-54	23,220,000	169,517	.0073
6.	55-64	18,590,000	308,373	.01659
7.	65-74	12,436,000	445,531	.03583
8.	75+	7,630,000	736,758	.09656

The standard population contains for each age stratum the total number of individuals (`pop`) and both the age-specific mortality rate (`rate`) and the number of deaths. The standard population need not contain all three. If we have only the age-specific mortality rate, we can use the `rate(`*ratevar*$_p$ *crudevar*$_p$`)` or `rate(`*ratevar*$_p$ *#*`)` option, where *crudevar*$_p$ refers to the variable containing the total population's crude death rate or *#* is the total population's crude death rate.

Now let's look at the states' data (study population):

```
. use http://www.stata-press.com/data/r12/kahn
. list, sep(4)
```

	state	age	populat~n	death	st	death_~e
1.	California	<15	5,524,000	166,285	1	.0016
2.	California	15-24	3,558,000	166,285	1	.0013
3.	California	25-34	2,677,000	166,285	1	.0015
4.	California	35-44	2,359,000	166,285	1	.0028
5.	California	45-54	2,330,000	166,285	1	.0067
6.	California	55-64	1,704,000	166,285	1	.0154
7.	California	65-74	1,105,000	166,285	1	.0328
8.	California	75+	696,000	166,285	1	.0917
9.	Maine	<15	286,000	11,051	2	.0019
10.	Maine	15-24	168,000	.	2	.0011
11.	Maine	25-34	110,000	.	2	.0014
12.	Maine	35-44	109,000	.	2	.0029
13.	Maine	45-54	110,000	.	2	.0069
14.	Maine	55-64	94,000	.	2	.0173
15.	Maine	65-74	69,000	.	2	.039
16.	Maine	75+	46,000	.	2	.1041

For each state, the number of individuals in each stratum (age group) is contained in the `pop` variable. The `death` variable is the total number of deaths observed in the state during the year. It must have the same value for all observations in the group, as for California, or it could be missing in all but one observation per group, as for Maine.

To match these two datasets, the strata variables must have the same name in both datasets and ideally the same levels. If a level is missing from either dataset, that level will not be included in the standardization.

With `kahn.dta` in memory, we now execute the command. We will use the `print` option to obtain the standard population's summary table, and because we have both the standard population's age-specific count and deaths, we will specify the `popvars(`*casevar*$_p$ *popvar*$_p$`)` option. Or, we could specify the `rate(rate 0.00945)` option because we know that 0.00945 is the U.S. crude death rate for 1970.

```
. istdize death pop age using http://www.stata-press.com/data/r12/popkahn,
> by(state) pop(deaths pop) print
-------Standard Population-------
  Stratum                 Rate
-----------------------------------
      <15                0.00178
    15-24                0.00128
    25-34                0.00157
    35-44                0.00315
    45-54                0.00730
    55-64                0.01659
    65-74                0.03583
      75+                0.09656
-----------------------------------
Standard population's crude rate:       0.00945
-------------------------------------------------------------------------------
-> state= California
                  Indirect Standardization
                  Standard
                 Population     Observed      Cases
  Stratum           Rate       Population    Expected
-------------------------------------------------------------------------------
      <15          0.0018       5524000      9832.72
    15-24          0.0013       3558000      4543.85
    25-34          0.0016       2677000      4212.46
    35-44          0.0031       2359000      7419.59
    45-54          0.0073       2330000     17010.10
    55-64          0.0166       1704000     28266.14
    65-74          0.0358       1105000     39587.63
      75+          0.0966        696000     67206.23
-------------------------------------------------------------------------------
Totals:                         19953000    178078.73

                                          Observed Cases:   166285
                                            SMR (Obs/Exp):     0.93
                          SMR exact 95% Conf. Interval: [0.9293, 0.9383]
                                              Crude Rate:   0.0083
                                            Adjusted Rate:   0.0088
                                  95% Conf. Interval: [0.0088, 0.0089]
-------------------------------------------------------------------------------
-> state= Maine
                  Indirect Standardization
                  Standard
                 Population     Observed      Cases
  Stratum           Rate       Population    Expected
-------------------------------------------------------------------------------
      <15          0.0018        286000       509.08
    15-24          0.0013        168000       214.55
    25-34          0.0016        110000       173.09
    35-44          0.0031        109000       342.83
    45-54          0.0073        110000       803.05
    55-64          0.0166         94000      1559.28
    65-74          0.0358         69000      2471.99
      75+          0.0966         46000      4441.79
-------------------------------------------------------------------------------
Totals:                           992000     10515.67

                                          Observed Cases:    11051
                                            SMR (Obs/Exp):     1.05
                          SMR exact 95% Conf. Interval: [1.0314, 1.0707]
                                              Crude Rate:   0.0111
                                            Adjusted Rate:   0.0099
                                  95% Conf. Interval: [0.0097, 0.0101]
```

```
Summary of Study Populations (Rates):
                Cases
    state     Observed      Crude    Adj_Rate  Confidence Interval
------------------------------------------------------------------------------
California      166285   0.008334    0.008824  [0.008782, 0.008866]
     Maine       11051   0.011140    0.009931  [0.009747, 0.010118]
Summary of Study Populations (SMR):
                Cases         Cases                      Exact
    state     Observed      Expected     SMR      Confidence Interval
------------------------------------------------------------------------------
California      166285     178078.73   0.934     [0.929290, 0.938271]
     Maine       11051      10515.67   1.051     [1.031405, 1.070688]
```

Saved results

`dstdize` saves the following in `r()`:

Scalars

`r(k)`	number of populations

Macros

`r(by)`	variable names specified in `by()`
`r(c#)`	values of `r(by)` for #th group

Matrices

`r(se)`	standard errors of adjusted rates
`r(ub)`	upper bounds of confidence intervals for adjusted rates
`r(lb)`	lower bounds of confidence intervals for adjusted rates
`r(Nobs)`	$1 \times k$ vector of number of observations
`r(crude)`	$1 \times k$ vector of crude rates (*)
`r(adj)`	$1 \times k$ vector of adjusted rates (*)

(*) If, in a group, the number of observations is 0, then 9 is stored for the corresponding crude and adjusted rates.

Methods and formulas

`dstdize` and `istdize` are implemented as ado-files.

The directly standardized rate, S_{R}, is defined by

$$S_{\mathrm{R}} = \frac{\sum_{i=1}^{k} w_i R_i}{\sum_{i=1}^{k} w_i}$$

(Rothman 1986, 44), where R_i is the stratum-specific rate in stratum i and w_i is the weight for stratum i derived from the standard population.

If n_i is the population of stratum i, the standard error, $\mathrm{se}(S_{\mathrm{R}})$, in stratified sampling for proportions (ignoring the finite population correction) is

$$\mathrm{se}(S_{\mathrm{R}}) = \frac{1}{\sum w_i} \sqrt{\sum_{i=1}^{k} \frac{{w_i}^2 R_i(1-R_i)}{n_i}}$$

(Cochran 1977, 108), from which the confidence intervals are calculated.

For indirect standardization, define O as the observed number of cases in each population to be standardized; $n_1, \ldots, n_k$ as the distribution across the various strata for the population being studied; $R_1, \ldots, R_k$ as the stratum-specific rates for the standard population; and C as the crude rate of the standard population. The expected number of cases (deaths), E, in each population is obtained by applying the standard population stratum-specific rates, $R_1, \ldots, R_k$, to the study populations:

$$E = \sum_{i=1}^{k} n_i R_i$$

The indirectly adjusted rate is then

$$R_{\text{indirect}} = C\frac{O}{E}$$

and O/E is the study population's SMR if death is the event of interest or the SIR for studies of disease (or other) incidence.

The exact confidence interval is calculated for each estimated SMR by assuming a Poisson process as described in Breslow and Day (1987, 69–71). These intervals are obtained by first calculating the upper and lower bounds for the confidence interval of the Poisson-distributed observed events, O—say, L and U, respectively—and then computing $\text{SMR}_L = L/E$ and $\text{SMR}_U = U/E$.

Acknowledgments

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Also see

[ST] **epitab** — Tables for epidemiologists

[SVY] **direct standardization** — Direct standardization of means, proportions, and ratios

Title

dydx — Calculate numeric derivatives and integrals

Syntax

Derivatives of numeric functions

`dydx` *yvar xvar* [*if*] [*in*] `,` `generate(`*newvar*`)` [*dydx_options*]

Integrals of numeric functions

`integ` *yvar xvar* [*if*] [*in*] [`,` *integ_options*]

dydx_options	Description
Main	
* `generate(`*newvar*`)`	create variable named *newvar*
`replace`	overwrite the existing variable

* `generate(`*newvar*`)` is required.

integ_options	Description
Main	
`generate(`*newvar*`)`	create variable named *newvar*
`trapezoid`	use trapezoidal rule to compute integrals; default is cubic splines
`initial(#)`	initial value of integral; default is `initial(0)`
`replace`	overwrite the existing variable

`by` is allowed with `dydx` and `integ`; see [D] **by**.

Menu

dydx

Data > Create or change data > Other variable-creation commands > Calculate numerical derivatives

integ

Data > Create or change data > Other variable-creation commands > Calculate numeric integrals

Description

`dydx` and `integ` calculate derivatives and integrals of numeric "functions".

Options

Main

`generate(`*newvar*`)` specifies the name of the new variable to be created. It must be specified with `dydx`.

`trapezoid` requests that the trapezoidal rule [the sum of $(x_i - x_{i-1})(y_i + y_{i-1})/2$] be used to compute integrals. The default is cubic splines, which give superior results for most smooth functions; for irregular functions, `trapezoid` may give better results.

`initial(#)` specifies the initial condition for calculating definite integrals; see *Methods and formulas* below. The default is `initial(0)`.

`replace` specifies that if an existing variable is specified for `generate()`, it should be overwritten.

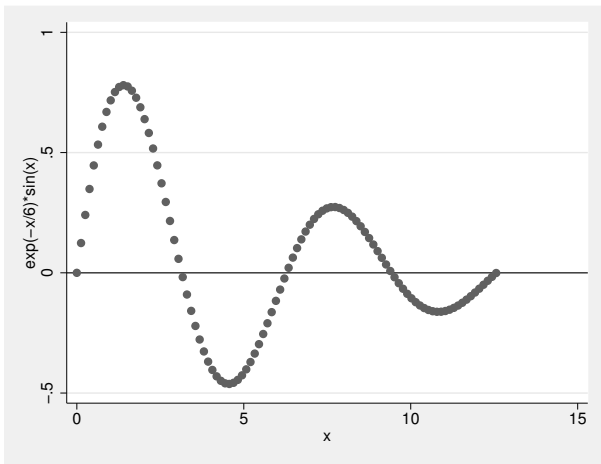
Remarks

`dydx` and `integ` lets you extend Stata's graphics capabilities beyond data analysis and into mathematics. (See Gould [1993] for another command that draws functions.)

▷ Example 1

We graph $y = e^{-x/6}\sin(x)$ over the interval $[0, 12.56]$:

```
. range x 0 12.56 100
obs was 0, now 100
. generate y = exp(-x/6)*sin(x)
. label variable y "exp(-x/6)*sin(x)"
. twoway connected y x, connect(i) yline(0)
```

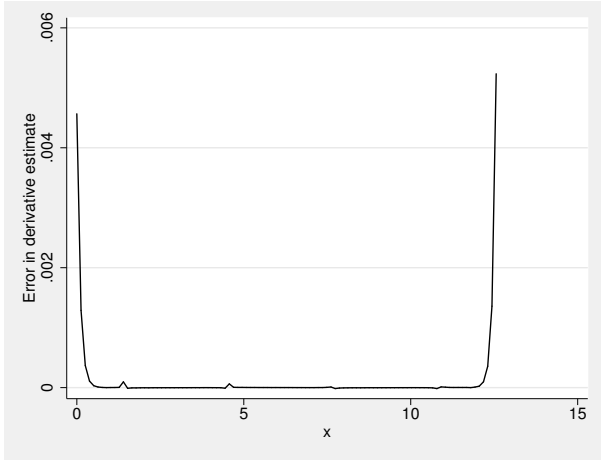


We estimate the derivative by using `dydx` and compute the relative difference between this estimate and the true derivative.

```
. dydx y x, gen(dy)
. generate dytrue = exp(-x/6)*(cos(x) - sin(x)/6)
. generate error = abs(dy - dytrue)/dytrue
```

The error is greatest at the endpoints, as we would expect. The error is approximately 0.5% at each endpoint, but the error quickly falls to less than 0.01%.

```
. label variable error "Error in derivative estimate"
. twoway line error x, ylabel(0(.002).006)
```

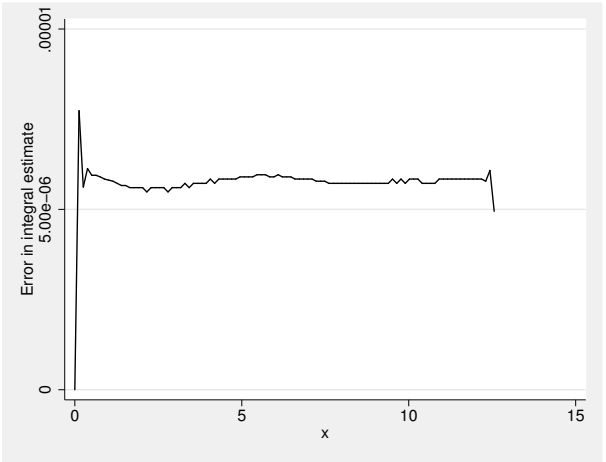


We now estimate the integral by using `integ`:

```
. integ y x, gen(iy)
number of points = 100
integral         = .85316396
. generate iytrue = (36/37)*(1 - exp(-x/6)*(cos(x) + sin(x)/6))
. display iytrue[_N]
.85315901
. display abs(r(integral) - iytrue[_N])/iytrue[_N]
5.799e-06
. generate diff = iy - iytrue
```

The relative difference between the estimate [stored in `r(integral)`] and the true value of the integral is about 6×10^{-6}. A graph of the absolute difference (`diff`) is shown below. Here error is cumulative. Again most of the error is due to a relatively poorer fit near the endpoints.

```
. label variable diff "Error in integral estimate"
. twoway line diff x, ylabel(0(5.00e-06).00001)
```



Saved results

`dydx` saves the following in `r()`:

Macros

`r(y)`	name of *yvar*

`integ` saves the following in `r()`:

Scalars

`r(N_points)`	number of unique x points
`r(integral)`	estimate of the integral

Methods and formulas

`dydx` and `integ` are implemented as ado-files.

Consider a set of data points, $(x_1, y_1), \ldots, (x_n, y_n)$, generated by a function $y = f(x)$. `dydx` and `integ` first fit these points with a cubic spline, which is then analytically differentiated (integrated) to give an approximation for the derivative (integral) of f.

The cubic spline (see, for example, Press et al. [2007]) consists of $n-1$ cubic polynomials $P_i(x)$, with the ith one defined on the interval $[x_i, x_{i+1}]$,

$$P_i(x) = y_i a_i(x) + y_{i+1} b_i(x) + y_i'' c_i(x) + y_{i+1}'' d_i(x)$$

where

$$a_i(x) = \frac{x_{i+1} - x}{x_{i+1} - x_i} \qquad b_i(x) = \frac{x - x_i}{x_{i+1} - x_i}$$

$$c_i(x) = \frac{1}{6}(x_{i+1} - x_i)^2 a_i(x)[\{a_i(x)\}^2 - 1] \qquad d_i(x) = \frac{1}{6}(x_{i+1} - x_i)^2 b_i(x)[\{b_i(x)\}^2 - 1]$$

and y_i'' and y_{i+1}'' are constants whose values will be determined as described below. The notation for these constants is justified because $P_i''(x_i) = y_i''$ and $P_i''(x_{i+1}) = y_{i+1}''$.

Because $a_i(x_i) = 1$, $a_i(x_{i+1}) = 0$, $b_i(x_i) = 0$, and $b_i(x_{i+1}) = 1$. Therefore, $P_i(x_i) = y_i$, and $P_i(x_{i+1}) = y_{i+1}$. Thus the P_i jointly define a function that is continuous at the interval boundaries. The first derivative should be continuous at the interval boundaries; that is,

$$P_i'(x_{i+1}) = P_{i+1}'(x_{i+1})$$

The above $n - 2$ equations (one equation for each point except the two endpoints) and the values of the first derivative at the endpoints, $P_1'(x_1)$ and $P_{n-1}'(x_n)$, determine the n constants y_i''.

The value of the first derivative at an endpoint is set to the value of the derivative obtained by fitting a quadratic to the endpoint and the two adjacent points; namely, we use

$$P_1'(x_1) = \frac{y_1 - y_2}{x_1 - x_2} + \frac{y_1 - y_3}{x_1 - x_3} - \frac{y_2 - y_3}{x_2 - x_3}$$

and a similar formula for the upper endpoint.

`dydx` approximates $f'(x_i)$ by using $P_i'(x_i)$.

`integ` approximates $F(x_i) = F(x_1) + \int_{x_1}^{x_i} f(x)\,dx$ by using

$$I_0 + \sum_{k=1}^{i-1} \int_{x_k}^{x_{k+1}} P_k(x)\,dx$$

where I_0 (an estimate of $F(x_1)$) is the value specified by the `initial(#)` option. If the `trapezoid` option is specified, `integ` approximates the integral by using the trapezoidal rule:

$$I_0 + \sum_{k=1}^{i-1} \frac{1}{2}\,(x_{k+1} - x_k)(y_{k+1} + y_k)$$

If there are ties among the x_i, the mean of y_i is computed at each set of ties and the cubic spline is fit to these values.

Acknowledgment

The present versions of `dydx` and `integ` were inspired by the `dydx2` command written by Patrick Royston of the MRC Clinical Trials Unit, London.

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Also see

[D] **obs** — Increase the number of observations in a dataset

[D] **range** — Generate numerical range

Title

***eform_option* — Displaying exponentiated coefficients**

Description

An *eform_option* causes the coefficient table to be displayed in exponentiated form: for each coefficient, e^b rather than b is displayed. Standard errors and confidence intervals (CIs) are also transformed.

An *eform_option* is one of the following:

eform_option	Description
`eform(`*string*`)`	use *string* for the column title
`eform`	exponentiated coefficient, *string* is `exp(b)`
`hr`	hazard ratio, *string* is `Haz. Ratio`
`shr`	subhazard ratio, *string* is `SHR`
`irr`	incidence-rate ratio, *string* is `IRR`
`or`	odds ratio, *string* is `Odds Ratio`
`rrr`	relative-risk ratio, *string* is `RRR`

Remarks

▷ Example 1

Here is a simple example of the `or` option with `svy: logit`. The CI for the odds ratio is computed by transforming (by exponentiating) the endpoints of the CI for the corresponding coefficient.

```
. use http://www.stata-press.com/data/r12/nhanes2d
. svy, or: logit highbp female black
(running logit on estimation sample)
```

(*output omitted*)

highbp	Odds Ratio	Linearized Std. Err.	t	P>|t|	[95% Conf.	Interval]
female	.693628	.048676	-5.21	0.000	.6011298	.8003593
black	1.509156	.2089571	2.97	0.006	1.137873	2.001588
_cons	.1350642	.0107783	-25.09	0.000	.1147774	.1589367

We also could have specified the following command and received the same results as above:

```
. svy: logit highbp female black, or
```

◁

Also see

[R] **ml** — Maximum likelihood estimation

Title

eivreg — Errors-in-variables regression

Syntax

`eivreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`reliab(`*indepvar* # [*indepvar* # [...]]`)`	specify measurement reliability for each *indepvar* measured with error
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Errors-in-variables regression

Description

`eivreg` fits errors-in-variables regression models.

Options

Model

`reliab(`*indepvar* # [*indepvar* # [...]]`)` specifies the measurement reliability for each independent variable measured with error. Reliabilities are specified as pairs consisting of an independent variable name (a name that appears in *indepvars*) and the corresponding reliability r, $0 < r \leq 1$. Independent variables for which no reliability is specified are assumed to have reliability 1. If the option is not specified, all variables are assumed to have reliability 1, and the result is thus the same as that produced by `regress` (the ordinary least-squares results).

Reporting

`level(#)`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `eivreg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

For an introduction to errors-in-variables regression, see Draper and Smith (1998, 89–91) or Kmenta (1997, 352–357). Treiman (2009, 258–261) compares the results of errors-in-variables regression with conventional regression.

Errors-in-variables regression models are useful when one or more of the independent variables are measured with additive noise. Standard regression (as performed by `regress`) would underestimate the effect of the variable, and the other coefficients in the model can be biased to the extent that they are correlated with the poorly measured variable. You can adjust for the biases if you know the reliability:

$$r = 1 - \frac{\text{noise variance}}{\text{total variance}}$$

That is, given the model $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{u}$, for some variable $\mathbf{x}_i$ in $\mathbf{X}$, the $\mathbf{x}_i$ is observed with error, $\mathbf{x}_i = \mathbf{x}_i^* + \mathbf{e}$, and the noise variance is the variance of $\mathbf{e}$. The total variance is the variance of $\mathbf{x}_i$.

▷ Example 1

Say that in our automobile data, the weight of cars was measured with error, and the reliability of our measured weight is 0.85. The result of this would be to underestimate the effect of `weight` in a regression of, say, `price` on `weight` and `foreign`, and it would also bias the estimate of the coefficient on `foreign` (because being of foreign manufacture is correlated with the weight of cars). We would ignore all of this if we fit the model with `regress`:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress price weight foreign
```

Source	SS	df	MS	Number of obs =	74
				F(2, 71) =	35.35
Model	316859273	2	158429637	Prob > F =	0.0000
Residual	318206123	71	4481776.38	R-squared =	0.4989
				Adj R-squared =	0.4848
Total	635065396	73	8699525.97	Root MSE =	2117

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	3.320737	.3958784	8.39	0.000	2.531378	4.110096
foreign	3637.001	668.583	5.44	0.000	2303.885	4970.118
_cons	-4942.844	1345.591	-3.67	0.000	-7625.876	-2259.812

With eivreg, we can account for our measurement error:

```
. eivreg price weight foreign, r(weight .85)
```

variable	assumed reliability
weight	0.8500
*	1.0000

Errors-in-variables regression

Number of obs	= 74
F(2, 71)	= 50.37
Prob > F	= 0.0000
R-squared	= 0.6483
Root MSE	= 1773.54

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	4.31985	.431431	10.01	0.000	3.459601	5.180099
foreign	4637.32	624.5362	7.43	0.000	3392.03	5882.609
_cons	-8257.017	1452.086	-5.69	0.000	-11152.39	-5361.639

The effect of weight is increased—as we knew it would be—and here the effect of foreign manufacture is also increased. A priori, we knew only that the estimate of foreign might be biased; we did not know the direction.

◁

❑ Technical note

Swept under the rug in our example is how we would determine the reliability, r. We can easily see that a variable is measured with error, but we may not know the reliability because the ingredients for calculating r depend on the unobserved noise.

For our example, we made up a value for r, and in fact we do not believe that weight is measured with error at all, so the reported eivreg results have no validity. The regress results were the statistically correct results here.

But let's say that we do suspect that weight is measured with error and that we do not know r. We could then experiment with various values of r to describe the sensitivity of our estimates to possible error levels. We may not know r, but r does have a simple interpretation, and we could probably produce a sensible range for r by thinking about how the data were collected.

If the reliability, r, is less than the R^2 from a regression of the poorly measured variable on all the other variables, including the dependent variable, the information might as well not have been collected; no adjustment to the final results is possible. For our automobile data, running a regression of weight on foreign and price would result in an R^2 of 0.6743. Thus the reliability must be at least 0.6743 here. If we specify a reliability that is too small, eivreg will inform us and refuse to fit the model:

```
. eivreg price weight foreign, r(weight .6742)
reliability r() too small
r(399);
```

Returning to our problem of how to estimate r, too small or not, if the measurements are summaries of scaled items, the reliability may be estimated using the alpha command; see [R] **alpha**. If the score is computed from factor analysis and the data are scored using predict's default options (see [MV] **factor postestimation**), the square of the standard deviation of the score is an estimate of the reliability.

❑

❑ Technical note

Consider a model with more than one variable measured with error. For instance, say that our model is that `price` is a function of `weight`, `foreign`, and `mpg` and that both `weight` and `mpg` are measured with error.

```
. eivreg price weight foreign mpg, r(weight .85 mpg .9)
                  assumed                      Errors-in-variables regression
    variable     reliability
-------------------------------                 Number of obs =        74
      weight          0.8500                    F(  3,    70) =    429.14
         mpg          0.9000                    Prob > F      =    0.0000
           *          1.0000                    R-squared     =    0.9728
                                                Root MSE      =    496.41
------------------------------------------------------------------------------
       price |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |   12.88302   .6820532    18.89   0.000     11.52271    14.24333
     foreign |   8268.951   352.8719    23.43   0.000      7565.17    8972.732
         mpg |   999.2043   73.60037    13.58   0.000      852.413    1145.996
       _cons |  -56473.19   3710.015   -15.22   0.000    -63872.58   -49073.8
------------------------------------------------------------------------------
```

❑

Saved results

`eivreg` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(df_m)`	model degrees of freedom
`e(df_r)`	residual degrees of freedom
`e(r2)`	R-squared
`e(F)`	F statistic
`e(rmse)`	root mean squared error
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`eivreg`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(rellist)`	*indepvars* and associated reliabilities
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(Cns)`	constraints matrix
`e(V)`	variance–covariance matrix of the estimators

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`eivreg` is implemented as an ado-file.

Let the model to be fit be

$$\mathbf{y} = \mathbf{X}^*\boldsymbol{\beta} + \mathbf{e}$$
$$\mathbf{X} = \mathbf{X}^* + \mathbf{U}$$

where $\mathbf{X}^*$ are the true values and $\mathbf{X}$ are the observed values. Let $\mathbf{W}$ be the user-specified weights. If no weights are specified, $\mathbf{W} = \mathbf{I}$. If weights are specified, let $\mathbf{v}$ be the specified weights. If `fweight` frequency weights are specified, then $\mathbf{W} = \text{diag}(\mathbf{v})$. If `aweight` analytic weights are specified, then $\mathbf{W} = \text{diag}\{\mathbf{v}/(\mathbf{1}'\mathbf{v})(\mathbf{1}'\mathbf{1})\}$, meaning that the weights are normalized to sum to the number of observations.

The estimates $\mathbf{b}$ of $\boldsymbol{\beta}$ are obtained as $\mathbf{A}^{-1}\mathbf{X}'\mathbf{W}\mathbf{y}$, where $\mathbf{A} = \mathbf{X}'\mathbf{W}\mathbf{X} - \mathbf{S}$. $\mathbf{S}$ is a diagonal matrix with elements $N(1-r_i)s_i^2$. N is the number of observations, r_i is the user-specified reliability coefficient for the ith explanatory variable or 1 if not specified, and s_i^2 is the (appropriately weighted) variance of the variable.

The variance–covariance matrix of the estimators is obtained as $s^2\mathbf{A}^{-1}\mathbf{X}'\mathbf{W}\mathbf{X}\mathbf{A}^{-1}$, where the root mean squared error $s^2 = (\mathbf{y}'\mathbf{W}\mathbf{y} - \mathbf{b}\mathbf{A}\mathbf{b}')/(N-p)$, where p is the number of estimated parameters.

References

Draper, N., and H. Smith. 1998. *Applied Regression Analysis*. 3rd ed. New York: Wiley.

Kmenta, J. 1997. *Elements of Econometrics*. 2nd ed. Ann Arbor: University of Michigan Press.

Treiman, D. J. 2009. *Quantitative Data Analysis: Doing Social Research to Test Ideas*. San Francisco, CA: Jossey-Bass.

Also see

[R] **eivreg postestimation** — Postestimation tools for eivreg

[R] **regress** — Linear regression

Stata Structural Equation Modeling Reference Manual

[U] **20 Estimation and postestimation commands**

Title

eivreg postestimation — Postestimation tools for eivreg

Description

The following postestimation commands are available after `eivreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	VCE and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic*]

statistic	Description
Main	
`xb`	linear prediction; the default
`residuals`	residuals
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`pr(`*a*`,`*b*`)`	$\Pr(a < y_j < b)$
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

where *a* and *b* may be numbers or variables; *a* missing ($a \geq .$) means $-\infty$, and *b* missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`residuals` calculates the residuals, that is, $y_j - \mathbf{x}_j\mathbf{b}$.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation and is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \,|\, a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated. *a* and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **eivreg** — Errors-in-variables regression

[U] **20 Estimation and postestimation commands**

Title

error messages — Error messages and return codes

Description

Whenever Stata detects that something is wrong—that what you typed is uninterpretable, that you are trying to do something you should not be trying to do, or that you requested the impossible—Stata responds by typing a message describing the problem, together with a *return code*. For instance,

```
. lsit
unrecognized command:  lsit
r(199);

. list myvar
variable myvar not found
r(111);

. test a=b
last estimates not found
r(301);
```

In each case, the message is probably sufficient to guide you to a solution. When we typed `lsit`, Stata responded with "unrecognized command". We meant to type `list`. When we typed `list myvar`, Stata responded with "variable myvar not found". There is no variable named `myvar` in our data. When we typed `test a=b`, Stata responded with "last estimates not found". `test` tests hypotheses about previously fit models, and we have not yet fit a model.

The numbers in parentheses in the `r(199)`, `r(111)`, and `r(301)` messages are called the *return codes*. To find out more about these messages, type `search rc #`, where # is the number returned in the parentheses.

▷ Example 1

```
. search rc 301
[P]     error messages . . . . . . . . . . . . . . . . . . . . Return code 301
        last estimates not found;
        You typed an estimation command such as regress without arguments
        or attempted to perform a test or typed predict, but there were no
        previous estimation results.
```

◁

Programmers should see [P] **error** for details on programming error messages.

Also see

[R] **search** — Search Stata documentation

Title

estat — Postestimation statistics

Syntax

Common subcommands

Display information criteria

```
estat ic [ , n(#) ]
```

Summarize estimation sample

```
estat summarize [ eqlist ] [ , estat_summ_options ]
```

Display covariance matrix estimates

```
estat vce [ , estat_vce_options ]
```

Command-specific subcommands

```
estat subcommand1 [ , options1 ]
estat subcommand2 [ , options2 ]
    ...
```

estat_summ_options	Description
`equation`	display summary by equation
`group`	display summary by group; only after `sem`
`labels`	display variable labels
`noheader`	suppress the header
`noweights`	ignore weights
display_options	control spacing and display of omitted variables and base and empty cells

eqlist is rarely used and specifies the variables, with optional equation name, to be summarized. *eqlist* may be *varlist* or (*eqname*$_1$`:` *varlist*) (*eqname*$_2$`:` *varlist*) .... *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

estat_vce_options	Description
`covariance`	display as covariance matrix; the default
`correlation`	display as correlation matrix
`equation(`*spec*`)`	display only specified equations
`block`	display submatrices by equation
`diag`	display submatrices by equation; diagonal blocks only
`format(%`*fmt*`)`	display format for covariances and correlations
`nolines`	suppress lines between equations
display_options	control display of omitted variables and base and empty cells

Menu

Statistics > Postestimation > Reports and statistics

Description

`estat` displays scalar- and matrix-valued statistics after estimation; it complements `predict`, which calculates variables after estimation. Exactly what statistics `estat` can calculate depends on the previous estimation command.

Three sets of statistics are so commonly used that they are available after all estimation commands that store the model log likelihood. `estat ic` displays Akaike's and Schwarz's Bayesian information criteria. `estat summarize` summarizes the variables used by the command and automatically restricts the sample to `e(sample)`; it also summarizes the weight variable and cluster structure, if specified. `estat vce` displays the covariance or correlation matrix of the parameter estimates of the previous model.

Option for estat ic

`n(#)` specifies the N to be used in calculating BIC; see [R] **BIC note**.

Options for estat summarize

`equation` requests that the dependent variables and the independent variables in the equations be displayed in the equation-style format of estimation commands, repeating the summary information about variables entered in more than one equation.

`group` displays summary information separately for each group. `group` is only allowed after `sem` with a `group()` variable specified.

`labels` displays variable labels.

`noheader` suppresses the header.

`noweights` ignores the weights, if any, from the previous estimation command. The default when weights are present is to perform a weighted `summarize` on all variables except the weight variable itself. An unweighted `summarize` is performed on the weight variable.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`; see [R] **estimation options**.

Options for estat vce

`covariance` displays the matrix as a variance–covariance matrix; this is the default.

`correlation` displays the matrix as a correlation matrix rather than a variance–covariance matrix. `rho` is a synonym.

`equation(`*spec*`)` selects part of the VCE to be displayed. If *spec* is *eqlist*, the VCE for the listed equations is displayed. If *spec* is *eqlist1* `\` *eqlist2*, the part of the VCE associated with the equations in *eqlist1* (rowwise) and *eqlist2* (columnwise) is displayed. If *spec* is `*`, all equations are displayed. `equation()` implies `block` if `diag` is not specified.

`block` displays the submatrices pertaining to distinct equations separately.

`diag` displays the diagonal submatrices pertaining to distinct equations separately.

`format(%`*fmt*`)` specifies the number format for displaying the elements of the matrix. The default is `format(%10.0g)` for covariances and `format(%8.4f)` for correlations. See [U] **12.5 Formats: Controlling how data are displayed** for more information.

`nolines` suppresses lines between equations.

display_options: `noomitted`, `noemptycells`, `baselevels`, `allbaselevels`; see [R] **estimation options**.

Remarks

`estat` displays a variety of scalar- and matrix-valued statistics after you have estimated the parameters of a model. Exactly what statistics `estat` can calculate depends on the estimation command used, and command-specific statistics are detailed in that command's postestimation manual entry. The rest of this entry discusses three sets of statistics that are available after all estimation commands.

Remarks are presented under the following headings:

estat ic
estat summarize
estat vce

estat ic

`estat ic` calculates two information criteria used to compare models. Unlike likelihood-ratio, Wald, and similar testing procedures, the models need not be nested to compare the information criteria. Because they are based on the log-likelihood function, information criteria are available only after commands that report the log likelihood.

In general, "smaller is better": given two models, the one with the smaller AIC fits the data better than the one with the larger AIC. As with the AIC, a smaller BIC indicates a better-fitting model. For AIC and BIC formulas, see *Methods and formulas*.

▷ Example 1

In [R] **mlogit**, we fit a model explaining the type of insurance a person has on the basis of age, gender, race, and site of study. Here we refit the model with and without the site dummies and compare the models.

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. mlogit insure age male nonwhite
  (output omitted)
. estat ic
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
.	615	-555.8545	-545.5833	8	1107.167	1142.54

Note: N=Obs used in calculating BIC; see **[R] BIC note**

```
. mlogit insure age male nonwhite i.site
  (output omitted)
```

```
. estat ic
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
.	615	-555.8545	-534.3616	12	1092.723	1145.783

Note: N=Obs used in calculating BIC; see **[R] BIC note**

The AIC indicates that the model including the site dummies fits the data better, whereas the BIC indicates the opposite. As is often the case, different model-selection criteria have led to conflicting conclusions.

◁

❑ Technical note

`glm` and `binreg, ml` report a slightly different version of AIC and BIC; see [R] **glm** for the formulas used. That version is commonly used within the GLM literature; see, for example, Hardin and Hilbe (2007). The literature on information criteria is vast; see, among others, Akaike (1973), Sawa (1978), and Raftery (1995). Judge et al. (1985) contains a discussion of using information criteria in econometrics. Royston and Sauerbrei (2008, chap. 2) examine the use of information criteria as an alternative to stepwise procedures for selecting model variables.

❑

estat summarize

Often when fitting a model, you will also be interested in obtaining summary statistics, such as the sample means and standard deviations of the variables in the model. `estat summarize` makes this process simple. The output displayed is similar to that obtained by typing

```
. summarize varlist if e(sample)
```

without the need to type the *varlist* containing the dependent and independent variables.

▷ Example 2

Continuing with the previous multinomial logit model, here we summarize the variables by using `estat summarize`.

```
. estat summarize, noomitted
Estimation sample mlogit                 Number of obs =    615
```

Variable	Mean	Std. Dev.	Min	Max
insure	1.596748	.6225846	1	3
age	44.46832	14.18523	18.1109	86.0725
male	.2504065	.4335998	0	1
nonwhite	.196748	.3978638	0	1
site				
2	.3707317	.4833939	0	1
3	.3138211	.4644224	0	1

◁

The output in the previous example contains all the variables in one table, though `mlogit` presents its results in a multiple-equation format. For models in which the same variables appear in all equations, that is fine; but for other multiple-equation models, we may prefer to have the variables separated by the equation in which they appear. The `equation` option makes this possible.

▷ Example 3

Systems of simultaneous equations typically have different variables in each equation, and the `equation` option of `estat summarize` is helpful in such situations. In example 2 of [R] **reg3**, we have a model of supply and demand. We first refit the model and then call `estat summarize`.

```
. use http://www.stata-press.com/data/r12/supDem
. reg3 (Demand:quantity price pcompete income) (Supply:quantity price praw),
> endog(price)
```

(*output omitted*)

```
. estat summarize, equation
Estimation sample reg3                    Number of obs =     49
```

Variable	Mean	Std. Dev.	Min	Max
depvar				
quantity	12.61818	2.774952	7.71069	20.0477
quantity	12.61818	2.774952	7.71069	20.0477
Demand				
price	32.70944	2.882684	26.3819	38.4769
pcompete	5.929975	3.508264	.207647	11.5549
income	7.811735	4.18859	.570417	14.0077
Supply				
price	32.70944	2.882684	26.3819	38.4769
praw	4.740891	2.962565	.151028	9.79881

The first block of the table contains statistics on the dependent (or, more accurately, left-hand-side) variables, and because we specified quantity as the left-hand-side variable in both equations, it is listed twice. The second block refers to the variables in the first equation we specified, which we labeled "Demand" in our call to `reg3`; and the final block refers to the supply equation.

◁

estat vce

`estat vce` allows you to display the VCE of the parameters of the previously fit model, as either a covariance matrix or a correlation matrix.

Example 4

Returning to the `mlogit` example, we type

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. mlogit insure age male nonwhite, nolog
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(6)      =      20.54
                                                Prob > chi2     =     0.0022
Log likelihood = -545.58328                     Pseudo R2       =     0.0185
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.0111915	.0060915	-1.84	0.066	-.0231305	.0007475
male	.5739825	.2005221	2.86	0.004	.1809665	.9669985
nonwhite	.7312659	.218978	3.34	0.001	.302077	1.160455
_cons	.1567003	.2828509	0.55	0.580	-.3976773	.7110778
Uninsure						
age	-.0058414	.0114114	-0.51	0.609	-.0282073	.0165245
male	.5102237	.3639793	1.40	0.161	-.2031626	1.22361
nonwhite	.4333141	.4106255	1.06	0.291	-.371497	1.238125
_cons	-1.811165	.5348606	-3.39	0.001	-2.859473	-.7628578

```
. estat vce, block
Covariance matrix of coefficients of mlogit model
  covariances of equation Indemnity
```

	age	male	nonwhite	_cons
age	0			
male	0	0		
nonwhite	0	0	0	
_cons	0	0	0	0

```
  covariances of equation Prepaid (row) by equation Indemnity (column)
```

	age	male	nonwhite	_cons
age	0			
male	0	0		
nonwhite	0	0	0	
_cons	0	0	0	0

```
  covariances of equation Prepaid
```

	age	male	nonwhite	_cons
age	.00003711			
male	-.00015303	.0402091		
nonwhite	-.00008948	.00470608	.04795135	
_cons	-.00159095	-.00398961	-.00628886	.08000462

```
  covariances of equation Uninsure (row) by equation Indemnity (column)
```

	age	male	nonwhite	_cons
age	0			
male	0	0		
nonwhite	0	0	0	
_cons	0	0	0	0

```
covariances of equation Uninsure (row) by equation Prepaid (column)
             |        age        male    nonwhite       _cons
-------------+--------------------------------------------------
         age |   .00001753  -.00007926  -.00004564  -.00076886
        male |  -.00007544   .02188398    .0023186  -.00145923
    nonwhite |  -.00004577   .00250588   .02813553  -.00263872
       _cons |  -.00077045  -.00130535  -.00257593   .03888032
covariances of equation Uninsure
             |        age        male    nonwhite       _cons
-------------+--------------------------------------------------
         age |   .00013022
        male |  -.00050406   .13248095
    nonwhite |  -.00026145   .01505449   .16861327
       _cons |  -.00562159  -.01686629  -.02474852   .28607591
```

The `block` option is particularly useful for multiple-equation estimators. The first block of output here corresponds to the VCE of the estimated parameters for the first equation—the square roots of the diagonal elements of this matrix are equal to the standard errors of the first equation's parameters. Similarly, the final block corresponds to the VCE of the parameters for the second equation. The middle block shows the covariances between the estimated parameters of the first and second equations. ◁

Saved results

`estat ic` saves the following in `r()`:

Matrices

`r(S)` 1 × 6 matrix of results:
1. sample size
2. log likelihood of null model
3. log likelihood of full model
4. degrees of freedom
5. AIC
6. BIC

`estat summarize` saves the following in `r()`:

Scalars

`r(N_groups)` number of groups (`group` only)

Matrices

`r(stats)` $k \times 4$ matrix of means, standard deviations, minimums, and maximums

`r(stats[_#])` $k \times 4$ matrix of means, standard deviations, minimums, and maximums for group # (`group` only)

`estat vce` saves the following in `r()`:

Matrices

`r(V)` VCE or correlation matrix

Methods and formulas

`estat` is implemented as an ado-file.

Akaike's (1974) information criterion is defined as

$$\mathrm{AIC} = -2\ln L + 2k$$

where $\ln L$ is the maximized log-likelihood of the model and k is the number of parameters estimated. Some authors define the AIC as the expression above divided by the sample size.

Schwarz's (1978) Bayesian information criterion is another measure of fit defined as

$$\text{BIC} = -2\ln L + k\ln N$$

where N is the sample size. See [R] **BIC note** for additional information on calculating and interpreting BIC.

Hirotugu Akaike (1927–2009) was born in Fujinomiya City, Shizuoka Prefecture, Japan. He was the son of a silkworm farmer. He gained BA and DSc degrees from the University of Tokyo. Akaike's career from 1952 at the Institute of Statistical Mathematics in Japan culminated in service as Director General; after 1994, he was Professor Emeritus. His best known work in a prolific career is on what is now known as the Akaike information criterion (AIC), which was formulated to help selection of the most appropriate model from a number of candidates.

Gideon E. Schwarz (1933–2007) was a professor of Statistics at the Hebrew University, Jerusalem. He was born in Salzburg, Austria, and obtained an MSc in 1956 from the Hebrew University and a PhD in 1961 from Columbia University. His interests included stochastic processes, sequential analysis, probability, and geometry. He is best known for the Bayesian information criterion (BIC).

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Also see

[R] **estimates** — Save and manipulate estimation results

[R] **summarize** — Summary statistics

[P] **estat programming** — Controlling estat after user-written commands

[U] **20 Estimation and postestimation commands**

Title

estimates — Save and manipulate estimation results

Syntax

Command	Reference
Save and use results from disk	
`estimates save` *filename*	[R] **estimates save**
`estimates use` *filename*	[R] **estimates save**
`estimates describe using` *filename*	[R] **estimates describe**
`estimates esample: ...`	[R] **estimates save**
Store and restore estimates in memory	
`estimates store` *name*	[R] **estimates store**
`estimates restore` *name*	[R] **estimates store**
`estimates query`	[R] **estimates store**
`estimates dir`	[R] **estimates store**
`estimates drop` *namelist*	[R] **estimates store**
`estimates clear`	[R] **estimates store**
Set titles and notes	
`estimates title:` *text*	[R] **estimates title**
`estimates title`	[R] **estimates title**
`estimates notes:` *text*	[R] **estimates notes**
`estimates notes`	[R] **estimates notes**
`estimates notes list ...`	[R] **estimates notes**
`estimates notes drop ...`	[R] **estimates notes**
Report	
`estimates describe` [*name*]	[R] **estimates describe**
`estimates replay` [*namelist*]	[R] **estimates replay**
Tables and statistics	
`estimates table` [*namelist*]	[R] **estimates table**
`estimates stats` [*namelist*]	[R] **estimates stats**
`estimates for` *namelist*`: ...`	[R] **estimates for**

Description

estimates allows you to store and manipulate estimation results:

- You can save estimation results in a file for use in later sessions.
- You can store estimation results in memory so that you can
    a. switch among separate estimation results and
    b. form tables combining separate estimation results.

Remarks

estimates is for use after you have fit a model, be it with regress, logistic, etc. You can use estimates after any estimation command, whether it be an official estimation command of Stata or a user-written one.

estimates has three separate but related capabilities:

1. You can save estimation results in a file on disk so that you can use them later, even in a different Stata session.
2. You can store up to 300 estimation results in memory so that they are at your fingertips.
3. You can make tables comparing any results you have stored in memory.

Remarks are presented under the following headings:

Saving and using estimation results
Storing and restoring estimation results
Comparing estimation results
Jargon

Saving and using estimation results

After you have fit a model, say, with regress, type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ foreign
  (output omitted)
```

You can save the results in a file:

```
. estimates save basemodel
(file basemodel.ster saved)
```

Later, say, in a different session, you can reload those results:

```
. estimates use basemodel
```

The situation is now nearly identical to what it was immediately after you fit the model. You can replay estimation results:

```
. regress
  (output omitted)
```

You can perform tests:

```
. test foreign==0
  (output omitted)
```

And you can use any postestimation command or postestimation capability of Stata. The only difference is that Stata no longer knows what the estimation sample, `e(sample)` in Stata jargon, was. When you reload the estimation results, you might not even have the original data in memory. That is okay. Stata will know to refuse to calculate anything that can be calculated only on the original estimation sample.

If it is important that you use a postestimation command that can be used only on the original estimation sample, there is a way you can do that. You `use` the original data and then use `estimates esample` to tell Stata what the original sample was.

See [R] **estimates save** for details.

Storing and restoring estimation results

Storing and restoring estimation results in memory is much like saving them to disk. You type

```
. estimates store base
```

to save the current estimation results under the name `base`, and you type

```
. estimates restore base
```

to get them back later. You can find out what you have stored by typing

```
. estimates dir
```

Saving estimation results to disk is more permanent than storing them in memory, so why would you want merely to store them? The answer is that, once they are stored, you can use other `estimates` commands to produce tables and reports from them.

See [R] **estimates store** for details about the `estimates store` and `restore` commands.

Comparing estimation results

Let's say that you have done the following:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ
  (output omitted)
. estimates store base
. regress mpg weight displ foreign
  (output omitted)
. estimates store alt
```

You can now get a table comparing the coefficients:

```
. estimates table base alt
```

Variable	base	alt
weight	-.00656711	-.00677449
displacement	.00528078	.00192865
foreign		-1.6006312
_cons	40.084522	41.847949

`estimates table` can do much more; see [R] **estimates table**. Also see [R] **estimates stats**. `estimates stats` works similarly to `estimates table` but produces model comparisons in terms of BIC and AIC.

Jargon

You know that if you fit a model, say, by typing

```
. regress mpg weight displacement
```

then you can later replay the results by typing

```
. regress
```

and you can do tests and calculate other postestimation statistics by typing

```
. test displacement==0
. estat vif
. predict mpghat
```

As a result, we often refer to the *estimation results* or the *current estimation results* or the *most recent estimation results* or the *last estimation results* or the *estimation results in memory*.

With `estimates store` and `estimates restore`, you can have many estimation results in memory. One set of those, the set most recently estimated, or the set most recently restored, are the *current* or *active* estimation results, which you can replay, which you can test, or from which you can calculate postestimation statistics.

Current and *active* are the two words we will use interchangeably from now on.

Also see

[P] **_estimates** — Manage estimation results

Title

estimates describe — Describe estimation results

Syntax

```
estimates describe
estimates describe name
estimates describe using filename [ , number(#) ]
```

Menu

Statistics > Postestimation > Manage estimation results > Describe results

Description

`estimates describe` describes the current (active) estimates. Reported are the command line that produced the estimates, any title that was set by `estimates title` (see [R] **estimates title**), and any notes that were added by `estimates notes` (see [R] **estimates notes**).

`estimates describe` *name* does the same but reports results for estimates stored by `estimates store` (see [R] **estimates store**).

`estimates describe using` *filename* does the same but reports results for estimates saved by `estimates save` (see [R] **estimates save**). If *filename* contains multiple sets of estimates (saved in it by `estimates save, append`), the number of sets of estimates is also reported. If *filename* is specified without an extension, `.ster` is assumed.

Option

`number(#)` specifies that the #th set of estimation results from *filename* be described. This assumes that multiple sets of estimation results have been saved in *filename* by `estimates save, append`. The default is `number(1)`.

Remarks

`estimates describe` can be used to describe the estimation results currently in memory,

```
. estimates describe
Estimation results produced by
    . regress mpg weight displ if foreign
```

or to describe results saved by `estimates save` in a `.ster` file:

```
. estimates describe using final
Estimation results "Final results" saved on 12apr2011 14:20, produced by
    . logistic myopic age sex drug1 drug2 if complete==1
Notes:
  1.  Used file patient.dta
  2.  "datasignature myopic age sex drug1 drug2 if complete==1"
      reports 148:5(58763):2252897466:3722318443
  3.  must be reviewed by rgg
```

▷ Example 1

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ if foreign
  (output omitted)
. estimates notes: file `c(filename)'
. datasignature
  74:12(71728):3831085005:1395876116
. estimates notes: datasignature report `r(datasignature)'
. estimates save foreign
file foreign.ster saved
. regress mpg weight displ if !foreign
  (output omitted)
. estimates describe using foreign
  Estimation results saved on 02may2011 10:33, produced by
     . regress mpg weight displ if foreign
  Notes:
    1.  file http://www.stata-press.com/data/r12/auto.dta
    2.  datasignature report 74:12(71728):3831085005:1395876116
```

◁

Saved results

`estimates describe` and `estimates describe` *name* save the following in `r()`:

Macros

`r(title)`	title
`r(cmdline)`	original command line

`estimates describe using` *filename* saves the above and the following in `r()`:

Scalars

`r(datetime)`	`%tc` value of date/time file saved
`r(nestresults)`	number of sets of estimation results in file

Methods and formulas

`estimates describe` is implemented as an ado-file.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates for — Repeat postestimation command across models

Syntax

estimates for *namelist* [, *options*]: *postestimation_command*

where *namelist* is a name, a list of names, _all, or *. A name may be ., meaning the current (active) estimates. _all and * mean the same thing.

options	Description
noheader	do not display title
nostop	do not stop if command fails

Description

estimates for performs *postestimation_command* on each estimation result specified.

Options

noheader suppresses the display of the header as *postestimation_command* is executed each time.

nostop specifies that execution of *postestimation_command* is to be performed on the remaining models even if it fails on some.

Remarks

In the example that follows, we fit a model two different ways, store the results, and then use estimates for to perform the same test on both of them:

▷ Example 1

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. gen fwgt = foreign*weight
. gen dwgt = !foreign*weight
. gen gpm = 1/mpg
. regress gpm fwgt dwgt displ foreign
  (output omitted)
. estimates store reg
. qreg gpm fwgt dwgt displ foreign
  (output omitted)
. estimates store qreg
```

```
. estimates for reg qreg: test fwgt==dwgt
-------------------------------------------------------------------------------
Model reg
-------------------------------------------------------------------------------
 ( 1)  fwgt - dwgt = 0
       F(  1,    69) =    4.87
            Prob > F =    0.0307
-------------------------------------------------------------------------------
Model qreg
-------------------------------------------------------------------------------
 ( 1)  fwgt - dwgt = 0
       F(  1,    69) =    0.07
            Prob > F =    0.7937
```

◁

Methods and formulas

`estimates for` is implemented as an ado-file.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates notes — Add notes to estimation results

Syntax

```
estimates notes: text

estimates notes

estimates notes list [ in noterange ]

estimates notes drop in noterange
```

where *noterange* is # or #/# and where # may be a number, the letter `f` (meaning first), or the letter `l` (meaning last).

Description

`estimates notes:` *text* adds a note to the current (active) estimation results.

`estimates notes` and `estimates notes list` list the current notes.

`estimates notes drop in` *noterange* eliminates the specified notes.

Remarks

After adding or removing notes, if estimates have been stored, do not forget to store them again. If estimates have been saved, do not forget to save them again.

Notes are most useful when you intend to save estimation results in a file; see [R] **estimates save**. For instance, after fitting a model, you might type

```
. estimates note:  I think these are final
. estimates save lock2
```

and then, later when going through your files, you could type

```
. estimates use lock2
. estimates notes
  1.  I think these are final
```

Up to 9,999 notes can be attached to estimation results. If estimation results are important, we recommend that you add a note identifying the `.dta` dataset you used. The best way to do that is to type

```
. estimates notes:  file `c(filename)'
```

because `` `c(filename)' `` will expand to include not just the name of the file but also its full path; see [P] **creturn**.

If estimation results took a long time to estimate—say, they were produced by `asmprobit` or `gllamm` (see [R] **asmprobit** and http://www.gllamm.org)—it is also a good idea to add a data signature. A data signature takes less time to compute than reestimation when you need proof that you really have the right dataset. The easy way to do that is to type

```
. datasignature
  74:12(71728):3831085005:1395876116
. estimates notes:  datasignature reports 'r(datasignature)'
```

Now when you ask to see the notes, you will see

```
. estimates notes
  1.  I think these are final
  2.  file C:\project\one\pat4.dta
  3.  datasignature reports 74:12(71728):3831085005:1395876116
```

See [D] **datasignature**.

Notes need not be positive. You might set a note to be, "I need to check that age is defined correctly."

▷ Example 1

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ if foreign
  (output omitted)
. estimates notes: file 'c(filename)'
. datasignature
  74:12(71728):3831085005:1395876116
. estimates notes: datasignature report 'r(datasignature)'
. estimates save foreign
file foreign.ster saved
. estimates notes list in 1/2
    1.  file http://www.stata-press.com/data/r12/auto.dta
    2.  datasignature report 74:12(71728):3831085005:1395876116
. estimates notes drop in 2
  (1 note dropped)
. estimates notes
    1.  file http://www.stata-press.com/data/r12/auto.dta
```

◁

Methods and formulas

`estimates notes` is implemented as an ado-file.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates replay — Redisplay estimation results

Syntax

```
estimates replay
```

```
estimates replay namelist
```

where *namelist* is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

Menu

Statistics > Postestimation > Manage estimation results > Redisplay estimation output

Description

`estimates replay` redisplays the current (active) estimation results, just as typing the name of the estimation command would do.

`estimates replay` *namelist* redisplays each specified estimation result. The active estimation results are left unchanged.

Remarks

In the example that follows, we fit a model two different ways, store the results, use `estimates for` to perform the same test on both of them, and then replay the results:

▷ Example 1

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. gen fwgt = foreign*weight
. gen dwgt = !foreign*weight
. gen gpm = 1/mpg
. regress gpm fwgt dwgt displ foreign
  (output omitted)
. estimates store reg
. qreg gpm fwgt dwgt displ foreign
  (output omitted)
. estimates store qreg
. estimates for reg qreg: test fwgt==dwgt
```

```
-------------------------------------------------------------------------------
Model reg
-------------------------------------------------------------------------------

 ( 1)  fwgt - dwgt = 0

       F(  1,    69) =    4.87
            Prob > F =    0.0307
```

```
Model qreg
------------------------------------------------------------------------------

 ( 1)  fwgt - dwgt = 0
       F(  1,    69) =    0.07
            Prob > F =    0.7937

. estimates replay
------------------------------------------------------------------------------
Model qreg
------------------------------------------------------------------------------

Median regression                               Number of obs =        74
  Raw sum of deviations .7555689 (about .05)
  Min sum of deviations .3201479                Pseudo R2     =    0.5763

------------------------------------------------------------------------------
         gpm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        fwgt |   .0000155   2.87e-06     5.40   0.000     9.76e-06    .0000212
        dwgt |   .0000147   1.88e-06     7.81   0.000     .0000109    .0000184
displacement |   .0000179   .0000147     1.22   0.226    -.0000113    .0000471
     foreign |   .0065352   .0078098     0.84   0.406     -.009045    .0221153
       _cons |   .0003134   .0042851     0.07   0.942    -.0082351    .0088618
------------------------------------------------------------------------------

. estimates replay reg
------------------------------------------------------------------------------
Model reg
------------------------------------------------------------------------------

      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  4,    69) =   61.62
       Model |  .009342436     4  .002335609           Prob > F      =  0.0000
    Residual |  .002615192    69  .000037901           R-squared     =  0.7813
-------------+------------------------------           Adj R-squared =  0.7686
       Total |  .011957628    73  .000163803           Root MSE      =  .00616

------------------------------------------------------------------------------
         gpm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        fwgt |     .00002   3.27e-06     6.12   0.000     .0000135    .0000265
        dwgt |   .0000123   2.30e-06     5.36   0.000     7.75e-06    .0000169
displacement |   .0000296   .0000187     1.58   0.119    -7.81e-06     .000067
     foreign |  -.0117756   .0086088    -1.37   0.176    -.0289497    .0053986
       _cons |   .0053352   .0046748     1.14   0.258    -.0039909    .0146612
------------------------------------------------------------------------------
```

◁

Methods and formulas

`estimates replay` is implemented as an ado-file.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates save — Save and use estimation results

Syntax

```
estimates save filename [, append replace]

estimates use filename [, number(#)]

estimates esample: [varlist] [if] [in] [weight]
    [, replace stringvars(varlist) zeroweight]

estimates esample
```

Menu

estimates save

Statistics > Postestimation > Manage estimation results > Save to disk

estimates use

Statistics > Postestimation > Manage estimation results > Load from disk

Description

`estimates save` *filename* saves the current (active) estimation results in *filename*.

`estimates use` *filename* loads the results saved in *filename* into the current (active) estimation results.

In both cases, if *filename* is specified without an extension, `.ster` is assumed.

`estimates esample:` (note the colon) resets `e(sample)`. After `estimates use` *filename*, `e(sample)` is set to contain 0, meaning that none of the observations currently in memory was used in obtaining the estimates.

`estimates esample` (without a colon) displays how `e(sample)` is currently set.

Options

`append`, used with `estimates save`, specifies that results be appended to an existing file. If the file does not already exist, a new file is created.

`replace`, used with `estimates save`, specifies that *filename* can be replaced if it already exists.

`number(#)`, used with `estimates use`, specifies that the #th set of estimation results from *filename* be loaded. This assumes that multiple sets of estimation results have been saved in *filename* by `estimates save, append`. The default is `number(1)`.

`replace`, used with `estimates esample:`, specifies that `e(sample)` can be replaced even if it is already set.

`stringvars(`*varlist*`)`, used with `estimates esample:`, specifies string variables. Observations containing variables that contain `""` will be omitted from `e(sample)`.

`zeroweight`, used with `estimates esample:`, specifies that observations with zero weights are to be included in `e(sample)`.

Remarks

See [R] **estimates** for an overview of the `estimates` commands.

For a description of `estimates save` and `estimates use`, see *Saving and using estimation results* in [R] **estimates**.

The rest of this entry concerns `e(sample)`.

Remarks are presented under the following headings:

Setting e(sample)
Resetting e(sample)
Determining who set e(sample)

Setting e(sample)

After `estimates use` *filename*, the situation is nearly identical to what it was immediately after you fit the model. The one difference is that `e(sample)` is set to 0.

`e(sample)` is Stata's function to mark which observations among those currently in memory were used in producing the estimates. For instance, you might type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ if foreign
  (output omitted)
. summarize mpg if e(sample)
  (output omitted)
```

and `summarize` would report the summary statistics for the observations `regress` in fact used, which would exclude not only observations for which `foreign` = 0 but also any observations for which `mpg`, `weight`, or `displ` was missing.

If you saved the above estimation results and then reloaded them, however, `summarize mpg if e(sample)` would produce

```
. summarize mpg if e(sample)
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
         mpg |         0
```

Stata thinks that none of these observations was used in producing the estimates currently loaded.

What else could Stata think? When you `estimates use` *filename*, you do not have to have the original data in memory. Even if you do have data in memory that look like the original data, it might not be. Setting `e(sample)` to 0 is the safe thing to do. There are some postestimation statistics, for instance, that are appropriate only when calculated on the estimation sample. Setting `e(sample)` to 0 ensures that, should you ask for one of them, you will get back a null result.

We recommend that you leave e(sample) set to 0. But what if you really need to calculate that postestimation statistic? Well, you can get it, but you are going to take responsibility for setting e(sample) correctly. Here we just happen to know that all the foreign observations were used, so we can type

```
. estimates esample:  if foreign
```

If all the observations had been used, we could simply type

```
. estimates esample:
```

The safe thing to do, however, is to look at the estimation command—estimates describe will show it to you—and then type

```
. estimates esample:  mpg weight displ if foreign
```

Resetting e(sample)

estimates esample: will allow you to not only set but also reset e(sample). If e(sample) has already been set (say that you just fit the model) and you try to set it, you will see

```
. estimates esample:  mpg weight displ if foreign
no; e(sample) already set
r(322);
```

Here you can specify the replace option:

```
. estimates esample:  mpg weight displ if foreign, replace
```

We do not recommend resetting e(sample), but the situation can arise where you need to. Imagine that you estimates use *filename*, you set e(sample), and then you realize that you set it wrong. Here you would want to reset it.

Determining who set e(sample)

estimates esample without a colon will report whether and how e(sample) was set. You might see

```
. estimates esample
  e(sample) set by estimation command
```

or

```
. estimates esample
  e(sample) set by user
```

or

```
. estimates esample
  e(sample) not set (0 assumed)
```

Saved results

estimates esample without the colon saves macro r(who), which will contain cmd, user, or zero'd.

Methods and formulas

`estimates save`, `estimates use`, `estimates esample:`, and `estimates esample` are implemented as ado-files.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates stats — Model statistics

Syntax

`estimates stats` [*namelist*] [`, n(#)`]

where *namelist* is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

Menu

Statistics > Postestimation > Manage estimation results > Table of fit statistics

Description

`estimates stats` reports model-selection statistics, including the Akaike information criterion (AIC) and the Bayesian information criterion (BIC). These measures are appropriate for maximum likelihood models.

If `estimates stats` is used for a non–likelihood-based model, such as `qreg`, missing values are reported.

Option

`n(#)` specifies the N to be used in calculating BIC; see [R] **BIC note**.

Remarks

If you type `estimates stats` without arguments, a table for the most recent estimation results will be shown:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. logistic foreign mpg weight displ
  (output omitted)
. estimates stats
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
.	74	-45.03321	-20.59083	4	49.18167	58.39793

Note: N=Obs used in calculating BIC; see **[R] BIC note**

Regarding the note at the bottom of the table, N is an ingredient in the calculation of BIC; see [R] **BIC note**. The note changes if you specify the `n()` option, which tells `estimates stats` what N to use. $N =$ `Obs` is the default.

Regarding the table itself, `ll(null)` is the log likelihood for the constant-only model, `ll(model)` is the log likelihood for the model, `df` is the number of degrees of freedom, and `AIC` and `BIC` are the Akaike and Bayesian information criteria.

Models with smaller values of an information criterion are considered preferable.

`estimates stats` can compare estimation results:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. logistic foreign mpg weight displ
  (output omitted)
. estimates store full
. logistic foreign mpg weight
  (output omitted)
. estimates store sub
. estimates stats full sub
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
full	74	-45.03321	-20.59083	4	49.18167	58.39793
sub	74	-45.03321	-27.17516	3	60.35031	67.26251

Note: N=Obs used in calculating BIC; see **[R] BIC note**

Saved results

`estimates stats` saves the following in `r()`:

Matrices

`r(S)` matrix with 6 columns (N, ll0, ll, df, AIC, and BIC) and rows corresponding to models in table

Methods and formulas

`estimates stats` is implemented as an ado-file.

See [R] **BIC note**.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates store — Store and restore estimation results

Syntax

```
estimates store name [, nocopy]

estimates restore name


estimates query

estimates dir [namelist]


estimates drop namelist

estimates clear
```

where *namelist* is a name, a list of names, `_all`, or `*`. `_all` and `*` mean the same thing.

Menu

estimates store

Statistics > Postestimation > Manage estimation results > Store in memory

estimates restore

Statistics > Postestimation > Manage estimation results > Restore from memory

estimates dir

Statistics > Postestimation > Manage estimation results > List results stored in memory

estimates drop

Statistics > Postestimation > Manage estimation results > Drop from memory

Description

`estimates store` *name* saves the current (active) estimation results under the name *name*.

`estimates restore` *name* loads the results saved under *name* into the current (active) estimation results.

`estimates query` tells you whether the current (active) estimates have been stored and, if so, the name.

`estimates dir` displays a list of the stored estimates.

`estimates drop` *namelist* drops the specified stored estimation results.

`estimates clear` drops all stored estimation results.

`estimates clear`, `estimates drop _all`, and `estimates drop *` do the same thing. `estimates drop` and `estimates clear` do not eliminate the current (active) estimation results.

Option

`nocopy`, used with `estimates store`, specifies that the current (active) estimation results are to be moved into *name* rather than copied. Typing

```
. estimates store hold, nocopy
```

is the same as typing

```
. estimates store hold
. ereturn clear
```

except that the former is faster. The `nocopy` option is sometimes used by programmers.

Remarks

`estimates store` stores estimation results in memory so that you can access them later.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ
  (output omitted)
. estimates store myreg
. ... you do other things, including fitting other models ...
. estimates restore myreg
. regress
  (same output shown again)
```

After `estimates restore myreg`, things are once again just as they were, estimationwise, just after you typed `regress mpg weight displ`.

`estimates store` stores results in memory. When you exit Stata, those stored results vanish. If you wish to make a permanent copy of your estimation results, see [R] **estimates save**.

The purpose of making copies in memory is 1) so that you can quickly switch between them and 2) so that you can make tables comparing estimation results. Concerning the latter, see [R] **estimates table** and [R] **estimates stats**.

Saved results

`estimates dir` saves the following in `r()`:

Macros
`r(names)` names of stored results

Methods and formulas

`estimates store`, `estimates restore`, `estimates query`, `estimates dir`, `estimates drop`, and `estimates clear` are implemented as ado-files.

References

Jann, B. 2005. Making regression tables from stored estimates. *Stata Journal* 5: 288–308.

——. 2007. Making regression tables simplified. *Stata Journal* 7: 227–244.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates table — Compare estimation results

Syntax

`estimates table` [*namelist*] [`,` *options*]

where *namelist* is a name, a list of names, `_all`, or `*`. A name may be `.`, meaning the current (active) estimates. `_all` and `*` mean the same thing.

options	Description
Main	
`stats(`*scalarlist*`)`	report *scalarlist* in table
`star[ (`*#1 #2 #3*`) ]`	use stars to denote significance levels
Options	
`keep(`*coeflist*`)`	report coefficients in order specified
`drop(`*coeflist*`)`	omit specified coefficients from table
`equations(`*matchlist*`)`	match equations of models as specified
Numerical formats	
`b[ (%`*fmt*`) ]`	how to format coefficients, which are always reported
`se[ (%`*fmt*`) ]`	report standard errors and use optional format
`t[ (%`*fmt*`) ]`	report t or z and use optional format
`p[ (%`*fmt*`) ]`	report p-values and use optional format
`stfmt(%`*fmt*`)`	how to format scalar statistics
General format	
`varwidth(#)`	use # characters to display variable names and statistics
`modelwidth(#)`	use # characters to display model names
`eform`	display coefficients in exponentiated form
`label`	display variable labels rather than variable names
`newpanel`	display statistics in separate table from coefficients
`style(oneline)`	put vertical line after variable names; the default
`style(columns)`	put vertical line separating every column
`style(noline)`	suppress all vertical lines
`coded`	display compact table
Reporting	
display_options	control row spacing and display of omitted variables and base and empty cells
`title(`*string*`)`	title for table

`title()` does not appear in the dialog box.

where

- A *scalarlist* is a list of any or all of the names of scalars stored in `e()`, plus `aic`, `bic`, and `rank`.
- *#1 #2 #3* are three numbers such as `.05 .01 .001`.
- A *coeflist* is a list of coefficient names, each name of which may be simple (for example, `price`), an equation name followed by a colon (for example, `mean:`), or a full name (for example, `mean:price`). Names are separated by blanks.
- A *matchlist* specifies how equations from different estimation results are to be matched. If you need to specify a *matchlist*, the solution is usually `1`, as in `equations(1)`. The full syntax is

$$matchlist \;:=\; term \;\left[\, \texttt{,}\; term \;\ldots\; \right]$$

$$term \;:=\; \left[\, eqname \;\texttt{=}\, \right]\; \#\texttt{:}\#\ldots\texttt{:}\#$$
$$\left[\, eqname \;\texttt{=}\, \right]\; \#$$

  See `equations()` under *Options* below.

Menu

Statistics > Postestimation > Manage estimation results > Table of estimation results

Description

`estimates table` displays a table of coefficients and statistics for one or more sets of estimation results.

Options

Main

`stats(`*scalarlist*`)` specifies one or more scalar statistics to be displayed in the table. *scalarlist* may contain

`aic`	Akaike's information criterion
`bic`	Schwarz's Bayesian information criterion
`rank`	rank of `e(V)` (# of free parameters in model)

along with the names of any scalars stored in `e()`. The specified statistics do not have to be available for all estimation results being displayed.

For example, `stats(N ll chi2 aic)` specifies that `e(N)`, `e(ll)`, `e(chi2)`, and AIC be included. In Stata, `e(N)` records the number of observations; `e(ll)`, the log likelihood; and `e(chi2)`, the chi-squared test that all coefficients in the first equation of the model are equal to zero.

`star` and `star(`*#1 #2 #3*`)` specify that stars (asterisks) are to be used to mark significance. The second syntax specifies the significance levels for one, two, and three stars. If you specify simply `star`, that is equivalent to specifying `star(.05 .01 .001)`, which means one star (*) if $p < 0.05$, two stars (**) if $p < 0.01$, and three stars (***) if $p < 0.001$.

The `star` and `star()` options may not be combined with `se`, `t`, or `p` option.

Options

`keep(`*coeflist*`)` and `drop(`*coeflist*`)` are alternatives; they specify coefficients to be included or omitted from the table. The default is to display all coefficients.

If `keep()` is specified, it specifies not only the coefficients to be included but also the order in which they appear.

A *coeflist* is a list of coefficient names, each name of which may be simple (for example, `price`), an equation name followed by a colon (for example, `mean:`), or a full name (for example, `mean:price`). Names are separated from each other by blanks.

When full names are not specified, all coefficients that match the partial specification are included. For instance, `drop(_cons)` would omit `_cons` for all equations.

`equations(`*matchlist*`)` specifies how the equations of the models in *namelist* are to be matched. The default is to match equations by name. Matching by name usually works well when all results were fit by the same estimation command. When you are comparing results from different estimation commands, however, specifying `equations()` may be necessary.

The most common usage is `equations(1)`, which indicates that all first equations are to be matched into one equation named `#1`.

matchlist has the syntax

term [, *term* ...]

where *term* is

[*eqname* =] #:#...:# (syntax 1)

[*eqname* =] # (syntax 2)

In syntax 1, each # is a number or a period (`.`). If a number, it specifies the position of the equation in the corresponding model; `1:3:1` would indicate that equation 1 in the first model matches equation 3 in the second, which matches equation 1 in the third. A period indicates that there is no corresponding equation in the model; `1:.:1` indicates that equation 1 in the first matches equation 1 in the third.

In syntax 2, you specify just one number, say, `1` or `2`, and that is shorthand for `1:1...:1` or `2:2...:2`, meaning that equation 1 matches across all models specified or that equation 2 matches across all models specified.

Now that you can specify a *term*, you can put that together into a *matchlist* by separating one term from the other by commas. In what follows, we will assume that three names were specified,

```
. estimates table alpha beta gamma, ...
```

`equations(1)` is equivalent to `equations(1:1:1)`; we would be saying that the first equations match across the board.

`equations(1:.:1)` would specify that equation 1 matches in models `alpha` and `gamma` but that there is nothing corresponding in model `beta`.

`equations(1,2)` is equivalent to `equations(1:1:1, 2:2:2)`. We would be saying that the first equations match across the board and so do the second equations.

`equations(1, 2:.:2)` would specify that the first equations match across the board, that the second equations match for models `alpha` and `gamma`, and that there is nothing equivalent to equation 2 in model `beta`.

If `equations()` is specified, equations not matched by position are matched by name.

Numerical formats

`b(%`*fmt*`)` specifies how the coefficients are to be displayed. You might specify `b(%9.2f)` to make decimal points line up. There is also a `b` option, which specifies that coefficients are to be displayed, but that is just included for consistency with the `se`, `t`, and `p` options. Coefficients are always displayed.

`se`, `t`, and `p` specify that standard errors, t or z statistics, and significance levels are to be displayed. The default is not to display them. `se(%`*fmt*`)`, `t(%`*fmt*`)`, and `p(%`*fmt*`)` specify that each is to be displayed and specifies the display format to be used to format them.

`stfmt(%`*fmt*`)` specifies the format for displaying the scalar statistics included by the `stats()` option.

General format

`varwidth(#)` specifies the number of character positions used to display the names of the variables and statistics. The default is 12.

`modelwidth(#)` specifies the number of character positions used to display the names of the models. The default is 12.

`eform` displays coefficients in exponentiated form. For each coefficient, $\exp(\beta)$ rather than β is displayed, and standard errors are transformed appropriately. Display of the intercept, if any, is suppressed.

`label` specifies that variable labels be displayed instead of variable names.

`newpanel` specifies that the statistics be displayed in a table separated by a blank line from the table with coefficients rather than in the style of another equation in the table of coefficients.

`style(`*stylespec*`)` specifies the style of the coefficient table.

`style(oneline)` specifies that a vertical line be displayed after the variables but not between the models. This is the default.

`style(columns)` specifies that vertical lines be displayed after each column.

`style(noline)` specifies that no vertical lines be displayed.

`coded` specifies that a compact table be displayed. This format is especially useful for comparing variables that are included in a large collection of models.

Reporting

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, and `allbaselevels`; see [R] **estimation options**.

The following option is available with `estimates table` but is not shown in the dialog box:

`title(`*string*`)` specifies the title to appear above the table.

Remarks

If you type `estimates table` without arguments, a table of the most recent estimation results will be shown:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ
  (output omitted)
```

```
. estimates table
```

Variable	active
weight	-.00656711
displacement	.00528078
_cons	40.084522

The real use of `estimates table`, however, is for comparing estimation results, and that requires using it after `estimates store`:

```
. regress mpg weight displ
  (output omitted)
. estimates store base
. regress mpg weight displ foreign
  (output omitted)
. estimates store alt
. qreg mpg weight displ foreign
  (output omitted)
. estimates store qreg
. estimates table base alt qreg, stats(r2)
```

Variable	base	alt	qreg
weight	-.00656711	-.00677449	-.00595056
displacement	.00528078	.00192865	.00018552
foreign		-1.6006312	-2.1326004
_cons	40.084522	41.847949	39.213348
r2	.6529307	.66287957	

Saved results

`estimates table` saves the following in `r()`:

Macros

`r(names)` names of results used

Matrices

`r(coef)` matrix M: $n \times 2{*}m$
$M[i, 2j-1]$ = ith parameter estimate for model j;
$M[i, 2j]$ = variance of $M[i, 2j-1]$; i=1,...,n; j=1,...,m

`r(stats)` matrix S: $k \times m$ (if option `stats()` specified)
$S[i, j]$ = ith statistic for model j; i=1,...,k; j=1,...,m

Methods and formulas

`estimates table` is implemented as an ado-file.

Reference

Weiss, M. 2010. Stata tip 90: Displaying partial results. *Stata Journal* 10: 500–502.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimates title — Set title for estimation results

Syntax

```
estimates title: [text]

estimates title
```

Menu

Statistics > Postestimation > Manage estimation results > Title/retitle results

Description

`estimates title:` (note the colon) sets or clears the title for the current estimation results. The title is used by `estimates table` and `estimates stats` (see [R] **estimates table** and [R] **estimates stats**).

`estimates title` without the colon displays the current title.

Remarks

After setting the title, if estimates have been stored, do not forget to store them again:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg gear turn
  (output omitted)
. estimates store reg
```

Now let's add a title:

```
. estimates title: "My regression"
. estimates store reg
```

Methods and formulas

`estimates title:` and `estimates title` are implemented as ado-files.

Also see

[R] **estimates** — Save and manipulate estimation results

Title

estimation options — Estimation options

Description

This entry describes the options common to many estimation commands. Not all the options documented below work with all estimation commands. See the documentation for the particular estimation command; if an option is listed there, it is applicable.

Options

Model

`noconstant` suppresses the constant term (intercept) in the model.

`offset(`*varname*`)` specifies that *varname* be included in the model with the coefficient constrained to be 1.

`exposure(`*varname*`)` specifies a variable that reflects the amount of exposure over which the *depvar* events were observed for each observation; ln(*varname*) with coefficient constrained to be 1 is entered into the log-link function.

`constraints(`*numlist* | *matname*`)` specifies the linear constraints to be applied during estimation. The default is to perform unconstrained estimation. See [R] **reg3** for the use of constraints in multiple-equation contexts.

`constraints(`*numlist*`)` specifies the constraints by number after they have been defined by using the `constraint` command; see [R] **constraint**. Some commands (for example, `slogit`) allow only `constraints(`*numlist*`)`.

`constraints(`*matname*`)` specifies a matrix containing the constraints; see [P] **makecns**.

`constraints(`*clist*`)` is used by some estimation commands, such as `mlogit`, where *clist* has the form #[-#] [, #[-#] ...].

`collinear` specifies that the estimation command not omit collinear variables. Usually, there is no reason to leave collinear variables in place, and, in fact, doing so usually causes the estimation to fail because of the matrix singularity caused by the collinearity. However, with certain models, the variables may be collinear, yet the model is fully identified because of constraints or other features of the model. In such cases, using the `collinear` option allows the estimation to take place, leaving the equations with collinear variables intact. This option is seldom used.

`force` specifies that estimation be forced even though the time variable is not equally spaced. This is relevant only for correlation structures that require knowledge of the time variable. These correlation structures require that observations be equally spaced so that calculations based on lags correspond to a constant time change. If you specify a time variable indicating that observations are not equally spaced, the (time dependent) model will not be fit. If you also specify `force`, the model will be fit, and it will be assumed that the lags based on the data ordered by the time variable are appropriate.

Correlation

`corr(`*correlation*`)` specifies the within-group correlation structure; the default corresponds to the equal-correlation model, `corr(exchangeable)`.

When you specify a correlation structure that requires a lag, you indicate the lag after the structure's name with or without a blank; for example, `corr(ar 1)` or `corr(ar1)`.

If you specify the fixed correlation structure, you specify the name of the matrix containing the assumed correlations following the word `fixed`, for example, `corr(fixed myr)`.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`noskip` specifies that a full maximum-likelihood model with only a constant for the regression equation be fit. This model is not displayed but is used as the base model to compute a likelihood-ratio test for the model test statistic displayed in the estimation header. By default, the overall model test statistic is an asymptotically equivalent Wald test of all the parameters in the regression equation being zero (except the constant). For many models, this option can substantially increase estimation time.

`nocnsreport` specifies that no constraints be reported. The default is to display user-specified constraints above the coefficient table.

`noomitted` specifies that variables that were omitted because of collinearity not be displayed. The default is to include in the table any variables omitted because of collinearity and to label them as "(omitted)".

`vsquish` specifies that the blank space separating factor-variable terms or time-series–operated variables from other variables in the model be suppressed.

`noemptycells` specifies that empty cells for interactions of factor variables not be displayed. The default is to include in the table interaction cells that do not occur in the estimation sample and to label them as "(empty)".

`baselevels` and `allbaselevels` control whether the base levels of factor variables and interactions are displayed. The default is to exclude from the table all base categories.

`baselevels` specifies that base levels be reported for factor variables and for interactions whose bases cannot be inferred from their component factor variables.

`allbaselevels` specifies that all base levels of factor variables and interactions be reported.

`cformat(%`*fmt*`)` specifies how to format coefficients, standard errors, and confidence limits in the coefficient table.

`pformat(%`*fmt*`)` specifies how to format p-values in the coefficient table.

`sformat(%`*fmt*`)` specifies how to format test statistics in the coefficient table.

`nolstretch` specifies that the width of the coefficient table not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the coefficient table up to the width of the Results window. To change the default, use `set lstretch off`. `nolstretch` is not shown in the dialog box.

Integration

`intmethod(`*intmethod*`)` specifies the integration method to be used for the random-effects model. It accepts one of three arguments: `mvaghermite`, the default, performs mean and variance adaptive Gauss–Hermite quadrature first on every and then on alternate iterations; `aghermite` performs mode and curvature adaptive Gauss–Hermite quadrature on the first iteration only; `ghermite` performs nonadaptive Gauss–Hermite quadrature.

`intpoints(#)` specifies the number of integration points to use for integration by quadrature. The default is `intpoints(12)`; the maximum is `intpoints(195)`. Increasing this value improves the accuracy but also increases computation time. Computation time is roughly proportional to its value.

The following option is not shown in the dialog box:

`coeflegend` specifies that the legend of the coefficients and how to specify them in an expression be displayed rather than displaying the statistics for the coefficients.

Also see

[U] **20 Estimation and postestimation commands**

Title

exit — Exit Stata

Syntax

```
exit [, clear]
```

Description

Typing `exit` causes Stata to stop processing and return control to the operating system. If the dataset in memory has changed since the last `save` command, you must specify the `clear` option before Stata will let you exit.

`exit` may also be used for exiting do-files or programs; see [P] **exit**.

Stata for Windows users may also exit Stata by clicking on the **Close** button or by pressing *Alt+F4*.

Stata for Mac users may also exit Stata by pressing *Command+Q*.

Stata(GUI) users may also exit Stata by clicking on the **Close** button.

Option

`clear` permits you to `exit`, even if the current dataset has not been `saved`.

Remarks

Type `exit` to leave Stata and return to the operating system. If the dataset in memory has changed since the last time it was saved, however, Stata will refuse. At that point, you can either `save` the dataset and then type `exit`, or type `exit, clear`:

```
. exit
no; data in memory would be lost
r(4);
. exit, clear
```

Also see

[P] **exit** — Exit from a program or do-file

Title

exlogistic — Exact logistic regression

Syntax

`exlogistic` *depvar indepvars* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`condvars(`*varlist*`)`	condition on variables in *varlist*
`group(`*varname*`)`	groups/strata are stratified by unique values of *varname*
`binomial(`*varname*`|#)`	data are in binomial form and the number of trials is contained in *varname* or in #
`estconstant`	estimate constant term; do not condition on the number of successes
`noconstant`	suppress constant term
Terms	
`terms(`*termsdef*`)`	terms definition
Options	
`memory(#[b|k|m|g])`	set limit on memory usage; default is `memory(10m)`
`saving(`*filename*`)`	save the joint conditional distribution to *filename*
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`coef`	report estimated coefficients
`test(`*testopt*`)`	report significance of observed sufficient statistic, conditional scores test, or conditional probabilities test
`mue(`*varlist*`)`	compute the median unbiased estimates for *varlist*
`midp`	use the mid-*p*-value rule
`nolog`	do not display the enumeration log

`by`, `statsby`, and `xi` are allowed; see [U] **11.1.10 Prefix commands**.
`fweights` are allowed; see [U] **11.1.6 weight**.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Exact statistics > Exact logistic regression

Description

`exlogistic` fits an exact logistic regression model of *depvar* on *indepvars*.

`exlogistic` is an alternative to `logistic`, the standard maximum-likelihood–based logistic regression estimator; see [R] **logistic**. `exlogistic` produces more-accurate inference in small samples because it does not depend on asymptotic results and `exlogistic` can better deal with one-way causation, such as the case where all females are observed to have a positive outcome.

exlogistic with the group(*varname*) option is an alternative to clogit, the conditional logistic regression estimator; see [R] **clogit**. Like clogit, exlogistic conditions on the number of positive outcomes within stratum.

depvar can be specified in two ways. It can be zero/nonzero, with zero indicating failure and nonzero representing positive outcomes (successes), or if you specify the binomial(*varname* | #) option, *depvar* may contain the number of positive outcomes within each trial.

exlogistic is computationally intensive. Unlike most estimators, rather than calculating coefficients for all independent variables at once, results for each independent variable are calculated separately with the other independent variables temporarily conditioned out. You can save considerable computer time by skipping the parameter calculations for variables that are not of direct interest. Specify such variables in the condvars() option rather than among the *indepvars*; see condvars() below.

Unlike Stata's other estimation commands, you may not use test, lincom, or other postestimation commands after exlogistic. Given the method used to calculate estimates, hypothesis tests must be performed during estimation by using exlogistic's terms() option; see terms() below.

Options

Model

condvars(*varlist*) specifies variables whose parameter estimates are not of interest to you. You can save substantial computer time and memory moving such variables from *indepvars* to condvars(). Understand that you will get the same results for x1 and x3 whether you type

```
. exlogistic y x1 x2 x3 x4
```

or

```
. exlogistic y x1 x3, condvars(x2 x4)
```

group(*varname*) specifies the variable defining the strata, if any. A constant term is assumed for each stratum identified in *varname*, and the sufficient statistics for *indepvars* are conditioned on the observed number of successes within each group. This makes the model estimated equivalent to that estimated by clogit, Stata's conditional logistic regression command (see [R] **clogit**). group() may not be specified with noconstant or estconstant.

binomial(*varname* | #) indicates that the data are in binomial form and *depvar* contains the number of successes. *varname* contains the number of trials for each observation. If all observations have the same number of trials, you can instead specify the number as an integer. The number of trials must be a positive integer at least as great as the number of successes. If binomial() is not specified, the data are assumed to be Bernoulli, meaning that *depvar* equaling zero or nonzero records one failure or success.

estconstant estimates the constant term. By default, the models are assumed to have an intercept (constant), but the value of the intercept is not calculated. That is, the conditional distribution of the sufficient statistics for the *indepvars* is computed given the number of successes in *depvar*, thus conditioning out the constant term of the model. Use estconstant if you want the estimate of the intercept reported. estconstant may not be specified with group().

noconstant; see [R] **estimation options**. noconstant may not be specified with group().

Terms

`terms(`*termname* `=` *variable* ... *variable* [`,` *termname* `=` *variable* ... *variable* ...]`)` defines additional terms of the model on which you want `exlogistic` to perform joint-significance hypothesis tests. By default, `exlogistic` reports tests individually on each variable in *indepvars*. For instance, if variables `x1` and `x3` are in *indepvars*, and you want to jointly test their significance, specify `terms(t1=x1 x3)`. To also test the joint significance of `x2` and `x4`, specify `terms(t1=x1 x3, t2=x2 x4)`. Each variable can be assigned to only one term.

Joint tests are computed only for the conditional scores tests and the conditional probabilities tests. See the `test()` option below.

Options

`memory(`*#*[`b` | `k` | `m` | `g`]`)` sets a limit on the amount of memory `exlogistic` can use when computing the conditional distribution of the parameter sufficient statistics. The default is `memory(10m)`, where `m` stands for megabyte, or 1,048,576 bytes. The following are also available: `b` stands for byte; `k` stands for kilobyte, which is equal to 1,024 bytes; and `g` stands for gigabyte, which is equal to 1,024 megabytes. The minimum setting allowed is `1m` and the maximum is `2048m` or `2g`, but do not attempt to use more memory than is available on your computer. Also see the first technical note under example 4 on counting the conditional distribution.

`saving(`*filename* [`, replace`]`)` saves the joint conditional distribution to *filename*. This distribution is conditioned on those variables specified in `condvars()`. Use `replace` to replace an existing file with *filename*. A Stata data file is created containing all the feasible values of the parameter sufficient statistics. The variable names are the same as those in *indepvars*, in addition to a variable named `_f_` containing the feasible value frequencies (sometimes referred to as the condition numbers).

Reporting

`level(#)`; see [R] **estimation options**. The `level(#)` option will not work on replay because confidence intervals are based on estimator-specific enumerations. To change the confidence level, you must refit the model.

`coef` reports the estimated coefficients rather than odds ratios (exponentiated coefficients). `coef` may be specified when the model is fit or upon replay. `coef` affects only how results are displayed and not how they are estimated.

`test(`<u>`s`</u>`ufficient` | `score` | <u>`p`</u>`robability)` reports the significance level of the observed sufficient statistics, the conditional scores tests, or the conditional probabilities tests, respectively. The default is `test(sufficient)`. If `terms()` is included in the specification, the conditional scores test and the conditional probabilities test are applied to each term providing conditional inference for several parameters simultaneously. All the statistics are computed at estimation time regardless of which is specified. Each statistic may thus also be displayed postestimation without having to refit the model; see [R] **exlogistic postestimation**.

`mue(`*varlist*`)` specifies that median unbiased estimates (MUEs) be reported for the variables in *varlist*. By default, the conditional maximum likelihood estimates (CMLEs) are reported, except for those parameters for which the CMLEs are infinite. Specify `mue(_all)` if you want MUEs for all the *indepvars*.

`midp` instructs `exlogistic` to use the mid-p-value rule when computing the MUEs, significance levels, and confidence intervals. This adjustment is for the discreteness of the distribution and halves the value of the discrete probability of the observed statistic before adding it to the p-value. The mid-p-value rule cannot be applied to MUEs whose corresponding parameter CMLE is infinite.

`nolog` prevents the display of the enumeration log. By default, the enumeration log is displayed, showing the progress of computing the conditional distribution of the sufficient statistics.

Remarks

Exact logistic regression is the estimation of the logistic model parameters by using the conditional distribution of the parameter sufficient statistics. The estimates are referred to as the conditional maximum likelihood estimates (CMLEs). This technique was first introduced by Cox and Snell (1989) as an alternative to using maximum likelihood estimation, which can perform poorly for small sample sizes. For stratified data, exact logistic regression is a small-sample alternative to conditional logistic regression. See [R] **logit**, [R] **logistic**, and [R] **clogit** to obtain maximum likelihood estimates (MLEs) for the logistic model and the conditional logistic model. For a comprehensive overview of exact logistic regression, see Mehta and Patel (1995).

Let Y_i denote a Bernoulli random variable where we observe the outcome $Y_i = y_i$, $i = 1, \ldots, n$. Associated with each independent observation is a $1 \times p$ vector of covariates, $\mathbf{x}_i$. We will denote $\pi_i = \Pr(\mathrm{Y_i} \mid \mathbf{x_i})$ and let the logit function model the relationship between Y_i and $\mathbf{x}_i$,

$$\log\left(\frac{\pi_i}{1-\pi_i}\right) = \theta + \mathbf{x}_i\boldsymbol{\beta}$$

where the constant term θ and the $p \times 1$ vector of regression parameters $\boldsymbol{\beta}$ are unknown. The probability of observing $Y_i = y_i$, $i = 1, \ldots, n$, is

$$\Pr(\mathbf{Y} = \mathbf{y}) = \prod_{i=1}^{n} \pi_i^{y_i} (1-\pi_i)^{1-y_i}$$

where $\mathbf{Y} = (Y_1, \ldots, Y_n)$ and $\mathbf{y} = (y_1, \ldots, y_n)$. The MLEs for θ and $\boldsymbol{\beta}$ maximize the log of this function.

The sufficient statistics for θ and β_j, $j = 1, \ldots, p$, are $M = \sum_{i=1}^{n} Y_i$ and $T_j = \sum_{i=1}^{n} Y_i x_{ij}$, respectively, and we observe $M = m$ and $T_j = t_j$. By default, `exlogistic` tallies the conditional distribution of $\mathbf{T} = (T_1, \ldots, T_p)$ given $M = m$. This distribution will have a size of $\binom{n}{m}$. (It would have a size of 2^n without conditioning on $M = m$.) Denote one of these vectors $\mathbf{T}^{(k)} = (t_1^{(k)}, \ldots, t_p^{(k)})$, $k = 1, \ldots, N$, with combinatorial coefficient (frequency) c_k, $\sum_{k=1}^{N} c_k = \binom{n}{m}$. For each independent variable x_j, $j = 1, \ldots, p$, we reduce the conditional distribution further by conditioning on all other observed sufficient statistics $T_l = t_l$, $l \neq j$. The conditional probability of observing $T_j = t_j$ has the form

$$\Pr(T_j = t_j \mid T_l = t_l, l \neq j, M = m) = \frac{c\, e^{t_j \beta_j}}{\sum_k c_k e^{t_j^{(k)} \beta_j}}$$

where the sum is over the subset of $\mathbf{T}$ vectors such that $(T_1^{(k)} = t_1, \ldots, T_j^{(k)} = t_j^{(k)}, \ldots, T_p^{(k)} = t_p)$ and c is the combinatorial coefficient associated with the observed $\mathbf{t}$. The CMLE for β_j maximizes the log of this function.

Specifying nuisance variables in `condvars()` will reduce the size of the conditional distribution by conditioning on their observed sufficient statistics as well as conditioning on $M = m$. This reduces the amount of memory consumed at the cost of not obtaining regression estimates for those variables specified in `condvars()`.

Inferences from MLEs rely on asymptotics, and if your sample size is small, these inferences may not be valid. On the other hand, inferences from the CMLEs are exact in the sense that they use the conditional distribution of the sufficient statistics outlined above.

For small datasets, it is common for the dependent variable to be completely determined by the data. Here the MLEs and the CMLEs are unbounded. `exlogistic` will instead compute the MUE, the regression estimate that places the observed sufficient statistic at the median of the conditional distribution.

▷ Example 1

One example presented by Mehta and Patel (1995) is data from a prospective study of perinatal infection and human immunodeficiency virus type 1 (HIV-1). We use a variation of this dataset. There was an investigation Hutto et al. (1991) into whether the blood serum levels of glycoproteins CD4 and CD8 measured in infants at 6 months of age might predict their development of HIV infection. The blood serum levels are coded as ordinal values 0, 1, and 2.

```
. use http://www.stata-press.com/data/r12/hiv1
(prospective study of perinatal infection of HIV-1)
. list
```

	hiv	cd4	cd8
1.	1	0	0
2.	0	0	0
3.	1	0	2
4.	1	1	0
5.	0	1	0
	(output omitted)		
46.	0	2	1
47.	0	2	2

We first obtain the MLEs from `logistic` so that we can compare the estimates and associated statistics with the CMLEs from `exlogistic`.

```
. logistic hiv cd4 cd8, coef
Logistic regression                               Number of obs   =         47
                                                  LR chi2(2)      =      15.75
                                                  Prob > chi2     =     0.0004
Log likelihood = -20.751687                       Pseudo R2       =     0.2751

------------------------------------------------------------------------------
         hiv |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         cd4 |  -2.541669   .8392231    -3.03   0.002    -4.186517   -.8968223
         cd8 |   1.658586    .821113     2.02   0.043     .0492344    3.267938
       _cons |   .5132389   .6809007     0.75   0.451    -.8213019     1.84778
------------------------------------------------------------------------------
```

```
. exlogistic hiv cd4 cd8, coef
Enumerating sample-space combinations:
observation 1:   enumerations =          2
observation 2:   enumerations =          3
  (output omitted)
observation 46:  enumerations =        601
observation 47:  enumerations =        326
Exact logistic regression                       Number of obs =         47
                                                Model score   =   13.34655
                                                Pr >= score   =     0.0006

------------------------------------------------------------------------------
         hiv |      Coef.       Score    Pr(Suff.)     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         cd4 |  -2.387632          10        0.0004    -4.699633   -.8221807
         cd8 |   1.592366          12        0.0528    -.0137905    3.907876
------------------------------------------------------------------------------
```

`exlogistic` produced a log showing how many records are generated as it processes each observation. The primary purpose of the log is to provide feedback because generating the distribution can be time consuming, but we also see from the last entry that the joint distribution for the sufficient statistics for `cd4` and `cd8` conditioned on the total number of successes has 326 unique values (but a size of $\binom{47}{14} = 341{,}643{,}774{,}795$).

The statistics for `logistic` are based on asymptotics: for a large sample size, each Z statistic will be approximately normally distributed (with a mean of zero and a standard deviation of one) if the associated regression parameter is zero. The question is whether a sample size of 47 is large enough.

On the other hand, the p-values computed by `exlogistic` are from the conditional distributions of the sufficient statistics for each parameter given the sufficient statistics for all other parameters. In this sense, these p-values are exact. By default, `exlogistic` reports the sufficient statistics for the regression parameters and the probability of observing a more extreme value. These are single-parameter tests for H_0: $\beta_{\text{cd4}} = 0$ and H_0: $\beta_{\text{cd8}} = 0$ versus the two-sided alternatives. The conditional scores test, located in the coefficient table header, is testing that both H_0: $\beta_{\text{cd4}} = 0$ and H_0: $\beta_{\text{cd8}} = 0$. We find these p-values to be in fair agreement with the Wald and likelihood-ratio tests from `logistic`.

The confidence intervals for `exlogistic` are computed from the exact conditional distributions. The exact confidence intervals are asymmetrical about the estimate and are wider than the normal-based confidence intervals from `logistic`.

Both estimation techniques indicate that the incidence of HIV infection decreases with increasing CD4 blood serum levels and increases with increasing CD8 blood serum levels. The constant term is missing from the exact logistic coefficient table because we conditioned out its observed sufficient statistic when tallying the joint distribution of the sufficient statistics for the `cd4` and `cd8` parameters.

The `test()` option provides two other test statistics used in exact logistic: the conditional scores test, `test(score)`, and the conditional probabilities test, `test(probability)`. For comparison, we display the individual parameter conditional scores tests.

```
. exlogistic, test(score) coef
Exact logistic regression                       Number of obs =         47
                                                Model score   =   13.34655
                                                Pr >= score   =     0.0006
```

hiv	Coef.	Score	Pr>=Score	[95% Conf.	Interval]
cd4	-2.387632	12.88022	0.0003	-4.699633	-.8221807
cd8	1.592366	4.604816	0.0410	-.0137905	3.907876

For the probabilities test, the probability statistic is computed from (1) in *Methods and formulas* with $\beta = 0$. For this example, the significance of the probabilities tests matches the scores tests so they are not displayed here.

◁

❑ Technical note

Typically, the value of θ, the constant term, is of little interest, as well as perhaps some of the parameters in β, but we need to include all parameters in the model to correctly specify it. By conditioning out the nuisance parameters, we can reduce the size of the joint conditional distribution that is used to estimate the regression parameters of interest. The `condvars()` option allows you to specify a *varlist* of nuisance variables. By default, `exlogistic` conditions on the sufficient statistic of θ, which is the number of successes. You can save computation time and computer memory by using the `condvars()` option because infeasible values of the sufficient statistics associated with the variables in `condvars()` can be dropped from consideration before all n observations are processed.

Specifying some of your independent variables in `condvars()` will not change the estimated regression coefficients of the remaining independent variables. For instance, in example 1, if we instead type

```
. exlogistic hiv cd4, condvars(cd8) coef
```

the regression coefficient for `cd4` (as well as all associated inference) will be identical.

One reason to have multiple variables in *indepvars* is to make conditional inference of several parameters simultaneously by using the `terms()` option. If you do not wish to test several parameters simultaneously, it may be more efficient to obtain estimates for individual variables by calling `exlogistic` multiple times with one variable in *indepvars* and all other variables listed in `condvars()`. The estimates will be the same as those with all variables in *indepvars*.

❑

❑ Technical note

If you fit a `clogit` (see [R] **clogit**) model to the HIV data from example 1, you will find that the estimates differ from those with `exlogistic`. (To fit the `clogit` model, you will have to create a group variable that includes all observations.) The regression estimates will be different because `clogit` conditions on the constant term only, whereas the estimates from `exlogistic` condition on the sufficient statistic of the other regression parameter as well as the constant term.

❑

▷ Example 2

The HIV data presented in table IV of Mehta and Patel (1995) are in a binomial form, where the variable `hiv` contains the HIV cases that tested positive and the variable `n` contains the number of individuals with the same CD4 and CD8 levels, the binomial number-of-trials parameter. Here *depvar* is `hiv`, and we use the `binomial(n)` option to identify the number-of-trials variable.

```
. use http://www.stata-press.com/data/r12/hiv_n
(prospective study of perinatal infection of HIV-1; binomial form)
. list
```

	cd4	cd8	hiv	n
1.	0	2	1	1
2.	1	2	2	2
3.	0	0	4	7
4.	1	1	4	12
5.	2	2	1	3
6.	1	0	2	7
7.	2	0	0	2
8.	2	1	0	13

Further, the `cd4` and `cd8` variables of the `hiv` dataset are actually factor variables, where each has the ordered levels of $(0, 1, 2)$. Another approach to the analysis is to use indicator variables, and following Mehta and Patel (1995), we used a 0–1 coding scheme that will give us the odds ratio of level 0 versus 2 and level 1 versus 2.

```
. gen byte cd4_0 = (cd4==0)
. gen byte cd4_1 = (cd4==1)
. gen byte cd8_0 = (cd8==0)
. gen byte cd8_1 = (cd8==1)
. exlogistic hiv cd4_0 cd4_1 cd8_0 cd8_1, terms(cd4=cd4_0 cd4_1,
> cd8=cd8_0 cd8_1) binomial(n) test(probability) saving(dist) nolog
note: saving distribution to file dist.dta
note: CMLE estimate for cd4_0 is +inf; computing MUE
note: CMLE estimate for cd4_1 is +inf; computing MUE
note: CMLE estimate for cd8_0 is -inf; computing MUE
note: CMLE estimate for cd8_1 is -inf; computing MUE
Exact logistic regression                       Number of obs =         47
Binomial variable: n                            Model prob.   =   3.19e-06
                                                Pr <= prob.   =     0.0011
```

hiv	Odds Ratio	Prob.	Pr<=Prob.	[95% Conf.	Interval]
cd4		.0007183	0.0055		
cd4_0	18.82831*	.007238	0.0072	1.714079	+Inf
cd4_1	11.53732*	.0063701	0.0105	1.575285	+Inf
cd8		.0053212	0.0323		
cd8_0	.1056887*	.0289948	0.0290	0	1.072531
cd8_1	.0983388*	.0241503	0.0242	0	.9837203

```
(*) median unbiased estimates (MUE)
. matrix list e(sufficient)
e(sufficient)[1,4]
    cd4_0  cd4_1  cd8_0  cd8_1
r1      5      8      6      4
. display e(n_possible)
1091475
```

Here we used `terms()` to specify two terms in the model, `cd4` and `cd8`, that make up the `cd4` and `cd8` indicator variables. By doing so, we obtained a conditional probabilities test for `cd4`, simultaneously testing both `cd4_0` and `cd4_1`, and for `cd8`, simultaneously testing both `cd8_0` and `cd8_1`. The significance levels for the two terms are 0.0055 and 0.0323, respectively.

This example also illustrates instances where the dependent variable is completely determined by the independent variables and CMLEs are infinite. If we try to obtain MLEs, `logistic` will drop each variable and then terminate with a no-data error, error number 2000.

```
. use http://www.stata-press.com/data/r12/hiv_n, clear
(prospective study of perinatal infection of HIV-1; binomial form)
. gen byte cd4_0 = (cd4==0)
. gen byte cd4_1 = (cd4==1)
. gen byte cd8_0 = (cd8==0)
. gen byte cd8_1 = (cd8==1)
. expand n
(39 observations created)
. logistic hiv cd4_0 cd4_1 cd8_0 cd8_1
note: cd4_0 != 0 predicts success perfectly
      cd4_0 dropped and 8 obs not used
note: cd4_1 != 0 predicts success perfectly
      cd4_1 dropped and 21 obs not used
note: cd8_0 != 0 predicts failure perfectly
      cd8_0 dropped and 2 obs not used
outcome = cd8_1 <= 0 predicts data perfectly
r(2000);
```

In the previous example, `exlogistic` generated the joint conditional distribution of $T_{\mathrm{cd4\_0}}$, $T_{\mathrm{cd4\_1}}$, $T_{\mathrm{cd8\_0}}$, and $T_{\mathrm{cd8\_1}}$ given $M = 14$ (the number of individuals that tested positive), and for reference, we listed the observed sufficient statistics that are stored in the matrix `e(sufficient)`. Below we take that distribution and further condition on $T_{\mathrm{cd4\_1}} = 8$, $T_{\mathrm{cd8\_0}} = 6$, and $T_{\mathrm{cd8\_1}} = 4$, giving the conditional distribution of $T_{\mathrm{cd4\_0}}$. Here we see that the observed sufficient statistic $T_{\mathrm{cd4\_0}} = 5$ is last in the sorted listing or, equivalently, $T_{\mathrm{cd4\_0}}$ is at the domain boundary of the conditional probability distribution. When this occurs, the conditional probability distribution is monotonically increasing in $\beta_{\mathrm{cd4\_0}}$ and a maximum does not exist.

```
. use dist, clear
. keep if cd4_1==8 & cd8_0==6 & cd8_1==4
(4139 observations deleted)
. list, sep(0)
```

	_f_	cd4_0	cd4_1	cd8_0	cd8_1
1.	1668667	0	8	6	4
2.	18945542	1	8	6	4
3.	55801053	2	8	6	4
4.	55867350	3	8	6	4
5.	17423175	4	8	6	4
6.	1091475	5	8	6	4

When the CMLEs are infinite, the MUEs are computed (Hirji, Tsiatis, and Mehta 1989). For the `cd4_0` estimate, we compute the value $\overline{\beta}_{\mathrm{cd4\_0}}$ such that

$$\Pr(T_{\mathrm{cd4\_0}} \geq 5 \mid \beta_{\mathrm{cd4\_0}} = \overline{\beta}_{\mathrm{cd4\_0}}, T_{\mathrm{cd4\_1}} = 8, T_{\mathrm{cd8\_0}} = 6, T_{\mathrm{cd8\_1}} = 4, M = 14) = 1/2$$

using (1) in *Methods and formulas*.

The output is in agreement with example 1: there is an increase in risk of HIV infection for a CD4 blood serum level of 0 relative to a level of 2 and for a level of 1 relative to a level of 2; there is a decrease in risk of HIV infection for a CD8 blood serum level of 0 relative to a level of 2 and for a level of 1 relative to a level of 2.

We also displayed `e(n_possible)`. This is the combinatorial coefficient associated with the observed sufficient statistics. The same value is found in the `_f_` variable of the conditional distribution dataset listed above. The size of the distribution is $\binom{47}{14} = 341{,}643{,}774{,}795$. This can be verified by summing the `_f_` variable of the generated conditional distribution dataset.

```
. use dist, clear
. summarize _f_, meanonly
. di %15.1f r(sum)
 341643774795.0
```

◁

▷ Example 3

One can think of exact logistic regression as a covariate-adjusted exact binomial. To demonstrate this point, we will use `exlogistic` to compute a binomial confidence interval for m successes of n trials, by fitting the constant-only model, and we will compare it with the confidence interval computed by `ci` (see [R] **ci**). We will use the `saving()` option to retain the dataset containing the feasible values for the constant term sufficient statistic, namely, the number of successes, m, given n trials and their associated combinatorial coefficients $\binom{n}{m}$, $m = 0, 1, \ldots, n$.

```
. input y
                y
  1. 1
  2. 0
  3. 1
  4. 0
  5. 1
  6. 1
  7. end
. ci y, binomial
```

				— Binomial Exact —	
Variable	Obs	Mean	Std. Err.	[95% Conf.	Interval]
y	6	.6666667	.1924501	.2227781	.9567281

```
. exlogistic y, estconstant nolog coef saving(binom)
note: saving distribution to file binom.dta
Exact logistic regression                       Number of obs =          6
```

y	Coef.	Suff.	2*Pr(Suff.)	[95% Conf.	Interval]
_cons	.6931472	4	0.6875	-1.24955	3.096017

We use the postestimation program `estat predict` to transform the estimated constant term and its confidence bounds by using the inverse logit function, `invlogit()` (see [D] **functions**). The standard error for the estimated probability is computed using the delta method.

```
. estat predict
```

y	Predicted	Std. Err.	[95% Conf.	Interval]
Probability	0.6667	0.1925	0.2228	0.9567

```
. use binom, replace
. list, sep(0)
```

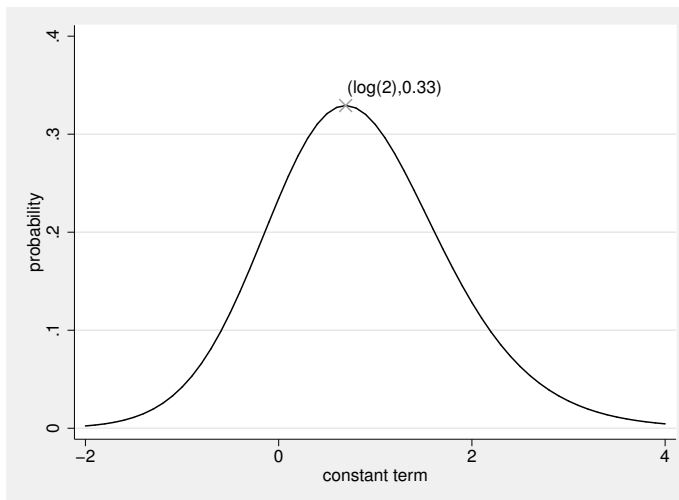
	_f_	_cons_
1.	1	0
2.	6	1
3.	15	2
4.	20	3
5.	15	4
6.	6	5
7.	1	6

Examining the listing of the generated data, the values contained in the variable `_cons_` are the feasible values of M, and the values contained in the variable `_f_` are the binomial coefficients $\binom{6}{m}$ with total $\sum_{m=0}^{6}\binom{6}{m} = 2^6 = 64$. In the coefficient table, the sufficient statistic for the constant term, labeled `Suff.`, is m = 4. This value is located at record 5 of the dataset. Therefore, the two-tailed probability of the sufficient statistic is computed as $0.6875 = 2(15 + 6 + 1)/64$.

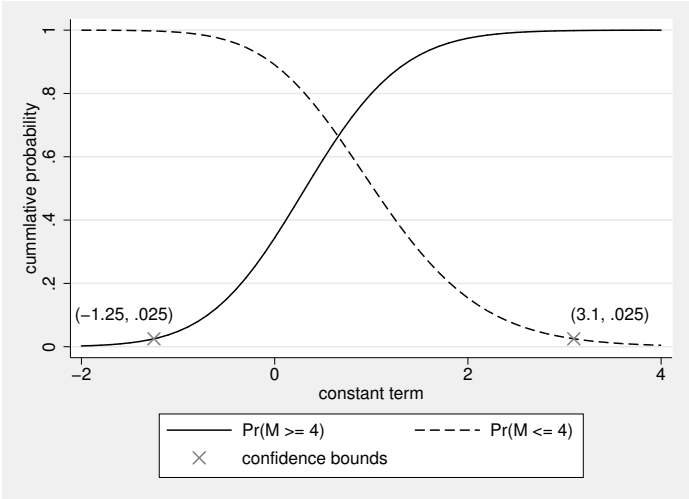
The constant term is the value of θ that maximizes the probability of observing $M = 4$; see (1) of *Methods and formulas*:

$$\Pr(M = 4|\theta) = \frac{15e^{4\alpha}}{1 + 6e^{\alpha} + 15e^{2\alpha} + 20e^{3\alpha} + 15e^{4\alpha} + 6e^{5\alpha} + e^{6\alpha}}$$

The maximum is at the value $\theta = \log 2$, which is demonstrated in the figure below.



The lower and upper confidence bounds are the values of θ such that $\Pr(M \geq 4|\theta) = 0.025$ and $\Pr(M \leq 4|\theta) = 0.025$, respectively. These probabilities are plotted in the figure below for $\theta \in [-2, 4]$.



Example 4

This example demonstrates the `group()` option, which allows the analysis of stratified data. Here the logistic model is

$$\log\left(\frac{\pi_{ik}}{1-\pi_{ik}}\right) = \theta_k + \mathbf{x}_{ki}\boldsymbol{\beta}$$

where k indexes the s strata, $k = 1, \ldots, s$, and θ_k is the strata-specific constant term whose sufficient statistic is $M_k = \sum_{i=1}^{n_k} Y_{ki}$.

Mehta and Patel (1995) use a case–control study to demonstrate this model, which is useful in comparing the estimates from `exlogistic` and `clogit`. This study was intended to determine the role of birth complications in people with schizophrenia (Garsd 1988). Siblings from seven families took part in the study, and each individual was classified as normal or schizophrenic. A birth complication index is recorded for each individual that ranges from 0, an uncomplicated birth, to 15, a very complicated birth. Some of the frequencies contained in variable `f` are greater than 1, and these count different births at different times where the individual has the same birth complications index, found in variable `BCindex`.

```
. use http://www.stata-press.com/data/r12/schizophrenia, clear
(case-control study on birth complications for people with schizophrenia)
. list, sepby(family)
```

	family	BCindex	schizo	f
1.	1	6	0	1
2.	1	7	0	1
3.	1	3	0	2
4.	1	2	0	3
5.	1	5	0	1
6.	1	0	0	1
7.	1	15	1	1
8.	2	2	1	1
9.	2	0	0	1
10.	3	2	0	1
11.	3	9	1	1
12.	3	1	0	1
13.	4	2	1	1
14.	4	0	0	4
15.	5	3	1	1
16.	5	6	0	1
17.	5	0	1	1
18.	6	3	0	1
19.	6	0	1	1
20.	6	0	0	2
21.	7	2	0	1
22.	7	6	1	1

```
. exlogistic schizo BCindex [fw=f], group(family) test(score) coef
Enumerating sample-space combinations:
observation 1:   enumerations =          2
observation 2:   enumerations =          3
observation 3:   enumerations =          4
observation 4:   enumerations =          5
observation 5:   enumerations =          6
    (output omitted)
observation 21:  enumerations =         72
observation 22:  enumerations =         40
Exact logistic regression                       Number of obs      =        29
Group variable: family                          Number of groups   =         7
                                                Obs per group: min =         2
                                                               avg =       4.1
                                                               max =        10
                                                Model score        =   6.32803
                                                Pr >= score        =    0.0167
```

schizo	Coef.	Score	Pr>=Score	[95% Conf.	Interval]
BCindex	.3251178	6.328033	0.0167	.0223423	.7408832

The asymptotic alternative for this model can be estimated using `clogit` (equivalently, `xtlogit, fe`) and is listed below for comparison. We must expand the data because `clogit` will not accept frequency weights if they are not constant within the groups.

```
. expand f
(7 observations created)
. clogit schizo BCindex, group(family) nolog
note: multiple positive outcomes within groups encountered.
Conditional (fixed-effects) logistic regression   Number of obs   =         29
                                                  LR chi2(1)      =       5.20
                                                  Prob > chi2     =     0.0226
Log likelihood = -6.2819819                       Pseudo R2       =     0.2927
```

schizo	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
BCindex	.3251178	.1678981	1.94	0.053	-.0039565	.654192

Both techniques compute the same regression estimate for the `BCindex`, which might not be too surprising because both estimation techniques condition on the total number of successes in each group. The difference lies in the p-values and confidence intervals. The p-value testing $H_0: \beta_{\text{BCindex}} = 0$ is approximately 0.0167 for the exact conditional scores test and 0.053 for the asymptotic Wald test. Moreover, the exact confidence interval is asymmetric about the estimate and does not contain zero.

◁

❑ Technical note

The `memory(#)` option limits the amount of memory that `exlogistic` will consume when computing the conditional distribution of the parameter sufficient statistics. `memory()` is independent of the data maximum memory setting (see `set max_memory` in [D] **memory**), and it is possible for `exlogistic` to exceed the memory limit specified in `set max_memory` without terminating. By default, a log is provided that displays the number of enumerations (the size of the conditional distribution) after processing each observation. Typically, you will see the number of enumerations increase, and then at some point they will decrease as the multivariate shift algorithm (Hirji, Mehta, and Patel 1987) determines that some of the enumerations cannot achieve the observed sufficient statistics of the conditioning variables. When the algorithm is complete, however, it is necessary to store the conditional distribution of the parameter sufficient statistics as a dataset. It is possible, therefore, to get a memory error when the algorithm has completed if there is not enough memory to store the conditional distribution.

❑

❑ Technical note

Computing the conditional distributions and reported statistics requires data sorting and numerical comparisons. If there is at least one single-precision variable specified in the model, `exlogistic` will make comparisons with a relative precision of 2^{-5}. Otherwise, a relative precision of 2^{-11} is used. Be careful if you use `recast` to promote a single-precision variable to double precision (see [D] **recast**). You might try listing the data in full precision (maybe `%20.15g`; see [D] **format**) to make sure that this is really what you want. See [D] **data types** for information on precision of numeric storage types.

❑

Saved results

exlogistic saves the following in e():

Scalars

e(N)	number of observations
e(k_groups)	number of groups
e(n_possible)	number of distinct possible outcomes where sum(sufficient) equals observed e(sufficient)
e(n_trials)	binomial number-of-trials parameter
e(sum_y)	sum of *depvar*
e(k_indvars)	number of independent variables
e(k_terms)	number of model terms
e(k_condvars)	number of conditioning variables
e(condcons)	conditioned on the constant(s) indicator
e(midp)	mid-p-value rule indicator
e(eps)	relative difference tolerance

Macros

e(cmd)	exlogistic
e(cmdline)	command as typed
e(title)	title in estimation output
e(depvar)	name of dependent variable
e(indvars)	independent variables
e(condvars)	conditional variables
e(groupvar)	group variable
e(binomial)	binomial number-of-trials variable
e(level)	confidence level
e(wtype)	weight type
e(wexp)	weight expression
e(datasignature)	the checksum
e(datasignaturevars)	variables used in calculation of checksum
e(properties)	b
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(mue_indicators)	indicator for elements of e(b) estimated using MUE instead of CMLE
e(se)	e(b) standard errors (CMLEs only)
e(ci)	matrix of e(level) confidence intervals for e(b)
e(sum_y_groups)	sum of e(depvar) for each group
e(N_g)	number of observations in each group
e(sufficient)	sufficient statistics for e(b)
e(p_sufficient)	p-value for e(sufficient)
e(scoretest)	conditional scores tests for *indepvars*
e(p_scoretest)	p-values for e(scoretest)
e(probtest)	conditional probabilities tests for *indepvars*
e(p_probtest)	p-value for e(probtest)
e(scoretest_m)	conditional scores tests for model terms
e(p_scoretest_m)	p-value for e(scoretest_m)
e(probtest_m)	conditional probabilities tests for model terms
e(p_probtest_m)	p-value for e(probtest_m)

Functions

e(sample)	marks estimation sample

Methods and formulas

exlogistic is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Sufficient statistics
Conditional distribution and CMLE
Median unbiased estimates and exact CI
Conditional hypothesis tests
Sufficient-statistic p-value

Sufficient statistics

Let $\{Y_1, Y_2, \ldots, Y_n\}$ be a set of n independent Bernoulli random variables, each of which can realize two outcomes, $\{0, 1\}$. For each $i = 1, \ldots, n$, we observe $Y_i = y_i$, and associated with each observation is the covariate row vector of length p, $\mathbf{x}_i = (x_{i1}, \ldots, x_{ip})$. Denote $\boldsymbol{\beta} = (\beta_1, \ldots, \beta_p)^T$ to be the column vector of regression parameters and θ to be the constant. The sufficient statistic for β_j is $T_j = \sum_{i=1}^n Y_i x_{ij}$, $j = 1, \ldots, p$, and for θ is $M = \sum_{i=1}^n Y_i$. We observe $T_j = t_j$, $t_j = \sum_{i=1}^n y_i x_{ij}$, and $M = m$, $m = \sum_{i=1}^n y_i$. The probability of observing $(Y_1 = y_1, Y_2 = y_2, \ldots, Y_n = y_n)$ is

$$\Pr(Y_1 = y_1, \ldots, Y_n = y_n \mid \boldsymbol{\beta}, \mathbf{X}) = \frac{\exp(m\theta + \mathbf{t}\boldsymbol{\beta})}{\prod_{i=1}^n \{1 + \exp(\theta + \mathbf{x}_i\boldsymbol{\beta})\}}$$

where $\mathbf{t} = (t_1, \ldots, t_p)$ and $\mathbf{X} = (\mathbf{x}_1^T, \ldots, \mathbf{x}_n^T)^T$.

The joint distribution of the sufficient statistics $\mathbf{T}$ is obtained by summing over all possible binary sequences $Y_1, \ldots, Y_n$ such that $\mathbf{T} = \mathbf{t}$ and $M = m$. This probability function is

$$\Pr(T_1 = t_1, \ldots, T_p = t_p, M = m \mid \boldsymbol{\beta}, \mathbf{X}) = \frac{c(\mathbf{t}, m)\exp(m\theta + \mathbf{t}\boldsymbol{\beta})}{\prod_{i=1}^n \{1 + \exp(\theta + \mathbf{x}_i\boldsymbol{\beta})\}}$$

where $c(\mathbf{t}, m)$ is the combinatorial coefficient of $(\mathbf{t}, m)$ or the number of distinct binary sequences $Y_1, \ldots, Y_n$ such that $\mathbf{T} = \mathbf{t}$ and $M = m$ (Cox and Snell 1989).

Conditional distribution and CMLE

Without loss of generality, we will restrict our discussion to computing the CMLE of β_1. If we condition on observing $M = m$ and $T_2 = t_2, \ldots, T_p = t_p$, the probability function of $(T_1 \mid \beta_1, T_2 = t_2, \ldots, T_p = t_p, M = m)$ is

$$\Pr(T_1 = t_1 \mid \beta_1, T_2 = t_2, \ldots, T_p = t_p, M = m) = \frac{c(\mathbf{t}, m)e^{t_1\beta_1}}{\sum_u c(u, t_2, \ldots, t_p, m)e^{u\beta_1}} \tag{1}$$

where the sum in the denominator is over all possible values of T_1 such that $M = m$ and $T_2 = t_2, \ldots, T_p = t_p$ and $c(u, t_2, \ldots, t_p, m)$ is the combinatorial coefficient of $(u, t_2, \ldots, t_p, m)$ (Cox and Snell 1989). The CMLE for β_1 is the value $\widehat{\beta}_1$ that maximizes the log of (1). This optimization task is carried out by `ml`, using the conditional frequency distribution of $(T_1 \mid T_2 = t_2, \ldots, T_p = t_p, M = m)$ as a dataset. Generating the joint conditional distribution is efficiently computed using the multivariate shift algorithm described by Hirji, Mehta, and Patel (1987).

Difficulties in computing $\widehat{\beta}_1$ arise if the observed $(T_1 = t_1, \ldots, T_p = t_p, M = m)$ lies on the boundaries of the distribution of $(T_1 \mid T_2 = t_2, \ldots, T_p = t_p, M = m)$, where the conditional probability function is monotonically increasing (or decreasing) in β_1. Here the CMLE is plus infinity if it is on the upper boundary, $\Pr(T_1 \leq t_1 \mid T_2 = t_2, \ldots, T_p = t_p, M = m) = 1$, and is minus infinity if it is on the lower boundary of the distribution, $\Pr(T_1 \geq t_1 \mid T_2 = t_2, \ldots, T_p = t_p, M = m) = 1$. This concept is demonstrated in example 2. When infinite CMLEs occur, the MUE is computed.

Median unbiased estimates and exact CI

The MUE is computed using the technique outlined by Hirji, Tsiatis, and Mehta (1989). First, we find the values of $\beta_1^{(u)}$ and $\beta_1^{(l)}$ such that

$$\begin{aligned}&\Pr(T_1 \le t_1 \mid \beta_1 = \beta_1^{(u)}, T_2 = t_2, \ldots, T_p = t_p, M = m) = \\ &\Pr(T_1 \ge t_1 \mid \beta_1 = \beta_1^{(l)}, T_2 = t_2, \ldots, T_p = t_p, M = m) = 1/2\end{aligned} \tag{2}$$

The MUE is then $\overline{\beta}_1 = \left(\beta_1^{(l)} + \beta_1^{(u)}\right)/2$. However, if T_1 is equal to the minimum of the domain of the conditional distribution, $\beta^{(l)}$ does not exist and $\overline{\beta}_1 = \beta^{(u)}$. If T_1 is equal to the maximum of the domain of the conditional distribution, $\beta^{(u)}$ does not exist and $\overline{\beta}_1 = \beta^{(l)}$.

Confidence bounds for β are computed similarly, except that we substitute $\alpha/2$ for $1/2$ in (2), where $1-\alpha$ is the confidence level. Here $\beta_1^{(l)}$ would then be the lower confidence bound and $\beta_1^{(u)}$ would be the upper confidence bound (see example 3).

Conditional hypothesis tests

To test H_0: $\beta_1 = 0$ versus H_1: $\beta_1 \neq 0$, we obtain the exact p-value from $\sum_{u\in E} f_1(u) - f_1(t_1)/2$ if the mid-p-value rule is used and $\sum_{u\in E} f_1(u)$ otherwise. Here E is a critical region, and we define $f_1(u) = \Pr(T_1 = u \mid \beta_1 = 0, T_2 = t_2, \ldots, T_p = t_p, M = m)$ for ease of notation. There are two popular ways to define the critical region: the conditional probabilities test and the conditional scores test (Mehta and Patel 1995). The critical region when using the conditional probabilities test is all values of the sufficient statistic for β_1 that have a probability less than or equal to that of the observed t_1, $E_p = \{u:\ f_1(u) \le f_1(t_1)\}$. The critical region of the conditional scores test is defined as all values of the sufficient statistic for β_1 such that its score is greater than or equal to that of t_1,

$$E_s = \left\{u:\ (u-\mu_1)^2/\sigma_1^2 \ge (t_1-\mu_1)^2/\sigma_1^2\right\}$$

Here μ_1 and σ_1^2 are the mean and variance of $(T_1 \mid \beta_1 = 0, T_2 = t_2, \ldots, T_p = t_p, M = m)$.

The score statistic is defined as

$$\left\{\frac{\partial \ell(\beta)}{\partial \beta}\right\}^2 \left[-E\left\{\frac{\partial^2 \ell(\beta)}{\partial \beta^2}\right\}\right]^{-1}$$

evaluated at H_0: $\beta = 0$, where ℓ is the log of (1). The score test simplifies to $(t - E[T|\beta])^2/\mathrm{var}(T|\beta)$ (Hirji 2006), where the mean and variance are computed from the conditional distribution of the sufficient statistic with $\beta = 0$ and t is the observed sufficient statistic.

Sufficient-statistic p-value

The p-value for testing H_0: $\beta_1 = 0$ versus the two-sided alternative when $(T_1 = t_1 | T_2 = t_2, \ldots, T_p = t_p)$ is computed as $2\times\min(p_l, p_u)$, where

$$p_l = \frac{\sum_{u\le t_1} c(u, t_2, \ldots, t_p, m)}{\sum_u c(u, t_2, \ldots, t_p, m)}$$

$$p_u = \frac{\sum_{u\ge t_1} c(u, t_2, \ldots, t_p, m)}{\sum_u c(u, t_2, \ldots, t_p, m)}$$

It is the probability of observing a more extreme T_1.

References

Cox, D. R., and E. J. Snell. 1989. *Analysis of Binary Data*. 2nd ed. London: Chapman & Hall.

Garsd, A. 1988. Schizophrenia and birth complications. Unpublished manuscript.

Hirji, K. F. 2006. *Exact Analysis of Discrete Data*. Boca Raton: Chapman & Hall/CRC.

Hirji, K. F., C. R. Mehta, and N. R. Patel. 1987. Computing distributions for exact logistic regression. *Journal of the American Statistical Association* 82: 1110–1117.

Hirji, K. F., A. A. Tsiatis, and C. R. Mehta. 1989. Median unbiased estimation for binary data. *American Statistician* 43: 7–11.

Hutto, C., W. P. Parks, S. Lai, M. T. Mastrucci, C. Mitchell, J. Muñoz, E. Trapido, I. M. Master, and G. B. Scott. 1991. A hospital-based prospective study of perinatal infection with human immunodeficiency virus type 1. *Journal of Pediatrics* 118: 347–353.

Mehta, C. R., and N. R. Patel. 1995. Exact logistic regression: Theory and examples. *Statistics in Medicine* 14: 2143–2160.

Also see

[R] **exlogistic postestimation** — Postestimation tools for exlogistic

[R] **binreg** — Generalized linear models: Extensions to the binomial family

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **expoisson** — Exact Poisson regression

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[U] **20 Estimation and postestimation commands**

Title

exlogistic postestimation — Postestimation tools for exlogistic

Description

The following postestimation commands are of special interest after `exlogistic`:

Command	Description
`estat predict`	single-observation prediction
`estat se`	report ORs or coefficients and their asymptotic standard errors

For information about these commands, see below.

The following standard postestimation command is also available:

Command	Description
`estat summarize`	estimation sample summary

`estat summarize` is not allowed if the `binomial()` option was specified in `exlogistic`.

See [R] **estat** for details.

Special-interest postestimation commands

`estat predict` computes a predicted probability (or linear predictor), its asymptotic standard error, and its exact confidence interval for 1 observation. Predictions are carried out by estimating the constant coefficient after shifting the independent variables and conditioned variables by the values specified in the `at()` option or by their medians. Therefore, predictions must be done with the estimation sample in memory. If a different dataset is used or if the dataset is modified, then an error will result.

`estat se` reports odds ratio or coefficients and their asymptotic standard errors. The estimates are stored in the matrix `r(estimates)`.

Syntax for estat predict

`estat predict` [, *options*]

options	Description
`pr`	probability; the default
`xb`	linear effect
`at(`*atspec*`)`	use the specified values for the *indepvars* and `condvars()`
`level(#)`	set confidence level for the predicted value; default is `level(95)`
`memory(#[b|k|m|g])`	set limit on memory usage; default is `memory(10m)`
`nolog`	do not display the enumeration log

These statistics are available only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for estat predict

`pr`, the default, calculates the probability.

`xb` calculates the linear effect.

`at(`*varname* `= #` [[*varname* `= #`] [...]]`)` specifies values to use in computing the predicted value. Here *varname* is one of the independent variables, *indepvars*, or the conditioned variables, `condvars()`. The default is to use the median of each independent and conditioned variable.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`memory(#`[`b`|`k`|`m`|`g`]`)` sets a limit on the amount of memory `estat predict` can use when generating the conditional distribution of the constant parameter sufficient statistic. The default is `memory(10m)`, where `m` stands for megabyte, or 1,048,576 bytes. The following are also available: `b` stands for byte; `k` stands for kilobyte, which is equal to 1,024 bytes; and `g` stands for gigabyte, which is equal to 1,024 megabytes. The minimum setting allowed is `1m` and the maximum is `512m` or `0.5g`, but do not attempt to use more memory than is available on your computer. Also see *Remarks* in [R] **exlogistic** for details on enumerating the conditional distribution.

`nolog` prevents the display of the enumeration log. By default, the enumeration log is displayed showing the progress of enumerating the distribution of the observed successes conditioned on the independent variables shifted by the values specified in `at()` (or by their medians). See *Methods and formulas* in [R] **exlogistic** for details of the computations.

Syntax for estat se

```
estat se [, coef]
```

Menu

Statistics > Postestimation > Reports and statistics

Option for estat se

`coef` requests that the estimated coefficients and their asymptotic standard errors be reported. The default is to report the odds ratios and their asymptotic standard errors.

Remarks

Predictions must be done using the estimation sample. This is because the prediction is really an estimated constant coefficient (the intercept) after shifting the independent variables and conditioned variables by the values specified in `at()` or by their medians. The justification for this approach can be seen by rewriting the model as

$$\log\left(\frac{\pi_i}{1-\pi_i}\right) = (\alpha + \mathbf{x}_0\boldsymbol{\beta}) + (\mathbf{x}_i - \mathbf{x}_0)\boldsymbol{\beta}$$

where $\mathbf{x}_0$ are the specified values for the *indepvars* (Mehta and Patel 1995). Because the estimation of the constant term is required, this technique is not appropriate for stratified models that used the `group()` option.

▷ Example 1

To demonstrate, we return to the example 2 in [R] **exlogistic** using data from a prospective study of perinatal infection and HIV-1. Here there was an investigation into whether the blood serum levels of CD4 and CD8 measured in infants at 6 months of age might predict their development of HIV infection. The blood serum levels are coded as ordinal values 0, 1, and 2. These data are used by Mehta and Patel (1995) as an exposition of exact logistic.

```
. use http://www.stata-press.com/data/r12/hiv_n
(prospective study of perinatal infection of HIV-1; binomial form)
. gen byte cd4_0 = (cd4==0)
. gen byte cd4_1 = (cd4==1)
. gen byte cd8_0 = (cd8==0)
. gen byte cd8_1 = (cd8==1)
. exlogistic hiv cd4_0 cd4_1 cd8_0 cd8_1, terms(cd4=cd4_0 cd4_1,
> cd8=cd8_0 cd8_1) binomial(n) test(probability) saving(dist, replace)
  (output omitted)
. estat predict
Enumerating sample-space combinations:
observation 1:   enumerations =          3
observation 2:   enumerations =         12
observation 3:   enumerations =          5
observation 4:   enumerations =          5
observation 5:   enumerations =          5
observation 6:   enumerations =         35
observation 7:   enumerations =         15
observation 8:   enumerations =         15
observation 9:   enumerations =          9
observation 10:  enumerations =          9
observation 11:  enumerations =          5
observation 12:  enumerations =         18
note: CMLE estimate for _cons is -inf; computing MUE
Predicted value at cd4_0 = 0, cd4_1 = 0, cd8_0 = 0, cd8_1 = 1
```

hiv	Predicted	Std. Err.	[95% Conf.	Interval]
Probability	0.0390*	N/A	0.0000	0.1962

```
(*) identifies median unbiased estimates (MUE); because an MUE
    is computed, there is no SE estimate
```

Because we did not specify values by using the `at()` option, the median values of the *indepvars* are used for the prediction. By default, medians are used instead of means because we want to use values that are observed in the dataset. If the means of the binary variables `cd4_0`–`cd8_1` were used, we would have created floating point variables in $(0, 1)$ that not only do not properly represent the indicator variables but also would be a source of computational inefficiency in generating the conditional distribution. Because the MUE is computed for the predicted value, there is no standard-error estimate.

From the example discussions in [R] **exlogistic**, the infants at highest risk are those with a CD4 level of 0 and a CD8 level of 2. Below we use the `at()` option to make a prediction at these blood serum levels.

```
. estat predict, at(cd4_0=1 cd4_1=0 cd8_0=0 cd8_1=0) nolog
note: CMLE estimate for _cons is +inf; computing MUE
Predicted value at cd4_0 = 1, cd4_1 = 0, cd8_0 = 0, cd8_1 = 0
```

hiv	Predicted	Std. Err.	[95% Conf.	Interval]
Probability	0.9063*	N/A	0.4637	1.0000

```
(*) identifies median unbiased estimates (MUE); because an MUE
    is computed, there is no SE estimate
```

◁

Saved results

`estat predict` saves the following in `r()`:

Scalars

`r(imue)`	`1` if `r(pred)` is an MUE and `0` if a CMLE
`r(pred)`	estimated probability or the linear effect
`r(se)`	asymptotic standard error of `r(pred)`

Macros

`r(estimate)`	prediction type: `pr` or `xb`
`r(level)`	confidence level

Matrices

`r(ci)`	confidence interval
`r(x)`	*indepvars* and `condvars()` values

Methods and formulas

All postestimation commands listed above are implemented as ado-files using Mata.

Reference

Mehta, C. R., and N. R. Patel. 1995. Exact logistic regression: Theory and examples. *Statistics in Medicine* 14: 2143–2160.

Also see

[R] **exlogistic** — Exact logistic regression

[U] **20 Estimation and postestimation commands**

Title

expoisson — Exact Poisson regression

Syntax

`expoisson` *depvar indepvars* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`condvars(`*varlist*`)`	condition on variables in *varlist*
`group(`*varname*`)`	groups/strata are stratified by unique values of *varname*
`exposure(`$varname_e$`)`	include ln($varname_e$) in model with coefficient constrained to 1
`offset(`$varname_o$`)`	include $varname_o$ in model with coefficient constrained to 1
Options	
`memory(#[b|k|m|g])`	set limit on memory usage; default is `memory(25m)`
`saving(`*filename*`)`	save the joint conditional distribution to *filename*
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`irr`	report incidence-rate ratios
`test(`*testopt*`)`	report significance of observed sufficient statistic, conditional scores test, or conditional probabilities test
`mue(`*varlist*`)`	compute the median unbiased estimates for *varlist*
`midp`	use the mid-*p*-value rule
`nolog`	do not display the enumeration log

`by`, `statsby`, and `xi` are allowed; see [U] **11.1.10 Prefix commands**.
`fweights` are allowed; see [U] **11.1.6 weight**.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Exact statistics > Exact Poisson regression

Description

`expoisson` fits an exact Poisson regression model of *depvar* on *indepvars*. Exact Poisson regression is an alternative to standard maximum-likelihood–based Poisson regression (see [R] **poisson**) that offers more accurate inference in small samples because it does not depend on asymptotic results. For stratified data, `expoisson` is an alternative to fixed-effects Poisson regression (see `xtpoisson, fe` in [XT] **xtpoisson**); like fixed-effects Poisson regression, exact Poisson regression conditions on the number of events in each stratum.

Exact Poisson regression is computationally intensive, so if you have regressors whose parameter estimates are not of interest (that is, nuisance parameters), you should specify those variables in the `condvars()` option instead of in *indepvars*.

Options

Model

`condvars(`*varlist*`)` specifies variables whose parameter estimates are not of interest to you. You can save substantial computer time and memory by moving such variables from *indepvars* to `condvars()`. Understand that you will get the same results for `x1` and `x3` whether you type

```
. expoisson y x1 x2 x3 x4
```

or

```
. expoisson y x1 x3, condvars(x2 x4)
```

`group(`*varname*`)` specifies the variable defining the strata, if any. A constant term is assumed for each stratum identified in *varname*, and the sufficient statistics for *indepvars* are conditioned on the observed number of successes within each group (as well as other variables in the model). The group variable must be integer valued.

`exposure(`*varname*$_e$`)`, `offset(`*varname*$_o$`)`; see [R] **estimation options**.

Options

`memory(#[ b | k | m | g ])` sets a limit on the amount of memory `expoisson` can use when computing the conditional distribution of the parameter sufficient statistics. The default is `memory(25m)`, where `m` stands for megabyte, or 1,048,576 bytes. The following are also available: `b` stands for byte; `k` stands for kilobyte, which is equal to 1,024 bytes; and `g` stands for gigabyte, which is equal to 1,024 megabytes. The minimum setting allowed is `1m` and the maximum is `2048m` or `2g`, but do not attempt to use more memory than is available on your computer. Also see the first technical note under example 3 on counting the conditional distribution.

`saving(`*filename* `[ , replace ])` saves the joint conditional distribution for each independent variable specified in *indepvars*. There is one file for each variable, and it is named using the prefix *filename* with the variable name appended. For example, `saving(mydata)` with an independent variable named `X` would generate a data file named `mydata_X.dta`. Use `replace` to replace an existing file. Each file contains the conditional distribution for one of the independent variables specified in *indepvars* conditioned on all other *indepvars* and those variables specified in `condvars()`. There are two variables in each data file: the feasible sufficient statistics for the variable's parameter and their associated weights. The weights variable is named `_w_`.

Reporting

`level(#)`; see [R] **estimation options**. The `level(#)` option will not work on replay because confidence intervals are based on estimator-specific enumerations. To change the confidence level, you must refit the model.

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, $\exp(\beta)$ rather than β. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. `irr` may be specified at estimation or when replaying previously estimated results.

`test(sufficient | score | probability)` reports the significance level of the observed sufficient statistic, the conditional scores test, or the conditional probabilities test. The default is `test(sufficient)`. All the statistics are computed at estimation time, and each statistic may be displayed postestimation; see [R] **expoisson postestimation**.

`mue(`*varlist*`)` specifies that median unbiased estimates (MUEs) be reported for the variables in *varlist*. By default, the conditional maximum likelihood estimates (CMLEs) are reported, except for those parameters for which the CMLEs are infinite. Specify `mue(_all)` if you want MUEs for all the *indepvars*.

`midp` instructs `expoisson` to use the mid-p-value rule when computing the MUEs, significance levels, and confidence intervals. This adjustment is for the discreteness of the distribution by halving the value of the discrete probability of the observed statistic before adding it to the p-value. The mid-p-value rule cannot be MUEs whose corresponding parameter CMLE is infinite.

`nolog` prevents the display of the enumeration log. By default, the enumeration log is displayed, showing the progress of computing the conditional distribution of the sufficient statistics.

Remarks

Exact Poisson regression estimates the model parameters by using the conditional distributions of the parameters' sufficient statistics, and the resulting parameter estimates are known as CMLEs. Exact Poisson regression is a small-sample alternative to the maximum-likelihood ML Poisson model. See [R] **poisson** and [XT] **xtpoisson** to obtain maximum likelihood estimates (MLEs) for the Poisson model and the fixed-effects Poisson model.

Let Y_i denote a Poisson random variable where we observe the outcome $Y_i = y_i$, $i = 1, \ldots, n$. Associated with each independent observation is a $1 \times p$ vector of covariates, $\mathbf{x}_i$. We will denote $\mu_i = E[Y_i \mid \mathbf{x}_i]$ and use the log linear model to model the relationship between Y_i and $\mathbf{x}_i$,

$$\log(\mu_i) = \theta + \mathbf{x}_i\boldsymbol{\beta}$$

where the constant term, θ, and the $p \times 1$ vector of regression parameters, $\boldsymbol{\beta}$, are unknown. The probability of observing $Y_i = y_i$, $i = 1, \ldots, n$, is

$$\Pr(\mathbf{Y} = \mathbf{y}) = \prod_{i=1}^{n} \frac{\mu_i^{y_i} e^{-\mu_i}}{y_i!}$$

where $\mathbf{Y} = (Y_1, \ldots, Y_n)$ and $\mathbf{y} = (y_1, \ldots, y_n)$. The MLEs for θ and $\boldsymbol{\beta}$ maximize the log of this function.

The sufficient statistics for θ and β_j, $j = 1, \ldots, p$, are $M = \sum_{i=1}^{n} Y_i$ and $T_j = \sum_{i=1}^{n} Y_i x_{ij}$, respectively, and we observe $M = m$ and $T_j = t_j$. `expoisson` tallies the conditional distribution for each T_j, given the other sufficient statistics $T_l = t_l$, $l \neq j$ and $M = m$. Denote one of these values to be $t_j^{(k)}$, $k = 1, \ldots, N$, with weight w_k that accounts for all the generated $\mathbf{Y}$ vectors that give rise to $t_j^{(k)}$. The conditional probability of observing $T_j = t_j$ has the form

$$\Pr(T_j = t_j \mid T_l = t_l, l \neq j, M = m) = \frac{w\ e^{t_j\beta_j}}{\sum_k w_k e^{t_j^{(k)}\beta_j}} \tag{1}$$

where the sum is over the subset of $\mathbf{T}$ vectors such that $(T_1^{(k)} = t_1, \ldots, T_j^{(k)} = t_j^{(k)}, \ldots, T_p^{(k)} = t_p)$ and w is the weight associated with the observed $\mathbf{t}$. The CMLE for β_j maximizes the log of this function.

Specifying nuisance variables in `condvars()` prevents `expoisson` from estimating their associated regression coefficients. These variables are still conditional variables when tallying the conditional distribution for the variables in *indepvars*.

Inferences from MLEs rely on asymptotics, and if your sample size is small, these inferences may not be valid. On the other hand, inferences from the CMLEs are exact in that they use the conditional distribution of the sufficient statistics outlined above.

For small datasets, the dependent variable can be completely determined by the data. Here the MLEs and the CMLEs are unbounded. When this occurs, `expoisson` will compute the MUE, the regression estimate that places the observed sufficient statistic at the median of the conditional distribution.

See [R] **exlogistic** for a more thorough discussion of exact estimation and related statistics.

▷ Example 1

Armitage, Berry, and Matthews (2002, 499–501) fit a log-linear model to data containing the number of cerebrovascular accidents experienced by 41 men during a fixed period, each of whom had recovered from a previous cerebrovascular accident and was hypertensive. Sixteen men received treatment, and in the original data, there are three age groups (40–49, 50–59, ≥60), but we pool the first two age groups to simplify the example. Armitage, Berry, and Matthews point out that this was not a controlled trial, but the data are useful to inquire whether there is evidence of fewer accidents for the treatment group and if age may be an important factor. The dependent variable `count` contains the number of accidents, variable `treat` is an indicator for the treatment group (1 = treatment, 0 = control), and variable `age` is an indicator for the age group (0 = 40−59; 1 = ≥60).

First, we load the data, list it, and tabulate the cerebrovascular accident counts by treatment and age group.

```
. use http://www.stata-press.com/data/r12/cerebacc
(cerebrovascular accidents in hypotensive-treated and control groups)
. list
```

	treat	count	age
1.	control	0	40/59
2.	control	0	>=60
3.	control	1	40/59
4.	control	1	>=60
5.	control	2	40/59
6.	control	2	>=60
7.	control	3	40/59

(*output omitted*)

35.	treatment	0	40/59
36.	treatment	0	40/59
37.	treatment	0	40/59
38.	treatment	0	40/59
39.	treatment	1	40/59
40.	treatment	1	40/59
41.	treatment	1	40/59

```
. tabulate treat age [fw=count]
```

hypotensive drug treatment	age group 40/59	>=60	Total
control	15	10	25
treatment	4	0	4
Total	19	10	29

Next we estimate the CMLE with `expoisson` and, for comparison, the MLE with `poisson`.

```
. expoisson count treat age
Estimating: treat
Enumerating sample-space combinations:
observation 1:   enumerations =         11
observation 2:   enumerations =         11
observation 3:   enumerations =         11
       (output omitted)
observation 39:  enumerations =        410
observation 40:  enumerations =        410
observation 41:  enumerations =         30
Estimating: age
Enumerating sample-space combinations:
observation 1:   enumerations =          5
observation 2:   enumerations =         15
observation 3:   enumerations =         15
       (output omitted)
observation 39:  enumerations =        455
observation 40:  enumerations =        455
observation 41:  enumerations =         30
Exact Poisson regression                                Number of obs =         41
```

count	Coef.	Suff.	2*Pr(Suff.)	[95% Conf.	Interval]
treat	-1.594306	4	0.0026	-3.005089	-.4701708
age	-.5112067	10	0.2794	-1.416179	.3429232

```
. poisson count treat age, nolog
Poisson regression                              Number of obs   =         41
                                                LR chi2(2)      =      10.64
                                                Prob > chi2     =     0.0049
Log likelihood =  -38.97981                     Pseudo R2       =     0.1201
```

count	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
treat	-1.594306	.5573614	-2.86	0.004	-2.686714	-.5018975
age	-.5112067	.4043525	-1.26	0.206	-1.303723	.2813096
_cons	.233344	.2556594	0.91	0.361	-.2677391	.7344271

`expoisson` generates an enumeration log for each independent variable in *indepvars*. The conditional distribution of the parameter sufficient statistic is tallied for each independent variable. The conditional distribution for `treat`, for example, has 30 records containing the weights, w_k, and feasible sufficient statistics, $t^{(k)}_{\text{treat}}$. In essence, the set of points $(w_k, t^{(k)}_{\text{treat}})$, $k = 1, \ldots, 30$, tallied by `expoisson` now become the data to estimate the regression coefficient for `treat`, using (1) as the likelihood. Remember that one of the 30 $(w_k, t^{(k)}_{\text{treat}})$ must contain the observed sufficient statistic, $t_{\text{treat}} = \sum_{i=1}^{41} \texttt{treat}_i \times \texttt{count}_i = 4$, and its relative position in the sorted set of points (sorted by $t^{(k)}_{\text{treat}}$) is how the sufficient-statistic significance is computed. This algorithm is repeated for the `age` variable.

The regression coefficients for `treat` and `age` are numerically identical for both Poisson models. Both models indicate that the treatment is significant at reducing the rate of cerebrovascular accidents, $\approx e^{-1.59} \approx 0.204$, or a reduction of about 80%. There is no significant age effect.

The p-value for the treatment regression-coefficient sufficient statistic indicates that the treatment effect is a bit more significant than for the corresponding asymptotic Z statistic from `poisson`. However, the exact confidence intervals are wider than their asymptotic counterparts.

◁

Example 2

Agresti (2002) used the data from Laird and Olivier (1981) to demonstrate the Poisson model for modeling rates. The data consist of patient survival after heart valve replacement operations. The sample consists of 109 patients that are classified by type of heart valve (aortic, mitral) and by age (<55, ≥ 55). Follow-up observations cover lengths from 3 to 97 months, and the time at risk, or exposure, is stored in the variable `TAR`. The response is whether the subject died. First, we take a look at the data and then estimate the incidence rates (IRs) with `expoisson` and `poisson`.

```
. use http://www.stata-press.com/data/r12/heartvalve
(heart valve replacement data)
. list
```

	age	valve	deaths	TAR
1.	< 55	aortic	4	1259
2.	< 55	mitral	1	2082
3.	>= 55	aortic	7	1417
4.	>= 55	mitral	9	1647

The `age` variable is coded 0 for age <55 and 1 for age ≥ 55, and the `valve` variable is coded 0 for the aortic valve and 1 for the mitral valve. The total number of deaths, $M = 21$, is small enough that enumerating the conditional distributions for age and valve type is feasible and asymptotic inferences associated with standard ML Poisson regression may be questionable.

```
. expoisson deaths age valve, exposure(TAR) irr
Estimating: age
Enumerating sample-space combinations:
observation 1:   enumerations =         11
observation 2:   enumerations =         11
observation 3:   enumerations =        132
observation 4:   enumerations =         22
Estimating: valve
Enumerating sample-space combinations:
observation 1:   enumerations =         17
observation 2:   enumerations =         17
observation 3:   enumerations =        102
observation 4:   enumerations =         22
Exact Poisson regression                        Number of obs =          4
```

deaths	IRR	Suff.	2*Pr(Suff.)	[95% Conf.	Interval]
age	3.390401	16	0.0194	1.182297	11.86935
valve	.7190197	10	0.5889	.2729881	1.870068
ln(TAR)	1	(exposure)			

```
. poisson deaths age valve, exposure(TAR) irr nolog
Poisson regression                              Number of obs   =          4
                                                LR chi2(2)      =       7.62
                                                Prob > chi2     =     0.0222
Log likelihood = -8.1747285                     Pseudo R2       =     0.3178

------------------------------------------------------------------------------
      deaths |        IRR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   3.390401   1.741967     2.38   0.017     1.238537    9.280965
       valve |   .7190197   .3150492    -0.75   0.452     .3046311      1.6971
       _cons |   .0018142   .0009191   -12.46   0.000     .0006722    .0048968
    ln(TAR)  |          1  (exposure)
------------------------------------------------------------------------------
```

The CMLE and the MLE are numerically identical. The death rate for the older age group is about 3.4 times higher than the younger age group, and this difference is significant at the 5% level. This means that for every death in the younger group each month, we would expect about three deaths in the older group. The IR estimate for valve type is approximately 0.72, but it is not significantly different from one. The exact Poisson confidence intervals are a bit wider than the asymptotic CIs.

You can use `ir` (see [ST] **epitab**) to estimate IRs and exact CIs for one covariate, and we compare these CIs with those from `expoisson`, where we estimate the incidence rate by using age only.

```
. ir deaths age TAR
                   | age of patient
                   |  Exposed   Unexposed |      Total
-------------------+----------------------+-----------
number of deaths   |        16           5 |         21
    time at risk   |      3064        3341 |       6405
-------------------+----------------------+-----------
  Incidence rate   |  .0052219    .0014966 |  .0032787
                   |      Point estimate  | [95% Conf. Interval]
-------------------+----------------------+-----------
 Inc. rate diff.   |        .0037254      |    .00085    .0066007
 Inc. rate ratio   |        3.489295      |  1.221441    12.17875 (exact)
 Attr. frac. ex.   |        .7134092      |  .1812948    .9178898 (exact)
 Attr. frac. pop   |        .5435498      |
-------------------+----------------------+-----------
                   (midp)   Pr(k>=16) =                 0.0049 (exact)
                   (midp) 2*Pr(k>=16) =                 0.0099 (exact)

. expoisson deaths age, exposure(TAR) irr midp nolog
Exact Poisson regression
                                                Number of obs =          4

------------------------------------------------------------------------------
      deaths |        IRR       Suff.  2*Pr(Suff.)     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   3.489295          16      0.0099      1.324926    10.64922
    ln(TAR)  |          1  (exposure)
------------------------------------------------------------------------------
mid-p-value computed for the probabilities and CIs
```

Both `ir` and `expoisson` give identical IRs and p-values. Both report the two-sided exact significance by using the mid-p-value rule that accounts for the discreteness in the distribution by subtracting $p_{1/2} = \Pr(T = t)/2$ from $p_l = \Pr(T \leq t)$ and $p_g = \Pr(T \geq t)$, computing $2 \times \min(p_l - p_{1/2}, p_g - p_{1/2})$. By default, `expoisson` will not use the mid-p-value rule (when you exclude the `midp` option), and here the two-sided exact significance would be $2 \times \min(p_l, p_g) = 0.0158$. The confidence intervals differ because `expoisson` uses the mid-p-value rule when computing the confidence intervals, yet

ir does not. You can verify this by executing expoisson without the midp option for this example; you will get the same CIs as ir.

You can replay expoisson to view the conditional scores test or the conditional probabilities test by using the test() option.

```
. expoisson, test(score) irr
Exact Poisson regression
                                                Number of obs =          4
```

deaths	IRR	Score	Pr>=Score	[95% Conf.	Interval]
age	3.489295	6.76528	0.0113	1.324926	10.64922
ln(TAR)	1	(exposure)			

```
mid-p-value computed for the probabilities and CIs
```

All the statistics for expoisson are defined in *Methods and formulas* of [R] **exlogistic**. Apart from enumerating the conditional distributions for the logistic and Poisson sufficient statistics, computationally, the primary difference between exlogistic and expoisson is the weighting values in the likelihood for the parameter sufficient statistics. ◁

▷ Example 3

In this example, we fabricate data that will demonstrate the difference between the CMLE and the MUE when the CMLE is not infinite. A difference in these estimates will be more pronounced when the probability of the coefficient sufficient statistic is skewed when plotted as a function of the regression coefficient.

```
. clear
. input y x
            y          x
  1. 0 2
  2. 1 1
  3. 1 0
  4. 0 0
  5. 0 .5
  6. 1 .5
  7. 2 .01
  8. 3 .001
  9. 4 .0001
 10. end
. expoisson y x, test(score)
Enumerating sample-space combinations:
observation 1:   enumerations =         13
observation 2:   enumerations =         91
observation 3:   enumerations =        169
observation 4:   enumerations =        169
observation 5:   enumerations =        313
observation 6:   enumerations =        313
observation 7:   enumerations =       1469
observation 8:   enumerations =       5525
observation 9:   enumerations =       5479
Exact Poisson regression
                                                Number of obs =          9
```

y	Coef.	Score	Pr>=Score	[95% Conf.	Interval]
x	-1.534468	2.955316	0.0810	-3.761718	.0485548

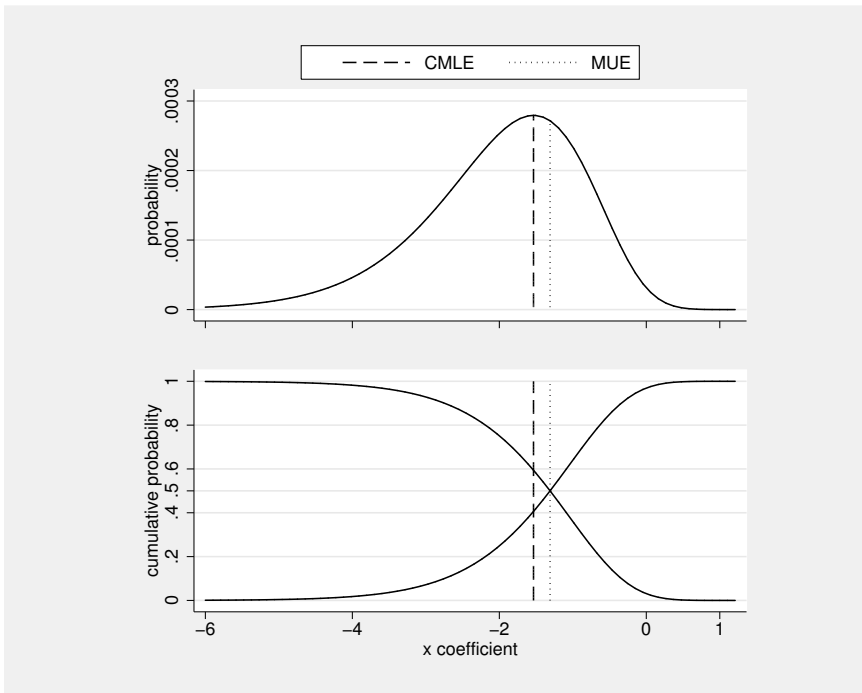
```
. expoisson y x, test(score) mue(x) nolog
Exact Poisson regression
                                                Number of obs =          9
```

y	Coef.	Score	Pr>=Score	[95% Conf.	Interval]
x	-1.309268*	2.955316	0.0810	-3.761718	.0485548

```
(*) median unbiased estimates (MUE)
```

We observe (x_i, y_i), $i = 1, \ldots, 9$. If we condition on $m = \sum_{i=1}^{9} y_i = 12$, the conditional distribution of $T_x = \sum_i Y_i x_i$ has a size of 5,479 elements. For each entry in this enumeration, a realization of $Y_i = y_i^{(k)}$, $k = 1, \ldots, 5{,}479$, is generated such that $\sum_i y_i^{(k)} = 12$. One of these realizations produces the observed $t_x = \sum_i y_i x_i \approx 1.5234$.

Below is a graphical display comparing the CMLE with the MUE. We plot $\Pr(T_x = t_x \mid M = 12, \beta_x)$ versus β_x, $-6 \leq \beta_x \leq 1$, in the upper panel and the cumulative probabilities, $\Pr(T_x \leq t_x \mid M = 12, \beta_x)$ and $\Pr(T_x \geq t_x \mid M = 12, \beta_x)$, in the lower panel.



The location of the CMLE, indicated by the dashed line, is at the mode of the probability profile, and the MUE, indicated by the dotted line, is to the right of the mode. If we solve for the $\beta_x^{(u)}$ and $\beta_x^{(l)}$ such that $\Pr(T_x \leq t_x \mid M = 12, \beta_x^{(u)}) = 1/2$ and $\Pr(T_x \geq t_x \mid M = 12, \beta_x^{(l)}) = 1/2$, the MUE is $(\beta_x^{(u)} + \beta_x^{(l)})/2$. As you can see in the lower panel, the MUE cuts through the intersection of these cumulative probability profiles.

◁

❑ Technical note

The memory(#) option limits the amount of memory that expoisson will consume when computing the conditional distribution of the parameter sufficient statistics. memory() is independent of the data maximum memory setting (see set max_memory in [D] **memory**), and it is possible for expoisson to exceed the memory limit specified in set max_memory without terminating. By default, a log is provided that displays the number of enumerations (the size of the conditional distribution) after processing each observation. Typically, you will see the number of enumerations increase, and then at some point they will decrease as the multivariate shift algorithm (Hirji, Mehta, and Patel 1987) determines that some of the enumerations cannot achieve the observed sufficient statistics of the conditioning variables. When the algorithm is complete, however, it is necessary to store the conditional distribution of the parameter sufficient statistics as a dataset. It is possible, therefore, to get a memory error when the algorithm has completed if there is not enough memory to store the conditional distribution.

❑

❑ Technical note

Computing the conditional distributions and reported statistics requires data sorting and numerical comparisons. If there is at least one single-precision variable specified in the model, expoisson will make comparisons with a relative precision of 2^{-5}. Otherwise, a relative precision of 2^{-11} is used. Be careful if you use recast to promote a single-precision variable to double precision (see [D] **recast**). You might try listing the data in full precision (maybe %20.15g; see [D] **format**) to make sure that this is really what you want. See [D] **data types** for information on precision of numeric storage types.

❑

Saved results

expoisson saves the following in e():

Scalars

e(N)	number of observations
e(k_groups)	number of groups
e(relative_weight)	relative weight for the observed e(sufficient) and e(condvars)
e(sum_y)	sum of *depvar*
e(k_indvars)	number of independent variables
e(k_condvars)	number of conditioning variables
e(midp)	mid-*p*-value rule indicator
e(eps)	relative difference tolerance

Macros

e(cmd)	expoisson
e(cmdline)	command as typed
e(title)	title in estimation output
e(depvar)	name of dependent variable
e(indvars)	independent variables
e(condvars)	conditional variables
e(groupvar)	group variable
e(exposure)	exposure variable
e(offset)	linear offset variable
e(level)	confidence level
e(wtype)	weight type
e(wexp)	weight expression
e(datasignature)	the checksum
e(datasignaturevars)	variables used in calculation of checksum
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

`e(b)`	coefficient vector
`e(mue_indicators)`	indicator for elements of `e(b)` estimated using MUE instead of CMLE
`e(se)`	`e(b)` standard errors (CMLEs only)
`e(ci)`	matrix of `e(level)` confidence intervals for `e(b)`
`e(sum_y_groups)`	sum of `e(depvar)` for each group
`e(N_g)`	number of observations in each group
`e(sufficient)`	sufficient statistics for `e(b)`
`e(p_sufficient)`	p-value for `e(sufficient)`
`e(scoretest)`	conditional scores tests for *indepvars*
`e(p_scoretest)`	p-values for `e(scoretest)`
`e(probtest)`	conditional probability tests for *indepvars*
`e(p_probtest)`	p-value for `e(probtest)`

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`expoisson` is implemented as an ado-file.

Let $\{Y_1, Y_2, \ldots, Y_n\}$ be a set of n independent Poisson random variables. For each $i = 1, \ldots, n$, we observe $Y_i = y_i \geq 0$, and associated with each observation is the covariate row vector of length p, $\mathbf{x}_i = (x_{i1}, \ldots, x_{ip})$. Denote $\boldsymbol{\beta} = (\beta_1, \ldots, \beta_p)^T$ to be the column vector of regression parameters and θ to be the constant. The sufficient statistic for β_j is $T_j = \sum_{i=1}^n Y_i x_{ij}$, $j = 1, \ldots, p$, and for θ is $M = \sum_{i=1}^n Y_i$. We observe $T_j = t_j$, $t_j = \sum_{i=1}^n y_i x_{ij}$, and $M = m$, $m = \sum_{i=1}^n y_i$. Let κ_i be the exposure for the ith observation. Then the probability of observing $(Y_1 = y_1, Y_2 = y_2, \ldots, Y_n = y_n)$ is

$$\Pr(Y_1 = y_1, \ldots, Y_n = y_n \mid \boldsymbol{\beta}, \mathbf{X}, \boldsymbol{\kappa}) = \frac{\exp(m\theta + \mathbf{t}\boldsymbol{\beta})}{\exp\{\sum_{i=1}^n \kappa_i \exp(\theta + \mathbf{x}_i\boldsymbol{\beta})\}} \prod_{i=1}^n \frac{\kappa_i^{y_i}}{y_i!}$$

where $\mathbf{t} = (t_1, \ldots, t_p)$, $\mathbf{X} = (\mathbf{x}_1^T, \ldots, \mathbf{x}_n^T)^T$, and $\boldsymbol{\kappa} = (\kappa_1, \ldots, \kappa_n)^T$.

The joint distribution of the sufficient statistics $(\mathbf{T}, M)$ is obtained by summing over all possible sequences $Y_1 \geq 0, \ldots, Y_n \geq 0$ such that $\mathbf{T} = \mathbf{t}$ and $M = m$. This probability function is

$$\Pr(T_1 = t_1, \ldots, T_p = t_p, M = m \mid \boldsymbol{\beta}, \mathbf{X}, \boldsymbol{\kappa}) = \frac{\exp(m\theta + \mathbf{t}\boldsymbol{\beta})}{\exp\{\sum_{i=1}^n \kappa_i \exp(\theta + \mathbf{x}_i\boldsymbol{\beta})\}} \left(\sum_{\mathbf{u}} \prod_{i=1}^n \frac{\kappa_i^{u_i}}{u_i!} \right)$$

where the sum $\sum_{\mathbf{u}}$ is over all nonnegative vectors $\mathbf{u}$ of length n such that $\sum_{i=1}^n u_i = m$ and $\sum_{i=1}^n u_i \mathbf{x}_i = \mathbf{t}$.

Conditional distribution

Without loss of generality, we will restrict our discussion to the conditional distribution of the sufficient statistic for β_1, T_1. If we condition on observing $M = m$ and $T_2 = t_2, \ldots, T_p = t_p$, the probability function of $(T_1 \mid \beta_1, T_2 = t_2, \ldots, T_p = t_p, M = m)$ is

$$\Pr(T_1 = t_1 \mid \beta_1, T_2 = t_2, \ldots, T_p = t_p, M = m) = \frac{\left(\sum_{\mathbf{u}} \prod_{i=1}^n \frac{\kappa_i^{u_i}}{u_i!} \right) e^{t_1\beta_1}}{\sum_{\mathbf{v}} \left(\prod_{i=1}^n \frac{\kappa_i^{v_i}}{v_i!} \right) e^{\beta_1 \sum_i v_i x_{i1}}} \tag{2}$$

where the sum $\sum_{\mathbf{u}}$ is over all nonnegative vectors $\mathbf{u}$ of length n such that $\sum_{i=1}^{n} u_i = m$ and $\sum_{i=1}^{n} u_i \mathbf{x}_i = \mathbf{t}$, and the sum $\sum_{\mathbf{v}}$ is over all nonnegative vectors $\mathbf{v}$ of length n such that $\sum_{i=1}^{n} v_i = m$, $\sum_{i=1}^{n} v_i x_{i2} = t_2, \ldots, \sum_{i=1}^{n} v_i x_{ip} = t_p$. The CMLE for β_1 is the value that maximizes the log of (1). This optimization task is carried out by `ml` (see [R] **ml**), using the conditional distribution of $(T_1 \mid T_2 = t_2, \ldots, T_p = t_p, M = m)$ as a dataset. This dataset consists of the feasible values and weights for T_1,

$$\left\{ \left(s_1, \prod_{i=1}^{n} \frac{\kappa_i^{v_i}}{v_i!} \right) : \sum_{i=1}^{n} v_i = m, \sum_{i=1}^{n} v_i x_{i1} = s_1, \sum_{i=1}^{n} v_i x_{i2} = t_2, \ldots, \sum_{i=1}^{n} v_i x_{ip} = t_p \right\}$$

Computing the CMLE, MUE, confidence intervals, conditional hypothesis tests, and sufficient statistic p-values is discussed in *Methods and formulas* of [R] **exlogistic**. The only difference between the two techniques is the use of the weights; that is, the weights for exact logistic are the combinatorial coefficients, $c(\mathbf{t}, m)$, in (1) of *Methods and formulas* in [R] **exlogistic**. `expoisson` and `exlogistic` use the same `ml` likelihood evaluator to compute the CMLEs as well as the same ado-programs and Mata functions to compute the MUEs and estimate statistics.

References

Agresti, A. 2002. *Categorical Data Analysis*. 2nd ed. Hoboken, NJ: Wiley.

Armitage, P., G. Berry, and J. N. S. Matthews. 2002. *Statistical Methods in Medical Research*. 4th ed. Oxford: Blackwell.

Cox, D. R., and E. J. Snell. 1989. *Analysis of Binary Data*. 2nd ed. London: Chapman & Hall.

Hirji, K. F., C. R. Mehta, and N. R. Patel. 1987. Computing distributions for exact logistic regression. *Journal of the American Statistical Association* 82: 1110–1117.

Laird, N. M., and D. Olivier. 1981. Covariance analysis of censored survival data using log-linear analysis techniques. *Journal of the American Statistical Association* 76: 231–240.

Also see

[R] **expoisson postestimation** — Postestimation tools for expoisson

[R] **poisson** — Poisson regression

[XT] **xtpoisson** — Fixed-effects, random-effects, and population-averaged Poisson models

[U] **20 Estimation and postestimation commands**

Title

expoisson postestimation — Postestimation tools for expoisson

Description

The following postestimation command is of special interest after `expoisson`:

Command	Description
`estat se`	report coefficients or IRRs and their asymptotic standard errors

For information about this command, see below.

The following standard postestimation command is also available:

Command	Description
`estat summarize`	estimation sample summary

See [R] **estat** for details.

Special-interest postestimation command

`estat se` reports regression coefficients or incidence-rate asymptotic standard errors. The estimates are stored in the matrix `r(estimates)`.

Syntax for estat se

```
estat se [, irr]
```

Menu

Statistics > Postestimation > Reports and statistics

Option for estat se

`irr` requests that the incidence-rate ratios and their asymptotic standard errors be reported. The default is to report the coefficients and their asymptotic standard errors.

Remarks

▷ Example 1

To demonstrate `estat se` after `expoisson`, we use the British physicians smoking data.

```
. use http://www.stata-press.com/data/r12/smokes
(cigarette smoking and lung cancer among British physicians (45-49 years))
. expoisson cases smokes, exposure(peryrs) irr nolog
Exact Poisson regression
                                                Number of obs =          7
------------------------------------------------------------------------------
       cases |        IRR       Suff.  2*Pr(Suff.)     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      smokes |   1.077718       797.4      0.0000       1.04552    1.111866
ln(peryrs)   |          1  (exposure)
------------------------------------------------------------------------------
. estat se, irr
------------------------------------
       cases |        IRR   Std. Err.
-------------+----------------------
      smokes |   1.077718   .0168547
------------------------------------
```

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **expoisson** — Exact Poisson regression

[U] **20 Estimation and postestimation commands**

Title

fracpoly — Fractional polynomial regression

Syntax

Fractional polynomial regression

```
fracpoly [ , fracpoly_options ] : regression_cmd [ yvar1 [ yvar2 ] ]
    xvar1 [ # [ #... ] ] [ xvar2 [ # [ #... ] ] ] [...] [ xvarlist ] [ if ] [ in ] [ weight ]
    [ , regression_cmd_options ]
```

Display table showing the best fractional polynomial model for each degree

```
fracpoly, compare
```

Create variables containing fractional polynomial powers

```
fracgen varname # [ # ... ] [ if ] [ in ] [ , fracgen_options ]
```

fracpoly_options	Description
Model	
`degree(#)`	degree of fractional polynomial to fit; default is `degree(2)`
Model 2	
`noscaling`	suppress scaling of first independent variable
`noconstant`	suppress constant term
`powers(`*numlist*`)`	list of fractional polynomial powers from which models are chosen
`center(`*cent_list*`)`	specification of centering for the independent variables
`all`	include out-of-sample observations in generated variables
Reporting	
`log`	display iteration log
`compare`	compare models by degree
display_options	control column formats and line width

regression_cmd_options	Description
Model 2	
regression_cmd_options	options appropriate to the regression command in use

All weight types supported by *regression_cmd* are allowed; see [U] **11.1.6 weight**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

where

cent_list is a comma-separated list with elements *varlist*:{mean|#|no}, except that the first element may optionally be of the form {mean|#|no} to specify the default for all variables.

regression_cmd may be clogit, glm, intreg, logistic, logit, mlogit, nbreg, ologit, oprobit, poisson, probit, qreg, regress, rreg, stcox, stcrreg, streg, or xtgee.

fracgen_options	Description
Main	
center(no|mean|#)	center *varname* as specified; default is center(no)
noscaling	suppress scaling of *varname*
restrict([*varname*] [*if*])	compute centering and scaling using specified subsample
replace	replace variables if they exist

Menu

fracpoly

Statistics > Linear models and related > Fractional polynomials > Fractional polynomial regression

fracgen

Statistics > Linear models and related > Fractional polynomials > Create fractional polynomial powers

Description

fracpoly fits fractional polynomials (FPs) in $xvar_1$ as part of the specified regression model. After execution, fracpoly leaves variables in the dataset named I*xvar*__1, I*xvar*__2, ..., where *xvar* represents the first four letters of the name of $xvar_1$. The new variables contain the best-fitting FP powers of $xvar_1$.

Covariates other than $xvar_1$, which are optional, are specified in $xvar_2$, ..., and *xvarlist*. They may be modeled linearly and with specified FP transformations. Fractional polynomial powers are specified by typing numbers after the variable's name. A variable name typed without numbers is entered linearly.

fracgen creates new variables named *varname*_1, *varname*_2, ..., containing FP powers of *varname* by using the powers (# [#...]) specified.

See [R] **fracpoly postestimation** for information on fracplot and fracpred.

See [R] **mfp** for multivariable FP model fitting.

Options for fracpoly

Model

degree(#) determines the degree of FP to be fit. The default is degree(2), that is, a model with two power terms.

Model 2

noscaling suppresses scaling of $xvar_1$ and its powers.

`noconstant` suppresses the regression constant if this is permitted by *regression_cmd*.

`powers(`*numlist*`)` is the set of FP powers from which models are to be chosen. The default is `powers(-2,-1,-.5,0,.5,1,2,3)` (0 means log).

`center(`*cent_list*`)` defines the centering for the covariates $xvar_1$, $xvar_2$, ..., *xvarlist*. The default is `center(mean)`. A typical item in *cent_list* is *varlist*`:{mean|#|no}`. Items are separated by commas. The first item is special because *varlist*`:` is optional, and if omitted, the default is (re)set to the specified value (`mean` or `#` or `no`). For example, `center(no, age:mean)` sets the default to `no` and sets the centering for `age` to `mean`.

regression_cmd_options are options appropriate to the regression command in use. For example, for `stcox`, *regression_cmd_options* may include `efron` or some alternate method for handling tied failures.

`all` includes out-of-sample observations when generating the best-fitting FP powers of $xvar_1$, $xvar_2$, etc. By default, the generated FP variables contain missing values outside the estimation sample.

Reporting

`log` displays deviances and (for `regress`) residual standard deviations for each FP model fit.

`compare` reports a closed-test comparison between FP models.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Options for fracgen

Main

`center(no|mean|#)` specifies whether *varname* is to be centered; the default is `center(no)`.

`noscaling` suppresses scaling of *varname*.

`restrict(`[*varname*] [*if*]`)` specifies that centering and scaling be computed using the subsample identified by *varname* and `if`.

The subsample is defined by the observations for which *varname* $\neq 0$ that also meet the `if` conditions. Typically, *varname* $= 1$ defines the subsample and *varname* $= 0$ indicates observations not belonging to the subsample. For observations whose subsample status is uncertain, *varname* should be set to a missing value; such observations are dropped from the subsample.

By default, `fracgen` computes the centering and scaling by using the sample of observations identified in the [*if*] [*in*] options. The `restrict()` option identifies a subset of this sample.

`replace` specifies that any existing variables named *varname*`_1`, *varname*`_2`, ... may be replaced.

Remarks

Remarks are presented under the following headings:

Introduction
fracpoly
Centering
Output with the compare option
fracgen
Models with several continuous covariates
Examples

Introduction

Regression models based on FP functions of a continuous covariate are described by Royston and Altman (1994b). Detailed examples using an earlier and rather more complex version of this set of commands are presented by Royston and Altman (1994a).

FPs increase the flexibility afforded by the family of conventional polynomial models. Although polynomials are popular in data analysis, linear and quadratic functions are severely limited in their range of curve shapes, whereas cubic and higher-order curves often produce undesirable artifacts, such as edge effects and waves.

A polynomial of degree m may be written as

$$\beta_0 + \beta_1 x + \beta_2 x^2 + \cdots + \beta_m x^m$$

whereas FP of degree m has m integer and/or fractional powers $p_1 < \cdots < p_m$,

$$\beta_0 + \beta_1 x^{(p_1)} + \beta_2 x^{(p_2)} + \cdots + \beta_m x^{(p_m)}$$

where for a power, p,

$$x^{(p)} = \begin{cases} x^p & \text{if } p \neq 0 \\ \log x & \text{if } p = 0 \end{cases}$$

x must be positive. An FP of first degree ($m = 1$) involves one power or log transformation of x.

This family of FP functions may be extended in a mathematically natural way to include repeated powers. An FP of degree m with exactly m repeated powers of p is defined as

$$\beta_0 + \beta_1 x^{(p)} + \beta_2 x^{(p)} \log x + \cdots + \beta_m x^{(p)} (\log x)^{m-1}$$

For example, an FP of second degree ($m = 2$) with repeated powers of 0.5 is

$$\beta_0 + \beta_1 x^{0.5} + \beta_2 x^{0.5} \log x$$

A general FP may include some unique and some repeated powers. For example, one with powers $(-1, 1, 3, 3)$ is

$$\beta_0 + \beta_1 x^{-1} + \beta_2 x + \beta_3 x^3 + \beta_4 x^3 \log x$$

The permitted powers are restricted to the set $\{-2, -1, -0.5, 0, 0.5, 1, 2, 3\}$ because our experience using FPs in data analysis indicates that including extra powers in the set is not often worthwhile.

Now we consider using FPs in regression modeling. If the values of the powers $p_1, \ldots, p_m$ were known, the FP would resemble a conventional multiple linear regression model with coefficients $\beta_0, \beta_1, \ldots, \beta_m$. However, the powers are not (usually) known and must be estimated, together with the coefficients, from the data. Estimation involves a systematic search for the best power or combination of powers from the permitted set. For each possible combination, a linear regression model as just described is fit, and the corresponding deviance (defined as minus twice the log likelihood) is noted. The model with the lowest deviance is deemed to have the best fit, and the corresponding powers and regression coefficients constitute the final FP model. In practice, $m = 2$ is often sufficient (Royston and Sauerbrei 2008, 76).

fracpoly

`fracpoly` finds and reports a multiple regression model comprising the best-fitting powers of $xvar_1$ together with other covariates specified by $xvar_2$, ..., *xvarlist*. The model that is fit depends on the type of *regression_cmd* used.

The regression output for the best-fitting model may be reproduced by typing *regression_cmd* without variables or options. `predict`, `test`, etc., may be used after `fracpoly`; the results will depend on *regression_cmd*.

The standard errors of the fitted values (as estimated after use of `fracpoly` by using `predict` or `fracpred` with the `stdp` option) are somewhat too low because no allowance has been made for the estimation of the powers.

If $xvar_1$ has any negative or zero values, `fracpoly` subtracts the minimum of *xvar* from *xvar* and then adds the rounding (or counting) interval. The interval is defined as the smallest positive difference between the ordered values of *xvar*. After this change of origin, the minimum value of $xvar_1$ is positive, so FPs (which require $xvar_1 > 0$) can be used. Unless the `noscaling` option is used, `fracpoly` scales the resulting variable by a power of 10 calculated from the data. The scaling is designed to improve numerical stability when fitting FP models.

After execution, `fracpoly` leaves in the dataset variables named `Ixvar__1`, `Ixvar__2`, ..., which are the best-fitting FP powers of $xvar_1$ (calculated, if necessary, after a change in origin and scale as just described, and if centering is specified, with a constant added to or subtracted from the values after FP transformation). Other variables, whose names follow the same convention, are left in the dataset if $xvar_2$ has been specified.

Centering

As discussed by Garrett (1995, 1998), covariate centering is a sensible, indeed often essential, step when reporting and interpreting the results of multiple regression models. For this and other reasons, centering has been introduced as the default option in `fracpoly`. As written, the familiar straight-line regression function $E[y|x] = \beta_0 + \beta_1 x$ is "centered" to 0 in that $\beta_0 = E[y|0]$. This is fine if $x = 0$ is a sensible base point. However, the sample values of x may not even encompass 0 (this is usually the case when FP models are contemplated). Then β_0 is a meaningless intercept, and the standard error of its estimate $\widehat{\beta}_0$ will be large. For FP model $E[y|x] = \beta_0 + \beta_1 x^{(p)}$, the point $x^{(p)} = 0$ may even correspond to $x = \infty$ (consider $p < 0$). The scheme adopted by `fracpoly` is to center on the mean of x. For example, for the FP $E[y|x] = \beta_0 + \beta_1 x^p + \beta_1 x^q$, `fracpoly` actually fits the model

$$E[y|x] = \beta_0 + \beta_1 \left(x^p - \overline{x}^p\right) + \beta_2 \left(x^q - \overline{x}^q\right)$$

where $\overline{x}$ is the sample mean of the x values and $E[y|\overline{x}] = \beta_0$, giving β_0 a respectable interpretation as the predicted value of y at the mean of x. This approach has the advantage that plots of the fitted values and 95% confidence intervals for $E[y|x]$ as a function of x, even within a multiple regression model, are always sensible (provided that the other predictors are suitably centered—otherwise, the confidence limits can be alarmingly wide).

Sometimes centering on the mean is not appropriate, an example being a binary covariate where often you will want to center on the lower value, usually 0 (that is, not center). You should then use the `center()` option to override the default. An example is `center(x1:mean,x2-x5:no,x6:1)`.

Output with the compare option

If the `compare` option is used, `fracpoly` displays a table showing the best FP model for each degree $k < m$ (including the model without x and the model linear in x). Deviance differences between each FP model and the degree m model are also reported along with the corresponding p-values (Royston and Altman 1994b; Royston and Sauerbrei 2008).

The `compare` option implements a closed-test approach to selecting an FP model. It has the advantage of preserving the type I error probability at a nominal value. For example, suppose a nominal 5% significance level was chosen, and the test of FP2 versus the null model (that is, omitting x) was not significant. No further tests among FP models would then be done, and x would be considered nonsignificant, regardless of the results of any further model comparisons.

fracgen

The basic syntax of `fracgen` is

`fracgen` *varname* # [# ...]

Each power (represented by # in the syntax diagram) should be separated by a space. `fracgen` creates new variables called *varname*_1, *varname*_2, etc. Each variable is labeled according to its power, preliminary linear transformation, and centering, if applied.

Positive or negative powers of *varname* are defined in the usual way. A power of zero is interpreted as log.

Models with several continuous covariates

`fracpoly` estimates powers for FP models in just one continuous covariate ($xvar_1$), though other covariates of any kind ($xvar_2$, ..., *xvarlist*) may be included as linear or predefined FP terms. An algorithm was suggested by Royston and Altman (1994b) for the joint estimation of FP models in several continuous covariates. It was later refined by Sauerbrei and Royston (1999) and is implemented in the Stata command `mfp`. See [R] **mfp** as well as Royston and Ambler (1998) and Royston and Sauerbrei (2008).

Examples

▷ Example 1

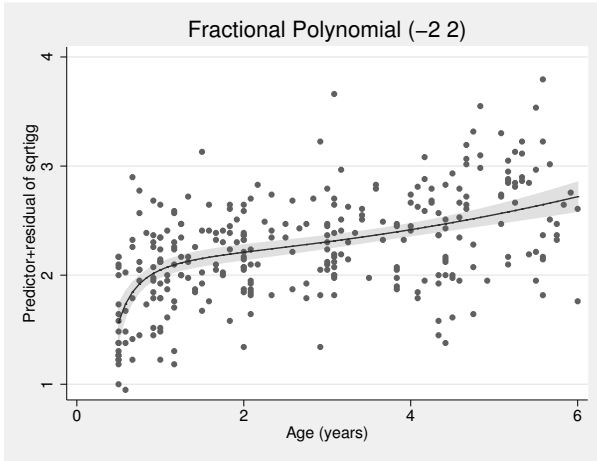
Consider the serum immunoglobulin G (IgG) dataset from Isaacs et al. (1983), which consists of 298 independent observations in young children. The dependent variable `sqrtigg` is the square root of the IgG concentration, and the independent variable `age` is the age of each child. (Preliminary Box–Cox analysis shows that a square root transformation removes the skewness in IgG.) The aim is to find a model that accurately predicts the mean of `sqrtigg` given `age`. We use `fracpoly` to find the best FP model of degree 2 (the default option) and graph the resulting fit and 95% confidence interval:

```
. use http://www.stata-press.com/data/r12/igg
(Immunoglobulin in children)
. fracpoly: regress sqrtigg age
........
-> gen double Iage__1 = age^-2-.1299486216 if e(sample)
-> gen double Iage__2 = age^2-7.695349038 if e(sample)
```

Source	SS	df	MS		
Model	22.2846976	2	11.1423488	Number of obs	= 298
Residual	50.9676492	295	.172771692	F(2, 295)	= 64.49
				Prob > F	= 0.0000
Total	73.2523469	297	.246640898	R-squared	= 0.3042
				Adj R-squared	= 0.2995
				Root MSE	= .41566

sqrtigg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
Iage__1	-.1562156	.027416	-5.70	0.000	-.2101713	-.10226
Iage__2	.0148405	.0027767	5.34	0.000	.0093757	.0203052
_cons	2.283145	.0305739	74.68	0.000	2.222974	2.343315

```
Deviance:  319.45. Best powers of age among 44 models fit: -2 2.
. fracplot age, msize(small)
```



The new variables created by `fracpoly` contain the best-fitting FP powers of `age`, as centered by `fracpoly`. For example, `Iage__1` is centered by subtracting the mean of `age` raised to the power -2. In general, the variables created by `fracpoly` are centered and possibly scaled, which is reflected in the estimated regression coefficients and intercept. Centering does have its advantages (see the *Centering* section earlier in this entry); however, sometimes you may want estimation for uncentered variables. To obtain regression results for uncentered and unscaled FP variables, specify options `center(no)` and `noscaling` to `fracpoly`. For a more detailed discussion, see Royston and Sauerbrei (2008, sec. 4.11).

The fitted curve has an asymmetric S shape. This model has powers $(-2, 2)$ and deviance 319.45. As many as 44 models have been quietly fit in the search for the best powers. Now let's look at models of degree ≤ 4:

```
. fracpoly, degree(4) compare: regress sqrtigg age
.....................................................................
> .....................................................................
> ........
-> gen double Iage__1 = ln(age)-1.020308063 if e(sample)
-> gen double Iage__2 = age^3-21.34727694 if e(sample)
-> gen double Iage__3 = age^3*ln(age)-21.78079878 if e(sample)
-> gen double Iage__4 = age^3*ln(age)^2-22.22312461 if e(sample)
```

Source	SS	df	MS		
Model	22.5754541	4	5.64386353	Number of obs =	298
Residual	50.6768927	293	.172958678	F(4, 293) =	32.63
				Prob > F =	0.0000
				R-squared =	0.3082
Total	73.2523469	297	.246640898	Adj R-squared =	0.2987
				Root MSE =	.41588

sqrtigg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
Iage__1	.8761824	.1898721	4.61	0.000	.5024962	1.249869
Iage__2	-.1922029	.0684934	-2.81	0.005	-.3270044	-.0574015
Iage__3	.2043794	.074947	2.73	0.007	.0568767	.3518821
Iage__4	-.0560067	.0212969	-2.63	0.009	-.097921	-.0140924
_cons	2.238735	.0482705	46.38	0.000	2.143734	2.333736

```
Deviance:  317.74. Best powers of age among 494 models fit: 0 3 3 3.
Fractional polynomial model comparisons:
```

age	df	Deviance	Res. SD	Dev. dif.	P (*)	Powers
Not in model	0	427.539	.49663	109.795	0.000	
Linear	1	337.561	.42776	19.818	0.006	1
m = 1	2	327.436	.420554	9.692	0.140	0
m = 2	4	319.448	.415658	1.705	0.794	-2 2
m = 3	6	319.275	.416243	1.532	0.473	-2 1 1
m = 4	8	317.744	.415883	—	—	0 3 3 3

```
(*) P-value from deviance difference comparing reported model with m = 4 model
```

It appears that the degree 4 FP model is not significantly different from the other FP models (at the 5% level).

Let's compare the curve shape from the $m = 2$ model with that from a conventional quartic polynomial, whose fit turns out to be significantly better than a cubic (not shown). We use the ability of `fracpoly` both to generate the required powers of `age`, namely, $(1, 2, 3, 4)$ for the quartic and $(-2, 2)$ for the second-degree FP, and to fit the model. We fit both models and graph the resulting curves:

```
. fracpoly: regress sqrtigg age 1 2 3 4
-> gen double Iage__1 = age-2.774049213 if e(sample)
-> gen double Iage__2 = age^2-7.695349038 if e(sample)
-> gen double Iage__3 = age^3-21.34727694 if e(sample)
-> gen double Iage__4 = age^4-59.21839681 if e(sample)
```

Source	SS	df	MS		
Model	22.5835458	4	5.64588646	Number of obs	= 298
Residual	50.668801	293	.172931061	F(4, 293)	= 32.65
				Prob > F	= 0.0000
Total	73.2523469	297	.246640898	R-squared	= 0.3083
				Adj R-squared	= 0.2989
				Root MSE	= .41585

sqrtigg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
Iage__1	2.047831	.4595962	4.46	0.000	1.143302	2.952359
Iage__2	-1.058902	.2822803	-3.75	0.000	-1.614456	-.5033479
Iage__3	.2284917	.0667591	3.42	0.001	.0971037	.3598798
Iage__4	-.0168534	.0053321	-3.16	0.002	-.0273475	-.0063594
_cons	2.240012	.0480157	46.65	0.000	2.145512	2.334511

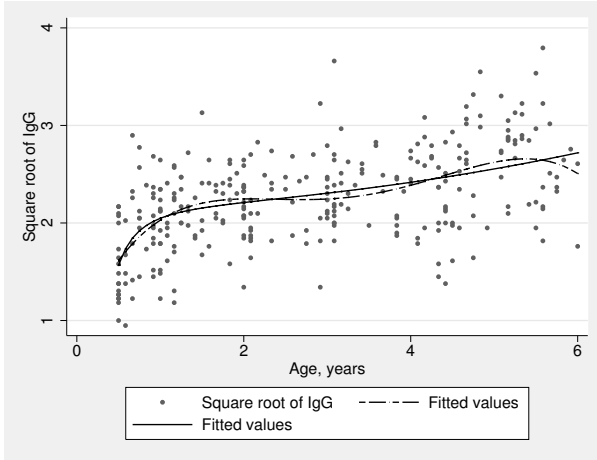
```
Deviance:   317.70.

. predict fit1
(option xb assumed; fitted values)

. fracpoly: regress sqrtigg age -2 2
-> gen double Iage__1 = age^-2-.1299486216 if e(sample)
-> gen double Iage__2 = age^2-7.695349038 if e(sample)
```

Source	SS	df	MS		
Model	22.2846976	2	11.1423488	Number of obs	= 298
Residual	50.9676492	295	.172771692	F(2, 295)	= 64.49
				Prob > F	= 0.0000
Total	73.2523469	297	.246640898	R-squared	= 0.3042
				Adj R-squared	= 0.2995
				Root MSE	= .41566

sqrtigg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
Iage__1	-.1562156	.027416	-5.70	0.000	-.2101713	-.10226
Iage__2	.0148405	.0027767	5.34	0.000	.0093757	.0203052
_cons	2.283145	.0305739	74.68	0.000	2.222974	2.343315

```
Deviance:   319.45.

. predict fit2
(option xb assumed; fitted values)
```

```
. scatter sqrtigg fit1 fit2 age, c(. l l) m(o i i) msize(small)
> clpattern(. -_.) ytitle("Square root of IgG") xtitle("Age, years")
```



The quartic curve has an unsatisfactory wavy appearance that is implausible for the known behavior of IgG, the serum level of which increases throughout early life. The FP curve increases monotonically and is therefore biologically the more plausible curve. The two models have approximately the same deviance.

◁

▷ Example 2

Data from Smith et al. (1992) contain times to complete healing of leg ulcers in a randomized controlled clinical trial of two treatments in 192 elderly patients. Several covariates were available, of which an important one is `mthson`, the number of months since the recorded onset of the ulcer. Because the response variable is time to an event of interest and some (in fact, about one-half) of the times are censored, using Cox regression to analyze the data is appropriate. We consider FPs in `mthson`, adjusting for four other covariates: `age`; `ulcarea`, the area of tissue initially affected by the ulcer; `deepppg`, a binary variable indicating the presence or absence of deep vein involvement; and `treat`, a binary variable indicating treatment type. We fit FPs of degree 1 and 2:

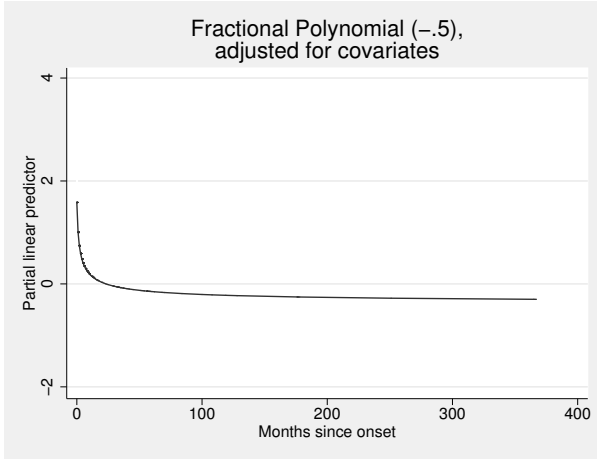
```
. use http://www.stata-press.com/data/r12/legulcer, clear
(Leg ulcer clinical trial)
. stset ttevent, fail(cens)
```

(*output omitted*)

```
. fracpoly, compare: stcox mthson age ulcarea deepppg treat, nohr
-> gen double Iage__1 = age-73.453125 if e(sample)
-> gen double Iulca__1 = ulcarea-1326.203125 if e(sample)
-> gen double Itrea__1 = treat-1 if e(sample)
........
-> gen double Imths__1 = X^.5-.4930242557 if e(sample)
-> gen double Imths__2 = X^.5*ln(X)+.6973304564 if e(sample)
   (where: X = (mthson+1)/100)

        failure _d:  censored
   analysis time _t:  ttevent

Iteration 0:   log likelihood = -422.65089
Iteration 1:   log likelihood = -390.49313
Iteration 2:   log likelihood = -383.44258
Iteration 3:   log likelihood = -374.28707
Iteration 4:   log likelihood = -369.31417
Iteration 5:   log likelihood = -368.38104
Iteration 6:   log likelihood = -368.35448
Iteration 7:   log likelihood = -368.35446
Refining estimates:
Iteration 0:   log likelihood = -368.35446

Cox regression -- Breslow method for ties

No. of subjects =          192                     Number of obs   =       192
No. of failures =           92
Time at risk    =        13825
                                                   LR chi2(6)      =    108.59
Log likelihood  =   -368.35446                     Prob > chi2     =    0.0000

------------------------------------------------------------------------------
          _t |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
    Imths__1 |  -2.81425   .6996385    -4.02   0.000    -4.185516   -1.442984
    Imths__2 |   1.541451  .4703143     3.28   0.001     .6196521    2.46325
     Iage__1 |  -.0261111  .0087983    -2.97   0.003    -.0433556   -.0088667
    Iulca__1 |  -.0017491   .000359    -4.87   0.000    -.0024527   -.0010455
     deepppg |  -.5850499  .2163173    -2.70   0.007    -1.009024   -.1610758
    Itrea__1 |  -.1624663  .2171048    -0.75   0.454    -.5879838    .2630513
------------------------------------------------------------------------------

Deviance:   736.71. Best powers of mthson among 44 models fit: .5 .5.

Fractional polynomial model comparisons:

------------------------------------------------------------------------------
mthson           df       Deviance   Dev. dif.  P (*)  Powers
------------------------------------------------------------------------------
Not in model      0        754.345    17.636    0.001
Linear            1        751.680    14.971    0.002  1
m = 1             2        738.969     2.260    0.323  -.5
m = 2             4        736.709         —        —  .5 .5
------------------------------------------------------------------------------
(*) P-value from deviance difference comparing reported model with m = 2 model
```

The best-fit FP of degree 2 has powers $(0.5, 0.5)$ and deviance 736.71. However, this model does not fit significantly better than the FP of degree 1 (at the 5% level), which has power -0.5 and deviance 738.97. We prefer the model with $m = 1$, for which the partial linear predictor is shown on the next page.

```
. quietly fracpoly, degree(1): stcox mthson age ulcarea deepppg treat, nohr
. fracplot, ytitle(Partial linear predictor) m(i) ciopts(bcolor(white))
```



The hazard for healing is much higher for patients whose ulcer is of recent onset than for those who have had an ulcer for many months.

`fracpoly` has automatically centered the predictors on their mean values, but because in Cox regression there is no constant term, we cannot see the effects of centering in the table of regression estimates. The effects would be present if we were to graph the baseline hazard or survival function because these functions are defined with all predictors set equal to 0.

A more appropriate analysis of this dataset, if one wished to model all the predictors, possibly with FP functions, would be to use `mfp`; see [R] **mfp**.

◁

Saved results

In addition to what *regression_cmd* saves, `fracpoly` saves the following in `e()`:

Scalars

`e(fp_N)`	number of nonmissing observations
`e(fp_dev)`	deviance for FP model of degree m
`e(fp_df)`	FP model degrees of freedom
`e(fp_d0)`	deviance for model without *xvar*$_1$
`e(fp_s0)`	residual SD for model without *xvar*$_1$
`e(fp_dlin)`	deviance for model linear in *xvar*$_1$
`e(fp_slin)`	residual SD for model linear in *xvar*$_1$
`e(fp_d1)`, `e(fp_d2)`, ...	deviances for FP models of degree 1,2,...,m
`e(fp_s1)`, `e(fp_s2)`, ...	residual SDs for FP models of degree 1,2,...,m

Macros

`e(fp_cmd)`	`fracpoly`
`e(cmdline)`	command as typed
`e(fp_depv)`	*yvar*$_1$ (*yvar*$_2$
`e(fp_rhs)`	*xvar*$_1$
`e(fp_base)`	variables in *xvar*$_2$, ..., *xvarlist* after centering and FP transformation
`e(fp_xp)`	I*xvar*__1, I*xvar*__2, etc.
`e(fp_fvl)`	variables in model finally estimated
`e(fp_wgt)`	weight type or `""`
`e(fp_wexp)`	weight expression if `'e(fp_wgt)' != ""`
`e(fp_pwrs)`	powers for FP model of degree m
`e(fp_x1)`, `e(fp_x2)`, ...	*xvar*$_1$ and variables in model
`e(fp_k1)`, `e(fp_k2)`, ...	powers for FP models of degree 1,2,...,m

Residual SDs are stored only when *regression_cmd* is `regress`.

Methods and formulas

`fracpoly` and `fracgen` are implemented as ado-files.

The general definition of an FP, accommodating possible repeated powers, may be written for functions $H_1(x), \ldots, H_m(x)$ as

$$\beta_0 + \sum_{j=1}^{m} \beta_j H_j(x)$$

where $H_1(x) = x^{(p_1)}$ and for $j = 2, \ldots, m$,

$$H_j(x) = \begin{cases} x^{(p_j)} & \text{if } p_j \neq p_{j-1} \\ H_{j-1}(x) \log x & \text{if } p_j = p_{j-1} \end{cases}$$

For example, an FP of degree 3 with powers $(1, 3, 3)$ has $H_1(x) = x$, $H_2(x) = x^3$, and $H_3(x) = x^3 \log x$ and equals $\beta_0 + \beta_1 x + \beta_2 x^3 + \beta_3 x^3 \log x$.

An FP model of degree m is taken to have $2m + 1$ degrees of freedom (df): one for β_0 and one for each β_j and its associated power. Because the powers in an FP are chosen from a finite set rather than from the entire real line, the df defined in this way are approximate.

The deviance D of a model is defined as -2 times its maximized log likelihood. For normal-errors models, we use the formula

$$D = n\left(1 - \bar{l} + \log \frac{2\pi \text{RSS}}{n}\right)$$

where n is the sample size, $\bar{l}$ is the mean of the lognormalized weights ($\bar{l} = 0$ if the weights are all equal), and RSS is the residual sum of squares as fit by `regress`.

The `compare` option causes `fracpoly` to report a table comparing FP models of degree $k < m$ to the degree m FP model. Suppose that we are comparing FP regression models with degrees k and m. The p-values reported by `compare` are calculated differently for normal and nonnormal regressions. Let D_k and D_m be the deviances of the models with degrees k and m, respectively. For normal-errors models such as `regress`, a variance ratio F is calculated as

$$F = \frac{n_2}{n_1}\left\{\exp\left(\frac{D_k - D_m}{n}\right) - 1\right\}$$

where n_1 is the numerator df (here, $2m - 2k$) and n_2 is the denominator df (equal to rdf $- 2m$, where rdf is the residual df for the regression model involving only the covariates in *xvar*$_2$, if any, but not x). The p-value is obtained by referring F to an F distribution on (n_1, n_2) df.

For nonnormal models (`clogit`, `glm`, `logistic`, ... `stcox`, or `streg`; not `regress`), the p-value is obtained by referring $D_k - D_m$ to a χ^2 distribution on $2m - 2k$ df. These p-values for comparing models are approximate and are typically somewhat conservative (Royston and Altman 1994b).

The component-plus-residual values graphed by `fracplot` are calculated as follows: let the data consist of triplets $(y_i, x_i, \mathbf{z}_i)$, $i = 1, \ldots, n$, where $\mathbf{z}_i$ is the vector of covariates for the ith observation, after applying possible FP transformation and centering as described earlier. Let $\widehat{\eta}_i = \widehat{\beta}_0 + \{\mathbf{H}(x_i) - \mathbf{H}(x_0)\}'\widehat{\boldsymbol{\beta}} + \mathbf{z}_i'\widehat{\boldsymbol{\gamma}}$ be the linear predictor from the FP model, as given by the `fracpred` command, or equivalently, by the `predict` command with the `xb` option, after the use of `fracpoly`. Here $\mathbf{H}(x_i) = \{H_1(x_i), \ldots, H_m(x_i)\}'$ is the vector of FP functions described above, $\mathbf{H}(x_0) = \{H_1(x_0), \ldots, H_m(x_0)\}'$ is the vector of centering to x_0 (x_0 is often chosen to be the mean of the x_i), $\widehat{\boldsymbol{\beta}}$ is the estimated parameter vector, and $\widehat{\boldsymbol{\gamma}}$ is the estimated parameter vector for the covariates. The values $\widehat{\eta}_i^* = \widehat{\beta}_0 + \{\mathbf{H}(x_i) - \mathbf{H}(x_0)\}'\widehat{\boldsymbol{\beta}}$ represent the behavior of the FP model for x at fixed values $\mathbf{z} = \mathbf{0}$ of the (centered) covariates. The ith component-plus-residual is defined as $\widehat{\eta}_i^* + d_i$, where d_i is the deviance residual for the ith observation. For normal-errors models, $d_i = \sqrt{w_i}(y_i - \widehat{\eta}_i)$, where w_i is the case weight (or 1, if *weight* is not specified). For logistic, Cox, and generalized linear regression models, see [R] **logistic**, [R] **probit**, [ST] **stcox**, and [R] **glm**, respectively, for the formula for d_i. The formula for `poisson` models is the same as that for `glm` with `family(poisson)`. For `stcox`, d_i is the partial martingale residual (see [ST] **stcox postestimation**).

Acknowledgment

`fracpoly` and `fracgen` were written by Patrick Royston, MRC Clinical Trials Unit, London.

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Also see

[R] **fracpoly postestimation** — Postestimation tools for fracpoly

[R] **mfp** — Multivariable fractional polynomial models

[U] **20 Estimation and postestimation commands**

Title

fracpoly postestimation — Postestimation tools for fracpoly

Description

The following postestimation commands are of special interest after `fracpoly`:

Command	Description
`fracplot`	plot data and fit from most recently fit fractional polynomial model
`fracpred`	create variable containing prediction, deviance residuals, or SEs of fitted values

For information about these commands, see below.

The following standard postestimation commands are also available if available after *regression_cmd*:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`	likelihood-ratio test
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation commands

`fracplot` plots the data and fit, with 95% confidence limits, from the most recently fit fractional polynomial (FP) model. The data and fit are plotted against *varname*, which may be $xvar_1$ or another of the covariates ($xvar_2$, ..., or a variable from *xvarlist*). If *varname* is not specified, $xvar_1$ is assumed.

`fracpred` creates *newvar* containing the fitted index or deviance residuals for the whole model, or the fitted index or its standard error for *varname*, which may be $xvar_1$ or another covariate.

Syntax for predict

The behavior of `predict` following `fracpoly` is determined by *regression_cmd*. See the corresponding *regression_cmd* **postestimation** entry for available `predict` options.

Also see information on `fracpred` below.

Syntax for fracplot and fracpred

Plot data and fit from most recently fit fractional polynomial model

`fracplot` [*varname*] [*if*] [*in*] [, *fracplot_options*]

Create variable containing the prediction, deviance residuals, or SEs of fitted values

`fracpred` *newvar* [, *fracpred_options*]

fracplot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Fitted line	
`lineopts(`*cline_options*`)`	affect rendition of the fitted line
CI plot	
`ciopts(`*area_options*`)`	affect rendition of the confidence bands
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

fracpred_options	Description
`for(`*varname*`)`	compute prediction for *varname*
`dresid`	compute deviance residuals
`stdp`	compute standard errors of the fitted values *varname*

`fracplot` is not allowed after `fracpoly` or `mfp` with `clogit`, `mlogit`, or `stcrreg`. `fracpred, dresid` is not allowed after `fracpoly` or `mfp` with `clogit`, `mlogit`, or `stcrreg`.

Menu

fracplot

Statistics > Linear models and related > Fractional polynomials > Fractional polynomial regression plot

fracpred

Statistics > Linear models and related > Fractional polynomials > Fractional polynomial prediction

Options for fracplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Fitted line

`lineopts(`*cline_options*`)` affect the rendition of the fitted line; see [G-3] ***cline_options***.

CI plot

`ciopts(`*area_options*`)` affect the rendition of the confidence bands; see [G-3] ***area_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Options for fracpred

`for(`*varname*`)` specifies (partial) prediction for variable *varname*. The fitted values are adjusted to the value specified by the `center()` option in `fracpoly`.

`dresid` specifies that deviance residuals be calculated.

`stdp` specifies calculation of the standard errors of the fitted values *varname*, adjusted for all the other predictors at the values specified by `center()`.

Remarks

`fracplot` actually produces a component-plus-residual plot. For normal-error models with constant weights and one covariate, this amounts to a plot of the observations with the fitted line inscribed. For other normal-error models, weighted residuals are calculated and added to the fitted values.

For models with additional covariates, the line is the partial linear predictor for the variable in question ($xvar_1$ or a covariate) and includes the intercept β_0.

For generalized linear and Cox models, the fitted values are plotted on the scale of the "index" (linear predictor). Deviance residuals are added to the (partial) linear predictor to give component-plus-residual values. These values are plotted as small circles.

See [R] **fracpoly** for examples using `fracplot`.

Methods and formulas

All postestimation commands listed above and `fracplot` and `fracpred` are implemented as ado-files.

See *Methods and formulas* in [R] **fracpoly** for notation.

The component-plus-residual values graphed by `fracplot` are calculated as follows: Let the data consist of triplets $(y_i, x_i, \mathbf{z}_i)$, $i = 1, \ldots, n$, where $\mathbf{z}_i$ is the vector of covariates for the ith observation, after applying possible fractional polynomial transformation and adjustment as described earlier. Let $\widehat{\eta}_i = \widehat{\beta}_0 + \{\mathbf{H}(x_i) - \mathbf{H}(x_0)\}' \widehat{\boldsymbol{\beta}} + \mathbf{z}_i' \widehat{\boldsymbol{\gamma}}$ be the linear predictor from the FP model, as given by the `fracpred` command or, equivalently, by the `predict` command with the `xb` option, following `fracpoly`. Here $\mathbf{H}(x_i) = \{H_1(x_i), \ldots, H_m(x_i)\}'$ is the vector of FP functions described above, $\mathbf{H}(x_0) = \{H_1(x_0), \ldots, H_m(x_0)\}'$ is the vector of adjustments to x_0 (often, x_0 is chosen to be the mean of the x_i), $\widehat{\boldsymbol{\beta}}$ is the estimated parameter vector, and $\widehat{\boldsymbol{\gamma}}$ is the estimated parameter vector for the covariates. The values $\widehat{\eta}_i^* = \widehat{\beta}_0 + \{\mathbf{H}(x_i) - \mathbf{H}(x_0)\}' \widehat{\boldsymbol{\beta}}$ represent the behavior of the FP model for x at fixed values $\mathbf{z} = \mathbf{0}$ of the (adjusted) covariates. The ith component-plus-residual is defined as $\widehat{\eta}_i^* + d_i$, where d_i is the deviance residual for the ith observation. For normal-errors models, $d_i = \sqrt{w_i}(y_i - \widehat{\eta}_i)$, where w_i is the case weight (or 1, if *weight* is not specified). For logistic, Cox, and generalized linear regression models, see [R] **logistic**, [R] **probit**, [ST] **stcox**, and [R] **glm** for the formula for d_i. The formula for `poisson` models is the same as that for `glm` with `family(poisson)`. For `stcox`, d_i is the partial martingale residual (see [ST] **stcox postestimation**).

`fracplot` plots the values of d_i and the curve represented by $\widehat{\eta}_i^*$ against x_i. The confidence interval for $\widehat{\eta}_i^*$ is obtained from the variance–covariance matrix of the entire model and takes into account the uncertainty in estimating β_0, $\boldsymbol{\beta}$, and $\boldsymbol{\gamma}$ (but not in estimating the FP powers for x).

`fracpred` with the `for(`*varname*`)` option calculates the predicted index at $x_i = x_0$ and $\mathbf{z}_i = \mathbf{0}$; that is, $\widehat{\eta}_i = \widehat{\beta}_0 + \{\mathbf{H}(x_i) - \mathbf{H}(x_0)\}' \widehat{\boldsymbol{\beta}}$. The standard error is calculated from the variance–covariance matrix of $(\widehat{\beta}_0, \widehat{\boldsymbol{\beta}})$, again ignoring estimation of the powers.

Acknowledgment

`fracplot` and `fracpred` were written by Patrick Royston of the MRC Clinical Trials Unit, London.

Also see

[R] **fracpoly** — Fractional polynomial regression

[U] **20 Estimation and postestimation commands**

Title

frontier — Stochastic frontier models

Syntax

```
frontier depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
distribution(hnormal)	half-normal distribution for the inefficiency term
distribution(exponential)	exponential distribution for the inefficiency term
distribution(tnormal)	truncated-normal distribution for the inefficiency term
ufrom(*matrix*)	specify untransformed log likelihood; only with d(tnormal)
cm(*varlist* [, noconstant])	fit conditional mean model; only with d(tnormal); use noconstant to suppress constant term
Model 2	
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
uhet(*varlist* [, noconstant])	explanatory variables for technical inefficiency variance function; use noconstant to suppress constant term
vhet(*varlist* [, noconstant])	explanatory variables for idiosyncratic error variance function; use noconstant to suppress constant term
cost	fit cost frontier model; default is production frontier model
SE	
vce(*vcetype*)	*vcetype* may be oim, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.
bootstrap, by, jackknife, rolling, and statsby are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Frontier models

Description

`frontier` fits stochastic production or cost frontier models; the default is a production frontier model. It provides estimators for the parameters of a linear model with a disturbance that is assumed to be a mixture of two components, which have a strictly nonnegative and symmetric distribution, respectively. `frontier` can fit models in which the nonnegative distribution component (a measurement of inefficiency) is assumed to be from a half-normal, exponential, or truncated-normal distribution. See Kumbhakar and Lovell (2000) for a detailed introduction to frontier analysis.

Options

Model

`noconstant`; see [R] **estimation options**.

`distribution(`*distname*`)` specifies the distribution for the inefficiency term as half-normal (`hnormal`), `exponential`, or truncated-normal (`tnormal`). The default is `hnormal`.

`ufrom(`*matrix*`)` specifies a $1 \times K$ matrix of untransformed starting values when the distribution is truncated-normal (`tnormal`). `frontier` can estimate the parameters of the model by maximizing either the log likelihood or a transformed log likelihood (see *Methods and formulas*). `frontier` automatically transforms the starting values before passing them on to the transformed log likelihood. The matrix must have the same number of columns as there are parameters to estimate.

`cm(`*varlist* [`, noconstant`]`)` may be used only with `distribution(tnormal)`. Here `frontier` will fit a conditional mean model in which the mean of the truncated-normal distribution is modeled as a linear function of the set of covariates specified in *varlist*. Specifying `noconstant` suppresses the constant in the mean function.

Model 2

`constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

By default, when fitting the truncated-normal model or the conditional mean model, `frontier` maximizes a transformed log likelihood. When constraints are applied, `frontier` will maximize the untransformed log likelihood with constraints defined in the untransformed metric.

`uhet(`*varlist*[`, noconstant`]`)` specifies that the technical inefficiency component is heteroskedastic, with the variance function depending on a linear combination of $varlist_u$. Specifying `noconstant` suppresses the constant term from the variance function. This option may not be specified with `distribution(tnormal)`.

`vhet(`*varlist*[`, noconstant`]`)` specifies that the idiosyncratic error component is heteroskedastic, with the variance function depending on a linear combination of $varlist_v$. Specifying `noconstant` suppresses the constant term from the variance function. This option may not be specified with `distribution(tnormal)`.

`cost` specifies that `frontier` fit a cost frontier model.

SE

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `frontier` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Stochastic production frontier models were introduced by Aigner, Lovell, and Schmidt (1977) and Meeusen and van den Broeck (1977). Since then, stochastic frontier models have become a popular subfield in econometrics. Kumbhakar and Lovell (2000) provide a good introduction.

`frontier` fits three stochastic frontier models with distinct parameterizations of the inefficiency term and can fit stochastic production or cost frontier models.

Let's review the nature of the stochastic frontier problem. Suppose that a producer has a production function $f(\mathbf{z}_i, \beta)$. In a world without error or inefficiency, the ith firm would produce

$$q_i = f(\mathbf{z}_i, \beta)$$

Stochastic frontier analysis assumes that each firm potentially produces less than it might due to a degree of inefficiency. Specifically,

$$q_i = f(\mathbf{z}_i, \beta)\xi_i$$

where ξ_i is the level of efficiency for firm i; ξ_i must be in the interval $(0, 1]$. If $\xi_i = 1$, the firm is achieving the optimal output with the technology embodied in the production function $f(\mathbf{z}_i, \beta)$. When $\xi_i < 1$, the firm is not making the most of the inputs $\mathbf{z}_i$ given the technology embodied in the production function $f(\mathbf{z}_i, \beta)$. Because the output is assumed to be strictly positive (that is, $q_i > 0$), the degree of technical efficiency is assumed to be strictly positive (that is, $\xi_i > 0$).

Output is also assumed to be subject to random shocks, implying that

$$q_i = f(\mathbf{z}_i, \beta)\xi_i \exp(v_i)$$

Taking the natural log of both sides yields

$$\ln(q_i) = \ln\{f(\mathbf{z}_i, \beta)\} + \ln(\xi_i) + v_i$$

Assuming that there are k inputs and that the production function is linear in logs, defining $u_i = -\ln(\xi_i)$ yields

$$\ln(q_i) = \beta_0 + \sum_{j=1}^{k} \beta_j \ln(z_{ji}) + v_i - u_i \tag{1}$$

Because u_i is subtracted from $\ln(q_i)$, restricting $u_i \geq 0$ implies that $0 < \xi_i \leq 1$, as specified above.

Kumbhakar and Lovell (2000) provide a detailed version of the above derivation, and they show that performing an analogous derivation in the dual cost function problem allows us to specify the problem as

$$\ln(c_i) = \beta_0 + \beta_q \ln(q_i) + \sum_{j=1}^{k} \beta_j \ln(p_{ji}) + v_i + u_i \tag{2}$$

where q_i is output, z_{ji} are input quantities, c_i is cost, and the p_{ji} are input prices.

Intuitively, the inefficiency effect is required to lower output or raise expenditure, depending on the specification.

❑ Technical note

The model that `frontier` actually fits is of the form

$$y_i = \beta_0 + \sum_{j=1}^{k} \beta_j x_{ji} + v_i - s u_i$$

where

$$s = \begin{cases} 1, & \text{for production functions} \\ -1, & \text{for cost functions} \end{cases}$$

so, in the context of the discussion above, $y_i = \ln(q_i)$, and $x_{ji} = \ln(z_{ji})$ for a production function; and for a cost function, $y_i = \ln(c_i)$, and the x_{ji} are the $\ln(p_{ji})$ and $\ln(q_i)$. You must take the natural logarithm of the data before fitting a stochastic frontier production or cost model. `frontier` performs no transformations on the data.

❑

Different specifications of the u_i and the v_i terms give rise to distinct models. `frontier` provides estimators for the parameters of three basic models in which the idiosyncratic component, v_i, is assumed to be independently $N(0, \sigma_v)$ distributed over the observations. The basic models differ in their specification of the inefficiency term, u_i, as follows:

`exponential`: the u_i are independently exponentially distributed with variance σ_u^2

`hnormal`: the u_i are independently half-normally $N^+(0, \sigma_u^2)$ distributed

`tnormal`: the u_i are independently $N^+(\mu, \sigma_u^2)$ distributed with truncation point at 0

For half-normal or exponential distributions, `frontier` can fit models with heteroskedastic error components, conditional on a set of covariates. For a truncated-normal distribution, `frontier` can also fit a conditional mean model in which the mean is modeled as a linear function of a set of covariates.

▷ Example 1

For our first example, we demonstrate the half-normal and exponential models by reproducing a study found in Greene (2003, 505), which uses data originally published in Zellner and Revankar (1969). In this study of the transportation-equipment manufacturing industry, observations on value added, capital, and labor are used to estimate a Cobb–Douglas production function. The variable `lnv` is the log-transformed value added, `lnk` is the log-transformed capital, and `lnl` is the log-transformed labor. OLS estimates are compared with those from stochastic frontier models using both the half-normal and exponential distribution for the inefficiency term.

```
. use http://www.stata-press.com/data/r12/greene9
. regress lnv lnk lnl
      Source |       SS       df       MS              Number of obs =      25
-------------+------------------------------           F(  2,    22) =  397.54
       Model |  44.1727741     2  22.086387             Prob > F      =  0.0000
    Residual |  1.22225984    22  .055557265           R-squared     =  0.9731
-------------+------------------------------           Adj R-squared =  0.9706
       Total |  45.3950339    24  1.89145975           Root MSE      =  .23571

------------------------------------------------------------------------------
         lnv |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         lnk |   .2454281   .1068574     2.30   0.032     .0238193    .4670368
         lnl |    .805183   .1263336     6.37   0.000     .5431831    1.067183
       _cons |   1.844416   .2335928     7.90   0.000     1.359974    2.328858
------------------------------------------------------------------------------

. frontier lnv lnk lnl
Iteration 0:   log likelihood =  2.3357572
Iteration 1:   log likelihood =  2.4673009
Iteration 2:   log likelihood =  2.4695125
Iteration 3:   log likelihood =  2.4695222
Iteration 4:   log likelihood =  2.4695222
Stoc. frontier normal/half-normal model          Number of obs   =        25
                                                 Wald chi2(2)    =    743.71
Log likelihood =  2.4695222                      Prob > chi2     =    0.0000

------------------------------------------------------------------------------
         lnv |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         lnk |   .2585478    .098764     2.62   0.009     .0649738    .4521218
         lnl |   .7802451   .1199399     6.51   0.000     .5451672    1.015323
       _cons |   2.081135    .281641     7.39   0.000     1.529128    2.633141
-------------+----------------------------------------------------------------
    /lnsig2v |   -3.48401   .6195353    -5.62   0.000    -4.698277   -2.269743
    /lnsig2u |  -3.014599    1.11694    -2.70   0.007    -5.203761   -.8254368
-------------+----------------------------------------------------------------
     sigma_v |   .1751688   .0542616                      .0954514    .3214633
     sigma_u |   .2215073   .1237052                       .074134    .6618486
      sigma2 |   .0797496   .0426989                     -.0039388     .163438
      lambda |   1.264536   .1678684                      .9355204    1.593552
------------------------------------------------------------------------------
Likelihood-ratio test of sigma_u=0: chibar2(01) = 0.43   Prob>=chibar2 = 0.256
. predict double u_h, u
```

```
. frontier lnv lnk lnl, distribution(exponential)
Iteration 0:   log likelihood =  2.7270659
Iteration 1:   log likelihood =  2.8551532
Iteration 2:   log likelihood =  2.8604815
Iteration 3:   log likelihood =  2.8604897
Iteration 4:   log likelihood =  2.8604897
Stoc. frontier normal/exponential model           Number of obs   =         25
                                                  Wald chi2(2)    =     845.68
Log likelihood =  2.8604897                       Prob > chi2     =     0.0000
```

lnv	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
lnk	.2624859	.0919988	2.85	0.004	.0821717	.4428002
lnl	.7703795	.1109569	6.94	0.000	.5529079	.9878511
_cons	2.069242	.2356159	8.78	0.000	1.607444	2.531041
/lnsig2v	-3.527598	.4486176	-7.86	0.000	-4.406873	-2.648324
/lnsig2u	-4.002457	.9274575	-4.32	0.000	-5.820241	-2.184674
sigma_v	.1713925	.0384448			.1104231	.2660258
sigma_u	.1351691	.0626818			.0544692	.3354317
sigma2	.0476461	.0157921			.016694	.0785981
lambda	.7886525	.087684			.616795	.9605101

```
Likelihood-ratio test of sigma_u=0: chibar2(01) = 1.21   Prob>=chibar2 = 0.135
. predict double u_e, u

. list state u_h u_e
```

	state	u_h	u_e
1.	Alabama	.2011338	.14592865
2.	California	.14480966	.0972165
3.	Connecticut	.1903485	.13478797
4.	Florida	.51753139	.5903303
5.	Georgia	.10397912	.07140994
6.	Illinois	.12126696	.0830415
7.	Indiana	.21128212	.15450664
8.	Iowa	.24933153	.20073081
9.	Kansas	.10099517	.06857629
10.	Kentucky	.05626919	.04152443
11.	Louisiana	.20332731	.15066405
12.	Maine	.22263164	.17245793
13.	Maryland	.13534062	.09245501
14.	Massachusetts	.15636999	.10932923
15.	Michigan	.15809566	.10756915
16.	Missouri	.10288047	.0704146
17.	NewJersey	.09584337	.06587986
18.	NewYork	.27787793	.22249416
19.	Ohio	.22914231	.16981857
20.	Pennsylvania	.1500667	.10302905
21.	Texas	.20297875	.14552218
22.	Virginia	.14000132	.09676078
23.	Washington	.11047581	.07533251
24.	WestVirginia	.15561392	.11236153
25.	Wisconsin	.14067066	.0970861

The parameter estimates and the estimates of the inefficiency terms closely match those published in Greene (2003, 505), but the standard errors of the parameter estimates are estimated differently (see the technical note below).

The output from `frontier` includes estimates of the standard deviations of the two error components, σ_v and σ_u, which are labeled `sigma_v` and `sigma_u`, respectively. In the log likelihood, they are parameterized as $\ln\sigma_v^2$ and $\ln\sigma_u^2$, and these estimates are labeled `/lnsig2v` and `/lnsig2u` in the output. `frontier` also reports two other useful parameterizations. The estimate of the total error variance, $\sigma_S^2 = \sigma_v^2 + \sigma_u^2$, is labeled `sigma2`, and the estimate of the ratio of the standard deviation of the inefficiency component to the standard deviation of the idiosyncratic component, $\lambda = \sigma_u/\sigma_v$, is labeled `lambda`.

At the bottom of the output, `frontier` reports the results of a test that there is no technical inefficiency component in the model. This is a test of the null hypothesis $H_0 : \sigma_u^2 = 0$ against the alternative hypotheses $H_1 : \sigma_u^2 > 0$. If the null hypothesis is true, the stochastic frontier model reduces to an OLS model with normal errors. However, because the test lies on the boundary of the parameter space of σ_u^2, the standard likelihood-ratio test is not valid, and a one-sided generalized likelihood-ratio test must be constructed; see Gutierrez, Carter, and Drukker (2001). For this example, the output shows LR = 0.43 with a p-value of 0.256 for the half-normal model and LR = 1.21 with a p-value of 0.135 for the exponential model. There are several possible reasons for the failure to reject the null hypothesis, but the fact that the test is based on an asymptotic distribution and the sample size was 25 is certainly a leading candidate among those possibilities.

◁

❑ Technical note

`frontier` maximizes the log-likelihood function of a stochastic frontier model by using the Newton–Raphson method, and the estimated variance–covariance matrix is calculated as the inverse of the negative Hessian (matrix of second partial derivatives); see [R] **ml**. When comparing the results with those published using other software, be aware of the difference in the optimization methods, which may result in different, yet asymptotically equivalent, variance estimates.

❑

▷ Example 2

Often the error terms may not have constant variance. `frontier` allows you to model heteroskedasticity in either error term as a linear function of a set of covariates. The variance of either the technical inefficiency or the idiosyncratic component may be modeled as

$$\sigma_i^2 = \exp(\mathbf{w}_i\boldsymbol{\delta})$$

The default constant included in $\mathbf{w}_i$ may be suppressed by appending a `noconstant` option to the list of covariates. Also, you can simultaneously specify covariates for both σ_{u_i} and σ_{v_i}.

In the example below, we use a sample of 756 observations of fictional firms producing a manufactured good by using capital and labor. The firms are hypothesized to use a constant returns-to-scale technology, but the sizes of the firms differ. Believing that this size variation will introduce heteroskedasticity into the idiosyncratic error term, we estimate the parameters of a Cobb–Douglas production function. To do this, we use a conditional heteroskedastic half-normal model, with the size of the firm as an explanatory variable in the variance function for the idiosyncratic error. We also perform a test of the hypothesis that the firms use a constant returns-to-scale technology.

```
. use http://www.stata-press.com/data/r12/frontier1, clear
. frontier lnoutput lnlabor lncapital, vhet(size)
Iteration 0:   log likelihood = -1508.3692
Iteration 1:   log likelihood =  -1501.583
Iteration 2:   log likelihood = -1500.3942
Iteration 3:   log likelihood = -1500.3794
Iteration 4:   log likelihood = -1500.3794
Stoc. frontier normal/half-normal model           Number of obs   =        756
                                                  Wald chi2(2)    =       9.68
Log likelihood = -1500.3794                       Prob > chi2     =     0.0079
```

lnoutput	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
lnoutput						
lnlabor	.7090933	.2349374	3.02	0.003	.2486244	1.169562
lncapital	.3931345	.5422173	0.73	0.468	-.6695919	1.455861
_cons	1.252199	3.14656	0.40	0.691	-4.914946	7.419344
lnsig2v						
size	-.0016951	.0004748	-3.57	0.000	-.0026256	-.0007645
_cons	3.156091	.9265826	3.41	0.001	1.340023	4.97216
lnsig2u						
_cons	1.947487	.1017653	19.14	0.000	1.748031	2.146943
sigma_u	2.647838	.134729			2.396514	2.925518

```
. test _b[lnlabor] + _b[lncapital] = 1
 ( 1)  [lnoutput]lnlabor + [lnoutput]lncapital = 1
           chi2(  1) =    0.03
         Prob > chi2 =    0.8622
```

The output above indicates that the variance of the idiosyncratic error term is a function of firm size. Also, we failed to reject the hypothesis that the firms use a constant returns-to-scale technology.

◁

❑ Technical note

In small samples, the conditional heteroskedastic estimators will lack precision for the variance parameters and may fail to converge altogether.

❑

▷ Example 3

Let's turn our attention to the truncated-normal model. Once again, we will use fictional data. For this example, we have 1,231 observations on the quantity of output, the total cost of production for each firm, the prices that each firm paid for labor and capital services, and a categorical variable measuring the quality of each firm's management. After taking the natural logarithm of the costs (`lncost`), prices (`lnp_k` and `lnp_l`), and output (`lnout`), we fit a stochastic cost frontier model and specify the distribution for the inefficiency term to be truncated normal.

```
. use http://www.stata-press.com/data/r12/frontier2
. frontier lncost lnp_k lnp_l lnout, distribution(tnormal) cost
Iteration 0:   log likelihood = -2386.9523
Iteration 1:   log likelihood = -2386.5146
Iteration 2:   log likelihood = -2386.2704
Iteration 3:   log likelihood = -2386.2504
Iteration 4:   log likelihood = -2386.2493
Iteration 5:   log likelihood = -2386.2493
Stoc. frontier normal/truncated-normal model      Number of obs   =       1231
                                                  Wald chi2(3)    =       8.82
Log likelihood = -2386.2493                       Prob > chi2     =     0.0318
```

lncost	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
lnp_k	.3410717	.2363861	1.44	0.149	-.1222366	.80438
lnp_l	.6608628	.4951499	1.33	0.182	-.3096131	1.631339
lnout	.7528653	.3468968	2.17	0.030	.0729601	1.432771
_cons	2.602609	1.083004	2.40	0.016	.4799595	4.725259
/mu	1.095705	.881517	1.24	0.214	-.632037	2.823446
/lnsigma2	1.5534	.1873464	8.29	0.000	1.186208	1.920592
/ilgtgamma	1.257862	.2589522	4.86	0.000	.7503255	1.765399
sigma2	4.727518	.8856833			3.274641	6.825001
gamma	.7786579	.0446303			.6792496	.8538846
sigma_u2	3.681119	.7503408			2.210478	5.15176
sigma_v2	1.046399	.2660035			.5250413	1.567756

```
H0: No inefficiency component:            z =   5.595          Prob>=z = 0.000
```

In addition to the coefficients, the output reports estimates for several parameters. `sigma_v2` is the estimate of σ_v^2. `sigma_u2` is the estimate of σ_u^2. `gamma` is the estimate of $\gamma = \sigma_u^2/\sigma_S^2$. `sigma2` is the estimate of $\sigma_S^2 = \sigma_v^2 + \sigma_u^2$. Because γ must be between 0 and 1, the optimization is parameterized in terms of the inverse logit of γ, and this estimate is reported as `ilgtgamma`. Because σ_S^2 must be positive, the optimization is parameterized in terms of $\ln(\sigma_S^2)$, whose estimate is reported as `lnsigma2`. Finally, `mu` is the estimate of μ, the mean of the truncated-normal distribution.

In the output above, the generalized log-likelihood test for the presence of the inefficiency term has been replaced with a test based on the third moment of the OLS residuals. When $\mu = 0$ and $\sigma_u = 0$, the truncated-normal model reduces to a linear regression model with normally distributed errors. However, the distribution of the test statistic under the null hypothesis is not well established, because it becomes impossible to evaluate the log likelihood as σ_u approaches zero, prohibiting the use of the likelihood-ratio test.

However, Coelli (1995) noted that the presence of an inefficiency term would negatively skew the residuals from an OLS regression. By identifying negative skewness in the residuals with the presence of an inefficiency term, Coelli derived a one-sided test for the presence of the inefficiency term. The results of this test are given at the bottom of the output. For this example, the null hypothesis of no inefficiency component is rejected.

In the example below, we fit a truncated model and detect a statistically significant inefficiency term in the model. We might question whether the inefficiency term is identically distributed over all firms or whether there might be heterogeneity across firms. `frontier` provides an extension to the truncated normal model by allowing the mean of the inefficiency term to be modeled as a linear function of a set of covariates. In our dataset, we have a categorical variable that measures the quality of a firm's management. We refit the model, including the `cm()` option, specifying a set of

binary indicator variables representing the different categories of the quality-measurement variable as covariates.

```
. frontier lncost lnp_k lnp_l lnout, distribution(tnormal) cm(i.quality) cost
Iteration 0:   log likelihood = -2386.9523
Iteration 1:   log likelihood =  -2384.936
Iteration 2:   log likelihood = -2382.3942
Iteration 3:   log likelihood =  -2382.324
Iteration 4:   log likelihood = -2382.3233
Iteration 5:   log likelihood = -2382.3233
Stoc. frontier normal/truncated-normal model      Number of obs   =       1231
                                                  Wald chi2(3)    =       9.31
Log likelihood = -2382.3233                       Prob > chi2     =     0.0254
```

lncost	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
lncost						
lnp_k	.3611204	.2359749	1.53	0.126	-.1013819	.8236227
lnp_l	.680446	.4934935	1.38	0.168	-.2867835	1.647675
lnout	.7605533	.3466102	2.19	0.028	.0812098	1.439897
_cons	2.550769	1.078911	2.36	0.018	.4361417	4.665396
mu						
quality						
2	.5056067	.3382907	1.49	0.135	-.1574309	1.168644
3	.783223	.376807	2.08	0.038	.0446947	1.521751
4	.5577511	.3355061	1.66	0.096	-.0998288	1.215331
5	.6792882	.3428073	1.98	0.048	.0073981	1.351178
_cons	.6014025	.990167	0.61	0.544	-1.339289	2.542094
/lnsigma2	1.541784	.1790926	8.61	0.000	1.190769	1.892799
/ilgtgamma	1.242302	.2588968	4.80	0.000	.734874	1.749731
sigma2	4.67292	.8368852			3.289611	6.637923
gamma	.7759645	.0450075			.6758739	.8519189
sigma_u2	3.62602	.7139576			2.226689	5.025351
sigma_v2	1.0469	.2583469			.5405491	1.553251

The conditional mean model was developed in the context of panel-data estimators, and we can apply `frontier`'s conditional mean model to panel data.

◁

Saved results

frontier saves the following in e():

Scalars

e(N)	number of observations
e(df_m)	model degrees of freedom
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(chi2)	χ^2
e(ll)	log likelihood
e(ll_c)	log likelihood for H_0: σ_u=0
e(z)	test for negative skewness of OLS residuals
e(sigma_u)	standard deviation of technical inefficiency
e(sigma_v)	standard deviation of v_i
e(p)	significance
e(chi2_c)	LR test statistic
e(p_z)	p-value for z
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	frontier
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(function)	production or cost
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(chi2type)	Wald; type of model χ^2 test
e(dist)	distribution assumption for u_i
e(het)	heteroskedastic components
e(u_hetvar)	*varlist* in uhet()
e(v_hetvar)	*varlist* in vhet()
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

frontier is implemented as an ado-file.

Consider an equation of the form

$$y_i = \mathbf{x}_i\boldsymbol{\beta} + v_i - su_i$$

where y_i is the dependent variable, $\mathbf{x}_i$ is a $1 \times k$ vector of observations on the independent variables included as indent covariates, $\boldsymbol{\beta}$ is a $k \times 1$ vector of coefficients, and

$$s = \begin{cases} 1, & \text{for production functions} \\ -1, & \text{for cost functions} \end{cases}$$

The log-likelihood functions are as follows.

Normal/half-normal model:

$$\ln L = \sum_{i=1}^{N} \left\{ \frac{1}{2}\ln\left(\frac{2}{\pi}\right) - \ln\sigma_S + \ln\Phi\left(-\frac{s\epsilon_i\lambda}{\sigma_S}\right) - \frac{\epsilon_i^2}{2\sigma_S^2} \right\}$$

Normal/exponential model:

$$\ln L = \sum_{i=1}^{N} \left\{ -\ln\sigma_u + \frac{\sigma_v^2}{2\sigma_u^2} + \ln\Phi\left(\frac{-s\epsilon_i - \frac{\sigma_v^2}{\sigma_u}}{\sigma_v}\right) + \frac{s\epsilon_i}{\sigma_u} \right\}$$

Normal/truncated-normal model:

$$\ln L = \sum_{i=1}^{N} \left\{ -\frac{1}{2}\ln(2\pi) - \ln\sigma_S - \ln\Phi\left(\frac{\mu}{\sigma_S\sqrt{\gamma}}\right) + \ln\Phi\left[\frac{(1-\gamma)\mu - s\gamma\epsilon_i}{\{\sigma_S^2\gamma(1-\gamma)\}^{1/2}}\right] - \frac{1}{2}\left(\frac{\epsilon_i + s\mu}{\sigma_S}\right)^2 \right\}$$

where $\sigma_S = (\sigma_u^2 + \sigma_v^2)^{1/2}$, $\lambda = \sigma_u/\sigma_v$, $\gamma = \sigma_u^2/\sigma_S^2$, $\epsilon_i = y_i - \mathbf{x}_i\boldsymbol{\beta}$, and $\Phi()$ is the cumulative distribution function of the standard normal distribution.

To obtain estimation for u_i, you can use either the mean or the mode of the conditional distribution $f(u|\epsilon)$.

$$E\left(u_i \mid \epsilon_i\right) = \mu_{*i} + \sigma_* \left\{ \frac{\phi(-\mu_{*i}/\sigma_*)}{\Phi(\mu_{*i}/\sigma_*)} \right\}$$

$$M\left(u_i \mid \epsilon_i\right) = \begin{cases} \mu_{*i}, & \text{if } \mu_{*i} \geq 0 \\ 0, & \text{otherwise} \end{cases}$$

Then the technical efficiency ($s = 1$) or cost efficiency ($s = -1$) will be estimated by

$$\begin{aligned} E_i &= E\left\{\exp(-su_i) \mid \epsilon_i\right\} \\ &= \left\{ \frac{1 - \Phi\left(s\sigma_* - \mu_{*i}/\sigma_*\right)}{1 - \Phi\left(-\mu_{*i}/\sigma_*\right)} \right\} \exp\left(-s\mu_{*i} + \frac{1}{2}\sigma_*^2 \right) \end{aligned}$$

where μ_{*i} and σ_* are defined for the normal/half-normal model as

$$\mu_{*i} = -s\epsilon_i\sigma_u^2/\sigma_S^2$$
$$\sigma_* = \sigma_u\sigma_v/\sigma_S$$

for the normal/exponential model as

$$\mu_{*i} = -s\epsilon_i - \sigma_v^2/\sigma_u$$
$$\sigma_* = \sigma_v$$

and for the normal/truncated-normal model as

$$\mu_{*i} = \frac{-s\epsilon_i\sigma_u^2 + \mu\sigma_v^2}{\sigma_S^2}$$
$$\sigma_* = \sigma_u\sigma_v/\sigma_S$$

In the half-normal and exponential models, when heteroskedasticity is assumed, the standard deviations, σ_u or σ_v, will be replaced in the above equations by

$$\sigma_i^2 = \exp(\mathbf{w}_i\boldsymbol{\delta})$$

where $\mathbf{w}$ is the vector of explanatory variables in the variance function.

In the conditional mean model, the mean parameter of the truncated normal distribution, μ, is modeled as a linear combination of the set of covariates, $\mathbf{w}$.

$$\mu = \mathbf{w}_i\boldsymbol{\delta}$$

Therefore, the log-likelihood function can be rewritten as

$$\ln L = \sum_{i=1}^{N}\left[-\frac{1}{2}\ln(2\pi) - \ln\sigma_S - \ln\Phi\left(\frac{\mathbf{w}_i\boldsymbol{\delta}}{\sqrt{\sigma_S^2\gamma}}\right) + \ln\Phi\left\{\frac{(1-\gamma)\,\mathbf{w}_i\boldsymbol{\delta} - s\gamma\epsilon_i}{\sqrt{\sigma_S^2\gamma\,(1-\gamma)}}\right\} - \frac{1}{2}\left(\frac{\epsilon_i + s\mathbf{w}_i\boldsymbol{\delta}}{\sigma_S}\right)^2\right]$$

The z test reported in the output of the truncated-normal model is a third-moment test developed by Coelli (1995) as an extension of a test previously developed by Pagan and Hall (1983). Coelli shows that under the null of normally distributed errors, the statistic

$$z = \frac{m_3}{\left(\frac{6m_2^3}{N}\right)^{1/2}}$$

has a standard normal distribution, where m_3 is the third moment from the OLS regression. Because the residuals are either negatively skewed (production function) or positively skewed (cost function), a one-sided p-value is used.

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Also see

[R] **frontier postestimation** — Postestimation tools for frontier

[R] **regress** — Linear regression

[XT] **xtfrontier** — Stochastic frontier models for panel data

[U] **20 Estimation and postestimation commands**

Title

frontier postestimation — Postestimation tools for frontier

Description

The following postestimation commands are available after `frontier`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic]

predict [type] { stub* | newvar_xb newvar_v newvar_u } [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the prediction
`u`	estimates of minus the natural log of the technical efficiency via $E(u_i \mid \epsilon_i)$
`m`	estimates of minus the natural log of the technical efficiency via $M(u_i \mid \epsilon_i)$
`te`	estimates of the technical efficiency via $E\{\exp(-su_i) \mid \epsilon_i\}$

$$s = \begin{cases} 1, & \text{for production functions} \\ -1, & \text{for cost functions} \end{cases}$$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`u` produces estimates of minus the natural log of the technical efficiency via $E(u_i \mid \epsilon_i)$.

`m` produces estimates of minus the natural log of the technical efficiency via $M(u_i \mid \epsilon_i)$.

`te` produces estimates of the technical efficiency via $E\{\exp(-su_i) \mid \epsilon_i\}$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_i\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\texttt{lnsig2v})$.

The third new variable will contain $\partial \ln L/\partial(\texttt{lnsig2u})$.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **frontier** — Stochastic frontier models

[U] **20 Estimation and postestimation commands**

Title

fvrevar — Factor-variables operator programming command

Syntax

`fvrevar` [*varlist*] [*if*] [*in*] [`,` `substitute` `tsonly` `list` `stub(`*stub*`)`]

You must `tsset` your data before using `fvrevar` if *varlist* contains time-series operators; see [TS] **tset**.

Description

`fvrevar` creates an equivalent, temporary variable list for a *varlist* that might contain factor variables, interactions, or time-series–operated variables so that the resulting variable list can be used by commands that do not otherwise support factor variables or time-series–operated variables. The resulting list also could be used in a program to speed execution at the cost of using more memory.

Options

`substitute` specifies that equivalent, temporary variables be substituted for any factor variables, interactions, or time-series–operated variables in *varlist*. `substitute` is the default action taken by `fvrevar`; you do not need to specify the option.

`tsonly` specifies that equivalent, temporary variables be substituted for only the time-series–operated variables in *varlist*.

`list` specifies that all factor-variable operators and time-series operators be removed from *varlist* and the resulting list of base variables be returned in `r(varlist)`. No new variables are created with this option.

`stub(`*stub*`)` specifies that `fvrevar` generate named variables instead of temporary variables. The new variables will be named *stub#*.

Remarks

`fvrevar` might create no new variables, one new variable, or many new variables, depending on the number of factor variables, interactions, and time-series operators appearing in *varlist*. Any new variables created are temporary. The new, equivalent varlist is returned in `r(varlist)`. The new varlist corresponds one to one with the original *varlist*.

▷ Example 1

Typing

```
. use http://www.stata-press.com/data/r12/auto
. fvrevar i.rep78 mpg turn
```

creates five temporary variables corresponding to the levels of `rep78`. No new variables are created for variables `mpg` and `turn` because they do not contain factor-variable or time-series operators.

The resulting variable list is

```
. display "`r(varlist)'"
__000000 __000001 __000002 __000003 __000004  mpg turn
```

(Your temporary variable names may be different, but that is of no consequence.)

Temporary variables automatically vanish when the program concludes.

◁

▷ Example 2

Suppose we want to create temporary variables for specific levels of a factor variable. To do this, we can use the parenthesis notation of factor-variable syntax.

```
. fvrevar i(2,3)bn.rep78 mpg
```

creates two temporary variables corresponding to levels 2 and 3 of `rep78`. Notice that we specified that neither level 2 nor 3 be set as the base level by using the `bn` notation. If we did not specify `bn`, level 2 would have been treated as the base level.

The resulting variable list is

```
. display "‘r(varlist)’"
__00000E __00000F mpg
```

We can see the results by listing the new variables alongside the original value of `rep78`.

```
. list rep78 ‘r(varlist)’  in 1/5
```

	rep78	__00000E	__00000F	mpg
1.	3	1	0	22
2.	3	1	0	17
3.	.	.	.	22
4.	3	1	0	20
5.	4	0	1	15

If we had needed only the base-variable names, we could have specified

```
. fvrevar i(2,3)bn.rep78 mpg, list
. display "‘r(varlist)’"
mpg rep78
```

The order of the list will probably differ from that of the original list; base variables are listed only once.

◁

▷ Example 3

Now let's assume we have a *varlist* containing both an interaction and time-series–operated variables. If we want to create temporary variables for the entire equivalent *varlist*, we can specify `fvrevar` with no options.

```
. generate t = _n
. tsset t
. fvrevar c.turn#i(2,3).rep78 L.mpg
```

The resulting variable list is

```
. display "‘r(varlist)’"
__00000I __00000K __00000M
```

If we want to create temporary variables only for the time-series–operated variables, we can specify the `tsonly` option.

```
. fvrevar c.turn#i(2,3).rep78 L.mpg, tsonly
```

The resulting variable list is

```
. display "`r(varlist)'"
2b.rep78#c.turn 3.rep78#c.turn __00000M
```

Notice that `fvrevar` returned the expanded factor-variable list with the `tsonly` option.

◁

❑ Technical note

`fvrevar, substitute` avoids creating duplicate variables. Consider

```
. fvrevar i.rep78 turn mpg i.rep78
```

`i.rep78` appears twice in the varlist. `fvrevar` will create only one set of new variables for the five levels of `rep78` and will use these new variables once in the resulting `r(varlist)`. Moreover, `fvrevar` will do this even across multiple calls:

```
. fvrevar i.rep78 turn mpg
. fvrevar i.rep78
```

`i.rep78` appears in two separate calls. At the first call, `fvrevar` creates five temporary variables corresponding to the five levels of `rep78`. At the second call, `fvrevar` remembers what it has done and uses the same temporary variables for `i.rep78`.

❑

Saved results

`fvrevar` saves the following in `r()`:

Macros

`r(varlist)`	the modified variable list or list of base-variable names

Also see

[P] **syntax** — Parse Stata syntax

[TS] **tsrevar** — Time-series operator programming command

[P] **unab** — Unabbreviate variable list

[U] **11 Language syntax**

[U] **11.4.4 Time-series varlists**

[U] **18 Programming Stata**

Title

fvset — Declare factor-variable settings

Syntax

Declare base settings

```
fvset base base_spec varlist
```

Declare design settings

```
fvset design design_spec varlist
```

Clear the current settings

```
fvset clear varlist
```

Report the current settings

```
fvset report [varlist] [, base(base_spec) design(design_spec)]
```

base_spec	Description
`default`	default base
`first`	lowest level value; the default
`last`	highest level value
`frequent`	most frequent level value
`none`	no base
#	nonnegative integer value

design_spec	Description
`default`	default base
`asbalanced`	accumulate using $1/k$, k = number of levels
`asobserved`	accumulate using observed relative frequencies; the default

Description

`fvset` declares factor-variable settings. Factor-variable settings identify the base level and how to accumulate statistics over levels.

`fvset base` specifies the base level for each variable in *varlist*. The default for factor variables without a declared base level is `first`.

`fvset design` specifies how to accumulate over the levels of a factor variable. The `margins` command is the only command aware of this setting; see [R] **margins**. By default, `margins` assumes that factor variables are `asobserved`, meaning that they are accumulated by weighting by the number of observations or the sum of the weights if weights have been specified.

`fvset clear` removes factor-variable settings for each variable in *varlist*. `fvset clear _all` removes all factor-variable settings from all variables.

`fvset report` reports the current factor-variable settings for each variable in *varlist*. `fvset` without arguments is a synonym for `fvset report`.

Options

`base(`*base_spec*`)` restricts `fvset report` to report only the factor-variable settings for variables with the specified *base_spec*.

`design(`*design_spec*`)` restricts `fvset report` to report only the factor-variable settings for variables with the specified *design_spec*.

Remarks

▷ Example 1

Using our `auto` dataset, we include factor variable `i.rep78` in a regression:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg i.rep78, baselevels
```

Source	SS	df	MS		
Model	549.415777	4	137.353944	Number of obs	= 69
Residual	1790.78712	64	27.9810488	F(4, 64)	= 4.91
				Prob > F	= 0.0016
Total	2340.2029	68	34.4147485	R-squared	= 0.2348
				Adj R-squared	= 0.1869
				Root MSE	= 5.2897

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
rep78						
1	0	(base)				
2	-1.875	4.181884	-0.45	0.655	-10.22927	6.479274
3	-1.566667	3.863059	-0.41	0.686	-9.284014	6.150681
4	.6666667	3.942718	0.17	0.866	-7.209818	8.543152
5	6.363636	4.066234	1.56	0.123	-1.759599	14.48687
_cons	21	3.740391	5.61	0.000	13.52771	28.47229

We specified the `baselevels` option so that the base level would be included in the output. By default, the first level is the base level. We can change the base level to `2`:

```
. fvset base 2 rep78
. regress mpg i.rep78, baselevels
```

Source	SS	df	MS	Number of obs =	69
				F(4, 64) =	4.91
Model	549.415777	4	137.353944	Prob > F =	0.0016
Residual	1790.78712	64	27.9810488	R-squared =	0.2348
				Adj R-squared =	0.1869
Total	2340.2029	68	34.4147485	Root MSE =	5.2897

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
rep78						
1	1.875	4.181884	0.45	0.655	-6.479274	10.22927
2	0	(base)				
3	.3083333	2.104836	0.15	0.884	-3.896559	4.513226
4	2.541667	2.247695	1.13	0.262	-1.948621	7.031954
5	8.238636	2.457918	3.35	0.001	3.32838	13.14889
_cons	19.125	1.870195	10.23	0.000	15.38886	22.86114

Let's set `rep78` to have no base level and fit a cell-means regression:

```
. fvset base none rep78
. regress mpg i.rep78, noconstant
```

Source	SS	df	MS	Number of obs =	69
				F(5, 64) =	227.47
Model	31824.2129	5	6364.84258	Prob > F =	0.0000
Residual	1790.78712	64	27.9810488	R-squared =	0.9467
				Adj R-squared =	0.9426
Total	33615	69	487.173913	Root MSE =	5.2897

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
rep78						
1	21	3.740391	5.61	0.000	13.52771	28.47229
2	19.125	1.870195	10.23	0.000	15.38886	22.86114
3	19.43333	.9657648	20.12	0.000	17.504	21.36267
4	21.66667	1.246797	17.38	0.000	19.1759	24.15743
5	27.36364	1.594908	17.16	0.000	24.17744	30.54983

◁

▷ Example 2

By default, `margins` accumulates a margin by using the observed relative frequencies of the factor levels.

```
. regress mpg i.foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =   13.18
       Model |  378.153515     1  378.153515            Prob > F      =  0.0005
    Residual |  2065.30594    72  28.6848048            R-squared     =  0.1548
-------------+------------------------------           Adj R-squared =  0.1430
       Total |  2443.45946    73  33.4720474            Root MSE      =  5.3558

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   1.foreign |    4.945804   1.362162     3.63   0.001     2.230384    7.661225
       _cons |    19.82692   .7427186    26.70   0.000     18.34634    21.30751
------------------------------------------------------------------------------

. margins
Predictive margins                                Number of obs   =         74
Model VCE    : OLS

Expression   : Linear prediction, predict()

------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    21.2973   .6226014    34.21   0.000     20.07702    22.51757
------------------------------------------------------------------------------
```

Let's set `foreign` to always accumulate using equal relative frequencies:

```
. fvset design asbalanced foreign
. regress mpg i.foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =   13.18
       Model |  378.153515     1  378.153515            Prob > F      =  0.0005
    Residual |  2065.30594    72  28.6848048            R-squared     =  0.1548
-------------+------------------------------           Adj R-squared =  0.1430
       Total |  2443.45946    73  33.4720474            Root MSE      =  5.3558

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   1.foreign |    4.945804   1.362162     3.63   0.001     2.230384    7.661225
       _cons |    19.82692   .7427186    26.70   0.000     18.34634    21.30751
------------------------------------------------------------------------------

. margins
Adjusted predictions                              Number of obs   =         74
Model VCE    : OLS

Expression   : Linear prediction, predict()
at           : foreign          (asbalanced)

------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |   22.29983   .6810811    32.74   0.000     20.96493    23.63472
------------------------------------------------------------------------------
```

Suppose that we issued the `fvset design` command earlier in our session and that we cannot remember which variables we set as `asbalanced`. We can retrieve this information by using the `fvset report` command:

```
. fvset report, design(asbalanced)
  Variable    Base    Design
  ------------------------------
  foreign             asbalanced
  ------------------------------
```

◁

❑ Technical note

`margins` is aware of a factor variable's design setting only through the estimation results it is working with. The design setting is stored by the estimation command; thus changing the design setting between the estimation command and `margins` will have no effect. For example, the output from the following two calls to `margins` yields the same results:

```
. fvset clear foreign
. regress mpg i.foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =   13.18
       Model |  378.153515     1  378.153515            Prob > F      =  0.0005
    Residual |  2065.30594    72  28.6848048            R-squared     =  0.1548
-------------+------------------------------           Adj R-squared =  0.1430
       Total |  2443.45946    73  33.4720474            Root MSE      =  5.3558

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   1.foreign |    4.945804   1.362162     3.63   0.001     2.230384    7.661225
       _cons |    19.82692   .7427186    26.70   0.000     18.34634    21.30751
------------------------------------------------------------------------------

. margins
Predictive margins                              Number of obs   =         74
Model VCE    : OLS

Expression   : Linear prediction, predict()

------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    21.2973   .6226014    34.21   0.000     20.07702    22.51757
------------------------------------------------------------------------------

. fvset design asbalanced foreign
. margins
Predictive margins                              Number of obs   =         74
Model VCE    : OLS

Expression   : Linear prediction, predict()

------------------------------------------------------------------------------
             |            Delta-method
             |     Margin   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |    21.2973   .6226014    34.21   0.000     20.07702    22.51757
------------------------------------------------------------------------------
```

❑

Saved results

`fvset` saves the following in `r()`:

Macros

`r(varlist)`	*varlist*
`r(baselist)`	base setting for each variable in *varlist*
`r(designlist)`	design setting for each variable in *varlist*

Methods and formulas

`fvset` is implemented as an ado-file.

Title

gllamm — Generalized linear and latent mixed models

Description

GLLAMM stands for generalized linear latent and mixed models, and `gllamm` is a Stata command for fitting such models written by Sophia Rabe-Hesketh (University of California–Berkeley) as part of joint work with Anders Skrondal (Norwegian Institute of Public Health) and Andrew Pickles (University of Manchester).

Remarks

Generalized linear latent and mixed models are a class of multilevel latent variable models, where a latent variable is a factor or a random effect (intercept or coefficient), or a disturbance (residual). The `gllamm` command for fitting such models is not an official command of Stata; it has been independently developed by highly regarded authors and is itself highly regarded. You can learn more about `gllamm` by visiting http://www.gllamm.org.

`gllamm` is available from the Statistical Software Components (SSC) archive. To install, type

```
. ssc describe gllamm
. ssc install gllamm
```

If you later wish to uninstall `gllamm`, type `ado uninstall gllamm`.

References

Miranda, A., and S. Rabe-Hesketh. 2006. Maximum likelihood estimation of endogenous switching and sample selection models for binary, ordinal, and count variables. *Stata Journal* 6: 285–308.

Rabe-Hesketh, S., and B. S. Everitt. 2007. *A Handbook of Statistical Analyses Using Stata*. 4th ed. Boca Raton, FL: Chapman & Hall/CRC.

Rabe-Hesketh, S., A. Pickles, and C. Taylor. 2000. sg129: Generalized linear latent and mixed models. *Stata Technical Bulletin* 53: 47–57. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 293–307. College Station, TX: Stata Press.

Rabe-Hesketh, S., and A. Skrondal. 2008. *Multilevel and Longitudinal Modeling Using Stata*. 2nd ed. College Station, TX: Stata Press.

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——. 2003. Maximum likelihood estimation of generalized linear models with covariate measurement error. *Stata Journal* 3: 386–411.

Skrondal, A., and S. Rabe-Hesketh. 2004. *Generalized Latent Variable Modeling: Multilevel, Longitudinal, and Structural Equation Models*. Boca Raton, FL: Chapman & Hall/CRC.

Zheng, X., and S. Rabe-Hesketh. 2007. Estimating parameters of dichotomous and ordinal item response models with gllamm. *Stata Journal* 7: 313–333.

The references above are restricted to works by the primary authors of `gllamm`. There are many other books and articles that use or discuss `gllamm`; see http://www.gllamm.org/pub.html for a list.

Also see

[XT] **xtmelogit** — Multilevel mixed-effects logistic regression

[XT] **xtmepoisson** — Multilevel mixed-effects Poisson regression

[XT] **xtmixed** — Multilevel mixed-effects linear regression

Title

glm — Generalized linear models

Syntax

`glm` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`family(`*familyname*`)`	distribution of *depvar*; default is `family(gaussian)`
`link(`*linkname*`)`	link function; default is canonical link for `family()` specified
Model 2	
`noconstant`	suppress constant term
`exposure(`*varname*`)`	include ln(*varname*) in model with coefficient constrained to 1
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
`mu(`*varname*`)`	use *varname* as the initial estimate for the mean of *depvar*
`init(`*varname*`)`	synonym for `mu(`*varname*`)`
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `eim`, `opg`, `bootstrap`, `jackknife`, `hac` *kernel*, `jackknife1`, or `unbiased`
`vfactor(#)`	multiply variance matrix by scalar #
`disp(#)`	quasilikelihood multiplier
`scale(x2 | dev | #)`	set the scale parameter
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`eform`	report exponentiated coefficients
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
`ml`	use maximum likelihood optimization; the default
`irls`	use iterated, reweighted least-squares optimization of the deviance
maximize_options	control the maximization process; seldom used
`fisher(#)`	use the Fisher scoring Hessian or expected information matrix (EIM)
`search`	search for good starting values
`noheader`	suppress header table from above coefficient table
`notable`	suppress coefficient table
`nodisplay`	suppress the output; iteration log is still displayed
`coeflegend`	display legend instead of statistics

familyname	Description
gaussian	Gaussian (normal)
igaussian	inverse Gaussian
binomial [*varname*$_N$ | #$_N$]	Bernoulli/binomial
poisson	Poisson
nbinomial [#$_k$ | ml]	negative binomial
gamma	gamma

linkname	Description
identity	identity
log	log
logit	logit
probit	probit
cloglog	cloglog
power #	power
opower #	odds power
nbinomial	negative binomial
loglog	log-log
logc	log-complement

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)`, `vce(jackknife)`, and `vce(jackknife1)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`vce()`, `vfactor()`, `disp()`, `scale()`, `irls`, `fisher()`, `noheader`, `notable`, `nodisplay`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `aweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`noheader`, `notable`, `nodisplay`, and `coeflegend` do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Generalized linear models > Generalized linear models (GLM)

Description

`glm` fits generalized linear models. It can fit models by using either IRLS (maximum quasilikelihood) or Newton–Raphson (maximum likelihood) optimization, which is the default.

See [I] **estimation commands** for a complete list of Stata's estimation commands, several of which fit models that can also be fit using `glm`.

Options

Model

`family(`*familyname*`)` specifies the distribution of *depvar*; `family(gaussian)` is the default.

`link(`*linkname*`)` specifies the link function; the default is the canonical link for the `family()` specified (except for `family(nbinomial)`).

Model 2

`noconstant`, `exposure(`*varname*`)`, `offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**. `constraints(`*constraints*`)` and `collinear` are not allowed with `irls`.

`mu(`*varname*`)` specifies *varname* as the initial estimate for the mean of *depvar*. This option can be useful with models that experience convergence difficulties, such as `family(binomial)` models with power or odds-power links. `init(`*varname*`)` is a synonym.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

In addition to the standard *vcetype*s, `glm` allows the following alternatives:

`vce(eim)` specifies that the EIM estimate of variance be used.

`vce(jackknife1)` specifies that the one-step jackknife estimate of variance be used.

`vce(hac` *kernel* $[$*#*$]$`)` specifies that a heteroskedasticity- and autocorrelation-consistent (HAC) variance estimate be used. HAC refers to the general form for combining weighted matrices to form the variance estimate. There are three kernels built into `glm`. *kernel* is a user-written program or one of

`nwest` | `gallant` | `anderson`

specifies the number of lags. If *#* is not specified, $N-2$ is assumed. If you wish to specify `vce(hac ...)`, you must `tsset` your data before calling `glm`.

`vce(unbiased)` specifies that the unbiased sandwich estimate of variance be used.

`vfactor(#)` specifies a scalar by which to multiply the resulting variance matrix. This option allows you to match output with other packages, which may apply degrees of freedom or other small-sample corrections to estimates of variance.

`disp(#)` multiplies the variance of *depvar* by *#* and divides the deviance by *#*. The resulting distributions are members of the quasilikelihood family.

`scale(x2` | `dev` | `#)` overrides the default scale parameter. This option is allowed only with Hessian (information matrix) variance estimates.

By default, `scale(1)` is assumed for the discrete distributions (binomial, Poisson, and negative binomial), and `scale(x2)` is assumed for the continuous distributions (Gaussian, gamma, and inverse Gaussian).

`scale(x2)` specifies that the scale parameter be set to the Pearson chi-squared (or generalized chi-squared) statistic divided by the residual degrees of freedom, which is recommended by McCullagh and Nelder (1989) as a good general choice for continuous distributions.

scale(dev) sets the scale parameter to the deviance divided by the residual degrees of freedom. This option provides an alternative to scale(x2) for continuous distributions and overdispersed or underdispersed discrete distributions.

scale(#) sets the scale parameter to #. For example, using scale(1) in family(gamma) models results in exponential-errors regression. Additional use of link(log) rather than the default link(power -1) for family(gamma) essentially reproduces Stata's streg, dist(exp) nohr command (see [ST] **streg**) if all the observations are uncensored.

Reporting

level(#); see [R] **estimation options**.

eform displays the exponentiated coefficients and corresponding standard errors and confidence intervals. For family(binomial) link(logit) (that is, logistic regression), exponentiation results in odds ratios; for family(poisson) link(log) (that is, Poisson regression), exponentiated coefficients are rate ratios.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

ml requests that optimization be carried out using Stata's ml commands and is the default.

irls requests iterated, reweighted least-squares (IRLS) optimization of the deviance instead of Newton–Raphson optimization of the log likelihood. If the irls option is not specified, the optimization is carried out using Stata's ml commands, in which case all options of ml maximize are also available.

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

fisher(#) specifies the number of Newton–Raphson steps that should use the Fisher scoring Hessian or EIM before switching to the observed information matrix (OIM). This option is useful only for Newton–Raphson optimization (and not when using irls).

search specifies that the command search for good starting values. This option is useful only for Newton–Raphson optimization (and not when using irls).

The following options are available with glm but are not shown in the dialog box:

noheader suppresses the header information from the output. The coefficient table is still displayed.

notable suppresses the table of coefficients from the output. The header information is still displayed.

nodisplay suppresses the output. The iteration log is still displayed.

coeflegend; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

General use
Variance estimators
User-defined functions

General use

`glm` fits generalized linear models of y with covariates $\mathbf{x}$:

$$g\{E(y)\} = \mathbf{x}\boldsymbol{\beta}, \qquad y \sim F$$

$g(\,)$ is called the link function, and F is the distributional family. Substituting various definitions for $g(\,)$ and F results in a surprising array of models. For instance, if y is distributed as Gaussian (normal) and $g(\,)$ is the identity function, we have

$$E(y) = \mathbf{x}\boldsymbol{\beta}, \qquad y \sim \text{Normal}$$

or linear regression. If $g(\,)$ is the logit function and y is distributed as Bernoulli, we have

$$\text{logit}\{E(y)\} = \mathbf{x}\boldsymbol{\beta}, \qquad y \sim \text{Bernoulli}$$

or logistic regression. If $g(\,)$ is the natural log function and y is distributed as Poisson, we have

$$\ln\{E(y)\} = \mathbf{x}\boldsymbol{\beta}, \qquad y \sim \text{Poisson}$$

or Poisson regression, also known as the log-linear model. Other combinations are possible.

Although `glm` can be used to perform linear regression (and, in fact, does so by default), this regression should be viewed as an instructional feature; `regress` produces such estimates more quickly, and many postestimation commands are available to explore the adequacy of the fit; see [R] **regress** and [R] **regress postestimation**.

In any case, you specify the link function by using the `link()` option and specify the distributional family by using `family()`. The available link functions are

Link function	`glm` option
identity	`link(identity)`
log	`link(log)`
logit	`link(logit)`
probit	`link(probit)`
complementary log-log	`link(cloglog)`
odds power	`link(opower #)`
power	`link(power #)`
negative binomial	`link(nbinomial)`
log-log	`link(loglog)`
log-complement	`link(logc)`

Define $\mu = E(y)$ and $\eta = g(\mu)$, meaning that $g(\cdot)$ maps $E(y)$ to $\eta = \mathbf{x}\boldsymbol{\beta} + \text{offset}$.

Link functions are defined as follows:

`identity` is defined as $\eta = g(\mu) = \mu$.

`log` is defined as $\eta = \ln(\mu)$.

`logit` is defined as $\eta = \ln\{\mu/(1-\mu)\}$, the natural log of the odds.

`probit` is defined as $\eta = \Phi^{-1}(\mu)$, where $\Phi^{-1}(\,)$ is the inverse Gaussian cumulative.

`cloglog` is defined as $\eta = \ln\{-\ln(1-\mu)\}$.

`opower` is defined as $\eta = \left[\{\mu/(1-\mu)\}^n - 1\right]/n$, the power of the odds. The function is generalized so that `link(opower 0)` is equivalent to `link(logit)`, the natural log of the odds.

`power` is defined as $\eta = \mu^n$. Specifying `link(power 1)` is equivalent to specifying `link(identity)`. The power function is generalized so that $\mu^0 \equiv \ln(\mu)$. Thus `link(power 0)` is equivalent to `link(log)`. Negative powers are, of course, allowed.

`nbinomial` is defined as $\eta = \ln\{\mu/(\mu+k)\}$, where $k = 1$ if `family(nbinomial)` is specified, $k = \#_k$ if `family(nbinomial` $\#_k$`)` is specified, and k is estimated via maximum likelihood if `family(nbinomial ml)` is specified.

`loglog` is defined as $\eta = -\ln\{-\ln(\mu)\}$.

`logc` is defined as $\eta = \ln(1-\mu)$.

The available distributional families are

Family	`glm` option
Gaussian (normal)	`family(gaussian)`
inverse Gaussian	`family(igaussian)`
Bernoulli/binomial	`family(binomial)`
Poisson	`family(poisson)`
negative binomial	`family(nbinomial)`
gamma	`family(gamma)`

`family(normal)` is a synonym for `family(gaussian)`.

The binomial distribution can be specified as 1) `family(binomial)`, 2) `family(binomial` $\#_N$`)`, or 3) `family(binomial` *varname*$_N$`)`. In case 2, $\#_N$ is the value of the binomial denominator N, the number of trials. Specifying `family(binomial 1)` is the same as specifying `family(binomial)`. In case 3, *varname*$_N$ is the variable containing the binomial denominator, allowing the number of trials to vary across observations.

The negative binomial distribution can be specified as 1) `family(nbinomial)`, 2) `family(nbinomial` $\#_k$`)`, or 3) `family(nbinomial ml)`. Omitting $\#_k$ is equivalent to specifying `family(nbinomial 1)`. In case 3, the value of $\#_k$ is estimated via maximum likelihood. The value $\#_k$ enters the variance and deviance functions. Typical values range between 0.01 and 2; see the technical note below.

You do not have to specify both `family()` and `link()`; the default `link()` is the canonical link for the specified `family()` (except for `nbinomial`):

Family	Default link
`family(gaussian)`	`link(identity)`
`family(igaussian)`	`link(power -2)`
`family(binomial)`	`link(logit)`
`family(poisson)`	`link(log)`
`family(nbinomial)`	`link(log)`
`family(gamma)`	`link(power -1)`

If you specify both `family()` and `link()`, not all combinations make sense. You may choose from the following combinations:

	identity	log	logit	probit	cloglog	power	opower	nbinomial	loglog	logc
Gaussian	x	x				x				
inverse Gaussian	x	x				x				
binomial	x	x	x	x	x	x	x		x	x
Poisson	x	x				x				
negative binomial	x	x				x		x		
gamma	x	x				x				

❑ Technical note

Some `family()` and `link()` combinations result in models already fit by Stata. These are

`family()`	`link()`	Options	Equivalent Stata command
`gaussian`	`identity`	*nothing* | `irls` | `irls vce(oim)`	`regress`
`gaussian`	`identity`	`t(`*var*`) vce(hac nwest #) vfactor(`$\#_v$`)`	`newey, t(`*var*`) lag(#)` (see note 1)
`binomial`	`cloglog`	*nothing* | `irls vce(oim)`	`cloglog` (see note 2)
`binomial`	`probit`	*nothing* | `irls vce(oim)`	`probit` (see note 2)
`binomial`	`logit`	*nothing* | `irls` | `irls vce(oim)`	`logit` or `logistic` (see note 3)
`poisson`	`log`	*nothing* | `irls` | `irls vce(oim)`	`poisson` (see note 3)
`nbinomial`	`log`	*nothing* | `irls vce(oim)`	`nbreg` (see note 4)
`gamma`	`log`	`scale(1)`	`streg, dist(exp) nohr` (see note 5)

Notes:

1. The variance factor $\#_v$ should be set to $n/(n-k)$, where n is the number of observations and k the number of regressors. If the number of regressors is not specified, the estimated standard errors will, as a result, differ by this factor.

2. Because the link is not the canonical link for the binomial family, you must specify the `vce(oim)` option if using `irls` to get equivalent standard errors. If `irls` is used without `vce(oim)`, the regression coefficients will be the same but the standard errors will be only asymptotically equivalent. If no options are specified (*nothing*), `glm` will optimize using Newton–Raphson, making it equivalent to the other Stata command.

   See [R] **cloglog** and [R] **probit** for more details about these commands.

3. Because the canonical link is being used, the standard errors will be equivalent whether the EIM or the OIM estimator of variance is used.

4. Family negative binomial, log-link models—also known as negative binomial regression models—are used for data with an overdispersed Poisson distribution. Although `glm` can be used to fit such models, using Stata's maximum likelihood `nbreg` command is probably better. In the GLM approach, you specify `family(nbinomial #k)` and then search for a $\#_k$ that results in the deviance-based dispersion being 1. You can also specify `family(nbinomial ml)` to estimate $\#_k$ via maximum likelihood, which will report the same value returned from `nbreg`. However, `nbreg` also reports a confidence interval for it; see [R] **nbreg** and Rogers (1993). Of course, `glm` allows links other than `log`, and for those links, including the canonical `nbinomial` link, you will need to use `glm`.

5. `glm` can be used to estimate parameters from exponential regressions, but this method requires specifying `scale(1)`. However, censoring is not available. Censored exponential regression may be modeled using `glm` with `family(poisson)`. The log of the original response is entered into a Poisson model as an offset, whereas the new response is the censor variable. The result of such modeling is identical to the log relative hazard parameterization of `streg, dist(exp) nohr`. See [ST] **streg** for details about the `streg` command.

In general, where there is overlap between a capability of `glm` and that of some other Stata command, we recommend using the other Stata command. Our recommendation is not because of some inferiority of the GLM approach. Rather, those other commands, by being specialized, provide options and ancillary commands that are missing in the broader `glm` framework. Nevertheless, `glm` does produce the same answers where it should.

Special note. When equivalence is expected, for some datasets, you may still see very slight differences in the results, most often only in the later digits of the standard errors. When you compare `glm` output to an equivalent Stata command, these tiny discrepancies arise for many reasons:

a. `glm` uses a general methodology for starting values, whereas the equivalent Stata command may be more specialized in its treatment of starting values.

b. When using a canonical link, `glm, irls` should be equivalent to the maximum likelihood method of the equivalent Stata command, yet the convergence criterion is different (one is for deviance, the other for log likelihood). These discrepancies are easily resolved by adjusting one convergence criterion to correspond to the other.

c. When both `glm` and the equivalent Stata command use Newton–Raphson, small differences may still occur if the Stata command has a different default convergence criterion from that of `glm`. Adjusting the convergence criterion will resolve the difference. See [R] **ml** and [R] **maximize** for more details.

❑

▷ Example 1

In example 1 of [R] **logistic**, we fit a model based on data from a study of risk factors associated with low birthweight (Hosmer and Lemeshow 2000, 25). We can replicate the estimation by using `glm`:

```
. use http://www.stata-press.com/data/r12/lbw
(Hosmer & Lemeshow data)
. glm low age lwt i.race smoke ptl ht ui, family(binomial) link(logit)
Iteration 0:   log likelihood =  -101.0213
Iteration 1:   log likelihood = -100.72519
Iteration 2:   log likelihood =   -100.724
Iteration 3:   log likelihood =   -100.724
Generalized linear models                         No. of obs      =       189
Optimization     : ML                             Residual df     =       180
                                                  Scale parameter =         1
Deviance         =  201.4479911                   (1/df) Deviance =  1.119156
Pearson          =  182.0233425                   (1/df) Pearson  =  1.011241
Variance function: V(u) = u*(1-u)                 [Bernoulli]
Link function    : g(u) = ln(u/(1-u))             [Logit]
                                                  AIC             =    1.1611
Log likelihood   = -100.7239956                   BIC             = -742.0665
```

low	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.0271003	.0364504	-0.74	0.457	-.0985418	.0443412
lwt	-.0151508	.0069259	-2.19	0.029	-.0287253	-.0015763
race						
2	1.262647	.5264101	2.40	0.016	.2309024	2.294392
3	.8620792	.4391532	1.96	0.050	.0013548	1.722804
smoke	.9233448	.4008266	2.30	0.021	.137739	1.708951
ptl	.5418366	.346249	1.56	0.118	-.136799	1.220472
ht	1.832518	.6916292	2.65	0.008	.4769494	3.188086
ui	.7585135	.4593768	1.65	0.099	-.1418484	1.658875
_cons	.4612239	1.20459	0.38	0.702	-1.899729	2.822176

`glm`, by default, presents coefficient estimates, whereas `logistic` presents the exponentiated coefficients—the odds ratios. `glm`'s `eform` option reports exponentiated coefficients, and `glm`, like Stata's other estimation commands, replays results.

```
. glm, eform
Generalized linear models                         No. of obs      =        189
Optimization     : ML                             Residual df     =        180
                                                  Scale parameter =          1
Deviance         =  201.4479911                   (1/df) Deviance =   1.119156
Pearson          =  182.0233425                   (1/df) Pearson  =   1.011241
Variance function: V(u) = u*(1-u)                 [Bernoulli]
Link function    : g(u) = ln(u/(1-u))             [Logit]
                                                  AIC             =     1.1611
Log likelihood   = -100.7239956                   BIC             = -742.0665
```

low	Odds Ratio	OIM Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.9732636	.0354759	-0.74	0.457	.9061578	1.045339
lwt	.9849634	.0068217	-2.19	0.029	.9716834	.9984249
race						
2	3.534767	1.860737	2.40	0.016	1.259736	9.918406
3	2.368079	1.039949	1.96	0.050	1.001356	5.600207
smoke	2.517698	1.00916	2.30	0.021	1.147676	5.523162
ptl	1.719161	.5952579	1.56	0.118	.8721455	3.388787
ht	6.249602	4.322408	2.65	0.008	1.611152	24.24199
ui	2.1351	.9808153	1.65	0.099	.8677528	5.2534
_cons	1.586014	1.910496	0.38	0.702	.1496092	16.8134

These results are the same as those reported in example 1 of [R] **logistic**.

Included in the output header are values for the Akaike (1973) information criterion (AIC) and the Bayesian information criterion (BIC) (Raftery 1995). Both are measures of model fit adjusted for the number of parameters that can be compared across models. In both cases, a smaller value generally indicates a better model fit. AIC is based on the log likelihood and thus is available only when Newton–Raphson optimization is used. BIC is based on the deviance and thus is always available. ◁

❑ Technical note

The values for AIC and BIC reported in the output after `glm` are different from those reported by `estat ic`:

```
. estat ic
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
.	189	.	-100.724	9	219.448	248.6237

Note: N=Obs used in calculating BIC; see **[R] BIC note**

There are various definitions of these information criteria (IC) in the literature; `glm` and `estat ic` use different definitions. `glm` bases its computation of the BIC on deviance, whereas `estat ic` uses the likelihood. Both `glm` and `estat ic` use the likelihood to compute the AIC; however, the AIC from `estat ic` is equal to N, the number of observations, times the AIC from `glm`. Refer to *Methods and formulas* in this entry and [R] **estat** for the references and formulas used by `glm` and `estat`, respectively, to compute AIC and BIC. Inferences based on comparison of IC values reported by `glm` for different GLM models will be equivalent to those based on comparison of IC values reported by `estat ic` after `glm`.

❑

▷ Example 2

We use data from an early insecticide experiment, given in Pregibon (1980). The variables are `ldose`, the log dose of insecticide; `n`, the number of flour beetles subjected to each dose; and `r`, the number killed.

```
. use http://www.stata-press.com/data/r12/ldose
. list, sep(4)
```

	ldose	n	r
1.	1.6907	59	6
2.	1.7242	60	13
3.	1.7552	62	18
4.	1.7842	56	28
5.	1.8113	63	52
6.	1.8369	59	53
7.	1.861	62	61
8.	1.8839	60	60

The aim of the analysis is to estimate a dose–response relationship between p, the proportion killed, and X, the log dose.

As a first attempt, we will formulate the model as a linear logistic regression of p on `ldose`; that is, we will take the logit of p and represent the dose–response curve as a straight line in X:

$$\ln\{p/(1-p)\} = \beta_0 + \beta_1 X$$

Because the data are grouped, we cannot use Stata's `logistic` command to fit the model. Stata does, however, already have a command for performing logistic regression on data organized in this way, so we could type

```
. blogit r n ldose
  (output omitted)
```

Instead, we will fit the model by using `glm`:

```
. glm r ldose, family(binomial n) link(logit)
Iteration 0:   log likelihood = -18.824848
Iteration 1:   log likelihood = -18.715271
Iteration 2:   log likelihood = -18.715123
Iteration 3:   log likelihood = -18.715123
Generalized linear models                         No. of obs      =         8
Optimization     : ML                             Residual df     =         6
                                                  Scale parameter =         1
Deviance         =  11.23220702                   (1/df) Deviance =  1.872035
Pearson          =   10.0267936                   (1/df) Pearson  =  1.671132
```

```
Variance function: V(u) = u*(1-u/n)              [Binomial]
Link function    : g(u) = ln(u/(n-u))            [Logit]

                                                 AIC             =  5.178781
Log likelihood   = -18.71512262                  BIC             = -1.244442
```

r	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
ldose	34.27034	2.912141	11.77	0.000	28.56265	39.97803
_cons	-60.71747	5.180713	-11.72	0.000	-70.87149	-50.56346

The only difference between `blogit` and `glm` here is how they obtain the answer. `blogit` expands the data to contain 481 observations (the sum of `n`) so that it can run Stata's standard, individual-level logistic command. `glm`, on the other hand, uses the information on the binomial denominator directly. We specified `family(binomial n)`, meaning that variable `n` contains the denominator. Parameter estimates and standard errors from the two approaches do not differ.

An alternative model, which gives asymmetric sigmoid curves for p, involves the complementary log-log, or cloglog, function:

$$\ln\{-\ln(1-p)\} = \beta_0 + \beta_1 X$$

We fit this model by using `glm`:

```
. glm r ldose, family(binomial n) link(cloglog)

Iteration 0:   log likelihood = -14.883594
Iteration 1:   log likelihood = -14.822264
Iteration 2:   log likelihood = -14.822228
Iteration 3:   log likelihood = -14.822228

Generalized linear models                        No. of obs      =         8
Optimization     : ML                            Residual df     =         6
                                                 Scale parameter =         1
Deviance         =  3.446418004                  (1/df) Deviance =   .574403
Pearson          =  3.294675153                  (1/df) Pearson  =  .5491125

Variance function: V(u) = u*(1-u/n)              [Binomial]
Link function    : g(u) = ln(-ln(1-u/n))         [Complementary log-log]

                                                 AIC             =  4.205557
Log likelihood   = -14.82222811                  BIC             = -9.030231
```

r	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
ldose	22.04118	1.793089	12.29	0.000	18.52679	25.55557
_cons	-39.57232	3.229047	-12.26	0.000	-45.90114	-33.24351

The complementary log-log model is preferred; the deviance for the logistic model, 11.23, is much higher than the deviance for the cloglog model, 3.45. This change also is evident by comparing log likelihoods, or equivalently, AIC values.

This example also shows the advantage of the `glm` command—we can vary assumptions easily. Note the minor difference in what we typed to obtain the logistic and cloglog models:

```
. glm r ldose, family(binomial n) link(logit)
. glm r ldose, family(binomial n) link(cloglog)
```

If we were performing this work for ourselves, we would have typed the commands in a more abbreviated form:

```
. glm r ldose, f(b n) l(l)
. glm r ldose, f(b n) l(cl)
```

◁

❑ Technical note

Factor variables may be used with `glm`. Say that, in the example above, we had `ldose`, the log dose of insecticide; `n`, the number of flour beetles subjected to each dose; and `r`, the number killed—all as before—except that now we have results for three different kinds of beetles. Our hypothetical data include `beetle`, which contains the values 1, 2, and 3.

```
. use http://www.stata-press.com/data/r12/beetle
. list, sep(0)
```

	beetle	ldose	n	r
1.	1	1.6907	59	6
2.	1	1.7242	60	13
3.	1	1.7552	62	18
4.	1	1.7842	56	28
5.	1	1.8113	63	52
	(*output omitted*)			
23.	3	1.861	64	23
24.	3	1.8839	58	22

Let's assume that, at first, we wish merely to add a shift factor for the type of beetle. We could type

```
. glm r i.beetle ldose, f(bin n) l(cloglog)
Iteration 0:   log likelihood = -79.012269
Iteration 1:   log likelihood =  -76.94951
Iteration 2:   log likelihood = -76.945645
Iteration 3:   log likelihood = -76.945645
Generalized linear models                         No. of obs      =         24
Optimization     : ML                             Residual df     =         20
                                                  Scale parameter =          1
Deviance         =  73.76505595                   (1/df) Deviance =   3.688253
Pearson          =   71.8901173                   (1/df) Pearson  =   3.594506
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(-ln(1-u/n))          [Complementary log-log]
                                                  AIC             =    6.74547
Log likelihood   = -76.94564525                   BIC             =   10.20398
```

r	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.0910396	.1076132	-0.85	0.398	-.3019576	.1198783
3	-1.836058	.1307125	-14.05	0.000	-2.09225	-1.579867
ldose	19.41558	.9954265	19.50	0.000	17.46458	21.36658
_cons	-34.84602	1.79333	-19.43	0.000	-38.36089	-31.33116

We find strong evidence that the insecticide works differently on the third kind of beetle. We now check whether the curve is merely shifted or also differently sloped:

```
. glm r beetle##c.ldose, f(bin n) l(cloglog)
Iteration 0:   log likelihood = -67.270188
Iteration 1:   log likelihood = -65.149316
Iteration 2:   log likelihood = -65.147978
Iteration 3:   log likelihood = -65.147978
Generalized linear models                         No. of obs      =         24
Optimization     : ML                             Residual df     =         18
                                                  Scale parameter =          1
Deviance         =  50.16972096                   (1/df) Deviance =  2.787207
Pearson          =  49.28422567                   (1/df) Pearson  =  2.738013
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(-ln(1-u/n))          [Complementary log-log]
                                                  AIC             =  5.928998
Log likelihood   = -65.14797776                   BIC             = -7.035248
```

r	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.79933	4.470882	-0.18	0.858	-9.562098	7.963438
3	17.78741	4.586429	3.88	0.000	8.798172	26.77664
ldose	22.04118	1.793089	12.29	0.000	18.52679	25.55557
beetle#c.ldose						
2	.3838708	2.478477	0.15	0.877	-4.473855	5.241596
3	-10.726	2.526412	-4.25	0.000	-15.67768	-5.774321
_cons	-39.57232	3.229047	-12.26	0.000	-45.90114	-33.24351

We find that the (complementary log-log) dose–response curve for the third kind of beetle has roughly half the slope of that for the first kind.

See [U] **25 Working with categorical data and factor variables**; what is said there concerning linear regression is applicable to any GLM model.

❑

Variance estimators

glm offers many variance options and gives different types of standard errors when used in various combinations. We highlight some of them here, but for a full explanation, see Hardin and Hilbe (2007).

▷ Example 3

Continuing with our flour beetle data, we rerun the most recently displayed model, this time requesting estimation via IRLS.

```
. use http://www.stata-press.com/data/r12/beetle
. glm r beetle##c.ldose, f(bin n) l(cloglog) ltol(1e-15) irls
Iteration 1:   deviance =  54.41414
Iteration 2:   deviance =  50.19424
Iteration 3:   deviance =  50.16973
  (output omitted)
Iteration 17:  deviance =  50.16972
Generalized linear models                         No. of obs      =        24
Optimization     : MQL Fisher scoring             Residual df     =        18
                   (IRLS EIM)                     Scale parameter =         1
Deviance         =  50.16972096                   (1/df) Deviance =  2.787207
Pearson          =  49.28422567                   (1/df) Pearson  =  2.738013
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(-ln(1-u/n))          [Complementary log-log]
                                                  BIC             = -7.035248
```

r	EIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.79933	4.586649	-0.17	0.862	-9.788997	8.190337
3	17.78741	4.624834	3.85	0.000	8.7229	26.85192
ldose	22.04118	1.799356	12.25	0.000	18.5145	25.56785
beetle#c.ldose						
2	.3838708	2.544068	0.15	0.880	-4.602411	5.370152
3	-10.726	2.548176	-4.21	0.000	-15.72033	-5.731665
_cons	-39.57232	3.240274	-12.21	0.000	-45.92314	-33.2215

Note our use of the ltol() option, which, although unrelated to our discussion on variance estimation, was used so that the regression coefficients would match those of the previous Newton–Raphson (NR) fit.

Because IRLS uses the EIM for optimization, the variance estimate is also based on EIM. If we want optimization via IRLS but the variance estimate based on OIM, we specify glm, irls vce(oim):

```
. glm r beetle##c.ldose, f(b n) l(cl) ltol(1e-15) irls vce(oim) noheader nolog
```

r	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.79933	4.470882	-0.18	0.858	-9.562098	7.963438
3	17.78741	4.586429	3.88	0.000	8.798172	26.77664
ldose	22.04118	1.793089	12.29	0.000	18.52679	25.55557
beetle#c.ldose						
2	.3838708	2.478477	0.15	0.877	-4.473855	5.241596
3	-10.726	2.526412	-4.25	0.000	-15.67768	-5.774321
_cons	-39.57232	3.229047	-12.26	0.000	-45.90114	-33.24351

This approach is identical to NR except for the convergence path. Because the cloglog link is not the canonical link for the binomial family, EIM and OIM produce different results. Both estimators, however, are asymptotically equivalent.

Going back to NR, we can also specify `vce(robust)` to get the Huber/White/sandwich estimator of variance:

```
. glm r beetle##c.ldose, f(b n) l(cl) vce(robust) noheader nolog
```

r	Robust Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.79933	5.733049	-0.14	0.889	-12.0359	10.43724
3	17.78741	5.158477	3.45	0.001	7.676977	27.89784
ldose	22.04118	.8998551	24.49	0.000	20.27749	23.80486
beetle#c.ldose						
2	.3838708	3.174427	0.12	0.904	-5.837892	6.605633
3	-10.726	2.800606	-3.83	0.000	-16.21508	-5.236912
_cons	-39.57232	1.621306	-24.41	0.000	-42.75003	-36.39462

The sandwich estimator gets its name from the form of the calculation—it is the multiplication of three matrices, with the outer two matrices (the "bread") set to the OIM variance matrix. When `irls` is used along with `vce(robust)`, the EIM variance matrix is instead used as the bread. Using a result from McCullagh and Nelder (1989), Newson (1999) points out that the EIM and OIM variance matrices are equivalent under the canonical link. Thus if `irls` is specified with the canonical link, the resulting variance is labeled "Robust". When the noncanonical link for the family is used, which is the case in the example below, the EIM and OIM variance matrices differ, so the resulting variance is labeled "Semirobust".

```
. glm r beetle##c.ldose, f(b n) l(cl) irls ltol(1e-15) vce(robust) noheader
> nolog
```

r	Coef.	Semirobust Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.79933	6.288963	-0.13	0.899	-13.12547	11.52681
3	17.78741	5.255307	3.38	0.001	7.487194	28.08762
ldose	22.04118	.9061566	24.32	0.000	20.26514	23.81721
beetle#c.ldose						
2	.3838708	3.489723	0.11	0.912	-6.455861	7.223603
3	-10.726	2.855897	-3.76	0.000	-16.32345	-5.128542
_cons	-39.57232	1.632544	-24.24	0.000	-42.77205	-36.3726

The outer product of the gradient (OPG) estimate of variance is one that avoids the calculation of second derivatives. It is equivalent to the "middle" part of the sandwich estimate of variance and can be specified by using `glm, vce(opg)`, regardless of whether NR or IRLS optimization is used.

```
. glm r beetle##c.ldose, f(b n) l(cl) vce(opg) noheader nolog
```

r	Coef.	OPG Std. Err.	z	P>|z|	[95% Conf.	Interval]
beetle						
2	-.79933	6.664045	-0.12	0.905	-13.86062	12.26196
3	17.78741	6.838505	2.60	0.009	4.384183	31.19063
ldose	22.04118	3.572983	6.17	0.000	15.03826	29.0441
beetle#c.ldose						
2	.3838708	3.700192	0.10	0.917	-6.868372	7.636114
3	-10.726	3.796448	-2.83	0.005	-18.1669	-3.285097
_cons	-39.57232	6.433101	-6.15	0.000	-52.18097	-26.96368

The OPG estimate of variance is a component of the BHHH (Berndt et al. 1974) optimization technique. This method of optimization is also available with `glm` with the `technique()` option; however, the `technique()` option is not allowed with the `irls` option.

◁

▷ Example 4

The Newey–West (1987) estimator of variance is a sandwich estimator with the "middle" of the sandwich modified to take into account possible autocorrelation between the observations. These estimators are a generalization of those given by the Stata command `newey` for linear regression. See [TS] **newey** for more details.

For example, consider the dataset given in [TS] **newey**, which has time-series measurements on `usr` and `idle`. We want to perform a linear regression with Newey–West standard errors.

```
. use http://www.stata-press.com/data/r12/idle2
. list usr idle time
```

	usr	idle	time
1.	0	100	1
2.	0	100	2
3.	0	97	3
4.	1	98	4
5.	2	94	5
	(*output omitted*)		
29.	1	98	29
30.	1	98	30

Examining *Methods and formulas* of [TS] **newey**, we see that the variance estimate is multiplied by a correction factor of $n/(n-k)$, where k is the number of regressors. `glm, vce(hac ...)` does not make this correction, so to get the same standard errors, we must use the `vfactor()` option within `glm` to make the correction manually.

```
. display 30/28
1.0714286
. tsset time
        time variable:  time, 1 to 30
                delta:  1 unit
. glm usr idle, vce(hac nwest 3) vfactor(1.0714286)
Iteration 0:   log likelihood = -71.743396
Generalized linear models                         No. of obs      =         30
Optimization     : ML                             Residual df     =         28
                                                  Scale parameter =   7.493297
Deviance         =  209.8123165                   (1/df) Deviance =   7.493297
Pearson          =  209.8123165                   (1/df) Pearson  =   7.493297
Variance function: V(u) = 1                       [Gaussian]
Link function    : g(u) = u                       [Identity]
HAC kernel (lags): Newey-West (3)
                                                  AIC             =   4.916226
Log likelihood   = -71.74339627                   BIC             =   114.5788
```

usr	Coef.	HAC Std. Err.	z	P>|z|	[95% Conf.	Interval]
idle	-.2281501	.0690928	-3.30	0.001	-.3635694	-.0927307
_cons	23.13483	6.327033	3.66	0.000	10.73407	35.53558

The `glm` command above reproduces the results given in [TS] **newey**. We may now generalize this output to models other than simple linear regression and to different kernel weights.

```
. glm usr idle, fam(gamma) link(log) vce(hac gallant 3)
Iteration 0:   log likelihood =  -61.76593
Iteration 1:   log likelihood = -60.963233
Iteration 2:   log likelihood =  -60.95097
Iteration 3:   log likelihood = -60.950965
Generalized linear models                         No. of obs      =         30
Optimization     : ML                             Residual df     =         28
                                                  Scale parameter =   .431296
Deviance         =  9.908506707                   (1/df) Deviance =  .3538752
Pearson          =  12.07628677                   (1/df) Pearson  =   .431296
Variance function: V(u) = u^2                     [Gamma]
Link function    : g(u) = ln(u)                   [Log]
HAC kernel (lags): Gallant (3)
                                                  AIC             =  4.196731
Log likelihood   = -60.95096484                   BIC             = -85.32502
------------------------------------------------------------------------------
             |                 HAC
         usr |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        idle |  -.0796609   .0184647    -4.31   0.000    -.115851   -.0434708
       _cons |   7.771011   1.510198     5.15   0.000    4.811078    10.73094
------------------------------------------------------------------------------
```

`glm` also offers variance estimators based on the bootstrap (resampling your data with replacement) and the jackknife (refitting the model with each observation left out in succession). Also included is the one-step jackknife estimate, which, instead of performing full reestimation when each observation is omitted, calculates a one-step NR estimate, with the full data regression coefficients as starting values.

```
. set seed 1
. glm usr idle, fam(gamma) link(log) vce(bootstrap, reps(100) nodots)
Generalized linear models                         No. of obs      =         30
Optimization     : ML                             Residual df     =         28
                                                  Scale parameter =   .431296
Deviance         =  9.908506707                   (1/df) Deviance =  .3538752
Pearson          =  12.07628677                   (1/df) Pearson  =   .431296
Variance function: V(u) = u^2                     [Gamma]
Link function    : g(u) = ln(u)                   [Log]
                                                  AIC             =  4.196731
Log likelihood   = -60.95096484                   BIC             = -85.32502
------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
         usr |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        idle |  -.0796609   .0216591    -3.68   0.000   -.1221119   -.0372099
       _cons |   7.771011    1.80278     4.31   0.000    4.237627     11.3044
------------------------------------------------------------------------------
```

See Hardin and Hilbe (2007) for a full discussion of the variance options that go with `glm` and, in particular, of how the different variance estimators are modified when `vce(cluster` *clustvar*`)` is specified. Finally, not all variance options are supported with all types of weights. See `help glm` for a current table of the variance options that are supported with the different weights.

User-defined functions

glm may be called with a user-written link function, variance (family) function, Newey–West kernel-weight function, or any combination of the three.

Syntax of link functions

```
program progname
        version 12
        args todo eta mu return
        if 'todo' == -1 {
                /* Set global macros for output */
                global SGLM_lt "title for link function"
                global SGLM_lf "subtitle showing link definition"
                exit
        }
        if 'todo' == 0 {
                /* set η=g(μ) */
                /* Intermediate calculations go here */
                generate double 'eta' = ...
                exit
        }
        if 'todo' == 1 {
                /* set μ=g^-1(η) */
                /* Intermediate calculations go here */
                generate double 'mu' = ...
                exit
        }
        if 'todo' == 2 {
                /* set return = ∂μ/∂η */
                /* Intermediate calculations go here */
                generate double 'return' = ...
                exit
        }
        if 'todo' == 3 {
                /* set return = ∂^2μ/∂η^2 */
                /* Intermediate calculations go here */
                generate double 'return' = ...
                exit
        }
        display as error "Unknown call to glm link function"
        exit 198
end
```

Syntax of variance functions

```
program progname
        version 12
        args todo eta mu return
        if `todo' == -1 {
                /*  Set global macros for output  */
                /*  Also check that depvar is in proper range */
                /*  Note: For this call,  eta contains indicator for whether each obs. is in est. sample  */
                global SGLM_vt "title for variance function"
                global SGLM_vf "subtitle showing function definition"
                global SGLM_mu "program to call to enforce boundary conditions on μ"
                exit
        }
        if `todo' == 0 {
                /*  set η to initial value.  */
                /*  Intermediate calculations go here  */
                generate double `eta' = ...
                exit
        }
        if `todo' == 1 {
                /*  set return = V(μ)  */
                /*  Intermediate calculations go here  */
                generate double `return' = ...
                exit
        }
        if `todo' == 2 {
                /*  set return = ∂V(μ)/∂μ  */
                /*  Intermediate calculations go here  */
                generate double `return' = ...
                exit
        }
        if `todo' == 3 {
                /*  set return =  squared deviance (per observation)  */
                /*  Intermediate calculations go here  */
                generate double `return' = ...
                exit
        }
        if `todo' == 4 {
                /*  set return =  Anscombe residual  */
                /*  Intermediate calculations go here  */
                generate double `return' = ...
                exit
        }
        if `todo' == 5 {
                /*  set return =  log likelihood  */
                /*  Intermediate calculations go here  */
                generate double `return' = ...
                exit
        }
        if `todo' == 6 {
                /*  set return =  adjustment for deviance residuals  */
                /*  Intermediate calculations go here  */
                generate double `return' = ...
                exit
        }
        display as error "Unknown call to glm variance function"
        exit 198
end
```

Syntax of Newey–West kernel-weight functions

```
program progname, rclass
        version 12
        args G j
        /* G  is the maximum lag */
        /* j  is the current lag */
        /*  Intermediate calculations go here */
        return scalar wt = computed weight
        return local setype "Newey-West"
        return local sewtype "name of kernel"
end
```

Global macros available for user-written programs

Global macro	Description
SGLM_V	program name of variance (family) evaluator
SGLM_L	program name of link evaluator
SGLM_y	dependent variable name
SGLM_m	binomial denominator
SGLM_a	negative binomial k
SGLM_p	power if power() or opower() is used, or an argument from a user-specified link function
SGLM_s1	indicator; set to one if scale is equal to one
SGLM_ph	value of scale parameter

▷ Example 5

Suppose that we wish to perform Poisson regression with a log-link function. Although this regression is already possible with standard glm, we will write our own version for illustrative purposes.

Because we want a log link, $\eta = g(\mu) = \ln(\mu)$, and for a Poisson family the variance function is $V(\mu) = \mu$.

The Poisson density is given by

$$f(y_i) = \frac{e^{-\exp(\mu_i)} e^{\mu_i y_i}}{y_i!}$$

resulting in a log likelihood of

$$L = \sum_{i=1}^{n} \{-e^{\mu_i} + \mu_i y_i - \ln(y_i!)\}$$

The squared deviance of the ith observation for the Poisson family is given by

$$d_i^2 = \begin{cases} 2\widehat{\mu}_i & \text{if } y_i = 0 \\ 2\{y_i \ln(y_i/\widehat{\mu}_i) - (y_i - \widehat{\mu}_i)\} & \text{otherwise} \end{cases}$$

We now have enough information to write our own Poisson-log `glm` module. We create the file `mylog.ado`, which contains

```
program mylog
        version 12
        args todo eta mu return
        if `todo' == -1 {
                global SGLM_lt "My Log"          // Titles for output
                global SGLM_lf "ln(u)"
                exit
        }
        if `todo' == 0  {
                gen double `eta' = ln(`mu')      // η = ln(μ)
                exit
        }
        if `todo' == 1  {
                gen double `mu' = exp(`eta')     // μ = exp(η)
                exit
        }
        if `todo' == 2 {
                gen double `return' = `mu'       // ∂μ/∂η = exp(η) = μ
                exit
        }
        if `todo' == 3 {
                gen double `return' = `mu'       // ∂²μ/∂η² = exp(η) = μ
                exit
        }
        di as error "Unknown call to glm link function"
        exit 198
end
```

and we create the file `mypois.ado`, which contains

```
program mypois
        version 12
        args todo eta mu return
        if `todo' == -1 {
                local y     "$SGLM_y"
                local touse "`eta'"                 // `eta' marks estimation sample here
                capture assert `y'>=0 if `touse'    // check range of y
                if _rc {
                        di as error `"dependent variable `y' has negative values"'
                        exit 499
                }
                global SGLM_vt "My Poisson"         // Titles for output
                global SGLM_vf "u"
                global SGLM_mu "glim_mu 0 ."        // see note 1
                exit
        }
        if `todo' == 0 {                            // Initialization of η; see note 2
                gen double `eta' = ln(`mu')
                exit
        }
```

```
        if `todo' == 1 {
                gen double `return' =  `mu'          //  V(μ) = μ
                exit
        }
        if `todo' == 2 {                             //  ∂V(μ)/∂μ
                gen byte `return' = 1
                exit
        }
        if `todo' == 3 {                             //  squared deviance, defined above
                local y "$SGLM_y"
                if "`y'" == "" {
                        local y "`e(depvar)'"
                }
                gen double `return' = cond(`y'==0, 2*`mu', /*
                          */ 2*(`y'*ln(`y'/`mu')-(`y'-`mu')))
                exit
        }
        if `todo' == 4 {                             //  Anscombe residual; see note 3
                local y "$SGLM_y"
                if "`y'" == "" {
                        local y "`e(depvar)'"
                }
                gen double `return' = 1.5*(`y'^(2/3)-`mu'^(2/3)) / `mu'^(1/6)
                exit
        }
        if `todo' == 5 {                             //  log likelihood; see note 4
                local y "$SGLM_y"
                if "`y'" == "" {
                        local y "`e(depvar)'"
                }
                gen double `return' = -`mu'+`y'*ln(`mu')-lngamma(`y'+1)
                exit
        }
        if `todo' == 6 {                             //  adjustment to residual; see note 5
                gen double `return' = 1/(6*sqrt(`mu'))
                exit
        }
        di as error "Unknown call to glm variance function"
        error 198
end
```

Notes:

1. `glim_mu` is a Stata program that will, at each iteration, bring $\widehat{\mu}$ back into its plausible range, should it stray out of it. Here `glim_mu` is called with the arguments zero and missing, meaning that zero is the lower bound of $\widehat{\mu}$ and there exists no upper bound—such is the case for Poisson models.

2. Here the initial value of η is easy because we intend to fit this model with our user-defined log link. In general, however, the initialization may need to vary according to the link to obtain convergence. If so, the global macro `SGLM_L` is used to determine which link is being utilized.

3. The Anscombe formula is given here because we know it. If we were not interested in Anscombe residuals, we could merely set `` `return' `` to missing. Also, the local macro `y` is set either to `SGLM_y` if it is in current estimation or to `e(depvar)` if this function is being accessed by `predict`.

4. If we were not interested in ML estimation, we could omit this code entirely and just leave an `exit` statement in its place. Similarly, if we were not interested in deviance or IRLS optimization, we could set `` `return' `` in the deviance portion of the code (`` `todo'==3 ``) to missing.

5. This code defines the term to be added to the predicted residuals if the `adjusted` option is specified. Again, if we were not interested, we could set `'return'` to missing.

We can now test our Poisson-log module by running it on the airline data presented in [R] **poisson**.

```
. use http://www.stata-press.com/data/r12/airline
. list airline injuries n XYZowned
```

	airline	injuries	n	XYZowned
1.	1	11	0.0950	1
2.	2	7	0.1920	0
3.	3	7	0.0750	0
4.	4	19	0.2078	0
5.	5	9	0.1382	0
6.	6	4	0.0540	1
7.	7	3	0.1292	0
8.	8	1	0.0503	0
9.	9	3	0.0629	1

```
. gen lnN=ln(n)
. glm injuries XYZowned lnN, fam(mypois) link(mylog) scale(1)
Iteration 0:   log likelihood = -22.557572
Iteration 1:   log likelihood = -22.332861
Iteration 2:   log likelihood = -22.332276
Iteration 3:   log likelihood = -22.332276
Generalized linear models                         No. of obs      =          9
Optimization     : ML                             Residual df     =          6
                                                  Scale parameter =          1
Deviance         =  12.70432823                   (1/df) Deviance =   2.117388
Pearson          =   12.7695081                   (1/df) Pearson  =   2.128251
Variance function: V(u) = u                       [My Poisson]
Link function    : g(u) = ln(u)                   [My Log]
                                                  AIC             =   5.629395
Log likelihood   = -22.33227605                   BIC             =  -.4790192
```

injuries	OIM Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
XYZowned	.6840668	.3895877	1.76	0.079	-.0795111	1.447645
lnN	1.424169	.3725155	3.82	0.000	.6940517	2.154286
_cons	4.863891	.7090501	6.86	0.000	3.474178	6.253603

```
(Standard errors scaled using dispersion equal to square root of 1.)
```

These are precisely the results given in [R] **poisson** and are those that would have been given had we run `glm, family(poisson) link(log)`. The only minor adjustment we needed to make was to specify the `scale(1)` option. If `scale()` is left unspecified, `glm` assumes `scale(1)` for discrete distributions and `scale(x2)` for continuous ones. By default, `glm` assumes that any user-defined family is continuous because it has no way of checking. Thus we needed to specify `scale(1)` because our model is discrete.

Because we were careful in defining the squared deviance, we could have fit this model with IRLS. Because log is the canonical link for the Poisson family, we would not only get the same regression coefficients but also the same standard errors.

◁

▷ Example 6

Suppose now that we wish to use our log link (`mylog.ado`) with `glm`'s binomial family. This task requires some modification because our current function is not equipped to deal with the binomial denominator, which we are allowed to specify. This denominator is accessible to our link function through the global macro `SGLM_m`. We now make the modifications and store them in `mylog2.ado`.

```
program mylog2                                                  // <-- changed
        version 12
        args todo eta mu return
        if `todo' == -1 {
                global SGLM_lt "My Log, Version 2"              // <-- changed
                if "$SGLM_m" == "1" {                           // <-- changed
                        global SGLM_lf "ln(u)"                  // <-- changed
                }                                               // <-- changed
                else    global SGLM_lf "ln(u/$SGLM_m)"          // <-- changed
                exit
        }
        if `todo' == 0  {
                gen double `eta' = ln(`mu'/$SGLM_m)             // <-- changed
                exit
        }
        if `todo' == 1  {
                gen double `mu' = $SGLM_m*exp(`eta')            // <-- changed
                exit
        }
        if `todo' == 2 {
                gen double `return' = `mu'
                exit
        }
        if `todo' == 3 {
                gen double `return' = `mu'
                exit
        }
        di as error "Unknown call to glm link function"
        exit 198
end
```

We can now run our new log link with `glm`'s binomial family. Using the flour beetle data from earlier, we have

```
. use http://www.stata-press.com/data/r12/beetle, clear
. glm r ldose, fam(bin n) link(mylog2) irls
Iteration 1:   deviance =  2212.108
Iteration 2:   deviance =  452.9352
Iteration 3:   deviance =    429.95
Iteration 4:   deviance =  429.2745
Iteration 5:   deviance =  429.2192
Iteration 6:   deviance =  429.2082
Iteration 7:   deviance =  429.2061
Iteration 8:   deviance =  429.2057
Iteration 9:   deviance =  429.2056
Iteration 10:  deviance =  429.2056
Iteration 11:  deviance =  429.2056
Iteration 12:  deviance =  429.2056
Generalized linear models                         No. of obs      =         24
Optimization     : MQL Fisher scoring             Residual df     =         22
                   (IRLS EIM)                     Scale parameter =          1
Deviance         =   429.205599                   (1/df) Deviance =   19.50935
Pearson          =   413.088142                   (1/df) Pearson  =   18.77673
Variance function: V(u) = u*(1-u/n)               [Binomial]
Link function    : g(u) = ln(u/n)                 [My Log, Version 2]
                                                  BIC             =   359.2884
------------------------------------------------------------------------------
             |                 EIM
           r |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       ldose |    8.478908   .4702808    18.03   0.000     7.557175    9.400642
       _cons |   -16.11006   .8723167   -18.47   0.000    -17.81977   -14.40035
------------------------------------------------------------------------------
```

◁

For a more detailed discussion on user-defined functions, and for an example of a user-defined Newey–West kernel weight, see Hardin and Hilbe (2007).

John Ashworth Nelder (1924–2010) was born in Somerset, England. He studied mathematics and statistics at Cambridge and worked as a statistician at the National Vegetable Research Station and then Rothamsted Experimental Station. In retirement, he was actively affiliated with Imperial College London. Nelder was especially well known for his contributions to the theory of linear models and to statistical computing. He was the principal architect of generalized and hierarchical generalized linear models and of the programs GenStat and GLIM.

Robert William Maclagan Wedderburn (1947–1975) was born in Edinburgh and studied mathematics and statistics at Cambridge. At Rothamsted Experimental Station, he developed the theory of generalized linear models with Nelder and originated the concept of quasilikelihood. He died of anaphylactic shock from an insect bite on a canal holiday.

Saved results

glm, ml saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(df)	residual degrees of freedom
e(phi)	scale parameter
e(aic)	model AIC
e(bic)	model BIC
e(ll)	log likelihood, if NR
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance
e(deviance)	deviance
e(deviance_s)	scaled deviance
e(deviance_p)	Pearson deviance
e(deviance_ps)	scaled Pearson deviance
e(dispers)	dispersion
e(dispers_s)	scaled dispersion
e(dispers_p)	Pearson dispersion
e(dispers_ps)	scaled Pearson dispersion
e(nbml)	1 if negative binomial parameter estimated via ML, 0 otherwise
e(vf)	factor set by vfactor(), 1 if not set
e(power)	power set by power(), opower()
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	glm
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(varfunc)	program to calculate variance function
e(varfunct)	variance title
e(varfuncf)	variance function
e(link)	program to calculate link function
e(linkt)	link title
e(linkf)	link function
e(m)	number of binomial trials
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald; type of model χ^2 test
e(cons)	set if noconstant specified
e(hac_kernel)	HAC kernel
e(hac_lag)	HAC lag
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	ml or irls
e(opt1)	optimization title, line 1
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

`glm, irls` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_eq_model)`	number of equations in overall model test
`e(df_m)`	model degrees of freedom
`e(df)`	residual degrees of freedom
`e(phi)`	scale parameter
`e(disp)`	dispersion parameter
`e(bic)`	model BIC
`e(N_clust)`	number of clusters
`e(deviance)`	deviance
`e(deviance_s)`	scaled deviance
`e(deviance_p)`	Pearson deviance
`e(deviance_ps)`	scaled Pearson deviance
`e(dispers)`	dispersion
`e(dispers_s)`	scaled dispersion
`e(dispers_p)`	Pearson dispersion
`e(dispers_ps)`	scaled Pearson dispersion
`e(nbml)`	`1` if negative binomial parameter estimated via ML, `0` otherwise
`e(vf)`	factor set by `vfactor()`, 1 if not set
`e(power)`	power set by `power()`, `opower()`
`e(rank)`	rank of `e(V)`
`e(rc)`	return code

Macros

`e(cmd)`	`glm`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(varfunc)`	program to calculate variance function
`e(varfunct)`	variance title
`e(varfuncf)`	variance function
`e(link)`	program to calculate link function
`e(linkt)`	link title
`e(linkf)`	link function
`e(m)`	number of binomial trials
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(clustvar)`	name of cluster variable
`e(offset)`	linear offset variable
`e(cons)`	set if `noconstant` specified
`e(hac_kernel)`	HAC kernel
`e(hac_lag)`	HAC lag
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(opt)`	`ml` or `irls`
`e(opt1)`	optimization title, line 1
`e(opt2)`	optimization title, line 2
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(marginsok)`	predictions allowed by `margins`
`e(marginsnotok)`	predictions disallowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(Cns)`	constraints matrix
`e(V)`	variance–covariance matrix of the estimators
`e(V_modelbased)`	model-based variance

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`glm` is implemented as an ado-file.

The canonical reference on GLM is McCullagh and Nelder (1989). The term "generalized linear model" is from Nelder and Wedderburn (1972). Many people use the acronym GLIM for GLM models because of the classic GLM software tool GLIM, by Baker and Nelder (1985). See Dobson and Barnett (2008) for a concise introduction and overview. See Rabe-Hesketh and Everitt (2007) for more examples of GLM using Stata. Hoffmann (2004) focuses on applying generalized linear models, using real-world datasets, along with interpreting computer output, which for the most part is obtained using Stata.

This discussion highlights the details of parameter estimation and predicted statistics. For a more detailed treatment, and for information on variance estimation, see Hardin and Hilbe (2007). `glm` supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

`glm` obtains results by IRLS, as described in McCullagh and Nelder (1989), or by maximum likelihood using Newton–Raphson. The implementation here, however, allows user-specified weights, which we denote as v_j for the jth observation. Let M be the number of "observations" ignoring weights. Define

$$w_j = \begin{cases} 1 & \text{if no weights are specified} \\ v_j & \text{if } \texttt{fweights} \text{ or } \texttt{iweights} \text{ are specified} \\ Mv_j/(\sum_k v_k) & \text{if } \texttt{aweights} \text{ or } \texttt{pweights} \text{ are specified} \end{cases}$$

The number of observations is then $N = \sum_j w_j$ if `fweights` are specified and $N = M$ otherwise. Each IRLS step is performed by `regress` using w_j as the weights.

Let d_j^2 denote the squared deviance residual for the jth observation:

For the Gaussian family, $d_j^2 = (y_j - \widehat{\mu}_j)^2$.

For the Bernoulli family (binomial with denominator 1),

$$d_j^2 = \begin{cases} -2\ln(1-\widehat{\mu}_j) & \text{if } y_j = 0 \\ -2\ln(\widehat{\mu}_j) & \text{otherwise} \end{cases}$$

For the binomial family with denominator m_j,

$$d_j^2 = \begin{cases} 2y_j\ln(y_j/\widehat{\mu}_j) + 2(m_j - y_j)\ln\{(m_j - y_j)/(m_j - \widehat{\mu}_j)\} & \text{if } 0 < y_j < m_j \\ 2m_j\ln\{m_j/(m_j - \widehat{\mu}_j)\} & \text{if } y_j = 0 \\ 2y_j\ln(y_j/\widehat{\mu}_j) & \text{if } y_j = m_j \end{cases}$$

For the Poisson family,

$$d_j^2 = \begin{cases} 2\widehat{\mu}_j & \text{if } y_j = 0 \\ 2\{y_j\ln(y_j/\widehat{\mu}_j) - (y_j - \widehat{\mu}_j)\} & \text{otherwise} \end{cases}$$

For the gamma family, $d_j^2 = -2\{\ln(y_j/\widehat{\mu}_j) - (y_j - \widehat{\mu}_j)/\widehat{\mu}_j\}$.

For the inverse Gaussian, $d_j^2 = (y_j - \widehat{\mu}_j)^2/(\widehat{\mu}_j^2 y_j)$.

For the negative binomial,

$$d_j^2 = \begin{cases} 2\ln(1+k\widehat{\mu}_j)/k & \text{if } y_j = 0 \\ 2y_j\ln(y_j/\widehat{\mu}_j) - 2\{(1+ky_j)/k\}\ln\{(1+ky_j)/(1+k\widehat{\mu}_j)\} & \text{otherwise} \end{cases}$$

Let $\phi = 1$ if the scale parameter is set to one; otherwise, define $\phi = \widehat{\phi}_0(n-k)/n$, where $\widehat{\phi}_0$ is the estimated scale parameter and k is the number of covariates in the model (including intercept).

Let $\ln L_j$ denote the log likelihood for the jth observation:

For the Gaussian family,

$$\ln L_j = -\frac{1}{2}\left[\left\{\frac{(y_j-\widehat{\mu}_j)^2}{\phi}\right\} + \ln(2\pi\phi)\right]$$

For the binomial family with denominator m_j (Bernoulli if all $m_j = 1$),

$$\ln L_j = \phi \times \begin{cases} \ln\{\Gamma(m_j+1)\} - \ln\{\Gamma(y_j+1)\} + \ln\{\Gamma(m_j-y_j+1)\} \\ \quad +(m_j-y_j)\ln(1-\widehat{\mu}_j/m_j) + y_j\ln(\widehat{\mu}_j/m_j) & \text{if } 0 < y_j < m_j \\ m_j\ln(1-\widehat{\mu}_j/m_j) & \text{if } y_j = 0 \\ m_j\ln(\widehat{\mu}_j/m_j) & \text{if } y_j = m_j \end{cases}$$

For the Poisson family,

$$\ln L_j = \phi\,[y_j\ln(\widehat{\mu}_j) - \widehat{\mu}_j - \ln\{\Gamma(y_j+1)\}]$$

For the gamma family, $\ln L_j = -y_j/\widehat{\mu}_j + \ln(1/\widehat{\mu}_j)$.

For the inverse Gaussian,

$$\ln L_j = -\frac{1}{2}\left\{\frac{(y_j-\widehat{\mu}_j)^2}{y_j\widehat{\mu}_j^2} + 3\ln(y_j) + \ln(2\pi)\right\}$$

For the negative binomial (let $m = 1/k$),

$$\begin{aligned}\ln L_j = &\phi\,[\ln\{\Gamma(m+y_j)\} - \ln\{\Gamma(y_j+1)\} - \ln\{\Gamma(m)\} \\ &-m\ln(1+\widehat{\mu}_j/m) + y_j\ln\{\widehat{\mu}_j/(\widehat{\mu}_j+m)\}]\end{aligned}$$

The overall deviance reported by `glm` is $D^2 = \sum_j w_j d_j^2$. The dispersion of the deviance is D^2 divided by the residual degrees of freedom.

The Akaike information criterion (AIC) and Bayesian information criterion (BIC) are given by

$$\begin{aligned}\text{AIC} &= \frac{-2\ln L + 2k}{N} \\ \text{BIC} &= D^2 - (N-k)\ln(N)\end{aligned}$$

where $\ln L = \sum_j w_j \ln L_j$ is the overall log likelihood.

The Pearson deviance reported by `glm` is $\sum_j w_j r_j^2$. The corresponding Pearson dispersion is the Pearson deviance divided by the residual degrees of freedom. `glm` also calculates the scaled versions of all these quantities by dividing by the estimated scale parameter.

Acknowledgments

`glm` was written by James Hardin, University of South Carolina, and Joseph Hilbe, Arizona State University. The previous version of this routine was written by Patrick Royston, MRC Clinical Trials Unit, London. The original version of this routine was published in Royston (1994). Royston's work, in turn, was based on a prior implementation by Joseph Hilbe, first published in Hilbe (1993). Roger Newson wrote an early implementation (Newson 1999) of robust variance estimates for GLM. Parts of this entry are excerpts from Hardin and Hilbe (2007).

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Also see

[R] **glm postestimation** — Postestimation tools for glm

[R] **cloglog** — Complementary log-log regression

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **nbreg** — Negative binomial regression

[R] **poisson** — Poisson regression

[R] **regress** — Linear regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtgee** — Fit population-averaged panel-data models by using GEE

[U] **20 Estimation and postestimation commands**

Title

glm postestimation — Postestimation tools for glm

Description

The following postestimation commands are available after `glm`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic options]
```

statistic	Description
Main	
mu	expected value of y; the default
xb	linear prediction $\eta = \mathbf{x}\widehat{\boldsymbol{\beta}}$
eta	synonym of xb
stdp	standard error of the linear prediction
anscombe	Anscombe (1953) residuals
cooksd	Cook's distance
deviance	deviance residuals
hat	diagonals of the "hat" matrix
likelihood	a weighted average of standardized deviance and standardized Pearson residuals
pearson	Pearson residuals
response	differences between the observed and fitted outcomes
score	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$
working	working residuals

options	Description
Options	
nooffset	modify calculations to ignore offset variable
adjusted	adjust deviance residual to speed up convergence
standardized	multiply residual by the factor $(1-h)^{-1/2}$
studentized	multiply residual by one over the square root of the estimated scale parameter
modified	modify denominator of residual to be a reasonable estimate of the variance of *depvar*

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`mu`, `xb`, `stdp`, and `score` are the only statistics allowed with `svy` estimation results.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`mu`, the default, specifies that `predict` calculate the expected value of y, equal to $g^{-1}(\mathbf{x}\widehat{\boldsymbol{\beta}})$ [$ng^{-1}(\mathbf{x}\widehat{\boldsymbol{\beta}})$ for the binomial family].

`xb` calculates the linear prediction $\eta = \mathbf{x}\widehat{\boldsymbol{\beta}}$.

`eta` is a synonym for `xb`.

`stdp` calculates the standard error of the linear prediction.

`anscombe` calculates the Anscombe (1953) residuals to produce residuals that closely follow a normal distribution.

`cooksd` calculates Cook's distance, which measures the aggregate change in the estimated coefficients when each observation is left out of the estimation.

`deviance` calculates the deviance residuals. Deviance residuals are recommended by McCullagh and Nelder (1989) and by others as having the best properties for examining the goodness of fit of a GLM. They are approximately normally distributed if the model is correct. They may be plotted against the fitted values or against a covariate to inspect the model's fit. Also see the `pearson` option below.

`hat` calculates the diagonals of the "hat" matrix as an analog to simple linear regression.

`likelihood` calculates a weighted average of standardized deviance and standardized Pearson residuals.

`pearson` calculates the Pearson residuals. Pearson residuals often have markedly skewed distributions for nonnormal family distributions. Also see the `deviance` option above.

`response` calculates the differences between the observed and fitted outcomes.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

`working` calculates the working residuals, which are response residuals weighted according to the derivative of the link function.

Options

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `glm`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`adjusted` adjusts the deviance residual to speed up the convergence to the limiting normal distribution. The adjustment deals with adding to the deviance residual a higher-order term that depends on the variance function family. This option is allowed only when `deviance` is specified.

`standardized` requests that the residual be multiplied by the factor $(1-h)^{-1/2}$, where h is the diagonal of the hat matrix. This operation is done to account for the correlation between *depvar* and its predicted value.

`studentized` requests that the residual be multiplied by one over the square root of the estimated scale parameter.

`modified` requests that the denominator of the residual be modified to be a reasonable estimate of the variance of *depvar*. The base residual is multiplied by the factor $(k/w)^{-1/2}$, where k is either one or the user-specified dispersion parameter and w is the specified weight (or one if left unspecified).

Remarks

Remarks are presented under the following headings:

Predictions
Other postestimation commands

Predictions

▷ Example 1

After `glm` estimation, `predict` may be used to obtain various predictions based on the model. In example 2 of [R] **glm**, we mentioned that the complementary log-log link seemed to fit the data better than the logit link. Now we go back and obtain the fitted values and deviance residuals:

```
. use http://www.stata-press.com/data/r12/ldose
. glm r ldose, f(binomial n) l(logit)
  (output omitted)
. predict mu_logit
(option mu assumed; predicted mean r)
. predict dr_logit, deviance
. quietly glm r ldose, f(binomial n) l(cloglog)
. predict mu_cl
(option mu assumed; predicted mean r)
. predict dr_cl, d
. format mu_logit dr_logit mu_cl dr_cl %9.5f
. list r mu_logit dr_logit mu_cl dr_cl, sep(4)
```

	r	mu_logit	dr_logit	mu_cl	dr_cl
1.	6	3.45746	1.28368	5.58945	0.18057
2.	13	9.84167	1.05969	11.28067	0.55773
3.	18	22.45139	-1.19611	20.95422	-0.80330
4.	28	33.89761	-1.59412	30.36942	-0.63439
5.	52	50.09584	0.60614	47.77644	1.28883
6.	53	53.29092	-0.12716	54.14273	-0.52366
7.	61	59.22216	1.25107	61.11331	-0.11878
8.	60	58.74297	1.59398	59.94723	0.32495

In six of the eight cases, $|$`dr_logit`$| > |$`dr_cl`$|$. The above represents only one of the many available options for `predict`. See Hardin and Hilbe (2007) for a more in-depth examination.

◁

Other postestimation commands

❑ Technical note

After `glm` estimation, you may perform any of the postestimation commands that you would perform after any other kind of estimation in Stata; see [U] **20 Estimation and postestimation commands**. Below we test the joint significance of all the interaction terms.

```
. use http://www.stata-press.com/data/r12/beetle, clear
. glm r beetle##c.ldose, f(bin n) l(cloglog)
  (output omitted)
. testparm i.beetle beetle#c.ldose
 ( 1)  [r]2.beetle = 0
 ( 2)  [r]3.beetle = 0
 ( 3)  [r]2.beetle#c.ldose = 0
 ( 4)  [r]3.beetle#c.ldose = 0
           chi2(  4) =  249.69
         Prob > chi2 =    0.0000
```

If you wanted to print the variance–covariance matrix of the estimators, you would type `estat vce`.

If you use the `linktest` postestimation command, you must also specify the `family()` and `link()` options; see [R] **linktest**.

❑

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

We follow the terminology used in *Methods and formulas* of [R] **glm**.

The deviance residual calculated by `predict` following `glm` is $d_j = \text{sign}(y_j - \widehat{\mu}_j)\sqrt{d_j^2}$.

The Pearson residual calculated by `predict` following `glm` is

$$r_j = \frac{y_j - \widehat{\mu}_j}{\sqrt{V(\widehat{\mu}_j)}}$$

where $V(\widehat{\mu}_j)$ is the family-specific variance function.

$$V(\widehat{\mu}_j) = \begin{cases} \widehat{\mu}_j(1 - \widehat{\mu}_j/m_j) & \text{if binomial or Bernoulli } (m_j = 1) \\ \widehat{\mu}_j^2 & \text{if gamma} \\ 1 & \text{if Gaussian} \\ \widehat{\mu}_j^3 & \text{if inverse Gaussian} \\ \widehat{\mu}_j + k\widehat{\mu}_j^2 & \text{if negative binomial} \\ \widehat{\mu}_j & \text{if Poisson} \end{cases}$$

The response residuals are given by $r_i^R = y_i - \mu_i$. The working residuals are

$$r_i^W = (y_i - \widehat{\mu}_i)\left(\frac{\partial \eta}{\partial \mu}\right)_i$$

and the score residuals are

$$r_i^S = \frac{y_i - \widehat{\mu}_i}{V(\widehat{\mu}_i)}\left(\frac{\partial \eta}{\partial \mu}\right)_i^{-1}$$

Define $\widehat{W} = V(\widehat{\mu})$ and X to be the covariate matrix. h_i, then, is the ith diagonal of the hat matrix given by

$$\widehat{H} = \widehat{W}^{1/2}X(X^T\widehat{W}X)^{-1}X^T\widehat{W}^{1/2}$$

As a result, the likelihood residuals are given by

$$r_i^L = \text{sign}(y_i - \widehat{\mu}_i)\left\{h_i(r_i^{'})^2 + (1 - h_i)(d_i^{'})^2\right\}^{1/2}$$

where $r_i^{'}$ and $d_i^{'}$ are the standardized Pearson and standardized deviance residuals, respectively. By *standardized*, we mean that the residual is divided by $\{1 - h_i\}^{1/2}$.

Cook's distance is an overall measure of the change in the regression coefficients caused by omitting the ith observation from the analysis. Computationally, Cook's distance is obtained as

$$C_i = \frac{(r_i')^2 h_i}{k(1 - h_i)}$$

where k is the number of regressors, including the constant.

Anscombe residuals are given by

$$r_i^A = \frac{A(y_i) - A(\widehat{\mu}_i)}{A'(\widehat{\mu}_i)\{V(\widehat{\mu}_i)\}^{1/2}}$$

where

$$A(\cdot) = \int \frac{d\mu}{V^{1/3}(\mu)}$$

Deviance residuals may be adjusted (`predict, adjusted`) to make the following correction:

$$d_i^a = d_i + \frac{1}{6}\rho_3(\theta)$$

where $\rho_3(\theta)$ is a family-specific correction. See Hardin and Hilbe (2007) for the exact forms of $\rho_3(\theta)$ for each family.

References

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Hardin, J. W., and J. M. Hilbe. 2007. *Generalized Linear Models and Extensions*. 2nd ed. College Station, TX: Stata Press.

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Also see

[R] **glm** — Generalized linear models

[R] **regress postestimation** — Postestimation tools for regress

[U] **20 Estimation and postestimation commands**

Title

glogit — Logit and probit regression for grouped data

Syntax

Logistic regression for grouped data

`blogit` *pos_var pop_var* [*indepvars*] [*if*] [*in*] [, *blogit_options*]

Probit regression for grouped data

`bprobit` *pos_var pop_var* [*indepvars*] [*if*] [*in*] [, *bprobit_options*]

Weighted least-squares logistic regression for grouped data

`glogit` *pos_var pop_var* [*indepvars*] [*if*] [*in*] [, *glogit_options*]

Weighted least-squares probit regression for grouped data

`gprobit` *pos_var pop_var* [*indepvars*] [*if*] [*in*] [, *gprobit_options*]

blogit_options	Description
Model	
`noconstant`	suppress constant term
`asis`	retain perfect predictor variables
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`or`	report odds ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`nocoef`	do not display coefficient table; seldom used
`coeflegend`	display legend instead of statistics

bprobit_options	Description
Model	
noconstant	suppress constant term
asis	retain perfect predictor variables
offset(*varname*)	include *varname* in model with coefficient constrained to 1
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
nocoef	do not display coefficient table; seldom used
coeflegend	display legend instead of statistics

glogit_options	Description
SE	
vce(*vcetype*)	*vcetype* may be ols, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
or	report odds ratios
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
coeflegend	display legend instead of statistics

gprobit_options	Description
SE	
vce(*vcetype*)	*vcetype* may be ols, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
coeflegend	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.

`nocoef` and `coeflegend` do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

blogit

Statistics > Binary outcomes > Grouped data > Logit regression for grouped data

bprobit

Statistics > Binary outcomes > Grouped data > Probit regression for grouped data

glogit

Statistics > Binary outcomes > Grouped data > Weighted least-squares logit regression

gprobit

Statistics > Binary outcomes > Grouped data > Weighted least-squares probit regression

Description

`blogit` and `bprobit` produce maximum-likelihood logit and probit estimates on grouped ("blocked") data; `glogit` and `gprobit` produce weighted least-squares estimates. In the syntax diagrams above, *pos_var* and *pop_var* refer to variables containing the total number of positive responses and the total population.

See [R] **logistic** for a list of related estimation commands.

Options for blogit and bprobit

Model

`noconstant`; see [R] **estimation options**.

`asis` forces retention of perfect predictor variables and their associated perfectly predicted observations and may produce instabilities in maximization; see [R] **probit**.

`offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

or (blogit only) reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. or may be specified at estimation or when replaying previously estimated results.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

The following options are available with blogit and bprobit but are not shown in the dialog box:

nocoef specifies that the coefficient table not be displayed. This option is sometimes used by program writers but is useless interactively.

coeflegend; see [R] **estimation options**.

Options for glogit and gprobit

SE

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory and that use bootstrap or jackknife methods; see [R] ***vce_option***.

vce(ols), the default, uses the standard variance estimator for ordinary least-squares regression.

Reporting

level(#); see [R] **estimation options**.

or (glogit only) reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. or may be specified at estimation or when replaying previously estimated results.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

The following option is available with glogit and gprobit but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Maximum likelihood estimates
Weighted least-squares estimates

Maximum likelihood estimates

`blogit` produces the same results as `logit` and `logistic`, and `bprobit` produces the same results as `probit`, but the "blocked" commands accept data in a slightly different "shape". Consider the following two datasets:

```
. use http://www.stata-press.com/data/r12/xmpl1
. list, sepby(agecat)
```

	agecat	exposed	died	pop
1.	0	0	0	115
2.	0	0	1	5
3.	0	1	0	98
4.	0	1	1	8
5.	1	0	0	69
6.	1	0	1	16
7.	1	1	0	76
8.	1	1	1	22

```
. use http://www.stata-press.com/data/r12/xmpl2
. list
```

	agecat	exposed	deaths	pop
1.	0	0	5	120
2.	0	1	8	106
3.	1	0	16	85
4.	1	1	22	98

These two datasets contain the same information; observations 1 and 2 of `xmpl1` correspond to observation 1 of `xmpl2`, observations 3 and 4 of `xmpl1` correspond to observation 2 of `xmpl2`, and so on.

The first observation of `xmpl1` says that for `agecat==0` and `exposed==0`, 115 subjects did not die (`died==0`). The second observation says that for the same `agecat` and `exposed` groups, five subjects did die (`died==1`). In `xmpl2`, the first observation says that there were five deaths of a population of 120 in `agecat==0` and `exposed==0`. These are two different ways of saying the same thing. Both datasets are transcriptions from the following table, reprinted in Rothman, Greenland, and Lash (2008, 260), for age-specific deaths from all causes for tolbutamide and placebo treatment groups (University Group Diabetes Program 1970):

	Age through 54		Age 55 and above	
	Tolbutamide	Placebo	Tolbutamide	Placebo
Dead	8	5	22	16
Surviving	98	115	76	79

The data in `xmpl1` are said to be "fully relational", which is computer jargon meaning that each observation corresponds to one cell of the table. Stata typically prefers data in this format. The second form of storing these data in `xmpl2` is said to be "folded", which is computer jargon for something less than fully relational.

`blogit` and `bprobit` deal with "folded" data and produce the same results that `logit` and `probit` would have if the data had been stored in the "fully relational" representation.

Example 1

For the tolbutamide data, the fully relational representation is preferred. We could then use `logistic`, `logit`, and any of the epidemiological table commands; see [R] **logistic**, [R] **logit**, and [ST] **epitab**. Nevertheless, there are occasions when the folded representation seems more natural. With `blogit` and `bprobit`, we avoid the tedium of having to unfold the data:

```
. use http://www.stata-press.com/data/r12/xmpl2
. blogit deaths pop agecat exposed, or
Logistic regression for grouped data              Number of obs   =        409
                                                  LR chi2(2)      =      22.47
                                                  Prob > chi2     =     0.0000
Log likelihood =  -142.6212                       Pseudo R2       =     0.0730

------------------------------------------------------------------------------
    _outcome | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      agecat |   4.216299   1.431519     4.24   0.000     2.167361    8.202223
     exposed |   1.404674   .4374454     1.09   0.275     .7629451    2.586175
       _cons |   .0513818   .0170762    -8.93   0.000     .0267868    .0985593
------------------------------------------------------------------------------
```

If we had not specified the `or` option, results would have been presented as coefficients instead of as odds ratios. The estimated odds ratio of death for tolbutamide exposure is 1.40, although the 95% confidence interval includes 1. (By comparison, these data, in fully relational form and analyzed using the `cs` command [see [ST] **epitab**], produce a Mantel–Haenszel weighted odds ratio of 1.40 with a 95% confidence interval of 0.76 to 2.59.)

We can see the underlying coefficients by replaying the estimation results and not specifying the `or` option:

```
. blogit
Logistic regression for grouped data              Number of obs   =        409
                                                  LR chi2(2)      =      22.47
                                                  Prob > chi2     =     0.0000
Log likelihood =  -142.6212                       Pseudo R2       =     0.0730

------------------------------------------------------------------------------
    _outcome |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      agecat |   1.438958   .3395203     4.24   0.000     .7735101    2.104405
     exposed |   .3398053   .3114213     1.09   0.275    -.2705692    .9501798
       _cons |  -2.968471     .33234    -8.93   0.000    -3.619846   -2.317097
------------------------------------------------------------------------------
```

▷ Example 2

`bprobit` works like `blogit`, substituting the probit for the logit-likelihood function.

```
. bprobit deaths pop agecat exposed
Probit regression for grouped data                Number of obs   =        409
                                                  LR chi2(2)      =      22.58
                                                  Prob > chi2     =     0.0000
Log likelihood = -142.56478                       Pseudo R2       =     0.0734

------------------------------------------------------------------------------
    _outcome |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      agecat |   .7542049   .1709692     4.41   0.000     .4191114    1.089298
     exposed |   .1906236   .1666059     1.14   0.253    -.1359179    .5171651
       _cons |  -1.673973   .1619594   -10.34   0.000    -1.991408   -1.356539
------------------------------------------------------------------------------
```

◁

Weighted least-squares estimates

▷ Example 3

We have state data for the United States on the number of marriages (`marriage`), the total population aged 18 years or more (`pop18p`), and the median age (`medage`). The dataset excludes Nevada, so it has 49 observations. We now wish to estimate a logit equation for the marriage rate. We will include age squared by specifying the term `c.medage#c.medage`:

```
. use http://www.stata-press.com/data/r12/census7
(1980 Census data by state)
. glogit marriage pop18p medage c.medage#c.medage
Weighted LS logistic regression for grouped data

      Source |       SS       df       MS              Number of obs =      49
-------------+------------------------------           F(  2,    46) =   12.89
       Model |  .71598314      2   .35799157           Prob > F      =  0.0000
    Residual |  1.27772858    46  .027776708           R-squared     =  0.3591
-------------+------------------------------           Adj R-squared =  0.3313
       Total |  1.99371172    48  .041535661           Root MSE      =  .16666

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     medage  |  -.6459349   .2828381    -2.28   0.027    -1.215258   -.0766114
             |
  c.medage#  |
  c.medage   |   .0095414   .0046608     2.05   0.046     .0001598    .0189231
             |
       _cons |   6.503833   4.288977     1.52   0.136    -2.129431    15.1371
------------------------------------------------------------------------------
```

◁

▷ Example 4

We could just as easily have fit a grouped-probit model by typing `gprobit` rather than `glogit`:

```
. gprobit marriage pop18p medage c.medage#c.medage
Weighted LS probit regression for grouped data
```

Source	SS	df	MS		
Model	.108222962	2	.054111481	Number of obs	= 49
Residual	.192322476	46	.004180923	F(2, 46)	= 12.94
				Prob > F	= 0.0000
Total	.300545438	48	.006261363	R-squared	= 0.3601
				Adj R-squared	= 0.3323
				Root MSE	= .06466

	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
medage	-.2755007	.1121042	-2.46	0.018	-.5011548	-.0498466
c.medage# c.medage	.0041082	.0018422	2.23	0.031	.0004001	.0078163
_cons	2.357708	1.704446	1.38	0.173	-1.073164	5.788579

◁

Saved results

`blogit` and `bprobit` save the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_cds)`	number of completely determined successes
`e(N_cdf)`	number of completely determined failures
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(r2_p)`	pseudo-R-squared
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance of model test
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	blogit or bprobit
e(cmdline)	command as typed
e(depvar)	variable containing number of positive responses and variable containing population size
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(mns)	vector of means of the independent variables
e(rules)	information about perfect predictors
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

glogit and gprobit save the following in e():

Scalars

e(N)	number of observations
e(mss)	model sum of squares
e(df_m)	model degrees of freedom
e(rss)	residual sum of squares
e(df_r)	residual degrees of freedom
e(r2)	R-squared
e(r2_a)	adjusted R-squared
e(F)	F statistic
e(rmse)	root mean squared error
e(rank)	rank of e(V)

Macros

e(cmd)	glogit or gprobit
e(cmdline)	command as typed
e(depvar)	variable containing number of positive responses and variable containing population size
e(model)	ols
e(title)	title in estimation output
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`blogit`, `bprobit`, `glogit`, and `gprobit` are implemented as ado-files.

Methods and formulas are presented under the following headings:

Maximum likelihood estimates
Weighted least-squares estimates

Maximum likelihood estimates

The results reported by `blogit` and `bprobit` are obtained by maximizing a weighted logit- or probit-likelihood function. Let $F(\,)$ denote the normal- or logistic-likelihood function. The likelihood of observing each observation in the data is then

$$F(\beta x)^s\{1-F(\beta x)\}^{t-s}$$

where s is the number of successes and t is the population. The term above is counted as contributing $s+(t-s)=t$ degrees of freedom. All of this follows directly from the definitions of logit and probit.

`blogit` and `bprobit` support the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

Weighted least-squares estimates

The logit function is defined as the log of the odds ratio. If there is one explanatory variable, the model can be written as

$$\log\left(\frac{p_j}{1-p_j}\right)=\beta_0+\beta_1 x_j+\epsilon_j \tag{1}$$

where p_j represents successes divided by population for the jth observation. (If there is more than one explanatory variable, we simply interpret β_1 as a row vector and x_j as a column vector.) The large-sample expectation of ϵ_j is zero, and its variance is

$$\sigma_j^2=\frac{1}{n_j p_j(1-p_j)}$$

where n_j represents the population for observation j. We can thus apply weighted least squares to the observations, with weights proportional to $n_j p_j(1-p_j)$.

As in any feasible generalized least-squares problem, estimation proceeds in two steps. First, we fit (1) by OLS and compute the predicted probabilities as

$$\widehat{p_j}=\frac{\exp(\widehat{\beta_0}+\widehat{\beta_1}x_j)}{1+\exp(\widehat{\beta_0}+\widehat{\beta_1}x_j)}$$

In the second step, we fit (1) by using analytic weights equal to $n_j\widehat{p_j}(1-\widehat{p_j})$.

For `gprobit`, write $\Phi(\cdot)$ for the cumulative normal distribution, and define z_j implicitly by $\Phi(z_j) = p_j$, where p_j is the fraction of successes for observation j. The probit model for one explanatory variable can be written as

$$\Phi^{-1}(p_j) = \beta_0 + \beta_1 x_j + \epsilon_j$$

(If there is more than one explanatory variable, we simply interpret β_1 as a row vector and x_j as a column vector.)

The expectation of ϵ_j is zero, and its variance is given by

$$\sigma_j^2 = \frac{p_j(1-p_j)}{n_j \phi^2\{\Phi^{-1}(p_j)\}}$$

where $\phi(\cdot)$ represents the normal density (Amemiya 1981, 1498). We can thus apply weighted least squares to the observations with weights proportional to $1/\sigma_j^2$. As for grouped logit, we use a two-step estimator to obtain the weighted least-squares estimates.

References

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Judge, G. G., W. E. Griffiths, R. C. Hill, H. Lütkepohl, and T.-C. Lee. 1985. *The Theory and Practice of Econometrics*. 2nd ed. New York: Wiley.

Rothman, K. J., S. Greenland, and T. L. Lash. 2008. *Modern Epidemiology*. 3rd ed. Philadelphia: Lippincott Williams & Wilkins.

University Group Diabetes Program. 1970. A study of the effects of hypoglycemic agents on vascular complications in patients with adult-onset diabetes, II: Mortality results. *Diabetes* 19, supplement 2: 789–830.

Also see

[R] **glogit postestimation** — Postestimation tools for glogit, gprobit, blogit, and bprobit

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **probit** — Probit regression

[R] **scobit** — Skewed logistic regression

[U] **20 Estimation and postestimation commands**

Title

glogit postestimation — Postestimation tools for glogit, gprobit, blogit, and bprobit

Description

The following postestimation commands are available after `glogit`, `gprobit`, `blogit`, and `bprobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
* `estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
* `lrtest`	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

* `estat ic` and `lrtest` are not appropriate after `glogit` and `gprobit`.

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [, *statistic*]

statistic	Description
Main	
`n`	predicted count; the default
`pr`	probability of a positive outcome
`xb`	linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`n`, the default, calculates the expected count, that is, the estimated probability times *pop_var*, which is the total population.

`pr` calculates the predicted probability of a positive outcome.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **glogit** — Logit and probit regression for grouped data

[U] **20 Estimation and postestimation commands**

Title

gmm — Generalized method of moments estimation

Syntax

Interactive version

`gmm` (*eqname*$_1$`:`]<*mexp*$_1$>) (*eqname*$_2$`:`]<*mexp*$_2$>)...[*if*] [*in*] [*weight*] [`,` *options*]

Moment-evaluator program version

`gmm` *moment_prog* [*if*] [*in*] [*weight*] `,` { `equations(`*namelist*`)` | `nequations(#)` }
{ `parameters(`*namelist*`)` | `nparameters(#)` } [*options*] [*program_options*]

where

mexp$_j$ is the substitutable expression for the jth moment equation and

moment_prog is a moment-evaluator program.

options	Description
Model	
`derivative(`<*dexp*$_{mn}$>`)`	specify derivative of *mexp*$_m$ with respect to parameter n; can be specified more than once (interactive version only)
* `twostep`	use two-step GMM estimator; the default
* `onestep`	use one-step GMM estimator
* `igmm`	use iterative GMM estimator
Instruments	
`instruments(`[<*eqlist*>`:`]*varlist*[`, noconstant`]`)`	specify instruments; can be specified more than once
`xtinstruments(`[<*eqlist*>`:`]*varlist*`, lags(`#$_1$`/`#$_2$`))`	specify panel-style instruments; can be specified more than once
Weight matrix	
`wmatrix(`*wmtype*[`, independent`]`)`	specify weight matrix; *wmtype* may be `robust`, `cluster` *clustvar*, `hac` *kernel* [*lags*], or `unadjusted`
`center`	center moments in weight-matrix computation
`winitial(`*iwtype*[`, independent`]`)`	specify initial weight matrix; *iwtype* may be `identity`, `unadjusted`, `xt` *xtspec*, or the name of a Stata matrix

Options

variables(*varlist*)	specify variables in model
nocommonesample	do not restrict estimation sample to be the same for all equations

SE/Robust

vce(*vcetype*[, independent])	*vcetype* may be robust, cluster *clustvar*, bootstrap, jackknife, hac *kernel lags*, or unadjusted

Reporting

level(#)	set confidence level; default is level(95)
title(*string*)	display *string* as title above the table of parameter estimates
title2(*string*)	display *string* as subtitle
display_options	control column formats and line width

Optimization

from(*initial_values*)	specify initial values for parameters
‡ igmmiterate(#)	specify maximum number of iterations for iterated GMM estimator
‡ igmmeps(#)	specify # for iterated GMM parameter convergence criterion; default is igmmeps(1e-6)
‡ igmmweps(#)	specify # for iterated GMM weight-matrix convergence criterion; default is igmmweps(1e-6)
optimization_options	control the optimization process; seldom used
coeflegend	display legend instead of statistics

* You can specify at most one of these options.

‡ These options may be specified only when igmm is specified.

program_options	Description

Model

evaluator_options	additional options to be passed to the moment-evaluator program
hasderivatives	moment-evaluator program can calculate derivatives
* equations(*namelist*)	specify moment-equation names
* nequations(#)	specify number of moment equations
‡ parameters(*namelist*)	specify parameter names
‡ nparameters(#)	specify number of parameters

* You must specify equations(*namelist*) or nequations(#); you may specify both.

‡ You must specify parameters(*namelist*) or nparameters(#); you may specify both.

bootstrap, by, jackknife, rolling, statsby, and xi are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
aweights are not allowed with the jackknife prefix; see [R] **jackknife**.
aweights, fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

<*mexp*$_j$> and <*dexp*$_{mn}$> are extensions of valid Stata expressions that also contain parameters to be estimated. The parameters are enclosed in curly braces and must otherwise satisfy the naming requirements for variables; `{beta}` is an example of a parameter. Also allowed is a notation of the form {<*eqname*>:*varlist*} for linear combinations of multiple covariates and their parameters. For example, `{xb: mpg price turn}` defines a linear combination of the variables `mpg`, `price`, and `turn`. See *Substitutable expressions* under *Remarks* below.

Menu

Statistics > Endogenous covariates > Generalized method of moments estimation

Description

`gmm` performs generalized method of moments (GMM) estimation. With the interactive version of the command, you enter the moment equations directly into the dialog box or on the command line using substitutable expressions. The moment-evaluator program version gives you greater flexibility in exchange for increased complexity; with this version, you write a program in an ado-file that calculates the moments based on a vector of parameters passed to it.

`gmm` can fit both single- and multiple-equation models, and it allows moment conditions of the form $E\{\mathbf{z}_i u_i(\beta)\} = \mathbf{0}$, where $\mathbf{z}_i$ is a vector of instruments and $u_i(\beta)$ is often an additive regression error term, as well as more general moment conditions of the form $E\{\mathbf{h}_i(\mathbf{z}_i;\beta)\} = \mathbf{0}$. `gmm` works with cross-sectional, time-series, and longitudinal (panel) data.

Options

Model

`derivative(`[*eqname* | #]`/`*name* `=` <*dexp*$_{mn}$>`)` specifies the derivative of moment equation *eqname* or # with respect to parameter *name*. If *eqname* or # is not specified, `gmm` assumes that the derivative applies to the first moment equation.

For a moment equation of the form $E\{\mathbf{z}_{mi}u_{mi}(\beta)\} = \mathbf{0}$, `derivative(`*m*`/`$\beta_j$ `=` <*dexp*$_{mn}$>`)` is to contain a substitutable expression for $\partial u_{mi}/\partial\beta_j$.

For a moment equation of the form $E\{h_{mi}(\mathbf{z}_i;\beta)\} = \mathbf{0}$, `derivative(`*m*`/`$\beta_j$ `=` <*dexp*$_{mn}$>`)` is to contain a substitutable expression for $\partial h_{mi}/\partial\beta_j$.

<*dexp*$_{mn}$> uses the same substitutable expression syntax as is used to specify moment equations. If you declare a linear combination in a moment equation, you provide the derivative for the linear combination; `gmm` then applies the chain rule for you. See *Specifying derivatives* under *Remarks* below for examples.

If you do not specify the `derivative()` option, `gmm` calculates derivatives numerically. You must either specify no derivatives or specify all the derivatives that are not identically zero; you cannot specify some analytic derivatives and have `gmm` compute the rest numerically.

`twostep`, `onestep`, and `igmm` specify which estimator is to be used. You can specify at most one of these options. `twostep` is the default.

`twostep` requests the two-step GMM estimator. `gmm` obtains parameter estimates based on the initial weight matrix, computes a new weight matrix based on those estimates, and then reestimates the parameters based on that weight matrix.

`onestep` requests the one-step GMM estimator. The parameters are estimated based on an initial weight matrix, and no updating of the weight matrix is performed except when calculating the appropriate variance–covariance (VCE) matrix.

`igmm` requests the iterative GMM estimator. `gmm` obtains parameter estimates based on the initial weight matrix, computes a new weight matrix based on those estimates, reestimates the parameters based on that weight matrix, computes a new weight matrix, and so on, to convergence. Convergence is declared when the relative change in the parameter vector is less than `igmmeps()`, the relative change in the weight matrix is less than `igmmweps()`, or `igmmiterate()` iterations have been completed. Hall (2005, sec. 2.4 and 3.6) mentions that there may be gains to finite-sample efficiency from using the iterative estimator.

Instruments

`instruments(`[*<eqlist>*`:`]*varlist*[`, noconstant`]`)` specifies a list of instrumental variables to be used. If you specify a single moment equation, then you do not need to specify the equations to which the instruments apply; you can omit the *eqlist* and simply specify `instruments(`*varlist*`)`. By default, a constant term is included in *varlist*; to omit the constant term, use the `noconstant` suboption: `instruments(`*varlist*`, noconstant)`.

If you specify a model with multiple moment conditions of the form

$$E\left\{\begin{array}{c}\mathbf{z}_{1i}u_{1i}(\beta)\\ \cdots\\ \mathbf{z}_{qi}u_{qi}(\beta)\end{array}\right\}=\mathbf{0}$$

then you can specify the equations to indicate the moment equations for which the list of variables is to be used as instruments if you do not want that list applied to all the moment equations. For example, you might type

```
gmm (main:<mexp1>) (<mexp2>) (<mexp3>), instruments(z1 z2) ///
  instruments(2: z3) instruments(main 3: z4)
```

Variables `z1` and `z2` will be used as instruments for all three equations, `z3` will be used as an instrument for the second equation, and `z4` will be used as an instrument for the first and third equations. Notice that we chose to supply a name for the first moment equation but not the second two.

`xtinstruments(`[*<eqlist>*`:`]*varlist*`, lags(`*#*$_1$`/`*#*$_2$`))` is for use with panel-data models in which the set of available instruments depends on the time period. As with `instruments()`, you can prefix the list of variables with equation names or numbers to target instruments to specific equations. Unlike with `instruments()`, a constant term is not included in *varlist*. You must `xtset` your data before using this option; see [XT] **xtset**.

If you specify

```
gmm ..., xtinstruments(x, lags(1/.)) ...
```

then for panel i and period t, `gmm` uses as instruments $x_{i,t-1}, x_{i,t-2}, \ldots, x_{i1}$. More generally, specifying `xtinstruments(x, lags(`*#*$_1$`, `*#*$_2$`))` uses as instruments $x_{i,t-\#_1}, \ldots, x_{i,t-\#_2}$; setting $\#_2$ `= .` requests all available lags. *#*$_1$ and *#*$_2$ must be zero or positive integers.

`gmm` automatically excludes observations for which no valid instruments are available. It does, however, include observations for which only a subset of the lags is available. For example, if you request that lags one through three be used, then `gmm` will include the observations for the second and third time periods even though fewer than three lags are available as instruments.

Weight matrix

`wmatrix(`*wmtype*[`, independent`]`)` specifies the type of weight matrix to be used in conjunction with the two-step and iterated GMM estimators.

Specifying `wmatrix(robust)` requests a weight matrix that is appropriate when the errors are independent but not necessarily identically distributed. `wmatrix(robust)` is the default.

Specifying `wmatrix(cluster` *clustvar*`)` requests a weight matrix that accounts for arbitrary correlation among observations within clusters identified by *clustvar*.

Specifying `wmatrix(hac` *kernel #*`)` requests a heteroskedasticity- and autocorrelation-consistent (HAC) weight matrix using the specified kernel (see below) with # lags. The bandwidth of a kernel is equal to the number of lags plus one.

Specifying `wmatrix(hac` *kernel* `opt)` requests an HAC weight matrix using the specified kernel, and the lag order is selected using Newey and West's (1994) optimal lag-selection algorithm.

Specifying `wmatrix(hac` *kernel*`)` requests an HAC weight matrix using the specified kernel and $N - 2$ lags, where N is the sample size.

There are three kernels available for HAC weight matrices, and you may request each one by using the name used by statisticians or the name perhaps more familiar to economists:

`bartlett` or `nwest` requests the Bartlett (Newey–West) kernel;

`parzen` or `gallant` requests the Parzen (Gallant) kernel; and

`quadraticspectral` or `andrews` requests the quadratic spectral (Andrews) kernel.

Specifying `wmatrix(unadjusted)` requests a weight matrix that is suitable when the errors are homoskedastic. In some applications, the GMM estimator so constructed is known as the (nonlinear) two-stage least-squares (2SLS) estimator.

Including the `independent` suboption creates a weight matrix that assumes moment equations are independent. This suboption is often used to replicate other models that can be motivated outside the GMM framework, such as the estimation of a system of equations by system-wide 2SLS. This suboption has no effect if only one moment equation is specified.

`wmatrix()` has no effect if `onestep` is also specified.

`center` requests that the sample moments be centered (demeaned) when computing GMM weight matrices. By default, centering is not done.

`winitial(`*wmtype*[`, independent`]`)` specifies the weight matrix to use to obtain the first-step parameter estimates.

Specifying `winitial(unadjusted)` requests a weighting matrix that assumes the moment equations are independent and identically distributed. This matrix is of the form $(\mathbf{Z}'\mathbf{Z})^{-1}$, where $\mathbf{Z}$ represents all the instruments specified in the `instruments()` option. To avoid a singular weight matrix, you should specify at least $q - 1$ moment equations of the form $E\{\mathbf{z}_{hi}u_{hi}(\beta)\} = \mathbf{0}$, where q is the number of moment equations, or you should specify the `independent` suboption.

Including the `independent` suboption creates a weight matrix that assumes moment equations are independent. Elements of the weight matrix corresponding to covariances between two moment equations are set equal to zero. This suboption has no effect if only one moment equation is specified.

`winitial(unadjusted)` is the default.

`winitial(xt` *xtspec*`)` is for use with dynamic panel-data models in which one of the moment equations is specified in first-differences form. *xtspec* is a string consisting of the letters "L" and "D", the length of which is equal to the number of moment equations in the model. You specify

"L" for a moment equation if that moment equation is written in levels, and you specify "D" for a moment equation if it is written in first-differences; *xtspec* is not case sensitive. When you specify this option, you can specify at most one moment equation in levels and one moment equation in first-differences. See the examples listed in *Dynamic panel-data models* under *Remarks* below.

`winitial(identity)` requests that the identity matrix be used.

`winitial(`*matname*`)` requests that Stata matrix *matname* be used. You cannot specify the `independent` suboption if you specify `winitial(`*matname*`)`.

Options

`variables(`*varlist*`)` specifies the variables in the model. `gmm` ignores observations for which any of these variables has a missing value. If you do not specify `variables()`, then `gmm` assumes all the observations are valid and issues an error message with return code 480 if any moment equations evaluate to missing for any observations at the initial value of the parameter vector.

`nocommonesample` requests that `gmm` not restrict the estimation sample to be the same for all equations. By default, `gmm` will restrict the estimation sample to observations that are available for all equations in the model, mirroring the behavior of other multiple-equation estimators such as `nlsur`, `sureg`, or `reg3`. For certain models, however, different equations can have different numbers of observations. For these models, you should specify `nocommonesample`. See *Dynamic panel-data models* below for one application of this option. You cannot specify weights if you specify `nocommonesample`.

SE/Robust

`vce(`*vcetype*`[ , independent ])` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(unadjusted)` specifies that an unadjusted (nonrobust) VCE matrix be used; this, along with the `twostep` option, results in the "optimal two-step GMM" estimates often discussed in textbooks.

The default *vcetype* is based on the *wmtype* specified in the `wmatrix()` option. If `wmatrix()` is specified but `vce()` is not, then *vcetype* is set equal to *wmtype*. To override this behavior and obtain an unadjusted (nonrobust) VCE matrix, specify `vce(unadjusted)`.

Specifying `vce(bootstrap)` or `vce(jackknife)` results in standard errors based on the bootstrap or jackknife, respectively. See [R] ***vce_option***, [R] **bootstrap**, and [R] **jackknife** for more information on these VCEs.

The syntax for *vcetype*s other than `bootstrap` and `jackknife` are identical to those for `wmatrix()`.

Reporting

`level(#)`; see [R] **estimation options**.

`title(`*string*`)` specifies an optional title that will be displayed just above the table of parameter estimates.

`title2(`*string*`)` specifies an optional subtitle that will be displayed between the title specified in `title()` and the table of parameter estimates. If `title2()` is specified but `title()` is not, `title2()` has the same effect as `title()`.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Optimization

`from(`*initial_values*`)` specifies the initial values to begin the estimation. You can specify a $1 \times k$ matrix, where k is the number of parameters in the model, or you can specify a parameter name, its initial value, another parameter name, its initial value, and so on. For example, to initialize `alpha` to 1.23 and `delta` to 4.57, you would type

```
gmm ..., from(alpha 1.23 delta 4.57) ...
```

Initial values declared using this option override any that are declared within substitutable expressions. If you specify a parameter that does not appear in your model, `gmm` exits with error code 480. If you specify a matrix, the values must be in the same order in which the parameters are declared in your model. `gmm` ignores the row and column names of the matrix.

`igmmiterate(#)`, `igmmeps(#)`, and `igmmweps(#)` control the iterative process for the iterative GMM estimator. These options can be specified only if you also specify `igmm`.

`igmmiterate(#)` specifies the maximum number of iterations to perform with the iterative GMM estimator. The default is the number set using `set maxiter` (set [R] **maximize**), which is 16,000 by default.

`igmmeps(#)` specifies the convergence criterion used for successive parameter estimates when the iterative GMM estimator is used. The default is `igmmeps(1e-6)`. Convergence is declared when the relative difference between successive parameter estimates is less than `igmmeps()` and the relative difference between successive estimates of the weight matrix is less than `igmmweps()`.

`igmmweps(#)` specifies the convergence criterion used for successive estimates of the weight matrix when the iterative GMM estimator is used. The default is `igmmweps(1e-6)`. Convergence is declared when the relative difference between successive parameter estimates is less than `igmmeps()` and the relative difference between successive estimates of the weight matrix is less than `igmmweps()`.

optimization_options: `technique()`, `conv_maxiter()`, `conv_ptol()`, `conv_vtol()`, `conv_nrtol()`, `tracelevel()`. `technique()` specifies the optimization technique to use; `gn` (the default), `nr`, `dfp`, and `bfgs` are allowed. `conv_maxiter()` specifies the maximum number of iterations; `conv_ptol()`, `conv_vtol()`, and `conv_nrtol()` specify the convergence criteria for the parameters, gradient, and scaled Hessian, respectively. `tracelevel()` allows you to obtain additional details during the iterative process. See [M-5] **optimize( )**.

The following options pertain only to the moment-evaluator program version of `gmm`.

Model

evaluator_options refer to any options allowed by your *moment_prog*.

`hasderivatives` indicates that you have written your moment-evaluator program to compute derivatives. If you do not specify this option, derivatives are computed numerically. If your moment-evaluator program does compute derivatives but you wish to use numerical derivatives instead (perhaps during debugging), do not specify this option.

`equations(`*namelist*`)` specifies the names of the moment equations in the model. If you specify both `equations()` and `nequations()`, the number of names in the former must match the number specified in the latter.

`nequations(#)` specifies the number of moment equations in the model. If you do not specify names with the `equations()` option, `gmm` numbers the moment equations 1, 2, 3, ... If you specify both `equations()` and `nequations()`, the number of names in the former must match the number specified in the latter.

`parameters(`*namelist*`)` specifies the names of the parameters in the model. The names of the parameters must adhere to the naming conventions of Stata's variables; see [U] **11.3 Naming conventions**. If you specify both `parameters()` and `nparameters()`, the number of names in the former must match the number specified in the latter.

`nparameters(#)` specifies the number of parameters in the model. If you do not specify names with the `parameters()` option, `gmm` names them `b1`, `b2`, ..., `b#`. If you specify both `parameters()` and `nparameters()`, the number of names in the former must match the number specified in the latter.

The following option is available with `gmm` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Substitutable expressions
The weight matrix and two-step estimation
Obtaining standard errors
Exponential (Poisson) regression models
Specifying derivatives
Exponential regression models with panel data
Rational-expectations models
System estimators
Dynamic panel-data models
Details of moment-evaluator programs

Introduction

The generalized method of moments (GMM) estimator is a workhorse of modern econometrics and is discussed in all the leading textbooks, including Cameron and Trivedi (2005, 2010), Davidson and MacKinnon (1993, 2004), Greene (2012, 468–506), Ruud (2000), Hayashi (2000), Wooldridge (2010), Hamilton (1994), and Baum (2006). An excellent treatise on GMM with a focus on time-series applications is Hall (2005). The collection of papers by Mátyás (1999) provides both theoretical and applied aspects of GMM. Here we give a brief introduction to the methodology and emphasize how the various options of `gmm` are used.

The starting point for the generalized method of moments (GMM) estimator is the analogy principle, which says we can estimate a parameter by replacing a population moment condition with its sample analogue. For example, the mean of an independent and identically distributed (i.i.d.) population is defined as the value μ such that the first (central) population moment is zero; that is, μ solves $E(y-\mu)=0$ where y is a random draw from the population. The analogy principle tells us that to obtain an estimate, $\widehat{\mu}$, of μ, we replace the population-expectations operator with its sample analogue (Manski 1988; Wooldridge 2010):

$$E(y-\mu)=0 \;\longrightarrow\; \frac{1}{N}\sum_{i=1}^{N}(y_i-\widehat{\mu})=0 \;\longrightarrow\; \widehat{\mu}=\frac{1}{N}\sum_{i=1}^{N}y_i$$

where N denotes sample size and y_i represents the ith observation of y in our dataset. The estimator $\widehat{\mu}$ is known as the method of moments (MM) estimator, because we started with a population moment condition and then applied the analogy principle to obtain an estimator that depends on the observed data.

Ordinary least-squares (OLS) regression can also be viewed as an MM estimator. In the model

$$y = \mathbf{x}'\beta + u$$

we assume that u has mean zero conditional on $\mathbf{x}$: $E(u|\mathbf{x}) = 0$. This conditional expectation implies the unconditional expectation $E(\mathbf{x}u) = \mathbf{0}$ because, using the law of iterated expectations,

$$E(\mathbf{x}u) = E_{\mathbf{x}}\left\{E(\mathbf{x}u|\mathbf{x})\right\} = E_{\mathbf{x}}\left\{\mathbf{x}\,E(u|\mathbf{x})\right\} = \mathbf{0}$$

(Using the law of iterated expectations to derive unconditional expectations based on conditional expectations, perhaps motivated by subject theory, is extremely common in GMM estimation.) Continuing,

$$E(\mathbf{x}u) = E\left\{\mathbf{x}(y - \mathbf{x}'\beta)\right\} = \mathbf{0}$$

Applying the analogy principle,

$$E\left\{\mathbf{x}(y - \mathbf{x}'\beta)\right\} \longrightarrow \frac{1}{N}\sum_{i=1}^{N}\mathbf{x}_i(y_i - \mathbf{x}_i'\beta) = \mathbf{0}$$

so that

$$\widehat{\beta} = \left(\sum\nolimits_i \mathbf{x}_i\mathbf{x}_i'\right)^{-1}\sum\nolimits_i \mathbf{x}_i y_i$$

which is just the more familiar formula $\widehat{\beta} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}$ written using summation notation.

In both the previous examples, the number of parameters we were estimating equaled the number of moment conditions. In the first example, we estimated one parameter, μ, and had one moment condition $E(y - \mu) = 0$. In the second example, the parameter vector β had k elements, as did the vector of regressors $\mathbf{x}$, yielding k moment conditions. Ignoring peculiar cases, a model of m equations in m unknowns has a unique solution, and because the moment equations in these examples were linear, we were able to solve for the parameters analytically. Had the moment conditions been nonlinear, we would have had to use numerical techniques to solve for the parameters, but that is not a significant limitation with modern computers.

What if we have more moment conditions than parameters? Say we have l moment conditions and k parameters. A model of $l > k$ equations in k unknowns does not have a unique solution. Any size-k subset of the moment conditions would yield a consistent parameter estimate, though the parameter estimate so obtained would in general be different based on which k moment conditions we used.

For concreteness, let's return to our regression model,

$$y = \mathbf{x}'\beta + u$$

but we no longer wish to assume that $E(\mathbf{x}u) = \mathbf{0}$; we suspect that the error term u affects one or more elements of $\mathbf{x}$. As a result, we can no longer use the OLS estimator. Suppose we have a vector $\mathbf{z}$ with the properties that $E(\mathbf{z}u) = \mathbf{0}$, that the rank of $E(\mathbf{z}'\mathbf{z})$ equals l, and that the rank of $E(\mathbf{z}'\mathbf{x}) = k$. The first assumption simply states that $\mathbf{z}$ is not correlated with the error term. The second assumption rules out perfect collinearity among the elements of $\mathbf{z}$. The third assumption, known as the *rank condition* in econometrics, ensures that $\mathbf{z}$ is sufficiently correlated with $\mathbf{x}$ and that the estimator is feasible. If some elements of $\mathbf{x}$ are not correlated with u, then they should also appear in $\mathbf{z}$.

If $l < k$, then the rank of $E(\mathbf{z}'\mathbf{x}) < k$, violating the rank condition.

If $l = k$, then we can use the simpler MM estimator we already discussed; we would obtain what is sometimes called the simple instrumental-variables estimator $\widehat{\beta} = (\sum_i \mathbf{z}_i\mathbf{x}_i')^{-1} \sum_i \mathbf{z}_i y_i$. The rank condition ensures that $\sum_i \mathbf{z}_i\mathbf{x}_i'$ is invertible, at least in the population.

If $l > k$, the GMM estimator chooses the value, $\widehat{\beta}$, that minimizes a quadratic function of the moment conditions. We could define

$$\widehat{\beta} \equiv \arg\min_\beta \left\{ \frac{1}{N}\sum\nolimits_i \mathbf{z}_i u_i(\beta) \right\}' \left\{ \frac{1}{N}\sum\nolimits_i \mathbf{z}_i u_i(\beta) \right\} \tag{1}$$

where for our linear regression example $u_i(\beta) = y_i - \mathbf{x}_i'\beta$. This estimator tries to make the moment conditions as close to zero as possible. This simple estimator, however, applies equal weight to each of the moment conditions; and as we shall see later, we can obtain more efficient estimators by choosing to weight some moment conditions more highly than others.

Consider the quadratic function

$$Q(\beta) = \left\{ \frac{1}{N}\sum\nolimits_i \mathbf{z}_i u_i(\beta) \right\}' \mathbf{W} \left\{ \frac{1}{N}\sum\nolimits_i \mathbf{z}_i u_i(\beta) \right\}$$

where $\mathbf{W}$ is a symmetric positive-definite matrix known as a weight matrix. Then we define the GMM estimator as

$$\widehat{\beta} \equiv \arg\min_\beta \; Q(\beta) \tag{2}$$

Continuing with our regression model example, if we choose

$$\mathbf{W} = \left(\frac{1}{N}\sum\nolimits_i \mathbf{z}_i\mathbf{z}_i' \right)^{-1} \tag{3}$$

then we obtain

$$\widehat{\beta} = \left\{ \left(\frac{1}{N}\sum\nolimits_i \mathbf{x}_i\mathbf{z}_i' \right) \left(\frac{1}{N}\sum\nolimits_i \mathbf{z}_i\mathbf{z}_i' \right)^{-1} \left(\frac{1}{N}\sum\nolimits_i \mathbf{z}_i\mathbf{x}_i' \right) \right\}^{-1} \times \left(\frac{1}{N}\sum\nolimits_i \mathbf{x}_i\mathbf{z}_i' \right) \left(\frac{1}{N}\sum\nolimits_i \mathbf{z}_i\mathbf{z}_i' \right)^{-1} \left(\frac{1}{N}\sum\nolimits_i \mathbf{z}_i y_i \right)$$

which is the well-known two-stage least-squares (2SLS) estimator. Our choice of weight matrix here was based on the assumption that u was homoskedastic. A feature of GMM estimation is that by selecting different weight matrices, we can obtain estimators that can tolerate heteroskedasticity, clustering, autocorrelation, and other features of u. See [R] **ivregress** for more information about the 2SLS and linear GMM estimators.

Returning to the case where the model is "just identified", meaning that $l = k$, if we apply the GMM estimator, we will obtain the same estimate, $\widehat{\boldsymbol{\beta}}$, regardless of our choice of $\mathbf{W}$. Because $l = k$, if a unique solution exists, it will set all the sample moment conditions to zero jointly, so $\mathbf{W}$ has no impact on the value of β that minimizes the objective function.

We will highlight other features of the GMM estimator and the `gmm` command as we proceed through examples. First, though, we discuss how to specify moment equations by using substitutable expressions.

Substitutable expressions

To use the interactive version of `gmm`, you define the moment equations by using substitutable expressions. In most applications, your moment conditions are of the form $E\{\mathbf{z}_i u_i(\boldsymbol{\beta})\}$, where $u_i(\boldsymbol{\beta})$ is a residual term that depends on the parameter vector $\boldsymbol{\beta}$ as well as variables in your dataset, though we suppress expressing the variables for notational simplicity; we refer to $u_i(\boldsymbol{\beta})$ as the moment equation to differentiate it from the moment conditions $E\{z_i' u_i(\boldsymbol{\beta})\} = \mathbf{0}$.

Substitutable expressions in `gmm` work much like those used in `nl` and `nlsur`, though with one important difference. For the latter two commands, you type the name of the dependent variable, an equal sign, and then the regression function. For example, in `nl`, if you want to fit the function $y = f(\mathbf{x};\boldsymbol{\beta}) + u$, you would type

```
nl (y = <expression for f(x; β)>), ...
```

On the other hand, `gmm` requires you to write a substitutable expression for u; in this example, $u = y - f(\mathbf{x};\boldsymbol{\beta})$, so you would type

```
gmm (y - <expression for f(x; β)>), ...
```

The advantage of writing the substitutable expression directly in terms of u is that you are not restricted to fitting models with additive error terms as you are with `nl` and `nlsur`.

You specify substitutable expressions just like any other mathematical expression involving scalars and variables, such as those you would use with Stata's `generate` command, except that the parameters to be estimated are bound in braces. See [U] **13.2 Operators** and [U] **13.3 Functions** for more information on expressions. Parameter names must follow the same conventions as variable names. See [U] **11.3 Naming conventions**.

For example, say that the tth observation on a sample moment is

$$u_t = 1 - \beta\left\{(1 + r_{t+1})(c_{t+1}/c_t)^{-\gamma}\right\}$$

where t denotes time period, β and γ are the parameters to be estimated, and r and c are variables in your dataset. Then you would type

```
gmm (1 - {beta}*((1 + F.r)*(F.c/c)^(-1*{gamma}))), ...
```

Because β and γ are parameters, we enclose them in braces. Also notice our use of the forward operator to refer to the values of r and c one period ahead; time-series operators are allowed in substitutable expressions as long as you have previously `tsset` (see [TS] **tsset**) your data. See [U] **13.9 Time-series operators** for more information on time-series operators.

To specify initial values for some parameters, you can include an equal sign and the initial value after a parameter:

```
gmm (1 - {beta}*((1 + F.r)*(F.c/c)^(-1*{gamma=1}))), ...
```

would initialize γ to be one. If you do not specify an initial value for a parameter, it is initialized to zero.

Frequently, even nonlinear functions contain linear combinations of variables. As an example, suppose you have this moment equation:

$$u = \{y - \exp(\beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3)\} / \exp(\beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3)$$

Instead of typing

```
gmm ((y - exp({beta1}*x1 + {beta2}*x2 + {beta3}*x3)) /     ///
      exp({beta1}*x1 + {beta2}*x2 + {beta3}*x3)) ...
```

you can type

```
gmm ((y - exp({xb:x1 x2 x3})) / exp({xb:})) .....
```

The notation {xb:x1 x2 x3} tells gmm that you want a linear combination of the variables x1, x2, and x3. We named this linear combination xb, so gmm will name the three parameters corresponding to the three variables xb_x1, xb_x2, and xb_x3. You can name the linear combination anything you wish (subject to Stata's naming conventions for variable names); gmm then names the parameter corresponding to variable x *lc*_x, where *lc* is the name of your linear combination. You cannot use the same name for both an individual parameter and a linear combination. You can, however, refer to one parameter in a linear combination after it has been declared as you would any other parameter by using the notation {*lc*_x}. Linear combinations do not include a constant term.

Once we have declared the variables in the linear combination xb, we can subsequently refer to the linear combination in our substitutable expression by using the notation xb:. The colon is not optional; it tells gmm that you are referring to a previously declared linear combination, not an individual parameter. This shorthand notation is also handy when specifying derivatives, as we will show later.

In general, there are three rules to follow when defining substitutable expressions:

1. Parameters of the model are bound in braces: {b0}, {param}, etc.
2. Initial values for parameters are given by including an equal sign and the initial value inside the braces: {b0=1}, {param=3.571}, etc.
3. Linear combinations of variables can be included using the notation {*eqname*:*varlist*}: {xb: mpg price weight}, {score: w x z}, etc. Parameters of linear combinations are initialized to zero.

If you specify initial values by using the from() option, they override whatever initial values are given within the substitutable expression. Substitutable expressions are so named because, once values are assigned to the parameters, the resulting expressions can be handled by generate and replace.

▷ Example 1: OLS regression

In *Introduction*, we stated that OLS is an MM estimator. Say that we want to fit the model

$$\texttt{mpg} = \beta_0 + \beta_1\texttt{weight} + \beta_2\texttt{length} + u$$

where u is an i.i.d. error term. We type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. gmm (mpg - {b1}*weight - {b2}*length - {b0}), instruments(weight length)
Step 1
Iteration 0:   GMM criterion Q(b) =   475.4138
Iteration 1:   GMM criterion Q(b) =  2.696e-20
Iteration 2:   GMM criterion Q(b) =  3.329e-27
Step 2
Iteration 0:   GMM criterion Q(b) =  5.109e-28
Iteration 1:   GMM criterion Q(b) =  7.237e-32
```

```
GMM estimation

Number of parameters =   3
Number of moments    =   3
Initial weight matrix: Unadjusted                 Number of obs   =        74
GMM weight matrix:     Robust
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/b1	-.0038515	.0019472	-1.98	0.048	-.0076678	-.0000351
/b2	-.0795935	.0677528	-1.17	0.240	-.2123866	.0531996
/b0	47.88487	7.50599	6.38	0.000	33.1734	62.59634

```
Instruments for equation 1: weight length _cons
```

Recall that the moment condition for OLS regression is $E(\mathbf{x}u) = \mathbf{0}$, where $\mathbf{x}$, the list of instruments, is the same as the list of regressors in the model. In our command, we defined the residual term, u, inside parentheses by using a substitutable expression; because linear combinations declared in substitutable expressions do not include a constant term, we included our own (`b0`). Inside the `instruments()` option, we listed our instruments; by default, `gmm` includes a constant term among the instrument list.

Because the number of moments equals the number of parameters we are estimating, the model is said to be "just identified" or "exactly identified." Therefore, the choice of weight matrix has no impact on the solution to (2), and the criterion function $Q(\boldsymbol{\beta})$ achieves its minimum value at zero.

The OLS estimator is a one-step GMM estimator, but we did not bother to specify the `onestep` option because the model is just identified. Doing a second step of GMM estimation affects neither the point estimates nor the standard errors, so to keep the syntax as simple as possible, we did not include the `onestep` option. The first step of estimation resulted in $Q(\beta) = 0$ as expected, and the second step of estimation did not change the minimized value of $Q(\beta)$. (3×10^{-27} and 7×10^{-32} are both zero for all practical purposes.)

When you do not specify either the `wmatrix()` or the `vce()` option, `gmm` reports heteroskedasticity-robust standard errors. The parameter estimates reported here match those that we would obtain from the command

```
. regress mpg weight length, vce(robust)
```

The standard errors reported by that `regress` command would be larger than those reported by `gmm` by a factor of $\text{sqrt}(74/71)$ because `regress` makes a small-sample adjustment to the estimated variance matrix while `gmm` does not. Likewise, had we specified the `vce(unadjusted)` option with our `gmm` command, then our standard errors would differ by a factor of $\text{sqrt}(74/71)$ from those reported by `regress` without the `vce(robust)` option.

Using the notation for linear combinations of parameters, we could have typed

```
. gmm (mpg - {xb: weight length} - {b0}), instruments(weight length)
```

and obtained identical results. Instead of having parameters `b1` and `b2`, with this syntax we would have parameters `xb_weight` and `xb_length`.

◁

▷ Example 2: Instrumental-variables regression

In *Introduction*, we mentioned that 2SLS can be viewed as a GMM estimator. In example 1 of [R] **ivregress**, we fit by 2SLS a model of rental rates (`rent`) as a function of the value of owner-occupied housing (`hsngval`) and the percentage of the population living in urban areas (`pcturban`):

$$\texttt{rent} = \beta_0 + \beta_1\texttt{hsngval} + \beta_2\texttt{pcturban} + u$$

by 2SLS. We argued that random shocks that affect rental rates likely also affect housing values, so we treated `hsngval` as an endogenous variable. As additional instruments, we used family income, `faminc`, and three regional dummies (`reg2`–`reg4`).

To replicate the results of `ivregress 2sls` by using `gmm`, we type

```
. use http://www.stata-press.com/data/r12/hsng2
(1980 Census housing data)
. gmm (rent - {xb:hsngval pcturban} - {b0}),
> instruments(pcturban faminc reg2-reg4) vce(unadjusted) onestep
Step 1
Iteration 0:   GMM criterion Q(b) =   56115.03
Iteration 1:   GMM criterion Q(b) =  110.91583
Iteration 2:   GMM criterion Q(b) =  110.91583
GMM estimation
Number of parameters =   3
Number of moments    =   6
Initial weight matrix: Unadjusted                 Number of obs   =       50
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
 /xb_hsngval |   .0022398   .0003284     6.82   0.000     .0015961    .0028836
/xb_pcturban |    .081516   .2987652     0.27   0.785    -.5040531     .667085
         /b0 |   120.7065   15.22839     7.93   0.000     90.85942    150.5536
------------------------------------------------------------------------------
Instruments for equation 1: pcturban faminc reg2 reg3 reg4 _cons
```

We specified `vce(unadjusted)` so that we would obtain an unadjusted VCE matrix and our standard errors would match those reported in [R] **ivregress**.

Pay attention to how we specified the `instruments()` option. In *Introduction*, we mentioned that the moment conditions for the 2SLS estimator are $E(\mathbf{z}u) = \mathbf{0}$, and we mentioned that if some elements of $\mathbf{x}$ (the regressors) are not endogenous, then they should also appear in $\mathbf{z}$. In this model, we assume the regressor `pcturban` is exogenous, so we included it in the list of instrumental variables. Commands like `ivregress`, `ivprobit`, and `ivtobit` accept standard *varlist*s, so they can deduce the exogenous regressors in the model. Because `gmm` accepts arbitrary functions in the form of substitutable expressions, it has no way of discerning the exogenous variables of the model on its own.

Also notice that we specified the `onestep` option. The 2SLS estimator is a one-step GMM estimator that is based on a weight matrix that assumes the error terms are i.i.d. Unlike the previous example, here we had more instruments than parameters, so the minimized value of $Q(\beta)$ is nonzero. We discuss the weight matrix and its relationship to two-step estimation next.

◁

The weight matrix and two-step estimation

Recall our definition of the GMM estimator given in (2). The estimator, $\widehat{\boldsymbol{\beta}}$, depends on the choice of the weight matrix, $\mathbf{W}$. Under relatively mild assumptions, our estimator, $\widehat{\boldsymbol{\beta}}$, is consistent regardless of the choice of $\mathbf{W}$, so how are we to decide what $\mathbf{W}$ to use? The most common solution is to use the two-step estimator, which we now describe.

A key result in Hansen's (1982) seminal paper is that if we denote by $\mathbf{S}$ the covariance matrix of the moment conditions, then the optimal (in a way we make precise later) GMM estimator is the one that uses a weight matrix equal to the inverse of the moment covariance matrix. That is, if we let $\mathbf{S} = \mathrm{Cov}(\mathbf{z}u)$, then we want to use $\mathbf{W} = \mathbf{S}^{-1}$. But how do we obtain $\mathbf{S}$ in the first place?

If we assume that the errors are i.i.d., then

$$\mathrm{Cov}(\mathbf{z}u) = E(u^2\mathbf{z}\mathbf{z}') = \sigma^2 E(\mathbf{z}\mathbf{z}')$$

where σ^2 is the variance of u. Because σ^2 is a positive scalar, we can ignore it when solving (2). Thus we compute

$$\widehat{\mathbf{W}}_1 = \left(\frac{1}{N}\sum\nolimits_i \mathbf{z}_i\mathbf{z}_i'\right)^{-1} \tag{4}$$

which does not depend on any unknown model parameters. (Notice that $\widehat{\mathbf{W}}_1$ is the same weight matrix used in 2SLS.) Given $\widehat{\mathbf{W}}_1$, we can solve (2) to obtain an initial estimate, say, $\widehat{\beta}_1$.

Our estimate, $\widehat{\beta}_1$, is consistent, so by Slutsky's theorem, the sample residuals $\widehat{u}$ computed at this value of β will also be consistent. Using virtually the same arguments used to justify the Huber/Eicker/White heteroskedasticity-robust VCE, if we assume that the residuals are independent though not identically distributed, we can estimate $\mathbf{S}$ as

$$\widehat{\mathbf{S}} = \frac{1}{N}\sum_i \widehat{u}_i^2\mathbf{z}_i\mathbf{z}_i'$$

Then, in the second step, we re-solve (2), using $\widehat{\mathbf{W}}_2 = \widehat{\mathbf{S}}^{-1}$, yielding the two-step GMM estimate $\widehat{\beta}_2$. If the residuals exhibit clustering, you can specify `wmatrix(cluster` *varname*`)` so that `gmm` computes a weight matrix that does not assume the u_i's are independent within clusters identified by *varname*. You can specify `wmatrix(hac ...)` to obtain weight matrices that are suitable for when the u_i's exhibit autocorrelation as well as heteroskedasticity.

We could take the point estimates from the second round of estimation and use them to compute yet another weight matrix, $\widehat{\mathbf{W}}_3$, say, re-solve (2) yet again, and so on, stopping when the parameters or weight matrix do not change much from one iteration to the next. This procedure is known as the iterative GMM estimator and is obtained with the `igmm` option. Asymptotically, the two-step and iterative GMM estimators have the same distribution. However, Hall (2005, 90) suggests that the iterative estimator may have better finite-sample properties.

Instead of computing $\widehat{\mathbf{W}}_1$ as in (4), we could simply choose $\widehat{\mathbf{W}}_1 = \mathbf{I}$, the identity matrix. The initial estimate, $\widehat{\beta}_1$, would still be consistent. You can request this behavior by specifying the `winitial(identity)` option. However, if you specify all your moment equations of the form $E(\mathbf{z}u) = \mathbf{0}$, we recommend using the default `winitial(unadjusted)` instead; the rescaling of the moment conditions implied by using a homoskedastic initial weight matrix makes the numerical routines used to solve (2) more stable.

If you fit a model with more than one of the moment equations of the form $E\{h(\mathbf{z};\beta)\} = \mathbf{0}$, then you must use `winitial(identity)` or `winitial(unadjusted, independent)`. With moment equations of that form, you do not specify a list of instruments, and `gmm` cannot evaluate (4)—the matrix expression in parentheses would necessarily be singular, so it cannot be inverted.

▷ Example 3: Two-step linear GMM estimator

From the previous discussion and the comments in *Introduction*, we see that the linear 2SLS estimator is a one-step GMM estimator where we use the weight matrix defined in (4) that assumes the errors are i.i.d. If we use the 2SLS estimate of β to obtain the sample residuals, compute a new weight matrix based on those residuals, and then do a second step of GMM estimation, we obtain the linear two-step GMM estimator as implemented by `ivregress gmm`.

In example 3 of [R] **ivregress**, we fit the model of rental rates as discussed in example 2 above. We now allow the residuals to be heteroskedastic, though we will maintain our assumption that they are independent. We type

```
. gmm (rent - {xb:hsngval pcturban} - {b0}), inst(pcturban faminc reg2-reg4)
Step 1
Iteration 0:   GMM criterion Q(b) =   56115.03
Iteration 1:   GMM criterion Q(b) =  110.91583
Iteration 2:   GMM criterion Q(b) =  110.91583
Step 2
Iteration 0:   GMM criterion Q(b) =   .2406087
Iteration 1:   GMM criterion Q(b) =  .13672801
Iteration 2:   GMM criterion Q(b) =  .13672801
GMM estimation
Number of parameters =   3
Number of moments    =   6
Initial weight matrix: Unadjusted                 Number of obs   =       50
GMM weight matrix:     Robust
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/xb_hsngval	.0014643	.0004473	3.27	0.001	.0005877	.002341
/xb_pcturban	.7615482	.2895105	2.63	0.009	.1941181	1.328978
/b0	112.1227	10.80234	10.38	0.000	90.95052	133.2949

```
Instruments for equation 1: pcturban faminc reg2 reg3 reg4 _cons
```

By default, `gmm` computes a heteroskedasticity-robust weight matrix before the second step of estimation, though we could have specified `wmatrix(robust)` if we wanted to be explicit. Because we did not specify the `vce()` option, `gmm` used a heteroskedasticity-robust one. Our results match those in example 3 of [R] **ivregress**. Moreover, the only difference between this example and the previous example of 2SLS is that here we did not use the `onestep` option.

◁

Obtaining standard errors

This section is a bit more theoretical and can be skipped on first reading. However, the information is sufficiently important that you should return to this section at some point.

So far in our discussion, we have focused on point estimation without much mention of how we obtain the standard errors of the estimates. We also mentioned that if we choose $\mathbf{W}$ to be the inverse of the covariance matrix of the moment conditions, then we obtain the "optimal" GMM estimator. We elaborate those points now.

Using mostly standard statistical arguments, we can show that for the GMM estimator defined in (2), the variance of $\widehat{\beta}$ is given by

$$\text{Var}(\widehat{\beta}) = \frac{1}{N}\left\{\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\right\}^{-1}\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\mathbf{S}\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\left\{\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\right\}^{-1} \tag{5}$$

where

$$\overline{\mathbf{G}}(\widehat{\beta}) = \frac{1}{N}\sum\nolimits_i \mathbf{z}_i \left.\frac{\partial u_i}{\partial \beta}\right|_{\beta=\widehat{\beta}} \qquad \text{or} \qquad \overline{\mathbf{G}}(\widehat{\beta}) = \frac{1}{N}\sum\nolimits_i \left.\frac{\partial \mathbf{h}_i}{\partial \beta}\right|_{\beta=\widehat{\beta}}$$

as the case may be and $\mathbf{S} = E(\mathbf{z}uu'\mathbf{z}')$.

Assuming the `vce(unadjusted)` option is not specified, `gmm` reports standard errors based on the robust variance matrix defined in (5). For the two-step estimator, $\mathbf{W}$ is the weight matrix requested using the `wmatrix()` option, and it is calculated based on the residuals obtained after the first estimation step. The second-step point estimates and residuals are obtained, and $\mathbf{S}$ is calculated based on the specification of the `vce()` option. For the iterated estimator, $\mathbf{W}$ is calculated based on the second-to-last round of estimation, while $\mathbf{S}$ is based on the residuals obtained after the last round of estimation. Computation of the covariance matrix for the one-step estimator is, perhaps surprisingly, more involved; we discuss the covariance matrix with the one-step estimator in the technical note at the end of this section.

If we choose the weight matrix to be the inverse of the covariance matrix of the moment conditions so that $\mathbf{W} = \mathbf{S}^{-1}$, then (5) simplifies substantially:

$$\text{Var}(\widehat{\beta}) = \frac{1}{N}\left\{\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\right\}^{-1} \tag{6}$$

The GMM estimator constructed using this choice of weight matrix along with the covariance matrix in (6) is known as the "optimal" GMM estimator. One can show that if in fact $\mathbf{W} = \mathbf{S}^{-1}$, then the variance in (6) is smaller than the variance in (5) of any other GMM estimator based on the same moment conditions but with a different choice of weight matrix. Thus the optimal GMM estimator is also known as the efficient GMM estimator, because it has the smallest variance of any estimator based on the given moment conditions.

To obtain standard errors from `gmm` based on the optimal GMM estimator, you specify the `vce(unadjusted)` option. We call that VCE unadjusted because we do not recompute the residuals after estimation to obtain the matrix $\mathbf{S}$ required in (5) or allow for the fact that those residuals may not be i.i.d. Some statistical packages by default report standard errors based on (6) and offer standard errors based on (5) only as an option or not at all. While the optimal GMM estimator is theoretically appealing, Cameron and Trivedi (2005, 177) suggest that in finite samples it need not perform better than the GMM estimator that uses (5) to obtain standard errors.

❑ Technical note

Computing the covariance matrix of the parameters after using the one-step estimator is actually a bit more complex than after using the two-step or iterative estimators. We can illustrate most of the intricacies by using linear regression with moment conditions of the form $E\{\mathbf{x}(y - \mathbf{x}'\beta)\} = \mathbf{0}$.

If you specify `winitial(unadjusted)` and `vce(unadjusted)`, then the initial weight matrix will be computed as

$$\widehat{\mathbf{W}}_1 = \left(\frac{1}{N}\sum_i \mathbf{x}_i\mathbf{x}_i'\right)^{-1} \tag{7}$$

Moreover, for linear regression, we can show that

$$\overline{\mathbf{G}}(\widehat{\beta}) = \frac{1}{N}\sum_i \mathbf{x}_i\mathbf{x}_i'$$

so that (6) becomes

$$\begin{aligned}\mathrm{Var}(\widehat{\beta}) &= \frac{1}{N}\left\{\left(\frac{1}{N}\sum_i \mathbf{x}_i\mathbf{x}_i'\right)\left(\frac{1}{N}\sum_i \mathbf{x}_i\mathbf{x}_i'\right)^{-1}\left(\frac{1}{N}\sum_i \mathbf{x}_i\mathbf{x}_i'\right)\right\}^{-1}\\ &= \left(\sum_i \mathbf{x}_i\mathbf{x}_i'\right)^{-1}\\ &= (\mathbf{X}'\mathbf{X})^{-1}\end{aligned} \tag{8}$$

However, we know that the nonrobust covariance matrix for the OLS estimator is actually $\widehat{\sigma}^2(\mathbf{X}'\mathbf{X})^{-1}$. What is missing from (8) is the scalar $\widehat{\sigma}^2$, the estimated variance of the residuals. When you use the one-step estimator and specify `winitial(unadjusted)`, the weight matrix (7) does not include the $\widehat{\sigma}^2$ term because `gmm` does not have a consistent estimate of β from which it can then estimate σ^2. The point estimates are still correct, because multiplying the weight matrix by a scalar factor does not affect the solution to the minimization problem.

To circumvent this issue, if you specify `winitial(unadjusted)` and `vce(unadjusted)`, `gmm` uses the estimated $\widehat{\beta}$ (which is consistent) to obtain a new unadjusted weight matrix that does include the term $\widehat{\sigma}^2$ so that evaluating (6) will yield correct standard errors.

If you use the two-step or iterated GMM estimators, this extra effort is not needed to obtain standard errors because the first-step (and subsequent steps') estimate of β is consistent and can be used to estimate σ^2 or some other weight matrix based on the `wmatrix()` option. Straightforward algebra shows that this extra effort is also not needed if you request any type of adjusted (robust) covariance matrix with the one-step estimator.

A similar issue arises when you specify `winitial(identity)` and `vce(unadjusted)` with the one-step estimator. Again the solution is to compute an unadjusted weight matrix after obtaining $\widehat{\beta}$ so that (6) provides the correct standard errors.

We have illustrated the problem and solution using a single-equation linear model. However, the problem arises whenever you use the one-step estimator with an unadjusted VCE, regardless of the number of equations; and `gmm` handles all the details automatically. Computation of Hansen's J statistic presents an identical issue, and `gmm` takes care of that as well.

If you supply your own initial weight matrix by using `winitial(`*matname*`)`, then the standard errors (as well as the J statistic reported by `estat overid`) are based on that weight matrix. You should verify that the weight matrix you provide will yield appropriate statistics.

❑

Exponential (Poisson) regression models

Exponential regression models are frequently encountered in applied work. For example, they can be used as alternatives to linear regression models on log-transformed dependent variables, obviating the need for post-hoc transformations to obtain predicted values in the original metric of the dependent variable. When the dependent variable represents a discrete count variable, they are also known as Poisson regression models; see Cameron and Trivedi (1998).

For now, we consider models of the form

$$y = \exp(\mathbf{x}'\beta) + u \tag{9}$$

where u is a zero-mean additive error term so that $E(y) = \exp(\mathbf{x}'\beta)$. Because the error term is additive, if $\mathbf{x}$ represents strictly exogenous regressors, then we have the population moment condition

$$E[\mathbf{x}\{y - \exp(\mathbf{x}'\beta)\}] = \mathbf{0} \tag{10}$$

Moreover, because the number of parameters in the model is equal to the number of instruments, there is no point to using the two-step GMM estimator.

▷ Example 4: Exponential regression

Cameron and Trivedi (2010, 323) fit a model of the number of doctor visits based on whether the patient has private insurance, whether the patient has a chronic disease, gender, and income. Here we fit that model by using `gmm`. To allow for potential excess dispersion, we will obtain a robust VCE matrix, which is the default for `gmm` anyway. We type

```
. use http://www.stata-press.com/data/r12/docvisits
. gmm (docvis - exp({xb:private chronic female income}+{b0})),
> instruments(private chronic female income) onestep
Step 1
Iteration 0:   GMM criterion Q(b) =  16.853973
Iteration 1:   GMM criterion Q(b) =  2.2706472
Iteration 2:   GMM criterion Q(b) =  .19088097
Iteration 3:   GMM criterion Q(b) =  .00041101
Iteration 4:   GMM criterion Q(b) =  3.939e-09
Iteration 5:   GMM criterion Q(b) =  6.572e-19
GMM estimation
Number of parameters =   5
Number of moments    =   5
Initial weight matrix: Unadjusted                     Number of obs   =      4412
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/xb_private	.7986654	.1089891	7.33	0.000	.5850507	1.01228
/xb_chronic	1.091865	.0559888	19.50	0.000	.9821291	1.201601
/xb_female	.4925481	.0585298	8.42	0.000	.3778317	.6072644
/xb_income	.003557	.0010824	3.29	0.001	.0014356	.0056784
/b0	-.2297263	.1108607	-2.07	0.038	-.4470093	-.0124434

```
Instruments for equation 1: private chronic female income _cons
```

Our point estimates agree with those reported by Cameron and Trivedi to at least six significant digits; the small discrepancies are attributable to different optimization techniques and convergence criteria being used by `gmm` and `poisson`. The standard errors differ by a factor of sqrt$(4412/4411)$ because `gmm` uses N in the denominator of the formula for the robust covariance matrix, while the robust covariance matrix estimator used by `poisson` uses $N - 1$.

◁

❑ Technical note

That the GMM and maximum likelihood estimators of the exponential regression model coincide is not a general property of these two classes of estimators. The maximum likelihood estimator solves the score equations

$$\frac{1}{N}\sum_{i=1}^{N}\frac{\partial \ln \ell_i}{\partial \beta} = \mathbf{0}$$

where l_i is the likelihood for the ith observation. These score equations can be viewed as the sample analogues of the population moment conditions

$$E\left\{\frac{\partial \ln \ell_i}{\partial \beta}\right\} = \mathbf{0}$$

establishing that maximum likelihood estimators represent a subset of the class of GMM estimators.

For the Poisson model,

$$\ln \ell_i = -\exp(\mathbf{x}_i'\beta) + y_i\mathbf{x}_i'\beta - \ln y_i!$$

so the score equations are

$$\frac{1}{N}\sum_{i=1}^{N}\mathbf{x}_i\{y_i - \exp(\mathbf{x}_i'\beta)\} = \mathbf{0}$$

which are just the sample moment conditions implied by (10) that we used in the previous example. That is why our results using `gmm` match Cameron and Trivedi's results using `poisson`.

On the other hand, an intuitive set of moment conditions to consider for GMM estimation of a probit model is

$$E[\mathbf{x}\{y - \Phi(\mathbf{x}'\beta)\}] = \mathbf{0}$$

where $\Phi()$ is the standard normal cumulative distribution function. Differentiating the likelihood function for the maximum likelihood probit estimator, we can show that the corresponding score equations are

$$\frac{1}{N}\sum_{i=1}^{N}\left[\mathbf{x}_i\left\{y_i\frac{\phi(\mathbf{x}_i'\beta)}{\Phi(\mathbf{x}_i'\beta)} - (1-y_i)\frac{\phi(\mathbf{x}_i'\beta)}{1-\Phi(\mathbf{x}_i'\beta)}\right\}\right] = \mathbf{0}$$

where $\phi()$ is the standard normal density function. These two moment conditions are not equivalent, so the maximum likelihood and GMM probit estimators are distinct.

❑

▷ Example 5: Comparison of GMM and maximum likelihood

Using the automobile dataset, here we fit a probit model of `foreign` on `gear_ratio`, `length`, and `headroom` using first the score equations and then the intuitive set of GMM equations. We type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. global xb "{b1}*gear_ratio + {b2}*length + {b3}*headroom + {b0}"
. global phi "normalden($xb)"
. global Phi "normal($xb)"
. gmm (foreign*$phi/$Phi - (1-foreign)*$phi/(1-$Phi)),
> instruments(gear_ratio length headroom) onestep
  (output omitted)
. estimates store ml
. gmm (foreign - $Phi), instruments(gear_ratio length headroom) onestep
  (output omitted)
. estimates store gmm
```

```
. estimates table ml gmm, b se
```

Variable	ml	gmm
b1		
_cons	2.9586277	2.8489213
	.64042341	.63570246
b2		
_cons	-.02148933	-.02056033
	.01382043	.01396954
b3		
_cons	.01136927	.02240761
	.27278528	.2849891
b0		
_cons	-6.0222289	-5.8595615
	3.5594588	3.5188028

legend: b/se

The coefficients on `gear_ratio` and `length` are close for the two estimators. The GMM estimate of the coefficient on `headroom` is twice that of the maximum likelihood estimate, though the relatively large standard errors imply that this difference is not significant. You can verify that the coefficients in the column marked "`ml`" match those you would obtain using `probit`. We have not discussed the differences among standard errors based on the various GMM and maximum-likelihood covariance matrix estimators to avoid tedious algebra, though you can verify that the robust covariance matrix after one-step GMM estimation differs by only a finite-sample adjustment factor of $(N/N-1)$ from the robust covariance matrix reported by `probit`. Both the maximum likelihood and GMM probit estimators require the normality assumption, and the maximum likelihood estimator is efficient if that normality assumption is correct; therefore, in this particular example, there is no reason to prefer the GMM estimator.

◁

We can modify (10) easily to allow for endogenous regressors. Suppose that x_j is endogenous in the sense that $E(u|x_j) \neq 0$. Then (10) is no longer a valid moment condition. However, suppose we have some variables other than $\mathbf{x}$ such that $E(u|\mathbf{z}) = \mathbf{0}$. We can instead use the moment conditions

$$E(\mathbf{z}u) = E[\mathbf{z}\{y - \exp(\mathbf{x}'\beta)\}] = \mathbf{0} \tag{11}$$

As usual, if some elements of $\mathbf{x}$ are exogenous, then they should appear in $\mathbf{z}$ as well.

▷ Example 6: Exponential regression with endogenous regressors

Returning to the model discussed in example 4, here we treat `income` as endogenous; unobservable factors that determine a person's income may also affect the number of times a person visits a doctor. We use a person's age and race as instruments. These are valid instruments if we believe that age and race influence a person's income but do not have a direct impact on the number of doctor visits. (Whether this belief is justified is another matter; we test that belief in [R] **gmm postestimation**.) Because we have more instruments (seven) than parameters (five), we have an overidentified model. Therefore, the choice of weight matrix does matter. We will utilize the default two-step GMM estimator. In the first step, we will use a weight matrix that assumes the errors are i.i.d. In the second step, we will use a weight matrix that assumes heteroskedasticity. When you specify `twostep`, these are the defaults for the first- and second-step weight matrices, so we do not have to use the `winitial()` or `wmatrix()` options. We will again obtain a robust VCE, which is also the default. We type

```
. use http://www.stata-press.com/data/r12/docvisits
. gmm (docvis - exp({xb:private chronic female income}+{b0})),
> instruments(private chronic female age black hispanic)
Step 1
Iteration 0:   GMM criterion Q(b) =  16.910173
Iteration 1:   GMM criterion Q(b) =  .82276104
Iteration 2:   GMM criterion Q(b) =  .21832032
Iteration 3:   GMM criterion Q(b) =  .12685935
Iteration 4:   GMM criterion Q(b) =  .12672369
Iteration 5:   GMM criterion Q(b) =  .12672365
Step 2
Iteration 0:   GMM criterion Q(b) =  .00234641
Iteration 1:   GMM criterion Q(b) =  .00215957
Iteration 2:   GMM criterion Q(b) =  .00215911
Iteration 3:   GMM criterion Q(b) =  .00215911
GMM estimation
Number of parameters =   5
Number of moments    =   7
Initial weight matrix: Unadjusted                 Number of obs   =      4412
GMM weight matrix:     Robust
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/xb_private	.535335	.1599039	3.35	0.001	.2219291	.8487409
/xb_chronic	1.090126	.0617659	17.65	0.000	.9690668	1.211185
/xb_female	.6636579	.0959884	6.91	0.000	.4755241	.8517918
/xb_income	.0142855	.0027162	5.26	0.000	.0089618	.0196092
/b0	-.5983477	.138433	-4.32	0.000	-.8696713	-.327024

```
Instruments for equation 1: private chronic female age black hispanic _cons
```

Once we control for the endogeneity of income, we find that its coefficient has quadrupled in size. Additionally, access to private insurance has less of an impact on the number of doctor visits and gender has more of an impact.

◁

❑ Technical note

Although perhaps at first tempting, unlike the Poisson model, you cannot simply replace $\mathbf{x}$ in the moment conditions for the probit (or logit) model with a vector of instruments, $\mathbf{z}$, if you have endogenous regressors. See Wilde (2008).

❑

Mullahy (1997) considers a slightly more complicated version of the exponential regression model that incorporates nonadditive unobserved heterogeneity. His model can be written as

$$y_i = \exp(\mathbf{x}_i'\beta)\eta_i + \epsilon_i$$

where $\eta_i > 0$ is an unobserved heterogeneity term that may be correlated with $\mathbf{x}_i$. One result from his paper is that instead of using the additive moment condition (10), we can use the multiplicative moment condition

$$E\left\{\mathbf{z}\frac{y - \exp(\mathbf{x}'\beta)}{\exp(\mathbf{x}'\beta)}\right\} = E[\mathbf{z}\{y\exp(-\mathbf{x}'\beta) - 1\}] = \mathbf{0} \tag{12}$$

Windmeijer and Santos Silva (1997) discuss the use of additive versus multiplicative moment conditions with endogenous regressors and note that a set of instruments that satisfies the additive moment conditions will not also satisfy the multiplicative moment conditions. They remark that which to use is an empirical issue that can at least partially be settled by using the test of overidentifying restrictions that is implemented by `estat overid` after `gmm` to ascertain whether the instruments for a given model are valid. See [R] **gmm postestimation** for information on the test of overidentifying restrictions.

Specifying derivatives

By default, `gmm` calculates derivatives numerically, and the method used produces accurate results for the vast majority of applications. However, if you refit the same model repeatedly or else have the derivatives available, then `gmm` will run more quickly if you supply it with analytic derivatives.

When you use the interactive version of `gmm`, you specify derivatives using substitutable expressions in much the same way you specify the moment equations. There are three rules you must follow:

1. As with the substitutable expressions that define residual equations, you bind parameters of the model in braces: `{b0}`, `{param}`, etc.
2. You must specify a derivative for each parameter that appears in each moment equation. If a parameter does not appear in a moment equation, then you do not specify a derivative for that parameter in that moment equation.
3. If you declare a linear combination in an equation, then you specify a derivative with respect to that linear combination. `gmm` applies the chain rule to obtain the derivatives with respect to the individual parameters encompassed by that linear combination.

We illustrate with several examples.

▷ Example 7: Derivatives for a single-equation model

Consider a simple exponential regression model with one exogenous regressor and a constant term. We have

$$u = y - \exp(\beta_0 + \beta_1 x)$$

Now

$$\frac{\partial u}{\partial \beta_0} = -\exp(\beta_0 + \beta_1 x) \qquad \text{and} \qquad \frac{\partial u}{\partial \beta_1} = -x\exp(\beta_0 + \beta_1 x)$$

In Stata, we type

```
. gmm (docvis - exp({b0} + {b1}*income)), instruments(income)
> deriv(/b0 = -1*exp({b0} + {b1}*income))
> deriv(/b1 = -1*income*exp({b0}+{b1}*income)) onestep
Step 1
Iteration 0:   GMM criterion Q(b) =  9.1548611
Iteration 1:   GMM criterion Q(b) =  3.5146131
Iteration 2:   GMM criterion Q(b) =  .01344695
Iteration 3:   GMM criterion Q(b) =  3.690e-06
Iteration 4:   GMM criterion Q(b) =  4.606e-13
Iteration 5:   GMM criterion Q(b) =  1.502e-26
```

```
GMM estimation
Number of parameters =   2
Number of moments    =   2
Initial weight matrix: Unadjusted                     Number of obs   =      4412
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/b0	1.204888	.0462355	26.06	0.000	1.114268	1.295507
/b1	.0046702	.0009715	4.81	0.000	.0027662	.0065743

```
Instruments for equation 1: income _cons
```

Notice how we specified the `derivative()` option for each parameter. We simply specified a slash, the name of the parameter, an equal sign, then a substitutable expression that represents the derivative. Because our model has only one residual equation, we do not need to specify equation numbers in the `derivative()` options.

◁

When you specify a linear combination of variables, your derivative should be with respect to the entire linear combination. For example, say we have the residual equation

$$u = y - \exp(\mathbf{x}'\beta + \beta_0)$$

for which we would type

```
. gmm (y - exp({xb: x1 x2 x3} + {b0}) ...
```

Then in addition to the derivative $\partial u/\partial\beta_0$, we are to compute and specify

$$\frac{\partial u}{\partial(\mathbf{x}'\beta)} = -\exp(\mathbf{x}'\beta + \beta_0)$$

Using the chain rule, $\partial u/\partial\beta_j = \partial u/\partial(\mathbf{x}'\beta) \times \partial(\mathbf{x}'\beta)/\partial\beta_j = -x_j\exp(\mathbf{x}'\beta + \beta_0)$. Stata does this last calculation automatically. It knows the variables in the linear combination, so all it needs is the derivative of the residual function with respect to the linear combination. This allows you to change the variables in your linear combination without having to change the derivatives.

▷ Example 8: Derivatives with a linear combination

We refit the model described in the example illustrating exponential regression with endogenous regressors, now providing analytic derivatives. We type

```
. gmm (docvis - exp({xb:private chronic female income}+{b0})),
> instruments(private chronic female age black hispanic)
> derivative(/xb = -1*exp({xb:} + {b0}))
> derivative(/b0 = -1*exp({xb:} + {b0}))
Step 1
Iteration 0:   GMM criterion Q(b) =  16.910173
Iteration 1:   GMM criterion Q(b) =  .82270871
Iteration 2:   GMM criterion Q(b) =  .21831995
Iteration 3:   GMM criterion Q(b) =  .12685934
Iteration 4:   GMM criterion Q(b) =  .12672369
Iteration 5:   GMM criterion Q(b) =  .12672365
Step 2
Iteration 0:   GMM criterion Q(b) =  .00234641
Iteration 1:   GMM criterion Q(b) =  .00215957
Iteration 2:   GMM criterion Q(b) =  .00215911
Iteration 3:   GMM criterion Q(b) =  .00215911
```

```
GMM estimation
Number of parameters =   5
Number of moments    =   7
Initial weight matrix: Unadjusted                 Number of obs   =      4412
GMM weight matrix:     Robust
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/xb_private	.535335	.159904	3.35	0.001	.221929	.848741
/xb_chronic	1.090126	.0617659	17.65	0.000	.9690668	1.211185
/xb_female	.6636579	.0959885	6.91	0.000	.475524	.8517918
/xb_income	.0142855	.0027162	5.26	0.000	.0089618	.0196092
/b0	-.5983477	.138433	-4.32	0.000	-.8696714	-.327024

```
Instruments for equation 1: private chronic female age black hispanic _cons
```

In the first `derivative()` option, we specified the name of the linear combination, `xb`, instead of an individual parameter's name. We already declared the variables of our linear combination in the substitutable expression for the residual equation, so in our substitutable expressions for the derivatives, we can use the shorthand notation `{xb:}` to refer to it.

Our point estimates are identical to those we obtained earlier. The standard errors and confidence intervals differ by only trivial amounts.

◁

Exponential regression models with panel data

In addition to supporting cross-sectional and time-series data, `gmm` also works with panel-data models. Here we illustrate `gmm`'s panel-data capabilities by expanding our discussion of exponential regression models to allow for panel data. This also provides us the opportunity to demonstrate the moment-evaluator program version of `gmm`. Our discussion is based on Blundell, Griffith, and Windmeijer (2002). Also see Wooldridge (1999) for further discussion of nonlinear panel-data models.

First, we expand (9) for panel data. With individual heterogeneity term η_i, we have

$$E(y_{it}|\mathbf{x}_{it}, \eta_i) = \exp(\mathbf{x}_{it}'\beta + \eta_i) = \mu_{it}\nu_i$$

where $\mu_{it} = \exp(\mathbf{x}_{it}'\beta)$ and $\nu_i = \exp(\eta_i)$. Note that there is no constant term in this model because its effect cannot be disentangled from ν_i. With an additive idiosyncratic error term, we have the regression model

$$y_{it} = \mu_{it}\nu_i + \epsilon_{it}$$

We do not impose the assumption $E(\mathbf{x}_{it}\eta_i) = \mathbf{0}$, so η_i can be considered a fixed effect in the sense that it may be correlated with the regressors.

As discussed by Blundell, Griffith, and Windmeijer (2002), if $\mathbf{x}_{it}$ is strictly exogenous, meaning $E(\mathbf{x}_{it}\epsilon_{is}) = \mathbf{0}$ for all t and s, then we can estimate the parameters of the model by using the sample moment conditions

$$\sum_i \sum_t \mathbf{x}_{it}\left(y_{it} - \mu_{it}\frac{\overline{y}_i}{\overline{\mu}_i}\right) = \mathbf{0} \tag{13}$$

where $\overline{y}_i$ and $\overline{\mu}_i$ are the means of y_{it} and μ_{it} for panel i, respectively. Because $\overline{\mu}_i$ depends on the parameters of the model, it must be recomputed each time `gmm` needs to evaluate the residual equation. Therefore, we cannot use the substitutable expression version of `gmm`. Instead, we must use the moment-evaluator program version.

The moment-evaluator program version of gmm functions much like the function-evaluator program versions of nl and nlsur. The program you write is passed one or more variables to be filled in with the residuals evaluated at the parameter values specified in an option passed to your program. For the fixed-effects Poisson model with strictly exogenous regressors, our first crack at a function-evaluator program is

```
program gmm_poi
        version 12
        syntax varlist if, at(name)
        quietly {
                tempvar mu mubar ybar
                gen double `mu' = exp(x1*`at'[1,1] + x2*`at'[1,2]       ///
                                                   + x3*`at'[1,3]) `if'
                egen double `mubar' = mean(`mu') `if', by(id)
                egen double `ybar' = mean(y) `if', by(id)
                replace `varlist' = y - `mu'*`ybar'/`mubar' `if'
        }
end
```

You can save your program in an ado-file named *name*.ado, where *name* is the name you use for your program; here we would save the program in the ado-file gmm_poi.ado. Alternatively, if you are working from within a do-file, you can simply define the program before calling gmm. The syntax statement declares that we are expecting to receive a *varlist*, containing the names of variables whose values we are to replace with the values of the residual equations, and an if expression that will mark the estimation sample; because our model has one residual equation, *varlist* will consist of one variable. at() is a required option to our program, and it will contain the name of a matrix containing the parameter values at which we are to evaluate the residual equation. All moment-evaluator programs must accept the *varlist*, if condition, and at() option.

The first part of our program computes μ_{it}. In the model we will fit shortly, we have three regressors, named x1, x2, and x3. The `at' vector will have three elements, one for each of those variables. Notice that we included `if' at the end of each statement that affects variables to restrict the computations to the relevant estimation sample. The two egen statements compute $\overline{\mu}_i$ and $\overline{y}_i$; in the example dataset we will use shortly, the panel variable is named id, and for simplicity we hardcoded that variable into our program as well. Finally, we compute the residual equation, which is the portion of (13) bound in parentheses.

▷ Example 9: Panel poisson with strictly exogenous regressors

To fit our model, we type

```
. use http://www.stata-press.com/data/r12/poisson1
. gmm gmm_poi, nequations(1) parameters(b1 b2 b3)
> instruments(x1 x2 x3, noconstant) vce(cluster id) onestep
Step 1
Iteration 0:   GMM criterion Q(b) =   51.99142
Iteration 1:   GMM criterion Q(b) =  .04345191
Iteration 2:   GMM criterion Q(b) =  8.720e-06
Iteration 3:   GMM criterion Q(b) =  7.115e-13
Iteration 4:   GMM criterion Q(b) =  5.130e-27
```

```
GMM estimation
Number of parameters =   3
Number of moments    =   3
Initial weight matrix: Unadjusted                     Number of obs   =       409
                                      (Std. Err. adjusted for 45 clusters in id)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         /b1 |     1.94866   .1000265    19.48   0.000     1.752612    2.144709
         /b2 |    -2.966119  .0923592   -32.12   0.000    -3.14714    -2.785099
         /b3 |     1.008634  .1156561     8.72   0.000      .781952    1.235315
------------------------------------------------------------------------------
Instruments for equation 1: x1 x2 x3
```

All three of our regressors are strictly exogenous, so they can serve as their own regressors. There is no constant term in the model (it would be unidentified), so we exclude a constant term from our list of instruments. We have one residual equation as indicated by `nequations(1)`, and we have three parameters, named `b1`, `b2`, and `b3`. The order in which you declare parameters in the `parameters()` option determines the order in which they appear in the `'at'` vector in the moment-evaluator program. We specified `vce(cluster id)` to obtain standard errors that allow for correlation among observations within each panel.

◁

❑ Technical note

The program we just wrote is sufficient to fit the model to the `poisson1` dataset, but if we want to fit that model to other datasets, we would need to change the variable names and perhaps account for having a different number of parameters as well. With a bit more programming, advanced users can write a more general program to work with arbitrary datasets. Any options not understood by `gmm` are passed along to the moment-evaluator program, and we can take advantage of that feature to pass the name of the dependent variable, list of regressors, and panel identifier variable. A better version of `gmm_poi` would be

```
program gmm_poi2
        version 12
        syntax varlist if, at(name) myrhs(varlist)  ///
               mylhs(varlist) myidvar(varlist)
        quietly {
                tempvar mu mubar ybar
                gen double `mu' = 0 `if'
                local j = 1
                foreach var of varlist `myrhs' {
                        replace `mu' = `mu' + `var'*`at'[1,`j'] `if'
                        local j = `j' + 1
                }
                replace `mu' = exp(`mu')
                egen double `mubar' = mean(`mu') `if', by(`myidvar')
                egen double `ybar' = mean(`mylhs') `if', by(`myidvar')
                replace `varlist' = `mylhs' - `mu'*`ybar'/`mubar' `if'
        }
end
```

Our program now accepts three more options. Our call to gmm is

```
. gmm gmm_poi2, mylhs(y) myrhs(x1 x2 x3) myidvar(id) nequations(1)
> parameters(b1 b2 b3) instruments(x1 x2 x3, noconstant) vce(cluster id) onestep
```

With mylhs(), myrhs(), and myidvar(), we are now able to fit our model to any panel dataset we wish without having to modify the gmm_poi2 program. In the section *Details of moment-evaluator programs* below, we show how to incorporate weights and derivatives in moment-evaluator programs. ❑

When past values of the idiosyncratic error term affect the value of a regressor, we say that regressor is *predetermined*. When one or more regressors are predetermined, sample moment condition (10) is no longer valid. However, Chamberlain (1992) shows that a simple alternative is to consider moment conditions of the form

$$\sum_i \sum_{t=2}^{T} \mathbf{x}_{i,t-1} \left(y_{i,t-1} - \mu_{i,t-1} \frac{y_{it}}{\mu_{it}} \right) = \mathbf{0} \tag{14}$$

Also see Wooldridge (1997) and Windmeijer (2000) for other moment conditions that can be used with predetermined regressors.

▷ Example 10: Panel Poisson with predetermined regressors

Here we refit the previous model, treating all the regressors as predetermined and using the moment conditions in (14). Our moment-evaluator program is

```
program gmm_poipre
        version 12
        syntax varlist if, at(name) myrhs(varlist) mylhs(varlist)
        quietly {
                tempvar mu mubar ybar
                gen double `mu' = 0 `if'
                local j = 1
                foreach var of varlist `myrhs' {
                        replace `mu' = `mu' + `var'*`at'[1,`j'] `if'
                        local j = `j' + 1
                }
                replace `mu' = exp(`mu')
                replace `varlist' = L.`mylhs' - L.`mu'*`mylhs'/`mu' `if'
        }
end
```

As before, the first part of our program computes μ_{it}; the only difference is in how we compute the residual equation. We used lag-operator notation so that Stata properly handles gaps in our dataset. Equation (14) shows that we are to use the first lags of the regressors as instruments, so we type

```
. gmm gmm_poipre, mylhs(y) myrhs(x1 x2 x3) nequations(1) parameters(b1 b2 b3)
> instruments(L.(x1 x2 x3), noconstant) vce(cluster id) onestep
(obs = 364)

Step 1
Iteration 0:   GMM criterion Q(b) =  52.997808
Iteration 1:   GMM criterion Q(b) =  2.1678071
Iteration 2:   GMM criterion Q(b) =  .08716503
Iteration 3:   GMM criterion Q(b) =  .00007136
Iteration 4:   GMM criterion Q(b) =  4.699e-11
Iteration 5:   GMM criterion Q(b) =  1.932e-23

GMM estimation

Number of parameters =   3
Number of moments    =   3
Initial weight matrix: Unadjusted                     Number of obs   =      364
                                      (Std. Err. adjusted for 45 clusters in id)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          /b1 |   2.035125   .2662377     7.64   0.000     1.513308    2.556941
          /b2 |  -2.929362   .2290397   -12.79   0.000    -3.378272   -2.480453
          /b3 |   1.235219   .1673295     7.38   0.000     .9072596    1.563179
------------------------------------------------------------------------------
Instruments for equation 1: L.x1 L.x2 L.x3
```

Here, like earlier with strictly exogenous regressors, the number of instruments equals the number of parameters, so there is no gain to using the two-step or iterated estimators. However, if you do have more instruments than parameters, you will most likely want to use one of those other estimators instead.

◁

In the previous example, we used $\mathbf{x}_{i,t-1}$ as instruments. A more efficient GMM estimator would also use $\mathbf{x}_{i,t-2}, \mathbf{x}_{i,t-3}, \ldots, \mathbf{x}_{i,1}$ as instruments in period t as well. `gmm`'s `xtinstruments()` option allows you to specify instrument lists that grow as t increases. Later we discuss the `xtinstruments()` option in detail in the context of linear dynamic panel-data models.

When a regressor is contemporaneously correlated with the idiosyncratic error term, we say that regressor is endogenous. Windmeijer (2000) shows that here we can use the moment condition

$$\sum_i \sum_{t=3}^{T} \mathbf{x}_{i,t-2} \left(\frac{y_{it}}{\mu_{it}} - \frac{y_{i,t-1}}{\mu_{i,t-1}} \right)$$

Here we use the second lag of the endogenous regressor as an instrument. If a variable is strictly exogenous, it can of course serve as its own instrument.

▷ Example 11: Panel Poisson with endogenous regressors

Here we refit the model, treating `x3` as endogenous and `x1` and `x2` as strictly exogenous. Our moment-evaluator program is

```
program gmm_poiend
        version 12
        syntax varlist if, at(name) myrhs(varlist) mylhs(varlist)
        quietly {
                tempvar mu mubar ybar
                gen double `mu' = 0 `if'
                local j = 1
                foreach var of varlist `myrhs' {
                        replace `mu' = `mu' + `var'*`at'[1,`j'] `if'
                        local j = `j' + 1
                }
                replace `mu' = exp(`mu')
                replace `varlist' = `mylhs'/`mu' - L.`mylhs'/L.`mu' `if'
        }
end
```

Now we call gmm using x1, x2, and L2.x3 as instruments:

```
. use http://www.stata-press.com/data/r12/poisson2
. gmm gmm_poiend, mylhs(y) myrhs(x1 x2 x3) nequations(1) parameters(b1 b2 b3)
> instruments(x1 x2 L2.x3, noconstant) vce(cluster id) onestep
Step 1
Iteration 0:   GMM criterion Q(b) =  47.376537
Iteration 1:   GMM criterion Q(b) =  .08115406
Iteration 2:   GMM criterion Q(b) =  .03477036
Iteration 3:   GMM criterion Q(b) =  .00041056
Iteration 4:   GMM criterion Q(b) =  1.189e-07
Iteration 5:   GMM criterion Q(b) =  1.298e-14
Iteration 6:   GMM criterion Q(b) =  1.574e-28
GMM estimation
Number of parameters =   3
Number of moments    =   3
Initial weight matrix: Unadjusted                     Number of obs   =      3766
                                  (Std. Err. adjusted for 500 clusters in id)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         /b1 |   1.844082   .1515252    12.17   0.000     1.547098    2.141066
         /b2 |  -2.904011    .108117   -26.86   0.000    -3.115916   -2.692105
         /b3 |   3.277512   2.459066     1.33   0.183    -1.542169    8.097193
------------------------------------------------------------------------------
Instruments for equation 1: x1 x2 L2.x3
```

As with the predetermined case previously, instead of using just $\mathbf{x}_{i,t-2}$ as an instrument, we could use all further lags of $\mathbf{x}_{it}$ as instruments as well.

◁

Rational-expectations models

Macroeconomic models typically assume that agents' expectations about the future are formed rationally. By rational expectations, we mean that agents use all information available when forming their forecasts, so the forecast error is uncorrelated with the information available when the forecast was made. Say that at time t, people make a forecast, $\widehat{y}_{t+1}$, of variable y in the next period. If Ω_t denotes all available information at time t, then rational expectations implies that $E\left\{(\widehat{y}_{t+1} - y_{t+1})|\Omega_t\right\} = 0$. If Ω_t denotes observable variables such as interest rates or prices, then this conditional expectation can serve as the basis of a moment condition for GMM estimation.

▷ Example 12: Fitting a Euler equation

In a well-known article, Hansen and Singleton (1982) consider a model of portfolio decision making and discuss parameter estimation using GMM. We will consider a simple example with one asset in which the agent can invest. A consumer wants to maximize the present value of his lifetime utility derived from consuming the good. On the one hand, the consumer is impatient, so he would rather consume today than wait until tomorrow. On the other hand, if he consumes less today, he can invest more of his money, earning more interest that he can then use to consume more of the good tomorrow. Thus there is a tradeoff between having his cake today or sacrificing a bit today to have more cake tomorrow.

If we assume a specific form for the agent's utility function, known as the constant relative-risk aversion utility function, we can show that the Euler equation is

$$E\left[\mathbf{z}_t\left\{1-\beta(1+r_{t+1})(c_{t+1}/c_t)^{-\gamma}\right\}\right]=\mathbf{0}$$

where β and γ are the parameters to estimate, r_t is the return to the financial asset, and c_t is consumption in period t. β measures the agent's discount factor. If β is near one, the agent is patient and is more willing to forgo consumption this period. If β is close to zero, the agent is less patient and prefers to consume more now. The parameter γ characterizes the agent's utility function. If γ equals one, the utility function is linear. As γ tends toward zero, the utility function tends toward $u=\log(c)$.

We have data on 3-month Treasury bills (r_t) and consumption expenditures (c_t). As instruments, we will use lagged rates of return and past growth rates of consumption. We will use the two-step estimator and a weight matrix that allows for heteroskedasticity and autocorrelation up to four lags with the Bartlett kernel. In Stata, we type

```
. use http://www.stata-press.com/data/r12/cr
. generate cgrowth = c / L.c
(1 missing value generated)
. gmm (1 - {b=1}*(1+F.r)*(F.c/c)^(-1*{gamma=1})), inst(L.r L2.r cgrowth L.cgrowth)
> wmat(hac nw 4) twostep
warning: 1 missing value returned for equation 1 at initial values
Step 1
Iteration 0:   GMM criterion Q(b) =  .00226482
Iteration 1:   GMM criterion Q(b) =  .00054369
Iteration 2:   GMM criterion Q(b) =  .00053904
Iteration 3:   GMM criterion Q(b) =  .00053904
Step 2
Iteration 0:   GMM criterion Q(b) =   .0600729
Iteration 1:   GMM criterion Q(b) =   .0596369
Iteration 2:   GMM criterion Q(b) =   .0596369
GMM estimation
Number of parameters =   2
Number of moments    =   5
Initial weight matrix: Unadjusted                     Number of obs   =       239
GMM weight matrix:     HAC Bartlett 4
```

	HAC Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/b	.9204617	.0134646	68.36	0.000	.8940716	.9468518
/gamma	-4.222361	1.473895	-2.86	0.004	-7.111143	-1.333579

```
HAC standard errors based on Bartlett kernel with 4 lags
Instruments for equation 1: L.r L2.r cgrowth L.cgrowth _cons
```

The warning message at the top of the output appears because the forward operator in our substitutable expression says that residuals can be computed only for 239 observations; our dataset contains 240 observations. Our estimate of β is near one, in line with expectations and published results.

◁

System estimators

In many economic models, two or more variables are determined jointly through a system of simultaneous equations. Indeed, some of the earliest work in econometrics, including that of the Cowles Commission, was centered around estimation of the parameters of simultaneous equations. The 2SLS and IV estimators we have already discussed are used in some circumstances to estimate such parameters. Here we focus on the joint estimation of all the parameters of systems of equations, and we begin with the well-known three-stage least-squares (3SLS) estimator.

Recall that the 2SLS estimator is based on the moment conditions $E(\mathbf{z}u) = \mathbf{0}$. The 2SLS estimator can be used to estimate the parameters of one equation of a system of structural equations. Moreover, with the 2SLS estimator, we do not even need to specify the structural relationship among all the endogenous variables; we need to specify only the equation on which interest focuses and simply assume reduced-form relationships among the endogenous regressors of the equation of interest and the exogenous variables of the model. If we are willing to specify the complete system of structural equations, then assuming our model is correctly specified, by estimating all the equations jointly, we can obtain estimates that are more efficient than equation-by-equation 2SLS.

In [R] **reg3**, we fit a simple two-equation macroeconomic model:

$$\texttt{consump} = \beta_0 + \beta_1\texttt{wagepriv} + \beta_2\texttt{wagegovt} + \epsilon_1 \tag{15}$$

$$\texttt{wagepriv} = \beta_3 + \beta_4\texttt{consump} + \beta_5\texttt{govt} + \beta_6\texttt{capital1} + \epsilon_2 \tag{16}$$

where `consump` represents aggregate consumption; `wagepriv` and `wagegovt` are total wages paid by the private and government sectors, respectively; `govt` is government spending; and `capital1` is the previous period's capital stock. We are not willing to assume that ϵ_1 and ϵ_2 are independent, so we must treat both `consump` and `wagepriv` as endogenous. Suppose that a random shock makes ϵ_2 positive. Then by (16), `wagepriv` will be higher than it otherwise would. Moreover, ϵ_1 will either be higher or lower, depending on the correlation between it and ϵ_2. The shock to ϵ_2 has made both `wagepriv` and ϵ_1 move, implying that in (15) `wagepriv` is an endogenous regressor. A similar argument shows that `consump` is an endogenous regressor in the second equation. In our model, `wagegovt`, `govt`, and `capital1` are all exogenous variables.

Let $\mathbf{z}_1$ and $\mathbf{z}_2$ denote the instruments for the first and second equations, respectively; we will discuss what comprises them shortly. We have two sets of moment conditions:

$$E\left\{\begin{array}{c}\mathbf{z}_1(\texttt{consump} - \beta_0 - \beta_1\texttt{wagepriv} - \beta_2\texttt{wagegovt}) \\ \mathbf{z}_2(\texttt{wagepriv} - \beta_3 - \beta_4\texttt{consump} - \beta_5\texttt{govt} - \beta_6\texttt{capital1})\end{array}\right\} = \mathbf{0} \tag{17}$$

One of the defining characteristics of 3SLS is that the errors are homoskedastic conditional on the instrumental variables. Using this assumption, we have

$$E\left[\left\{\begin{array}{c}\mathbf{z}_1\epsilon_1 \\ \mathbf{z}_2\epsilon_2\end{array}\right\}\left\{\begin{array}{cc}\mathbf{z}_1'\epsilon_1 & \mathbf{z}_2'\epsilon_2\end{array}\right\}\right] = \left\{\begin{array}{cc}\sigma_{11}E(\mathbf{z}_1\mathbf{z}_1') & \sigma_{12}E(\mathbf{z}_1\mathbf{z}_2') \\ \sigma_{21}E(\mathbf{z}_2\mathbf{z}_1') & \sigma_{22}E(\mathbf{z}_2\mathbf{z}_2')\end{array}\right\} \tag{18}$$

where $\sigma_{ij} = \mathrm{cov}(\epsilon_i, \epsilon_j)$. Let $\mathbf{\Sigma}$ denote the 2×2 matrix with typical element σ_{ij}.

The second defining characteristic of the 3SLS estimator is that it uses all the exogenous variables as instruments for all equations; here $\mathbf{z}_1 = \mathbf{z}_2 = (\texttt{wagegovt}, \texttt{govt}, \texttt{capital1}, 1)$, where the 1 indicates a constant term. From our discussion on the weight matrix and two-step estimation, we want to use the sample analogue of the matrix inverse of the right-hand side of (18) as our weight matrix.

To implement the 3SLS estimator, we apparently need to know $\mathbf{\Sigma}$ or at least have a consistent estimator of it. The solution is to fit (15) and (16) by 2SLS, use the sample residuals $\widehat{\epsilon_1}$ and $\widehat{\epsilon_2}$ to estimate $\mathbf{\Sigma}$, then estimate the parameters of (17) via GMM by using the weight matrix just discussed.

▷ Example 13: 3SLS estimation

3SLS is easier to do using `gmm` than it sounds. The 3SLS estimator is a two-step GMM estimator. In the first step, we do the equivalent of 2SLS on each equation, and then we compute a weight matrix based on (18). Finally, we perform a second step of GMM with this weight matrix.

In Stata, we type

```
. use http://www.stata-press.com/data/r12/klein, clear
. gmm (eq1:consump - {b0} - {xb: wagepriv wagegovt})
>     (eq2:wagepriv - {c0} - {xc: consump govt capital1}),
> instruments(eq1 eq2: wagegovt govt capital1) winitial(unadjusted, independent)
> wmatrix(unadjusted) twostep
Step 1
Iteration 0:   GMM criterion Q(b) =  4195.4487
Iteration 1:   GMM criterion Q(b) =  .22175631
Iteration 2:   GMM criterion Q(b) =  .22175631
Step 2
Iteration 0:   GMM criterion Q(b) =  .09716589
Iteration 1:   GMM criterion Q(b) =  .07028208
Iteration 2:   GMM criterion Q(b) =  .07028208
GMM estimation
Number of parameters =   7
Number of moments    =   8
Initial weight matrix: Unadjusted                 Number of obs   =       22
GMM weight matrix:     Unadjusted
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/b0	19.3559	3.583772	5.40	0.000	12.33184	26.37996
/xb_wagepriv	.8012754	.1279329	6.26	0.000	.5505314	1.052019
/xb_wagegovt	1.029531	.3048424	3.38	0.001	.432051	1.627011
/c0	14.63026	10.26693	1.42	0.154	-5.492552	34.75306
/xc_consump	.4026076	.2567312	1.57	0.117	-.1005764	.9057916
/xc_govt	1.177792	.5421253	2.17	0.030	.1152461	2.240338
/xc_capital1	-.0281145	.0572111	-0.49	0.623	-.1402462	.0840173

```
Instruments for equation 1: wagegovt govt capital1 _cons
Instruments for equation 2: wagegovt govt capital1 _cons
```

The `independent` suboption of the `winitial()` option tells `gmm` to assume that the residuals are independent across equations; this suboption sets $\sigma_{21} = \sigma_{12} = 0$ in (18). Assuming both homoskedasticity and cross-equation independence is equivalent to fitting the two equations of our model independently by 2SLS. The `wmatrix()` option controls how the weight matrix is computed based on the first-step parameter estimates before the second step of estimation; here we request a weight matrix that assumes conditional homoskedasticity but that does not impose the cross-equation independence like the initial weight matrix we used. In this example, we also illustrated how to

name equations and how equation names can be used in the `instruments()` option. Our results are identical to those in [R] **reg3**.

We could have specified our instruments with the syntax

```
instruments(wagegovt govt capital1)
```

because `gmm` uses the variables listed in the `instruments()` option for all equations unless you use the `equations()` suboption to restrict those variables to certain equations. However, we wanted to emphasize that the same instruments are being used for both equations; in a moment, we will discuss an estimator that does not use the same instruments in all equations.

◁

In the previous example, if we omit the `twostep` option, the resulting coefficients will be equivalent to equation-by-equation 2SLS, which Wooldridge (2010, 216) calls the "system 2SLS estimator". Eliminating the `twostep` option makes the `wmatrix()` option irrelevant, so that option can be eliminated as well.

So far, we have developed the traditional 3SLS estimator. Wooldridge (2010, chap. 8) discusses the "GMM 3SLS" estimator that extends the traditional 3SLS estimator by allowing for heteroskedasticity and different instruments for different equations.

Generalizing (18) to an arbitrary number of equations, we have

$$E\left(\mathbf{Z}'\epsilon\epsilon'\mathbf{Z}\right) = E\left(\mathbf{Z}'\mathbf{\Sigma}\mathbf{Z}\right) \tag{19}$$

where

$$\mathbf{Z} = \begin{bmatrix} \mathbf{z}_1 & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{0} & \mathbf{z}_2 & \cdots & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \mathbf{z}_m \end{bmatrix}$$

and $\mathbf{\Sigma}$ is now $m \times m$. Equation (19) is the multivariate analogue of a homoskedasticity assumption; for each equation, the error variance is constant for all observations, as is the covariance between any two equations' errors.

We can relax this homoskedasticity assumption by considering different weight matrices. For example, if we continue to assume that observations are independent but not necessarily identically distributed, then by specifying `wmatrix(robust)`, we would obtain a weight matrix that allows for heteroskedasticity:

$$\widehat{W} = \frac{1}{N}\sum_i \mathbf{Z}_i'\widehat{\epsilon}_i\widehat{\epsilon}_i'\mathbf{Z}_i$$

This is the weight matrix in Wooldridge's (2010, 218) Procedure 8.1, "GMM with Optimal Weighting Matrix". By default, `gmm` would report standard errors based on his covariance matrix (8.27); specifying `vce(unadjusted)` would provide the optimal GMM standard errors. If you have multiple observations for each individual or firm in your dataset, you could specify `wmatrix(cluster` *id*`)`, where *id* identifies individuals or firms. This would allow arbitrary within-individual correlation, though it does not account for an individual-specific fixed or random effect. In both cases, we would continue to use `winitial(unadjusted, independent)` so that the first-step estimates are the system 2SLS estimates.

Wooldridge (2010, sec. 9.6) discusses instances where it is necessary to use different instruments in different equations. The GMM 3SLS estimator with different instruments in different equations but with conditional homoskedasticity is what Hayashi (2000, 275) calls the "full-information instrumental

variables efficient" (FIVE) estimator. Implementing the FIVE estimator is easy with gmm. For example, say we have a two-equation system, where kids, age, income, and education are all valid instruments for the first equation; but education is not a valid instrument for the second equation. Then our syntax would take the form

```
gmm (<mexp_1>) (<mexp_2>), instruments(1:kids age income education)
     instruments(2:kids age income)
```

The following syntax is equivalent:

```
gmm (<mexp_1>) (<mexp_2>), instruments(kids age income)
     instruments(1:education)
```

Because we did not specify a list of equations in the second example's first instruments() option, those variables are used as instruments in both equations. You can use whichever syntax you prefer. The first requires a bit more typing but is arguably more transparent.

If all the regressors in the model are exogenous, then the traditional 3SLS estimator is the seemingly unrelated regression (SUR) estimator. Here you would specify all the regressors as instruments.

Dynamic panel-data models

Commands in Stata that work with panel data expect the data to be in the "long" format, meaning that each row of the dataset consists of one subobservation that is a member of a logical observation (represented by the panel identifier variable). See [D] **reshape** for a discussion of the long versus "wide" data forms. gmm is no exception in this respect when used with panel data. From a theoretical perspective, however, it is sometimes easier to view GMM estimators for panel data as system estimators in which we have N observations on a system of T equations, where N and T are the number of observations and panels, respectively, rather than a single-equation estimator with NT observations. Usually, each of the T equations will in fact be the same, though we will want to specify different instruments for each of these equations.

In a dynamic panel-data model, lagged values of the dependent variable are included as regressors. Here we consider a simple model with one lag of the dependent variable y as a regressor and a vector of strictly exogenous regressors, $\mathbf{x}_{it}$:

$$y_{it} = \rho y_{i,t-1} + \mathbf{x}_{it}'\beta + u_i + \epsilon_{it} \tag{20}$$

u_i can be either a fixed- or a random-effect term, in the sense that we do not require $\mathbf{x}_{it}$ to be independent of it. Even with the assumption that ϵ_{it} is i.i.d., the presence of both $y_{i,t-1}$ and u_i in (20) renders both the standard fixed- and random-effects estimators to be inconsistent because of the well-known Nickell (1981) bias. OLS regression of y_{it} on $y_{i,t-1}$ and $\mathbf{x}_{it}$ also produces inconsistent estimates, because $y_{i,t-1}$ will be correlated with the error term.

❑ Technical note

Stata has the xtabond, xtdpd, and xtdpdsys commands (see [XT] **xtabond**, [XT] **xtdpd**, and [XT] **xtdpdsys**) to fit equations like (20), and for everyday use those commands are preferred because they offer features such as Windmeijer (2005) bias-corrected standard errors to account for the bias of traditional two-step GMM standard errors seen in dynamic panel-data models and, being linear estimators, only require you to specify variable names instead of complete equations. However, using gmm has several pedagogical advantages, including the ability to tie those model-specific commands into a more general framework, a clear illustration of how certain types of instrument matrices for panel-data models are formed, and demonstrations of several advanced features of gmm.

❑

First-differencing (20) removes the panel-specific u_i term:

$$y_{it} - y_{i,t-1} = \rho(y_{i,t-1} - y_{i,t-2}) + (\mathbf{x}_{it} - \mathbf{x}_{i,t-1})'\beta + (\epsilon_{it} - \epsilon_{i,t-1}) \tag{21}$$

However, now $(y_{i,t-1} - y_{i,t-2})$ is correlated with $(\epsilon_{it} - \epsilon_{i,t-1})$. Thus we need an instrument that is correlated with the former but not the latter. The lagged variables in (21) mean that equation is not estimable for $t < 3$, so consider when $t = 3$. We have

$$y_{i3} - y_{i2} = \rho(y_{i2} - y_{i1}) + (\mathbf{x}_{i3} - \mathbf{x}_{i2})'\beta + (\epsilon_{i3} - \epsilon_{i2}) \tag{22}$$

In the Arellano–Bond (1991) estimator, lagged levels of the dependent variable are used as instruments. With our assumption that the ϵ_{it} are i.i.d., (20) intimates that y_{i1} can serve as an instrumental variable when we fit (22).

Next consider (21) when $t = 4$. We have

$$y_{i4} - y_{i3} = \rho(y_{i3} - y_{i2}) + (\mathbf{x}_{i4} - \mathbf{x}_{i3})'\beta + (\epsilon_{i4} - \epsilon_{i3})$$

Now (20) shows that both y_{i1} and y_{i2} are uncorrelated with the error term $(\epsilon_{i4} - \epsilon_{i3})$, so we have two instruments available. For $t = 5$, you can show that y_{i1}, y_{i2}, and y_{i3} can serve as instruments. As may now be apparent, one of the key features of these dynamic panel-data models is that the available instruments depend on the time period, t, as was the case for some of the panel Poisson models we considered earlier. Because the $\mathbf{x}_{it}$ are strictly exogenous by assumption, they can serve as their own instruments.

The initial weight matrix that is appropriate for the GMM dynamic panel-data estimator is slightly more involved than the unadjusted matrix we have used in most of our previous examples that assumes the errors are i.i.d. First, rewrite (21) for panel i as

$$\mathbf{y}_i - \mathbf{y}_i^L = \rho\,(\mathbf{y}_i^L - \mathbf{y}_i^{LL}) + (\mathbf{X}_i - \mathbf{X}_i^L)\beta + (\epsilon_i - \epsilon_i^L)$$

where $\mathbf{y}_i = (y_{i3}, \ldots, y_{iT})$ and $\mathbf{y}_i^L = (y_{i2}, \ldots, y_{i,T-1})$, $\mathbf{y}_i^{LL} = (y_{i1}, \ldots, y_{i,T-2})$, and $\mathbf{X}_i$, $\mathbf{X}_i^L$, ϵ_i, and ϵ_i^L are defined analogously. Let $\mathbf{Z}$ denote the full matrix of instruments for panel i, including the variables specified in both the `instruments()` and `xtinstruments()` options; the exact structure is detailed in *Methods and formulas*.

By assumption, ϵ_{it} is i.i.d., so the first-difference $(\epsilon_{it} - \epsilon_{i,t-1})$ is necessarily autocorrelated with correlation -0.5. Therefore, we should not use a weight matrix that assumes the errors are independent. For dynamic panel-data models, we can show that the appropriate initial weight matrix is

$$\widehat{\mathbf{W}} = \left(\frac{1}{N}\sum\nolimits_i \mathbf{Z}_i'\mathbf{H}_D\mathbf{Z}_i\right)^{-1}$$

where

$$\mathbf{H}_D = \begin{bmatrix} 1 & -0.5 & 0 & \ldots & 0 & 0 \\ -0.5 & 1 & -0.5 & \ldots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \ldots & 1 & -0.5 \\ 0 & 0 & 0 & \ldots & -0.5 & 1 \end{bmatrix}$$

We can obtain this initial weight matrix by specifying `winitial(xt D)`. The letter `D` indicates that the equation we are estimating is specified in first-differences.

▷ Example 14: Arellano–Bond estimator

Say we want to fit the model

$$\mathtt{n}_{it} = \rho\,\mathtt{n}_{i,t-1} + \beta_1\mathtt{w}_{it} + \beta_2\mathtt{w}_{i,t-1} + \beta_3\mathtt{k}_{it} + \beta_4\mathtt{k}_{i,t-1} + u_i + \epsilon_{it} \tag{23}$$

where we assume that $\mathtt{w}_{it}$ and $\mathtt{k}_{it}$ are strictly exogenous. First-differencing, our residual equation is

$$\begin{aligned}\epsilon^*_{it} = (\epsilon_{it} - \epsilon_{i,t-1}) =& \mathtt{n}_{it} - \mathtt{n}_{i,t-1} - \rho\,(\mathtt{n}_{i,t-1} - \mathtt{n}_{i,t-2}) - \beta_1(\mathtt{w}_{it} - \mathtt{w}_{i,t-1}) \\ &- \beta_2(\mathtt{w}_{i,t-1} - \mathtt{w}_{i,t-2}) - \beta_3(\mathtt{k}_{it} - \mathtt{k}_{i,t-1}) - \beta_4(\mathtt{k}_{i,t-1} - \mathtt{k}_{i,t-2})\end{aligned} \tag{24}$$

In Stata, we type

```
. use http://www.stata-press.com/data/r12/abdata
. gmm (D.n - {rho}*LD.n - {xb:D.w LD.w D.k LD.k}), xtinstruments(n, lags(2/.))
> instruments(D.w LD.w D.k LD.k, noconstant) deriv(/rho = -1*LD.n)
> deriv(/xb = -1) winitial(xt D) onestep
Step 1
Iteration 0:   GMM criterion Q(b) =   .0011455
Iteration 1:   GMM criterion Q(b) =  .00009103
Iteration 2:   GMM criterion Q(b) =  .00009103
GMM estimation
Number of parameters =   5
Number of moments    =  32
Initial weight matrix: XT D                         Number of obs   =      751
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
/rho	.8041712	.1199819	6.70	0.000	.5690111	1.039331
/xb_D_w	-.5600476	.1619472	-3.46	0.001	-.8774583	-.242637
/xb_LD_w	.3946699	.1092229	3.61	0.000	.1805969	.6087429
/xb_D_k	.3520286	.0536546	6.56	0.000	.2468676	.4571897
/xb_LD_k	-.2160435	.0679689	-3.18	0.001	-.3492601	-.0828269

```
Instruments for equation 1:
        XT-style: L(2/.).n
        Standard: D.w LD.w D.k LD.k
```

Because `w` and `k` are strictly exogenous, we specified the variants of them that appear in (24) in the `instruments()` option; because there is no constant term in the model, we specified `noconstant` to omit the constant from the instrument list.

We specified `xtinstruments(n, lags(2/.))` to tell `gmm` what instruments to use for the lagged dependent variable included as a regressor in (23). Based on our previous discussion, lags two and higher of $\mathtt{n}_{it}$ can serve as instruments. The `lags(2/.)` suboption tells `gmm` that the first available instrument for $\mathtt{n}_{it}$ is the lag-two value $\mathtt{n}_{i,t-2}$. The "`.`" tells `gmm` to use all further lags of $\mathtt{n}_{it}$ as instruments as well. The instrument matrices in dynamic panel-data models can become large if the dataset has many time periods per panel. In those cases, you could specify, for example, `lags(2/4)` to use just lags two through four instead of using all available lags.

Our results are identical to those we would obtain using `xtabond` with the syntax

```
xtabond n L(0/1).w L(0/1).k, lags(1) noconstant vce(robust)
```

Had we left off the `vce(robust)` option in our call to `xtabond`, we would have had to specify `vce(unadjusted)` in our call to `gmm` to obtain the same standard errors.

◁

❑ Technical note

gmm automatically excludes observations for which there are no valid observations for the panel-style instruments. However, it keeps in the estimation sample those observations for which fewer than the maximum number of instruments you requested are available. For example, if you specify the lags(2/4) suboption, you have requested three instruments, but gmm will keep observations even if only one or two instruments are available.

❑

▷ Example 15: Two-step Arellano–Bond estimator

Here we refit the model in the previous example, using the two-step GMM estimator.

```
. gmm (D.n - {rho}*LD.n - {xb:D.w LD.w D.k LD.k}),
> xtinstruments(n, lags(2/.)) instruments(D.w LD.w D.k LD.k, noconstant)
> deriv(/rho = -1*LD.n) deriv(/xb = -1) winitial(xt D) wmatrix(robust)
> vce(unadjusted)

Step 1
Iteration 0:   GMM criterion Q(b) =   .0011455
Iteration 1:   GMM criterion Q(b) =  .00009103
Iteration 2:   GMM criterion Q(b) =  .00009103

Step 2
Iteration 0:   GMM criterion Q(b) =  .44107941
Iteration 1:   GMM criterion Q(b) =   .4236729
Iteration 2:   GMM criterion Q(b) =   .4236729

GMM estimation

Number of parameters =   5
Number of moments    =  32
Initial weight matrix: XT D                          Number of obs   =       751
GMM weight matrix:     Robust

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        /rho |   .8044783   .0534763    15.04   0.000     .6996667      .90929
     /xb_D_w |  -.5154978   .0335506   -15.36   0.000    -.5812557   -.4497399
    /xb_LD_w |   .4059309   .0637294     6.37   0.000     .2810235    .5308384
     /xb_D_k |   .3556204   .0390892     9.10   0.000     .2790071    .4322337
    /xb_LD_k |  -.2204521    .046439    -4.75   0.000    -.3114709   -.1294332
------------------------------------------------------------------------------
Instruments for equation 1:
        XT-style: L(2/.).n
        Standard: D.w LD.w D.k LD.k
```

Our results match those you would obtain with the command

```
xtabond n L(0/1).(w k), lags(1) noconstant twostep
```

◁

❑ Technical note

Had we specified vce(robust) in our call to gmm, we would have obtained the traditional sandwich-based robust covariance matrix, but our standard errors would not match those we would obtain by specifying vce(robust) with the xtabond command. The xtabond, xtdpd, and xtdpdsys commands implement a bias-corrected robust VCE for the two-step GMM dynamic panel-data estimator. Traditional VCEs computed after the two-step dynamic panel-data estimator have been shown to exhibit often-severe bias; see Windmeijer (2005).

❑

Neither of the two dynamic panel-data examples we have fit so far include a constant term. When a constant term is included, the dynamic panel-data estimator is in fact a two-equation system estimator. For notational simplicity, consider a simple model containing just a constant term and one lag of the dependent variable:

$$y_{it} = \alpha + \rho y_{i,t-1} + u_i + \epsilon_{it}$$

First-differencing to remove the u_i term, we have

$$y_{it} - y_{i,t-1} = \rho(y_{i,t-1} - y_{i,t-2}) + (\epsilon_{it} - \epsilon_{i,t-1}) \tag{25}$$

This has also eliminated the constant term. If we assume $E(u_i) = 0$, which is reasonable if a constant term is included in the model, then we can recover α by including the moment condition

$$y_{it} = \alpha + \rho y_{i,t-1} + \epsilon'_{it} \tag{26}$$

where $\epsilon'_{it} = u_i + \epsilon_{it}$. The parameter ρ continues to be identified by (25), so the only instrument we use with (26) is a constant term. As before, the error term $(\epsilon_{i,t} - \epsilon_{i,t-1})$ is necessarily autocorrelated with correlation coefficient -0.5, though the error term ϵ'_{it} is white noise. Therefore, our initial weight matrix should be

$$\widehat{\mathbf{W}} = \left(\frac{1}{N}\sum\nolimits_i \mathbf{Z}_i'\mathbf{H}\mathbf{Z}_i\right)^{-1}$$

where

$$\mathbf{H} = \begin{bmatrix} \mathbf{H}_D & \mathbf{0} \\ \mathbf{0} & \mathbf{I} \end{bmatrix}$$

and $\mathbf{I}$ is a conformable identity matrix.

One complication arises concerning the relevant estimation sample. Looking at (25), we apparently lose the first two observations from each panel because of the presence of $y_{i,t-2}$, but in (26) we need only to sacrifice one observation, for $y_{i,t-1}$. For most multiple-equation models, we need to use the same estimation sample for all equations. However, in dynamic panel-data models, we can use more observations to fit the equation in level form [(26) here] than the equation in first-differences [equation (25)]. To request this behavior, we specify the `nocommonesample` option to `gmm`. That option tells `gmm` to use as many observations as possible for each equation, ignoring the loss of observations due to lagging or differencing.

▷ Example 16: Arellano–Bond estimator with constant term

Here we fit the model

$$\mathtt{n}_{it} = \alpha + \rho\,\mathtt{n}_{i,t-1} + u_i + \epsilon_{it}$$

Without specifying derivatives, our command would be

```
. gmm (D.n - {rho}*LD.n) (n - {alpha} - {rho}*L.n),
> xtinstruments(1: n, lags(2/.)) instruments(1:, noconstant) onestep
> winitial(xt DL) vce(unadj) nocommonesample
```

We would specify `winitial(xt DL)` to obtain the required initial weight matrix. The notation `DL` indicates that our first moment equation is in first-differences and the second moment equation is in levels (not first-differenced). We exclude a constant in the instrument list for the first equation, because first-differencing removed the constant term. Because we do not specify the `instruments()` option for the second moment equation, a constant is used by default.

This example also provides us the opportunity to illustrate how to specify derivatives for multiple-equation GMM models. Within the `derivative()` option, instead of specifying just the parameter name, now you must specify the equation name or number, a slash, and the parameter name to which the derivative applies. In Stata, we type

```
. gmm (D.n - {rho}*LD.n) (n - {alpha} - {rho}*L.n),
> xtinstruments(1: n, lags(2/.)) instruments(1:, noconstant)
> derivative(1/rho = -1*LD.n) derivative(2/alpha = -1)
> derivative(2/rho = -1*L.n) winitial(xt DL) vce(unadj) nocommonesample onestep
Step 1
Iteration 0:   GMM criterion Q(b) =  .09894466
Iteration 1:   GMM criterion Q(b) =  .00023508
Iteration 2:   GMM criterion Q(b) =  .00023508
GMM estimation
Number of parameters =   2
Number of moments    =  29
Initial weight matrix: XT DL                          Number of obs  =   *
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        /rho |   1.023349   .0608293    16.82   0.000     .9041259    1.142572
      /alpha |  -.0690864   .0660343    -1.05   0.295    -.1985112    .0603384
------------------------------------------------------------------------------
* Number of observations for equation 1: 751
  Number of observations for equation 2: 891
------------------------------------------------------------------------------
Instruments for equation 1:
        XT-style: L(2/.).n
Instruments for equation 2:
        Standard: _cons
```

These results are identical to those we would obtain by typing

```
xtabond n, lags(1)
```

Because we specified `nocommonesample`, `gmm` did not report the number of observations used in the header of the output. In this dataset, there are in fact 1,031 observations on 140 panels. In the second equation, the presence of the lagged value of `n` reduces the sample size for that equation to $1031 - 140 = 891$. In the first equation, we lose the first two observations per panel due to lagging and differencing, leading to 751 usable observations. These tallies are listed after the coefficient table in the output.

◁

❑ Technical note

Specifying

```
xtinstruments(x1 x2 x3, lags(1/3))
```

differs from

```
instruments(L(1/3).(x1 x2 x3))
```

in how observations are excluded from the estimation sample. When you use the latter syntax, `gmm` must exclude the first three observations from each panel when computing the moment equation: you requested three lags of each regressor be used as instruments, so the first residual that could be interacted with those instruments is the one for $t = 4$. On the other hand, when you use `xtinstruments()`, you are telling `gmm` that you would like to use up to the first three lags of `x1`, `x2`, and `x3` as instruments

but that using just one lag is acceptable. Because most panel datasets have a relatively modest number of observations per panel, dynamic instrument lists are typically used so that the number of usable observations is maximized. Dynamic instrument lists also accommodate the fact that there are more valid instruments for later time periods than earlier time periods.

Specifying panel-style instruments using the `xtinstruments()` option also affects how the standard instruments specified in the `instruments()` option are treated. To illustrate, suppose we have a balanced panel dataset with $T = 5$ observations per panel and we specify

```
. gmm ..., xtinstruments(w, lags(1/2)) instruments(x)
```

We will lose the first observation because we need at least one lag of `w` to serve as an instrument. Our instrument matrix for panel i will therefore be

$$\mathbf{Z}_i = \begin{bmatrix} w_{i1} & 0 & 0 & 0 \\ 0 & w_{i1} & 0 & 0 \\ 0 & w_{i2} & 0 & 0 \\ 0 & 0 & w_{i2} & 0 \\ 0 & 0 & w_{i3} & 0 \\ 0 & 0 & 0 & w_{i3} \\ 0 & 0 & 0 & w_{i4} \\ x_{i2} & x_{i3} & x_{i4} & x_{i5} \\ 1 & 1 & 1 & 1 \end{bmatrix} \tag{27}$$

The vector of ones in the final row represents the constant term implied by the `instruments()` option. Because we lost the first observation, the residual vector $\mathbf{u}_i$ will be 4×1. Thus our moment conditions for the ith panel can be written in matrix notation as

$$E\{\mathbf{Z}_i \mathbf{u}_i(\beta)\} = E\left\{ \mathbf{Z}_i \begin{bmatrix} u_{i2}(\beta) \\ u_{i3}(\beta) \\ u_{i4}(\beta) \\ u_{i5}(\beta) \end{bmatrix} \right\} = \mathbf{0}$$

The moment conditions corresponding to the final two rows of (27) say that

$$E\left\{ \sum_{t=2}^{T=4} x_{it} u_{it}(\beta) \right\} = 0 \qquad \text{and} \qquad E\left\{ \sum_{t=2}^{T=4} u_{it}(\beta) \right\} = 0$$

Because we specified panel-style instruments with the `xtinstruments()` option, `gmm` no longer uses moment conditions for strictly exogenous variables of the form $E\{x_{it} u_{it}(\beta)\} = 0$ for each t. Instead, the moment conditions now stipulate that the average (over t) of $x_{it} u_{it}(\beta)$ has expectation zero. This corresponds to the approach proposed by Arellano and Bond (1991, 280) and others.

When you request panel-style instruments with the `xtinstruments()` option, the number of instruments in the $\mathbf{Z}_i$ matrix increases quadratically in the number of periods. The dynamic panel-data estimators we have discussed in this section are designed for datasets that contain a large number of panels and a modest number of time periods. When the number of time periods is large, estimators that use standard (non–panel-style) instruments are more appropriate.

❑

We have focused on the Arellano–Bond dynamic panel-data estimator because of its relative simplicity. gmm can additionally fit any models that can be formulated using the xtdpd and xtdpdsys commands; see [XT] **xtdpd** and [XT] **xtdpdsys**. The key is to determine the appropriate instruments to use for the level and difference equations. You may find it useful to fit a version of your model with those commands to determine what instruments and XT-style instruments to use. We conclude this section with an example using the Arellano–Bover/Blundell–Bond estimator.

▷ Example 17: Arellano–Bover/Blundell–Bond estimator

We fit a small model that includes one lag of the dependent variable n as a regressor as well as the contemporaneous and first lag of w, which we assume are strictly exogenous. We could fit our model using xtdpdsys using the syntax

```
xtdpdsys n L(0/1).w, lags(1) twostep
```

Applying virtually all the syntax issues we have discussed so far, the equivalent gmm command is

```
. gmm (n - {rho}*L.n - {w}*w - {lagw}*L.w - {c})
>     (D.n - {rho}*LD.n - {w}*D.w - {lagw}*LD.w),
>     xtinst(1: D.n, lags(1/1)) xtinst(2: n, lags(2/.))
>     inst(2: D.w LD.w, noconstant)
>     deriv(1/rho = -1*L.n)
>     deriv(1/w = -1*w)
>     deriv(1/lagw = -1*L.w)
>     deriv(1/c = -1)
>     deriv(2/rho = -1*LD.n)
>     deriv(2/w = -1*D.w)
>     deriv(2/lagw = -1*LD.w)
>     winit(xt LD) wmatrix(robust) vce(unadjusted) nocommonesample
Step 1
Iteration 0:   GMM criterion Q(b) =  .10170339
Iteration 1:   GMM criterion Q(b) =  .00022772
Iteration 2:   GMM criterion Q(b) =  .00022772
Step 2
Iteration 0:   GMM criterion Q(b) =  .59965014
Iteration 1:   GMM criterion Q(b) =  .56578186
Iteration 2:   GMM criterion Q(b) =  .56578186
GMM estimation
Number of parameters =   4
Number of moments    =  39
Initial weight matrix: XT LD                         Number of obs   =   *
GMM weight matrix:     Robust
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/rho	1.122738	.0206512	54.37	0.000	1.082263	1.163214
/w	-.6719909	.0246148	-27.30	0.000	-.7202351	-.6237468
/lagw	.571274	.0403243	14.17	0.000	.4922398	.6503083
/c	.154309	.17241	0.90	0.371	-.1836084	.4922263

```
* Number of observations for equation 1: 891
  Number of observations for equation 2: 751
Instruments for equation 1:
        XT-style: LD.n
        Standard: _cons
Instruments for equation 2:
        XT-style: L(2/.).n
        Standard: D.w LD.w
```

◁

Details of moment-evaluator programs

In examples 9, 10, and 11, we used moment-evaluator programs to evaluate moment conditions that could not be specified using the interactive version of `gmm`. In the technical note after example 9, we showed how to make our program accept optional arguments so that we could pass the name of our dependent and independent variables and panel identifier variable. Here we discuss how to make moment-evaluator programs accept weights and provide derivatives.

The complete specification for a moment-evaluator program's `syntax` statement is

```
syntax varlist if [weight], at(name) options [derivatives(varlist)]
```

The macro `'varlist'` contains the list of variables that we are to fill in with the values of our residual equations. The macro `'if'` represents an `if` condition that restricts the estimation sample. The macro `'at'` represents a vector containing the parameter values at which we are to evaluate our residual equations. `options` represent other options that you specify in your call to `gmm` and want to have passed to your moment-evaluator programs. In our previous examples, we included the `mylhs()`, `myrhs()`, and `myidvar()` options.

Two new elements of the `syntax` statement allow for weights and derivatives. `weight` specifies the types of weights your program allows. The interactive version of `gmm` allows for `fweight`s, `aweight`s, and `pweight`s. However, unless you explicitly allow your moment evaluator program to accept weights, you cannot specify weights in your call to `gmm` with the moment-evaluator program version.

The `derivatives()` option is used to pass to your program a set of variables that you are to fill in with the derivatives of your residual equations with respect to the parameters. Say you specify k parameters in the `nparameters()` or `parameters()` option and q equations in the `nequations()` or `equations()` option. Then `'derivatives'` will contain $k \times q$ variables. The first k variables are for the derivatives of the first residual equation with respect to the k parameters, the second k variables are for the derivatives of the second residual equation, and so on.

▷ Example 18: Panel Poisson with strictly exogenous regressors and derivatives

To focus on how to specify derivatives, we return to the simple moment-evaluator program we used in example 9, in which we had three regressors, and extend it to supply derivatives. The error equation corresponding to moment condition (13) is

$$u_{it}(\beta) = y_{it} - \mu_{it}\frac{\overline{y}_i}{\overline{\mu}_i}$$

where μ_{it}, $\overline{\mu}_i$, and $\overline{y}_i$ were defined previously. Now

$$\frac{\partial}{\partial \beta_j} u_{it}(\beta) = -\mu_{it}\frac{\overline{y}_i}{\overline{\mu}_i^2}\left(x_{it}^{(j)}\overline{\mu}_i - \frac{1}{T}\sum_{l=1}^{l=T} x_{il}^{(j)}\mu_{il}\right) \tag{28}$$

where $x_{it}^{(j)}$ represents the jth element of $\mathbf{x}_{it}$.

Our moment-evaluator program is

```
program gmm_poideriv
        version 12
        syntax varlist if, at(name) [derivatives(varlist)]
        quietly {
                // Calculate residuals as before
                tempvar mu mubar ybar
                gen double `mu' = exp(x1*`at'[1,1] + x2*`at'[1,2]       ///
                                                   + x3*`at'[1,3]) `if'
                egen double `mubar' = mean(`mu') `if', by(id)
                egen double `ybar' = mean(y) `if', by(id)
                replace `varlist' = y - `mu'*`ybar'/`mubar' `if'
                // Did -gmm- request derivatives?
                if "`derivatives'" == "" {
                        exit                    // no, so we are done
                }
                // Calculate derivatives
                // We need the panel means of x1*mu, x2*mu, and x3*mu
                tempvar work x1mubar x2mubar x3mubar
                generate double `work' = x1*`mu' `if'
                egen double `x1mubar' = mean(`work') `if', by(id)
                replace `work' = x2*`mu' `if'
                egen double `x2mubar' = mean(`work') `if', by(id)
                replace `work' = x3*`mu' `if'
                egen double `x3mubar' = mean(`work') `if', by(id)
                local d1: word 1 of `derivatives'
                local d2: word 2 of `derivatives'
                local d3: word 3 of `derivatives'
                replace `d1' = -1*`mu'*`ybar'/`mubar'^2*(x1*`mubar' - `x1mubar')
                replace `d2' = -1*`mu'*`ybar'/`mubar'^2*(x2*`mubar' - `x2mubar')
                replace `d3' = -1*`mu'*`ybar'/`mubar'^2*(x3*`mubar' - `x3mubar')
        }
end
```

The `derivatives()` option is made optional in the `syntax` statement by placing it in square brackets. If `gmm` needs to evaluate your moment equations but does not need derivatives at that time, then the `derivatives()` option will be empty. In our program, we check to see if that is the case, and, if so, `exit` without calculating derivatives. As is often the case with [R] **ml** as well, the portion of our program devoted to derivatives is longer than the code to compute the objective function.

The first part of our derivative code computes the term

$$\frac{1}{T}\sum_{l=1}^{l=T} x_{il}^{(j)}\mu_{il} \tag{29}$$

for $x_{it}^{(j)} =$ `x1`, `x2`, and, `x3`. The `` `derivatives' `` macro contains three variable names, corresponding to the three parameters of the `` `at' `` matrix. We extract those names into local macros `` `d1' ``, `` `d2' ``, and `` `d3' ``, and then fill in the variables those macros represent with the derivatives shown in (28).

With our program written, we fit our model by typing

```
. use http://www.stata-press.com/data/r12/poisson1
. gmm gmm_poideriv, nequations(1) parameters(b1 b2 b3)
> instructments(x1 x2 x3, noconstant) vce(cluster id) onestep hasderivatives
Step 1
Iteration 0:   GMM criterion Q(b) =   51.99142
Iteration 1:   GMM criterion Q(b) =  .04345191
Iteration 2:   GMM criterion Q(b) =  8.720e-06
Iteration 3:   GMM criterion Q(b) =  7.115e-13
Iteration 4:   GMM criterion Q(b) =  5.130e-27
GMM estimation
Number of parameters =   3
Number of moments    =   3
Initial weight matrix: Unadjusted                     Number of obs   =      409
                                  (Std. Err. adjusted for 45 clusters in id)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         /b1 |     1.94866   .1000265    19.48   0.000     1.752612    2.144709
         /b2 |    -2.966119  .0923592   -32.12   0.000    -3.14714    -2.785099
         /b3 |     1.008634  .1156561     8.72   0.000      .781952    1.235315
------------------------------------------------------------------------------
Instruments for equation 1: x1 x2 x3
```

Our results are identical to those in example 9. Another way to verify that our program calculates derivatives correctly would be to type

```
. gmm gmm_poideriv, nequations(1) parameters(b1 b2 b3)
>  instruments(x1 x2 x3, noconstant) vce(cluster id) onestep
```

Without the `hasderivatives` option, `gmm` will not request derivatives from your program, even if it contains code to compute them. If you have trouble obtaining convergence with the `hasderivatives` option but do not have trouble without that option, then you need to recheck your derivatives.

◁

In the technical note after example 9, we modified the `gmm_poi` program so that we could specify the name of our dependent variable and a list of regressors. Here is the analogous version that computes analytic derivatives:

```
program gmm_poideriv2
        version 12
        syntax varlist if, at(name) myrhs(varlist)                      ///
                           mylhs(varlist) myidvar(varlist)              ///
                           [ derivatives(varlist) ]
        quietly {
                tempvar mu mubar ybar
                gen double `mu' = 0 `if'
                local j = 1
                foreach var of varlist `myrhs' {
                        replace `mu' = `mu' + `var'*`at'[1,`j'] `if'
                        local j = `j' + 1
                }
                replace `mu' = exp(`mu')
                egen double `mubar' = mean(`mu') `if', by(`myidvar')
                egen double `ybar' = mean(`mylhs') `if', by(`myidvar')
                replace `varlist' = `mylhs' - `mu'*`ybar'/`mubar' `if'
                if "`derivatives'" == "" {
                        exit
                }
                tempvar work xmubar
                local j = 1
                foreach var of varlist `myrhs' {
                        generate double `work' = `var'*`mu' `if'
                        egen double `xmubar' = mean(`work') `if' `wt'`exp', ///
                                by(`myidvar')
                        local deriv : word `j' of `derivatives'
                        replace `deriv' = -1*`mu'*`ybar'/`mubar'^2*     ///
                                (`var'*`mubar' - `xmubar')
                        local `++j'
                        drop `work' `xmubar'
                }
        }
end
```

To use this program, we type

```
gmm gmm_poideriv2, mylhs(y) myrhs(x1 x2 x3)
        nequations(1) parameters(b1 b2 b3)
        instruments(x1 x2 x3, noconstant)
        vce(cluster id) myidvar(id) onestep
        hasderivatives
```

We obtain results identical to those shown in example 18.

Depending on your model, allowing your moment-evaluator program to accept weights may be as easy as modifying the `syntax` command to allow them, or it may require significantly more work. If your program uses only commands like `generate` and `replace`, then just modifying the `syntax` command is all you need to do; `gmm` takes care of applying the weights to the observation-level residuals when computing the sample moments, derivatives, and weight matrices. On the other hand, if your moment-evaluator program computes residuals using statistics that depend on multiple observations, then you must apply the weights passed to your program when computing those statistics.

In our examples of panel Poisson with strictly exogenous regressors, we used the statistics $\overline{\mu}_i$ and $\overline{y}_i$ when computing the residuals. If we are to allow weights with our moment-evaluator program, then we must incorporate those weights when computing $\overline{\mu}_i$ and $\overline{y}_i$. Moreover, looking at the derivative in (28), the term highlighted in (29) is in fact a sample mean, so we must incorporate weights when computing it.

▷ Example 19: Panel Poisson with derivatives and weights

Here we modify the program in example 18. to accept frequency weights. One complication immediately arises: we had been using `egen` to compute $\overline{\mu}_i$ and $\overline{y}_i$. `egen` does not accept weights, so we must compute $\overline{\mu}_i$ and $\overline{y}_i$ ourselves, incorporating any weights the user may specify. Our program is

```
program gmm_poiderivfw
        version 12
        syntax varlist if [fweight/], at(name) [derivatives(varlist)]
        quietly {
                if "`exp'" == "" {        // no weights
                        local exp 1       // weight each observation equally
                }
                // Calculate residuals as before
                tempvar mu mubar ybar sumwt
                gen double `mu' = exp(x1*`at'[1,1] + x2*`at'[1,2]      ///
                                                   + x3*`at'[1,3]) `if'
                bysort id: gen double `sumwt' = sum(`exp')
                by id: gen double `mubar' = sum(`mu'*`exp')
                by id: gen double `ybar' = sum(y*`exp')
                by id: replace `mubar' = `mubar'[_N] / `sumwt'[_N]
                by id: replace `ybar' = `ybar'[_N] / `sumwt'[_N]
                replace `varlist' = y - `mu'*`ybar'/`mubar' `if'
                // Did -gmm- request derivatives?
                if "`derivatives'" == "" {
                        exit        // no, so we are done
                }
                // Calculate derivatives
                // We need the panel means of x1*mu, x2*mu, and x3*mu
                tempvar work x1mubar x2mubar x3mubar
                generate double `work' = x1*`mu' `if'
                by id: generate double `x1mubar' = sum(`work'*`exp')
                by id: replace `x1mubar' = `x1mubar'[_N] / `sumwt'[_N]
                replace `work' = x2*`mu' `if'
                by id: generate double `x2mubar' = sum(`work'*`exp')
                by id: replace `x2mubar' = `x2mubar'[_N] / `sumwt'[_N]
                replace `work' = x3*`mu' `if'
                by id: generate double `x3mubar' = sum(`work'*`exp')
                by id: replace `x3mubar' = `x3mubar'[_N] / `sumwt'[_N]
                local d1: word 1 of `derivatives'
                local d2: word 2 of `derivatives'
                local d3: word 3 of `derivatives'
                replace `d1' = -1*`mu'*`ybar'/`mubar'^2*(x1*`mubar' - `x1mubar')
                replace `d2' = -1*`mu'*`ybar'/`mubar'^2*(x2*`mubar' - `x2mubar')
                replace `d3' = -1*`mu'*`ybar'/`mubar'^2*(x3*`mubar' - `x3mubar')
        }
end
```

Our `syntax` command now indicates that `fweights` are allowed. The first part of our code looks at the macro `` `exp' ``. If it is empty, then the user did not specify weights in their call to `gmm`; and we set the macro equal to 1, so that we weight each observation equally. After we compute μ_{it}, we calculate $\overline{\mu}_i$ and $\overline{y}_i$, taking into account weights. To compute frequency-weighted means for each panel, we just multiply each observation by its respective weight, sum over all observations in the panel, then divide by the sum of the weights for the panel. (See [U] **20.22 Weighted estimation** for information on how to handle `aweights` and `pweights`.) We use the same procedure to compute the frequency-weighted variant of expression (29) in the derivative calculations.

To use our program, we type

```
. use http://www.stata-press.com/data/r12/poissonwts
. gmm gmm_poiderivfw [fw=fwt], nequations(1) parameters(b1 b2 b3)
> instruments(x1 x2 x3, noconstant) vce(cluster id) onestep hasderivatives
(sum of wgt is 819)
Step 1
Iteration 0:   GMM criterion Q(b) =    49.8292
Iteration 1:   GMM criterion Q(b) =  .11136736
Iteration 2:   GMM criterion Q(b) =  .00008519
Iteration 3:   GMM criterion Q(b) =  7.110e-11
Iteration 4:   GMM criterion Q(b) =  5.596e-23
GMM estimation
Number of parameters =   3
Number of moments    =   3
Initial weight matrix: Unadjusted                     Number of obs   =        819
                                  (Std. Err. adjusted for 45 clusters in id)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          /b1 |    1.967766    .111795    17.60   0.000     1.748652    2.186881
          /b2 |   -3.060838   .0935561   -32.72   0.000    -3.244205   -2.877472
          /b3 |    1.037594   .1184227     8.76   0.000       .80549    1.269698
------------------------------------------------------------------------------
Instruments for equation 1: x1 x2 x3
```

Testing whether our program works correctly with frequency weights is easy. A frequency-weighted dataset is just a compact form of a larger dataset in which identical observations are omitted and a frequency-weight variable is included to tell us how many times each observation in the smaller dataset appears in the larger dataset. Therefore, we can `expand` our smaller dataset by the frequency-weight variable and then refit our model without specifying frequency weights. If we obtain the same results, our program works correctly. When we type

```
. expand fw
(410 observations created)
. gmm gmm_poiderivfw, nequations(1) parameters(b1 b2 b3)
> instruments(x1 x2 x3, noconstant) vce(cluster id) onestep
```

we obtain the same results as before.

◁

Saved results

gmm saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_aux)	number of auxiliary parameters
e(n_moments)	number of moments
e(n_eq)	number of equations in moment-evaluator program
e(Q)	criterion function
e(J)	Hansen J χ^2 statistic
e(J_df)	J statistic degrees of freedom
e(k_*i*)	number of parameters in equation i
e(has_xtinst)	1 if panel-style instruments specified, 0 otherwise
e(N_clust)	number of clusters
e(type)	1 if interactive version, 2 if moment-evaluator program version
e(rank)	rank of e(V)
e(ic)	number of iterations used by iterative GMM estimator
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	gmm
e(cmdline)	command as typed
e(title)	title specified in title()
e(title_2)	title specified in title2()
e(clustvar)	name of cluster variable
e(inst_*i*)	equation i instruments
e(eqnames)	equation names
e(winit)	initial weight matrix used
e(winitname)	name of user-supplied initial weight matrix
e(estimator)	onestep, twostep, or igmm
e(rhs)	variables specified in variables()
e(params_*i*)	equation i parameters
e(wmatrix)	*wmtype* specified in wmatrix()
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(params)	parameter names
e(sexp_*i*)	substitutable expression for equation i
e(evalprog)	moment-evaluator program
e(evalopts)	options passed to moment-evaluator program
e(nocommonesample)	nocommonesample, if specified
e(technique)	optimization technique
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(init)	initial values of the estimators
e(Wuser)	user-supplied initial weight matrix
e(W)	weight matrix used for final round of estimation
e(S)	moment covariance matrix used in robust VCE computations
e(N_byequation)	number of observations per equation, if nocommonesample specified
e(V)	variance–covariance matrix
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

gmm is implemented as an ado-file.

Let q denote the number of moment equations. For observation i, $i = 1, \ldots, N$, write the jth moment equation as $\mathbf{z}_{ij}u_{ij}(\beta_j)$ for $j = 1, \ldots, q$. $\mathbf{z}_{ij}$ is a $1 \times m_j$ vector, where m_j is the number of instruments specified for equation j. Let $m = m_1 + \cdots + m_q$.

Our notation can incorporate moment conditions of the form $h_{ij}(\mathbf{w}_{ij}; \beta_j)$ with instruments $\mathbf{w}_{ij}$ by defining $\mathbf{z}_{ij} = 1$ and $u_{ij}(\beta_j) = h_{ij}(\mathbf{w}_{ij}; \beta_j)$, so except when necessary we do not distinguish between the two types of moment conditions. We could instead use notation so that all our moment conditions are of the form $h_{ij}(\mathbf{w}_{ij}; \beta_j)$, or we could adopt notation that explicitly combines both forms of moment equations. However, because moment conditions of the form $\mathbf{z}'_{ij}u_{ij}(\beta_j)$ are arguably more common, we use that notation.

Let β denote a $k \times 1$ vector of parameters, consisting of all the unique parameters of $\beta_1, \ldots, \beta_q$. Then we can stack the moment conditions and write them more compactly as $\mathbf{Z}'_i\mathbf{u}_i(\beta)$, where

$$\mathbf{Z}_i = \begin{bmatrix} \mathbf{z}_{i1} & \mathbf{0} & \cdots & \mathbf{0} \\ \mathbf{0} & \mathbf{z}_{i2} & \cdots & \mathbf{0} \\ \vdots & \vdots & \ddots & \vdots \\ \mathbf{0} & \mathbf{0} & \cdots & \mathbf{z}_{iq} \end{bmatrix} \quad \text{and} \quad \mathbf{u}_i(\beta) = \begin{bmatrix} u_{i1}(\beta_1) \\ u_{i2}(\beta_2) \\ \vdots \\ u_{iq}(\beta_j) \end{bmatrix}$$

The GMM estimator $\widehat{\beta}$ is the value of β that minimizes

$$Q(\beta) = \left\{ N^{-1} \sum_{i=1}^{N} \mathbf{Z}'_i\mathbf{u}_i(\beta) \right\}' \mathbf{W} \left\{ N^{-1} \sum_{i=1}^{N} \mathbf{Z}'_i\mathbf{u}_i(\beta) \right\} \tag{A1}$$

for $q \times q$ weight matrix $\mathbf{W}$.

By default, gmm minimizes (A1) using the Gauss–Newton method. See Hayashi (2000, 498) for a derivation. This technique is typically faster than quasi-Newton methods and does not require second-order derivatives.

Methods and formulas are presented under the following headings:

Initial weight matrix
Weight matrix
Variance–covariance matrix
Hansen's J statistic
Panel-style instruments

Initial weight matrix

If you specify `winitial(identity)`, then we set $\mathbf{W} = \mathbf{I}_q$.

If you specify `winitial(unadjusted)`, then we create matrix $\mathbf{\Lambda}$ with typical submatrix

$$\mathbf{\Lambda}_{rs} = N^{-1} \sum_{i=1}^{N} \mathbf{z}'_{ir}\mathbf{z}_{is}$$

for $r = 1, \ldots, q$ and $s = 1, \ldots, q$. If you include the `independent` suboption, then we set $\mathbf{\Lambda}_{rs} = \mathbf{0}$ for $r \neq s$. The weight matrix $\mathbf{W}$ equals $\mathbf{\Lambda}^{-1}$.

If you specify `winitial(`*matname*`)`, then we set $\mathbf{W}$ equal to Stata matrix *matname*.

If you specify `winitial(xt` *xtspec*`)`, then you must specify one or two items in *xtspec*, one for each equation. `gmm` allows you to specify at most two moment equations when you specify `winitial(xt` *xtspec*`)`, one in first-differences and one in levels. We create the block-diagonal matrix $\mathbf{H}$ with typical block $\mathbf{H}_j$. If the jth element of *xtspec* is "L", then $\mathbf{H}_j$ is the identity matrix of suitable dimension. If the jth element of *xtspec* is "D", then

$$\mathbf{H}_j = \begin{bmatrix} 1 & -0.5 & 0 & \dots & 0 & 0 \\ -0.5 & 1 & -0.5 & \dots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \dots & 1 & -0.5 \\ 0 & 0 & 0 & \dots & -0.5 & 1 \end{bmatrix}$$

Then

$$\mathbf{\Lambda}_H = N_g^{-1} \sum_{g=1}^{g=N_G} \mathbf{Z}_g' \mathbf{H} \mathbf{Z}_g$$

where g indexes panels in the dataset, N_G is the number of panels, $\mathbf{Z}_g$ is the full instrument matrix for panel g, and $\mathbf{W} = \mathbf{\Lambda}_H^{-1}$. See *Panel-style instruments* below for a discussion of how $\mathbf{Z}_g$ is formed.

Weight matrix

Specification of the weight matrix applies only to the two-step and iterative estimators. When you use the `onestep` option, the `wmatrix()` option is ignored.

We first evaluate (A1) using the initial weight matrix described above and then compute $\mathbf{u}_i(\widehat{\beta})$. In all cases, $\mathbf{W} = \mathbf{\Lambda}^{-1}$. If you specify `wmatrix(unadjusted)`, then we create $\mathbf{\Lambda}$ to have typical submatrix

$$\mathbf{\Lambda}_{rs} = \sigma_{rs}\, N^{-1} \sum_{i=1}^{N} \mathbf{z}_{ir}' \mathbf{z}_{is}$$

where

$$\sigma_{rs} = N^{-1} \sum_{i=1}^{N} u_{ir}(\widehat{\beta}) u_{is}(\widehat{\beta})$$

and r and s index moment equations. For all types of weight matrices, if the `independent` suboption is specified, then $\mathbf{\Lambda}_{rs} = \mathbf{0}$ for $r \neq s$, where $\mathbf{\Lambda}_{rs}$ measures the covariance between moment conditions for equations r and s.

If you specify `wmatrix(robust)`, then

$$\mathbf{\Lambda} = N^{-1} \sum_{i=1}^{N} \mathbf{Z}_i \mathbf{u}_i(\widehat{\beta}) \mathbf{u}_i'(\widehat{\beta}) \mathbf{Z}_i'$$

If you specify `wmatrix(cluster` *clustvar*`)`, then

$$\mathbf{\Lambda} = N^{-1} \sum_{c=1}^{c=N_C} \mathbf{q}_c \mathbf{q}_c'$$

where c indexes clusters, N_C is the number of clusters, and

$$\mathbf{q}_c = \sum_{i \in c_j} \mathbf{Z}_i \mathbf{u}_i(\widehat{\beta})$$

If you specify `wmatrix(hac` *kernel* `[#])`, then

$$\begin{aligned}\mathbf{\Lambda} =& N^{-1} \sum_{i=1}^{N} \mathbf{Z}_i \mathbf{u}_i(\widehat{\beta}) \mathbf{u}_i(\widehat{\beta})' \mathbf{Z}_i' \quad + \\ & N^{-1} \sum_{l=1}^{l=n-1} \sum_{i=l+1}^{N} K(l,m) \left\{ \mathbf{Z}_i \mathbf{u}_i(\widehat{\beta}) \mathbf{u}_{i-l}'(\widehat{\beta}) \mathbf{Z}_{i-l}' + \mathbf{Z}_{i-l} \mathbf{u}_{i-l}(\widehat{\beta}) \mathbf{u}_i'(\widehat{\beta}) \mathbf{Z}_i' \right\}\end{aligned}$$

where $m = \#$ if # is specified and $m = N - 2$ otherwise. Define $z = l/(m+1)$. If *kernel* is `bartlett` or `nwest`, then

$$K(l,m) = \begin{cases} 1 - z & 0 \le z \le 1 \\ 0 & \text{otherwise} \end{cases}$$

If *kernel* is `parzen` or `gallant`, then

$$K(l,m) = \begin{cases} 1 - 6z^2 + 6z^3 & 0 \le z \le 0.5 \\ 2(1-z)^3 & 0.5 < z \le 1 \\ 0 & \text{otherwise} \end{cases}$$

If *kernel* is `quadraticspectral` or `andrews`, then

$$K(l,m) = \begin{cases} 1 & z = 0 \\ 3\{\sin(\theta)/\theta - \cos(\theta)\}/\theta^2 & \text{otherwise} \end{cases}$$

where $\theta = 6\pi z/5$.

If `wmatrix(hac` *kernel* `opt)` is specified, then `gmm` uses Newey and West's (1994) automatic lag-selection algorithm, which proceeds as follows. Define $\mathbf{h}$ to be an $m \times 1$ vector of ones. Note that this definition of $\mathbf{h}$ is slightly different than the one used by `ivregress`. There, the element of $\mathbf{h}$ corresponding to the constant term equals zero, effectively ignoring the effect of the constant in determining the optimal lag length. Here we include the effect of the constant term. Now define

$$\begin{aligned} f_i &= \{\mathbf{Z}_i' \mathbf{u}_i(\beta)\}' \mathbf{h} \\ \widehat{\sigma}_j &= N^{-1} \sum_{i=j+1}^{N} f_i f_{i-j} \qquad j = 0, \ldots, m^* \\ \widehat{s}^{(q)} &= 2 \sum_{j=1}^{j=m^*} \widehat{\sigma}_j j^q \\ \widehat{s}^{(0)} &= \widehat{\sigma}_0 + 2 \sum_{j=1}^{j=m^*} \widehat{\sigma}_j \\ \widehat{\gamma} &= c_\gamma \left\{ \left(\frac{\widehat{s}^{(q)}}{\widehat{s}^{(0)}} \right)^2 \right\}^{1/(2q+1)} \\ m &= \widehat{\gamma} N^{1/(2q+1)} \end{aligned}$$

where q, m^*, and c_γ depend on the kernel specified:

Kernel	q	m^*	c_γ
Bartlett/Newey–West	1	int $\{20(T/100)^{2/9}\}$	1.1447
Parzen/Gallant	2	int $\{20(T/100)^{4/25}\}$	2.6614
Quadratic spectral/Andres	2	int $\{20(T/100)^{2/25}\}$	1.3221

where int(x) denotes the integer obtained by truncating x toward zero. For the Bartlett and Parzen kernels, the optimal lag is min$\{$int$(m), m^*\}$. For the quadratic spectral kernel, the optimal lag is min$\{m, m^*\}$.

Variance–covariance matrix

If you specify `vce(unadjusted)`, then the VCE matrix is computed as

$$\text{Var}(\widehat{\beta}) = N^{-1}\left\{\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\right\}^{-1} \tag{A2}$$

where

$$\overline{\mathbf{G}}(\widehat{\beta}) = N^{-1}\sum_{i=1}^{N}\mathbf{Z}_i'\left.\frac{\partial \mathbf{u}_i(\beta)}{\partial \beta'}\right|_{\beta=\widehat{\beta}}$$

For the two-step and iterated estimators, we use the weight matrix $\mathbf{W}$ that was used to compute the final-round estimate $\widehat{\beta}$.

For the one-step estimator, how the unadjusted VCE is computed depends on the type of initial weight matrix requested and the form of the moment equations. If you specify two or more moment equations of the form $h_{ij}(\mathbf{w}_{ij};\beta_j)$, then `gmm` issues a warning message and computes a heteroskedasticity-robust VCE because here the matrix $\mathbf{Z}'\mathbf{Z}$ is necessarily singular; moreover, here you must use the identity matrix as the initial weight matrix. Otherwise, if you specify `winitial(identity)` or `winitial(unadjusted)`, then `gmm` first computes an unadjusted weight matrix based on $\widehat{\beta}$ before evaluating (A2). If you specify `winitial(`*matname*`)`, then (A2) is evaluated based on *matname*; the user is responsible for verifying that the VCE and other statistics so produced are appropriate.

All types of robust VCEs computed by `gmm` take the form

$$\text{Var}(\widehat{\beta}) = N^{-1}\left\{\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\right\}^{-1}\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\mathbf{S}\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\left\{\overline{\mathbf{G}}(\widehat{\beta})'\mathbf{W}\overline{\mathbf{G}}(\widehat{\beta})\right\}^{-1}$$

For the one-step estimator, $\mathbf{W}$ represents the initial weight matrix requested using the `winitial()` option, and $\mathbf{S}$ is computed based on the specification of the `vce()` option. The formulas for the $\mathbf{S}$ matrix are identical to the ones that define the $\mathbf{\Lambda}$ matrix in *Weight matrix* above, except that $\mathbf{S}$ is computed after the moment equations are reevaluated using the final estimate of $\widehat{\beta}$. For the two-step and iterated GMM estimators, computation of $\mathbf{W}$ is controlled by the `wmatrix()` option based on the penultimate estimate of $\widehat{\beta}$.

For details on computation of the VCE matrix with dynamic panel-data models, see *Panel-style instruments* below.

Hansen's J statistic

Hansen's (1982) J test of overidentifying restrictions is $J = N \times Q(\widehat{\beta})$. $J \sim \chi^2(m-k)$. If $m < k$, `gmm` issues an error message without estimating the parameters. If $m = k$, the model is just-identified and J is saved as missing ("."). For the two-step and iterated GMM estimators, the J statistic is based on the last-computed weight matrix as determined by the `wmatrix()` option. For the one-step estimator, `gmm` recomputes a weight matrix as described in the second paragraph of *Variance–covariance matrix* above. To obtain Hansen's J statistic, you use `estat overid`; see [R] **gmm postestimation**.

Panel-style instruments

Here we discuss several issues that arise only when you specify panel-style instruments by using the `xtinstruments()` option. When you specify the `xtinstruments()` option, we can no longer consider the instruments for one observation in isolation; instead, we must consider the instrument matrix for an entire panel at once. In the following discussion, we let T denote the number of time periods in a panel. To accommodate unbalanced datasets, conceptually we simply use zeros as instruments and residuals for time periods that are missing in a panel.

We consider the case where you specify both an equation in levels and an equation in differences, yielding two residual equations. Let $u^L_{pt}(\beta)$ denote the residual for the level equation for panel p in period t, and let $u^D_{pt}(\beta)$ denote the residual for the corresponding difference equation. Now define the $2T \times 1$ vector $\mathbf{u}_p(\beta)$ as

$$\mathbf{u}_p(\beta) = [u^L_{p1}(\beta), u^L_{p2}(\beta), \ldots, u^L_{pT}(\beta), u^D_{p2}(\beta), u^D_{p3}(\beta), \ldots, u^D_{pT}(\beta)]$$

The $T+1$ element of $\mathbf{u}_p$ is $u^D_{p2}(\beta)$ since we lose the first observation of the difference equation because of differencing.

We write the moment conditions for the pth panel as $\mathbf{Z}_p\mathbf{u}_p(\beta)$. To see how $\mathbf{Z}_p$ is defined, let $\mathbf{w}^L_{pt}$ and $\mathbf{w}^D_{pt}$ denote the vectors of panel-style instruments for the level and difference equations, respectively, and let time be denoted by t; we discuss their dimensions momentarily. Also let $\mathbf{x}^L_{pt}$ and $\mathbf{x}^D_{pt}$ denote the vectors of instruments specified in `instruments()` for the level and difference equations at time t. Without loss of generality, for our discussion we assume that you specify the level equation first. Then $\mathbf{Z}_p$ has the form

$$\mathbf{Z}_p = \begin{bmatrix}
\mathbf{w}^L_1 & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} \\
\mathbf{0} & \mathbf{w}^L_2 & \cdots & \mathbf{0} & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} \\
\vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\
\mathbf{0} & \mathbf{0} & \cdots & \mathbf{w}^L_T & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} \\
\mathbf{x}^L_1 & \mathbf{x}^L_2 & \cdots & \mathbf{x}^L_T & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} \\
\mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{w}^D_1 & \mathbf{0} & \cdots & \mathbf{0} \\
\mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{0} & \mathbf{w}^D_2 & \cdots & \mathbf{0} \\
\vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\
\mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{0} & \mathbf{0} & \cdots & \mathbf{w}^D_T \\
\mathbf{0} & \mathbf{0} & \cdots & \mathbf{0} & \mathbf{x}^D_1 & \mathbf{x}^D_2 & \cdots & \mathbf{x}^D_T
\end{bmatrix} \tag{A3}$$

To see how the $\mathbf{w}$ vectors are formed, suppose you specify

```
xtinstruments(eq(1): d, lags(a/b))
```

Then $\mathbf{w}_t^L$ will be a $(b-a+1)\times 1$ vector consisting of $d_{t-a},\ldots,d_{t-b}$. If $(t-a)\leq 0$, then instead we set $\mathbf{w}_t^L=0$. If $(t-a)>0$ but $(t-b)\leq 0$, then we create $\mathbf{w}_t^L$ to consist of $d_{t-a},\ldots,d_1$. With this definition, $(b-a+1)$ defines the maximum number of lags of d used, but `gmm` will proceed with fewer lags if all $(b-a+1)$ lags are not available. If you specify two panel-style instruments, `d` and `e`, say, then $\mathbf{w}_t^L$ will consist of $d_{t-a},\ldots,d_{t-b},e_{t-a},\ldots,e_{t-b}$. $\mathbf{w}_t^D$ is handled analogously.

The $\mathbf{x}_t^L$ vectors are simply $j\times 1$ vectors, where j is the number of regular instruments specified with the `instruments()` option; these vectors include a "1" unless you specify the `noconstant` suboption.

Looking carefully at (A3), you will notice that for dynamic panel-data models, moment conditions corresponding to the instruments $\mathbf{x}_{pt}^L$ take the form

$$E\left[\sum_{t=1}^{t=T}\mathbf{x}_{pt}^L u_{pt}^L(\beta)\right]=\mathbf{0}$$

and likewise for $\mathbf{x}_{pt}^D$. Instead of having separate moment conditions for each time period, there is one moment condition equal to the average of individual periods' moments. See Arellano and Bond (1991, 280). To include separate moment conditions for each time period, instead of specifying, say,

```
instruments(1: x)
```

you could instead first generate a variable called `one` equal to unity for all observations and specify

```
xtinstruments(1: x one)
```

(Creating the variable `one` is necessary because a constant is not automatically included in variable lists specified in `xtinstruments()`.)

Unbalanced panels are essentially handled by including zeros rows and columns of $\mathbf{Z}_p$ and $\mathbf{u}_p(\beta)$ corresponding to missing time periods. However, the numbers of instruments and moment conditions reported by `gmm` do not reflect this trickery and instead reflect the numbers of instruments and moment conditions that are not manipulated in this way. Moreover, `gmm` includes code to work through these situations efficiently without actually having to fill in zeros.

When you specify `winitial(xt ...)`, the one-step unadjusted VCE is computed as

$$\mathrm{Var}(\widehat{\beta})=\widehat{\sigma}_1^2\mathbf{\Lambda}_H$$

where $\mathbf{\Lambda}_H$ was defined previously,

$$\widehat{\sigma}_1^2=(N-k)^{-1}\sum_{p=1}^{p=P}\mathbf{u}_p^D(\widehat{\beta})$$

and $\mathbf{u}_p^D(\widehat{\beta})=[u_{p2}^D(\widehat{\beta}),\ldots,u_{pT}^D(\widehat{\beta})]$. Here we use $(N-k)^{-1}$ instead of N^{-1} to match `xtdpd`.

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Also see

[R] **gmm postestimation** — Postestimation tools for gmm

[R] **ivregress** — Single-equation instrumental-variables regression

[R] **ivprobit** — Probit model with continuous endogenous regressors

[R] **ivtobit** — Tobit model with continuous endogenous regressors

[R] **nl** — Nonlinear least-squares estimation

[R] **nlsur** — Estimation of nonlinear systems of equations

[R] **regress** — Linear regression

[XT] **xtdpd** — Linear dynamic panel-data estimation

[U] **20 Estimation and postestimation commands**

Title

gmm postestimation — Postestimation tools for gmm

Description

The following postestimation command is of special interest after gmm:

Command	Description
estat overid	perform test of overidentifying restrictions

For information about this command, see below.

The following standard postestimation commands are also available:

Command	Description
estat	VCE
estimates	cataloging estimation results
lincom	point estimates, standard errors, testing, and inference for linear combinations of coefficients
nlcom	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
predict	residuals
predictnl	point estimates, standard errors, testing, and inference for generalized predictions
test	Wald tests of simple and composite linear hypotheses
testnl	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation command

`estat overid` reports Hansen's J statistic, which is used to determine the validity of the overidentifying restrictions in a GMM model. If the model is correctly specified in the sense that $E\{\mathbf{z}_i u_i(\boldsymbol{\beta})\} = \mathbf{0}$, then the sample analog to that condition should hold at the estimated value of $\boldsymbol{\beta}$. Hansen's J statistic is valid only if the weight matrix is optimal, meaning that it equals the inverse of the covariance matrix of the moment conditions. Therefore, `estat overid` only reports Hansen's J statistic after two-step or iterated estimation, or if you specified `winitial(`*matname*`)` when calling gmm. In the latter case, it is your responsibility to determine the validity of the J statistic.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`, equation(#`*eqno* | *eqname*`)`]

`predict` [*type*] { *stub*`*` | *newvar*$_1$ ... *newvar*$_q$ } [*if*] [*in*]

Residuals are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

You specify one new variable and (optionally) `equation()`, or you specify *stub*`*` or q new variables, where q is the number of moment equations.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Option for predict

Main

`equation(#`*eqno* | *eqname*`)` specifies the equation for which residuals are desired. Specifying `equation(#1)` indicates that the calculation is to be made for the first moment equation. Specifying `equation(demand)` would indicate that the calculation is to be made for the moment equation named `demand`, assuming there is an equation named `demand` in the model.

If you specify one new variable name and omit `equation()`, results are the same as if you had specified `equation(#1)`.

For more information on using `predict` after multiple-equation estimation commands, see [R] **predict**.

Syntax for estat overid

```
estat overid
```

Menu

Statistics > Postestimation > Reports and statistics

Remarks

As we noted in *Introduction* of [R] **gmm**, underlying generalized method of moments (GMM) estimators is a set of l moment conditions, $E\{\mathbf{z}_i u_i(\beta)\} = \mathbf{0}$. When l is greater than the number of parameters, k, any size-k subset of the moment conditions would yield a consistent parameter estimate. We remarked that the parameter estimates we would obtain would in general depend on which k moment conditions we used. However, if all our moment conditions are indeed valid, then the parameter estimates should not differ too much regardless of which k moment conditions we used to estimate the parameters. The test of overidentifying restrictions is a model specification test based on this observation. The test of overidentifying restrictions requires that the number of moment conditions be greater than the number of parameters in the model.

Recall that the GMM criterion function is

$$Q = \left\{ \frac{1}{N} \sum_i \mathbf{z}_i u_i(\beta) \right\}' \mathbf{W} \left\{ \frac{1}{N} \sum_i \mathbf{z}_i u_i(\beta) \right\}$$

The test of overidentifying restrictions is remarkably simple. If $\mathbf{W}$ is an optimal weight matrix, under the null hypothesis $H_0\colon E\{\mathbf{z}_i u_i(\beta)\} = \mathbf{0}$, the test statistic $J = N \times Q \sim \chi^2(l-k)$. A large test statistic casts doubt on the null hypothesis.

For the test to be valid, $\mathbf{W}$ must be optimal, meaning that $\mathbf{W}$ must be the inverse of the covariance matrix of the moment conditions:

$$\mathbf{W}^{-1} = E\{\mathbf{z}_i u_i(\beta) u_i'(\beta) \mathbf{z}_i'\}$$

Therefore, `estat overid` works only after the two-step and iterated estimators, or if you supplied your own initial weight matrix by using the `winitial(`*matname*`)` option to `gmm` and used the one-step estimator.

Often the overidentifying restrictions test is interpreted as a test of the validity of the instruments **z**. However, other forms of model misspecification can sometimes lead to a significant test statistic. See Hall (2005, sec. 5.1) for a discussion of the overidentifying restrictions test and its behavior in correctly and misspecified models.

▷ Example 1

In example 6 of [R] **gmm**, we fit an exponential regression model of the number of doctor visits based on the person's gender, income, possession of private health insurance, and presence of a chronic disease. We argued that the variable `income` may be endogenous; we used the person's age and race as additional instrumental variables. Here we refit the model and test the specification of the model. We type

```
. use http://www.stata-press.com/data/r12/docvisits
. gmm (docvis - exp({xb:private chronic female income} + {b0})),
> instruments(private chronic female age black hispanic)
(output omitted)
. estat overid
  Test of overidentifying restriction:
  Hansen's J chi2(2) = 9.52598 (p = 0.0085)
```

The J statistic is significant even at the 1% significance level, so we conclude that our model is misspecified. One possibility is that age and race directly affect the number of doctor visits, so we are not justified in excluding them from the model.

A simple technique to explore whether any of the instruments is invalid is to examine the statistics

$$r_j = \mathbf{W}_{jj}^{1/2} \left\{ \frac{1}{N} \sum_{i=1}^{N} z_{ij} u_i(\widehat{\beta}) \right\}$$

for $j = 1, \ldots, k$, where $\mathbf{W}_{jj}$ denotes the jth diagonal element of $\mathbf{W}$, $u_i(\widehat{\beta})$ denotes the sample residuals, and k is the number of instruments. If all the instruments are valid, then the scaled sample moments should at least be on the same order of magnitude. If one (or more) instrument's r_j is large in absolute value relative to the others, then that could be an indication that instrument is not valid.

In Stata, we type

```
. predict double r if e(sample)   // obtain residual from the model
. matrix W = e(W)                 // retrieve weight matrix
. local i 1
. // loop over each instrument and compute r_j
. foreach var of varlist private chronic female age black hispanic {
  2.         generate double r`var' = r*`var'*sqrt(W[`i', `i'])
  3.         local `++i'
  4. }
```

```
. summarize r*
```

Variable	Obs	Mean	Std. Dev.	Min	Max
r	4412	.0344373	8.26176	-151.1847	113.059
rprivate	4412	.007988	3.824118	-72.66254	54.33852
rchronic	4412	.0026947	2.0707	-43.7311	32.703
rfemale	4412	.0028168	1.566397	-12.7388	24.43621
rage	4412	.0360978	4.752986	-89.74112	55.58143
rblack	4412	-.0379317	1.062027	-24.39747	27.34512
rhispanic	4412	-.017435	1.08567	-5.509386	31.53512

We notice that the r_j statistics for `age`, `black`, and `hispanic` are larger than those for the other instruments in our model, supporting our suspicion that age and race may have a direct impact on the number of doctor visits.

◁

Saved results

`estat overid` saves the following in `r()`:

Scalars

`r(J)`	Hansen's J statistic
`r(J_df)`	J statistic degrees of freedom
`r(J_p)`	J statistic p-value

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Reference

Hall, A. R. 2005. *Generalized Method of Moments*. Oxford: Oxford University Press.

Also see

[R] **gmm** — Generalized method of moments estimation

[U] **20 Estimation and postestimation commands**

Title

grmeanby — Graph means and medians by categorical variables

Syntax

`grmeanby` *varlist* [*if*] [*in*] [*weight*] , `summarize(`*varname*`)` [*options*]

options	Description
Main	
* `summarize(`*varname*`)`	graph mean (or median) of *varname*
`median`	graph medians; default is to graph means
Plot	
cline_options	change the look of the lines
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

*`summarize(`*varname*`)` is required.

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Graph means/medians by groups

Description

`grmeanby` graphs the (optionally weighted) means or medians of *varname* according to the values of the variables in *varlist*. The variables in *varlist* may be string or numeric and, if numeric, may be labeled.

Options

Main

`summarize(`*varname*`)` is required; it specifies the name of the variable whose mean or median is to be graphed.

`median` specifies that the graph is to be of medians, not means.

Plot

cline_options affect the rendition of the lines through the markers, including their color, pattern, and width; see [G-3] ***cline_options***.

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

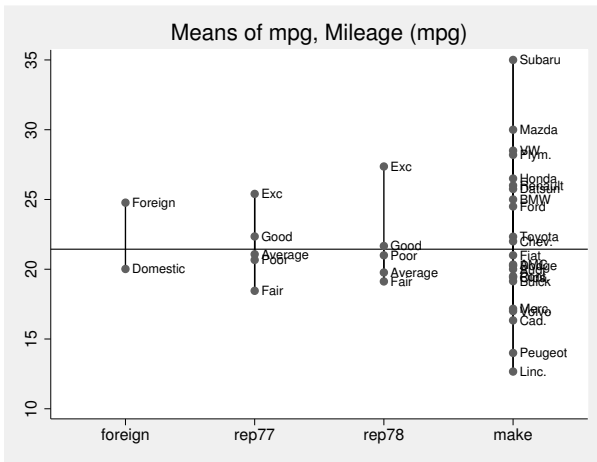
Remarks

The idea of graphing means of categorical variables was shown in Chambers and Hastie (1992, 3). Because this was shown in the context of an S function for making such graphs, it doubtless has roots going back further than that. `grmeanby` is, in any case, another implementation of what we will assume is their idea.

▷ Example 1

Using a variation of our auto dataset, we graph the mean of `mpg` by `foreign`, `rep77`, `rep78`, and `make`:

```
. use http://www.stata-press.com/data/r12/auto1
(Automobile Models)
. grmeanby foreign rep77 rep78 make, sum(mpg)
```



If we had wanted a graph of medians rather than means, we could have typed

```
. grmeanby foreign rep77 rep78 make, sum(mpg) median
```

◁

Methods and formulas

`grmeanby` is implemented as an ado-file.

References

Chambers, J. M., and T. J. Hastie, ed. 1992. *Statistical Models in S*. Pacific Grove, CA: Wadsworth and Brooks/Cole.

Gould, W. W. 1993. gr12: Graphs of means and medians by categorical variables. *Stata Technical Bulletin* 12: 13. Reprinted in *Stata Technical Bulletin Reprints*, vol. 2, pp. 44–45. College Station, TX: Stata Press.

Title

hausman — Hausman specification test

Syntax

`hausman` *name-consistent* [*name-efficient*] [, *options*]

options	Description
Main	
`constant`	include estimated intercepts in comparison; default is to exclude
`alleqs`	use all equations to perform test; default is first equation only
`skipeqs(`*eqlist*`)`	skip specified equations when performing test
`equations(`*matchlist*`)`	associate/compare the specified (by number) pairs of equations
`force`	force performance of test, even though assumptions are not met
`df(#)`	use # degrees of freedom
`sigmamore`	base both (co)variance matrices on disturbance variance estimate from efficient estimator
`sigmaless`	base both (co)variance matrices on disturbance variance estimate from consistent estimator
Advanced	
`tconsistent(`*string*`)`	consistent estimator column header
`tefficient(`*string*`)`	efficient estimator column header

where *name-consistent* and *name-efficient* are names under which estimation results were saved via `estimates store`; see [R] **estimates store**.

A period (`.`) may be used to refer to the last estimation results, even if these were not already stored.

Not specifying *name-efficient* is equivalent to specifying the last estimation results as ".".

Menu

Statistics > Postestimation > Tests > Hausman specification test

Description

`hausman` performs Hausman's (1978) specification test.

Options

Main

`constant` specifies that the estimated intercept(s) be included in the model comparison; by default, they are excluded. The default behavior is appropriate for models in which the constant does not have a common interpretation across the two models.

`alleqs` specifies that all the equations in the models be used to perform the Hausman test; by default, only the first equation is used.

`skipeqs(`*eqlist*`)` specifies in *eqlist* the names of equations to be excluded from the test. Equation numbers are not allowed in this context, because the equation names, along with the variable names, are used to identify common coefficients.

`equations(`*matchlist*`)` specifies, by number, the pairs of equations that are to be compared.

The *matchlist* in `equations()` should follow the syntax

$$\#_c{:}\#_e\ \left[,\#_c{:}\#_e\left[,\ldots\right]\right]$$

where $\#_c$ ($\#_e$) is an equation number of the always-consistent (efficient under H_0) estimator. For instance, `equations(1:1)`, `equations(1:1, 2:2)`, or `equations(1:2)`.

If `equations()` is not specified, then equations are matched on equation names.

`equations()` handles the situation in which one estimator uses equation names and the other does not. For instance, `equations(1:2)` means that equation 1 of the always-consistent estimator is to be tested against equation 2 of the efficient estimator. `equations(1:1, 2:2)` means that equation 1 is to be tested against equation 1 and that equation 2 is to be tested against equation 2. If `equations()` is specified, the `alleqs` and `skipeqs` options are ignored.

`force` specifies that the Hausman test be performed, even though the assumptions of the Hausman test seem not to be met, for example, because the estimators were `pweighted` or the data were clustered.

`df(#)` specifies the degrees of freedom for the Hausman test. The default is the matrix rank of the variance of the difference between the coefficients of the two estimators.

`sigmamore` and `sigmaless` specify that the two covariance matrices used in the test be based on a common estimate of disturbance variance (σ^2).

`sigmamore` specifies that the covariance matrices be based on the estimated disturbance variance from the efficient estimator. This option provides a proper estimate of the contrast variance for so-called tests of exogeneity and overidentification in instrumental-variables regression.

`sigmaless` specifies that the covariance matrices be based on the estimated disturbance variance from the consistent estimator.

These options can be specified only when both estimators save `e(sigma)` or `e(rmse)`, or with the `xtreg` command. `e(sigma_e)` is saved after the `xtreg` command with the option `fe` or `mle` option. `e(rmse)` is saved after the `xtreg` command with the `re` option.

`sigmamore` or `sigmaless` are recommended when comparing fixed-effects and random-effects linear regression because they are much less likely to produce a non–positive-definite-differenced covariance matrix (although the tests are asymptotically equivalent whether or not one of the options is specified).

Advanced

`tconsistent(`*string*`)` and `tefficient(`*string*`)` are formatting options. They allow you to specify the headers of the columns of coefficients that default to the names of the models. These options will be of interest primarily to programmers.

Remarks

`hausman` is a general implementation of Hausman's (1978) specification test, which compares an estimator $\widehat{\theta}_1$ that is known to be consistent with an estimator $\widehat{\theta}_2$ that is efficient under the assumption being tested. The null hypothesis is that the estimator $\widehat{\theta}_2$ is indeed an efficient (and consistent) estimator of the true parameters. If this is the case, there should be no systematic difference between the two estimators. If there exists a systematic difference in the estimates, you have reason to doubt the assumptions on which the efficient estimator is based.

The assumption of efficiency is violated if the estimator is `pweighted` or the data are clustered, so `hausman` cannot be used. The test can be forced by specifying the `force` option with `hausman`. For an alternative to using `hausman` in these cases, see [R] **suest**.

To use `hausman`, you

```
. (compute the always-consistent estimator)
. estimates store name-consistent
. (compute the estimator that is efficient under H_0)
. hausman name-consistent .
```

Alternatively, you can turn this around:

```
. (compute the estimator that is efficient under H_0)
. estimates store name-efficient
. (fit the less-efficient model)
. (compute the always-consistent estimator)
. hausman . name-efficient
```

You can, of course, also compute and store both the always-consistent and efficient-under-H_0 estimators and perform the Hausman test with

```
. hausman name-consistent name-efficient
```

▷ Example 1

We are studying the factors that affect the wages of young women in the United States between 1970 and 1988, and we have a panel-data sample of individual women over that time span.

```
. use http://www.stata-press.com/data/r12/nlswork4
(National Longitudinal Survey.  Young Women 14-26 years of age in 1968)
. describe
Contains data from http://www.stata-press.com/data/r12/nlswork4.dta
  obs:        28,534                          National Longitudinal Survey.
                                                Young Women 14-26 years of age
                                                in 1968
 vars:             6                          29 Jan 2011 16:35
 size:       370,942
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
idcode          int    %8.0g                  NLS ID
year            byte   %8.0g                  interview year
age             byte   %8.0g                  age in current year
msp             byte   %8.0g                  1 if married, spouse present
ttl_exp         float  %9.0g                  total work experience
ln_wage         float  %9.0g                  ln(wage/GNP deflator)
-------------------------------------------------------------------------------
Sorted by:  idcode  year
```

We believe that a random-effects specification is appropriate for individual-level effects in our model. We fit a fixed-effects model that will capture all temporally constant individual-level effects.

```
. xtreg ln_wage age msp ttl_exp, fe
Fixed-effects (within) regression               Number of obs      =     28494
Group variable: idcode                          Number of groups   =      4710

R-sq:  within  = 0.1373                         Obs per group: min =         1
       between = 0.2571                                        avg =       6.0
       overall = 0.1800                                        max =        15

                                                F(3,23781)         =   1262.01
corr(u_i, Xb)  = 0.1476                         Prob > F           =    0.0000

------------------------------------------------------------------------------
     ln_wage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   -.005485    .000837    -6.55   0.000    -.0071256   -.0038443
         msp |   .0033427   .0054868     0.61   0.542    -.0074118    .0140971
     ttl_exp |   .0383604   .0012416    30.90   0.000     .0359268    .0407941
       _cons |   1.593953   .0177538    89.78   0.000     1.559154    1.628752
-------------+----------------------------------------------------------------
     sigma_u |  .37674223
     sigma_e |  .29751014
         rho |  .61591044   (fraction of variance due to u_i)
------------------------------------------------------------------------------
F test that all u_i=0:     F(4709, 23781) =     7.76         Prob > F = 0.0000
```

We assume that this model is consistent for the true parameters and save the results by using `estimates store` under a name, `fixed`:

```
. estimates store fixed
```

Now we fit a random-effects model as a fully efficient specification of the individual effects under the assumption that they are random and follow a normal distribution. We then compare these estimates with the previously saved results by using the `hausman` command.

```
. xtreg ln_wage age msp ttl_exp, re
Random-effects GLS regression                   Number of obs      =     28494
Group variable: idcode                          Number of groups   =      4710

R-sq:  within  = 0.1373                         Obs per group: min =         1
       between = 0.2552                                        avg =       6.0
       overall = 0.1797                                        max =        15

Random effects u_i ~ Gaussian                   Wald chi2(3)       =   5100.33
corr(u_i, X)       = 0 (assumed)                Prob > chi2        =    0.0000

------------------------------------------------------------------------------
     ln_wage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |  -.0069749   .0006882   -10.13   0.000    -.0083238   -.0056259
         msp |   .0046594   .0051012     0.91   0.361    -.0053387    .0146575
     ttl_exp |   .0429635   .0010169    42.25   0.000     .0409704    .0449567
       _cons |   1.609916   .0159176   101.14   0.000     1.578718    1.641114
-------------+----------------------------------------------------------------
     sigma_u |  .32648519
     sigma_e |  .29751014
         rho |  .54633481   (fraction of variance due to u_i)
------------------------------------------------------------------------------
```

```
. hausman fixed ., sigmamore
                 ---- Coefficients ----
              |      (b)          (B)            (b-B)     sqrt(diag(V_b-V_B))
              |    fixed            .          Difference          S.E.
--------------+----------------------------------------------------------------
          age |   -.005485    -.0069749         .0014899        .0004803
          msp |    .0033427    .0046594        -.0013167        .0020596
      ttl_exp |    .0383604    .0429635        -.0046031        .0007181
--------------------------------------------------------------------------------
                           b = consistent under Ho and Ha; obtained from xtreg
            B = inconsistent under Ha, efficient under Ho; obtained from xtreg

    Test:  Ho:  difference in coefficients not systematic

                  chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                          =      260.40
                Prob>chi2 =      0.0000
```

Under the current specification, our initial hypothesis that the individual-level effects are adequately modeled by a random-effects model is resoundingly rejected. This result is based on the rest of our model specification, and random effects might be appropriate for some alternate model of wages.

◁

Jerry Allen Hausman was born in West Virginia in 1946. He studied economics at Brown and Oxford, has been at MIT since 1972, and has made many outstanding contributions to econometrics and applied microeconometrics.

▷ Example 2

A stringent assumption of multinomial and conditional logit models is that outcome categories for the model have the property of independence of irrelevant alternatives (IIA). Stated simply, this assumption requires that the inclusion or exclusion of categories does not affect the relative risks associated with the regressors in the remaining categories.

One classic example of a situation in which this assumption would be violated involves the choice of transportation mode; see McFadden (1974). For simplicity, postulate a transportation model with the four possible outcomes: rides a train to work, takes a bus to work, drives the Ford to work, and drives the Chevrolet to work. Clearly, "drives the Ford" is a closer substitute to "drives the Chevrolet" than it is to "rides a train" (at least for most people). This means that excluding "drives the Ford" from the model could be expected to affect the relative risks of the remaining options and that the model would not obey the IIA assumption.

Using the data presented in [R] **mlogit**, we will use a simplified model to test for IIA. The choice of insurance type among indemnity, prepaid, and uninsured is modeled as a function of age and gender. The indemnity category is allowed to be the base category, and the model including all three outcomes is fit. The results are then stored under the name `allcats`.

```
. use http://www.stata-press.com/data/r12/sysdsn3
(Health insurance data)
. mlogit insure age male
Iteration 0:   log likelihood = -555.85446
Iteration 1:   log likelihood = -551.32973
Iteration 2:   log likelihood = -551.32802
Iteration 3:   log likelihood = -551.32802
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(4)      =       9.05
                                                Prob > chi2     =     0.0598
Log likelihood = -551.32802                     Pseudo R2       =     0.0081
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.0100251	.0060181	-1.67	0.096	-.0218204	.0017702
male	.5095747	.1977893	2.58	0.010	.1219147	.8972346
_cons	.2633838	.2787575	0.94	0.345	-.2829708	.8097383
Uninsure						
age	-.0051925	.0113821	-0.46	0.648	-.0275011	.0171161
male	.4748547	.3618462	1.31	0.189	-.2343508	1.18406
_cons	-1.756843	.5309602	-3.31	0.001	-2.797506	-.7161803

```
. estimates store allcats
```

Under the IIA assumption, we would expect no systematic change in the coefficients if we excluded one of the outcomes from the model. (For an extensive discussion, see Hausman and McFadden [1984].) We reestimate the parameters, excluding the uninsured outcome, and perform a Hausman test against the fully efficient full model.

```
. mlogit insure age male if insure != "Uninsure":insure
Iteration 0:   log likelihood =  -394.8693
Iteration 1:   log likelihood =  -390.4871
Iteration 2:   log likelihood = -390.48643
Iteration 3:   log likelihood = -390.48643
Multinomial logistic regression                 Number of obs   =        570
                                                LR chi2(2)      =       8.77
                                                Prob > chi2     =     0.0125
Log likelihood = -390.48643                     Pseudo R2       =     0.0111
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.0101521	.0060049	-1.69	0.091	-.0219214	.0016173
male	.5144003	.1981735	2.60	0.009	.1259874	.9028133
_cons	.2678043	.2775563	0.96	0.335	-.276196	.8118046

```
. hausman . allcats, alleqs constant
                 ---- Coefficients ----
              |      (b)          (B)            (b-B)     sqrt(diag(V_b-V_B))
              |        .       allcats       Difference          S.E.
--------------+----------------------------------------------------------------
          age |   -.0101521    -.0100251       -.0001269              .
         male |    .5144003     .5095747        .0048256        .0123338
        _cons |    .2678043     .2633838        .0044205              .
------------------------------------------------------------------------------
                    b = consistent under Ho and Ha; obtained from mlogit
     B = inconsistent under Ha, efficient under Ho; obtained from mlogit

  Test:  Ho:  difference in coefficients not systematic

                chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                        =         0.08
              Prob>chi2 =       0.9944
              (V_b-V_B is not positive definite)
```

The syntax of the `if` condition on the `mlogit` command simply identified the `"Uninsured"` category with the `insure` value label; see [U] **12.6.3 Value labels**. On examining the output from `hausman`, we see that there is no evidence that the IIA assumption has been violated.

Because the Hausman test is a standardized comparison of model coefficients, using it with `mlogit` requires that the base outcome be the same in both competing models. In particular, if the most-frequent category (the default base outcome) is being removed to test for IIA, you must use the `baseoutcome()` option in `mlogit` to manually set the base outcome to something else. Or you can use the `equation()` option of the `hausman` command to align the equations of the two models.

Having the missing values for the square root of the diagonal of the covariance matrix of the differences is not comforting, but it is also not surprising. This covariance matrix is guaranteed to be positive definite only asymptotically (it is a consequence of the assumption that one of the estimators is efficient), and assurances are not made about the diagonal elements. Negative values along the diagonal are possible, and the fourth column of the table is provided mainly for descriptive use.

We can also perform the Hausman IIA test against the remaining alternative in the model:

```
. mlogit insure age male if insure != "Prepaid":insure
Iteration 0:   log likelihood = -132.59913
Iteration 1:   log likelihood = -131.78009
Iteration 2:   log likelihood = -131.76808
Iteration 3:   log likelihood = -131.76807
Multinomial logistic regression                 Number of obs   =        338
                                                LR chi2(2)      =       1.66
                                                Prob > chi2     =     0.4356
Log likelihood = -131.76807                     Pseudo R2       =     0.0063

------------------------------------------------------------------------------
      insure |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
Indemnity    |  (base outcome)
-------------+----------------------------------------------------------------
Uninsure     |
         age |  -.0041055   .0115807    -0.35   0.723    -.0268033    .0185923
        male |   .4591074   .3595663     1.28   0.202    -.2456296    1.163844
       _cons |  -1.801774   .5474476    -3.29   0.001    -2.874752   -.7287968
------------------------------------------------------------------------------
```

```
. hausman . allcats, alleqs constant
                 ---- Coefficients ----
              |      (b)          (B)            (b-B)     sqrt(diag(V_b-V_B))
              |        .       allcats       Difference          S.E.
--------------+----------------------------------------------------------------
          age |  -.0041055    -.0051925         .001087        .0021355
         male |   .4591074     .4748547        -.0157473              .
        _cons |  -1.801774    -1.756843        -.0449311        .1333421
------------------------------------------------------------------------------
                    b = consistent under Ho and Ha; obtained from mlogit
     B = inconsistent under Ha, efficient under Ho; obtained from mlogit

  Test:  Ho:  difference in coefficients not systematic

                chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                        =    -0.18    chi2<0 ==> model fitted on these
                                      data fails to meet the asymptotic
                                      assumptions of the Hausman test;
                                      see suest for a generalized test
```

Here the χ^2 statistic is actually negative. We might interpret this result as strong evidence that we cannot reject the null hypothesis. Such a result is not an unusual outcome for the Hausman test, particularly when the sample is relatively small—there are only 45 uninsured individuals in this dataset.

Are we surprised by the results of the Hausman test in this example? Not really. Judging from the z statistics on the original multinomial logit model, we were struggling to identify any structure in the data with the current specification. Even when we were willing to assume IIA and computed the efficient estimator under this assumption, few of the effects could be identified as statistically different from those on the base category. Trying to base a Hausman test on a contrast (difference) between two poor estimates is just asking too much of the existing data.

◁

In example 2, we encountered a case in which the Hausman was not well defined. Unfortunately, in our experience this happens fairly often. Stata provides an alternative to the Hausman test that overcomes this problem through an alternative estimator of the variance of the difference between the two estimators. This other estimator is guaranteed to be positive semidefinite. This alternative estimator also allows a widening of the scope of problems to which Hausman-type tests can be applied by relaxing the assumption that one of the estimators is efficient. For instance, you can perform Hausman-type tests to clustered observations and survey estimators. See [R] **suest** for details.

Saved results

`hausman` saves the following in `r()`:

Scalars

`r(chi2)`	χ^2
`r(df)`	degrees of freedom for the statistic
`r(p)`	p-value for the χ^2
`r(rank)`	rank of `(V_b-V_B)^(-1)`

Methods and formulas

`hausman` is implemented as an ado-file.

The Hausman statistic is distributed as χ^2 and is computed as

$$H = (\beta_c - \beta_e)'(V_c - V_e)^{-1}(\beta_c - \beta_e)$$

where

β_c	is the coefficient vector from the consistent estimator
β_e	is the coefficient vector from the efficient estimator
V_c	is the covariance matrix of the consistent estimator
V_e	is the covariance matrix of the efficient estimator

When the difference in the variance matrices is not positive definite, a Moore–Penrose generalized inverse is used. As noted in Gourieroux and Monfort (1995, 125–128), the choice of generalized inverse is not important asymptotically.

The number of degrees of freedom for the statistic is the rank of the difference in the variance matrices. When the difference is positive definite, this is the number of common coefficients in the models being compared.

Acknowledgment

Portions of `hausman` are based on an early implementation by Jeroen Weesie, Utrecht University, The Netherlands.

References

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Gourieroux, C., and A. Monfort. 1995. *Statistics and Econometric Models, Vol 2: Testing, Confidence Regions, Model Selection, and Asymptotic Theory*. Trans. Q. Vuong. Cambridge: Cambridge University Press.

Hausman, J. A. 1978. Specification tests in econometrics. *Econometrica* 46: 1251–1271.

Hausman, J. A., and D. L. McFadden. 1984. Specification tests for the multinomial logit model. *Econometrica* 52: 1219–1240.

McFadden, D. L. 1974. Measurement of urban travel demand. *Journal of Public Economics* 3: 303–328.

Also see

[R] **lrtest** — Likelihood-ratio test after estimation

[R] **suest** — Seemingly unrelated estimation

[R] **test** — Test linear hypotheses after estimation

[XT] **xtreg** — Fixed-, between-, and random-effects and population-averaged linear models

Title

heckman — Heckman selection model

Syntax

Basic syntax

```
heckman depvar [indepvars], select(varlist_s) [twostep]
```

or

```
heckman depvar [indepvars], select(depvar_s = varlist_s) [twostep]
```

Full syntax for maximum likelihood estimates only

```
heckman depvar [indepvars] [if] [in] [weight],
    select([depvar_s =] varlist_s [, offset(varname) noconstant])
    [heckman_ml_options]
```

Full syntax for Heckman's two-step consistent estimates only

```
heckman depvar [indepvars] [if] [in], twostep
    select([depvar_s =] varlist_s [, noconstant]) [heckman_ts_options]
```

heckman_ml_options	Description
Model	
* `select()`	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`first`	report first-step probit estimates
`noskip`	perform likelihood-ratio test
`nshazard(`*newvar*`)`	generate nonselection hazard variable
`mills(`*newvar*`)`	synonym for `nshazard()`
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells

Maximization

maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

*select() is required.
The full specification is select([*depvar*$_s$ =] *varlist*$_s$ [, offset(*varname*) noconstant]) .

heckman_ts_options	Description
Model	
*select()	specify selection equation: dependent and independent variables; whether to have constant term
*twostep	produce two-step consistent estimate
noconstant	suppress constant term
rhosigma	truncate ρ to $[-1, 1]$ with consistent σ
rhotrunc	truncate ρ to $[-1, 1]$
rholimited	truncate ρ in limited cases
rhoforce	do not truncate ρ
SE	
vce(*vcetype*)	*vcetype* may be conventional, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
first	report first-step probit estimates
nshazard(*newvar*)	generate nonselection hazard variable
mills(*newvar*)	synonym for nshazard()
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
coeflegend	display legend instead of statistics

*select() and twostep are required.
The full specification is select([*depvar*$_s$ =] *varlist*$_s$ [, noconstant])

indepvars and *varlist*$_s$ may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar, *indepvars*, *varlist*$_s$, and *depvar*$_s$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
bootstrap, by, jackknife, rolling, statsby, and svy are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
aweights are not allowed with the jackknife prefix; see [R] **jackknife**.
twostep, vce(), first, noskip, and weights are not allowed with the svy prefix; see [SVY] **svy**.
pweights, aweights, fweights, and iweights are allowed with maximum likelihood estimation; see [U] **11.1.6 weight**. No weights are allowed if twostep is specified.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

heckman for maximum likelihood estimates

Statistics > Sample-selection models > Heckman selection model (ML)

heckman for two-step consistent estimates

Statistics > Sample-selection models > Heckman selection model (two-step)

Description

`heckman` fits regression models with selection by using either Heckman's two-step consistent estimator or full maximum likelihood.

Options for Heckman selection model (ML)

Model

`select(...)` specifies the variables and options for the selection equation. It is an integral part of specifying a Heckman model and is required. The selection equation should contain at least one variable that is not in the outcome equation.

If $depvar_s$ is specified, it should be coded as 0 or 1, with 0 indicating an observation not selected and 1 indicating a selected observation. If $depvar_s$ is not specified, observations for which *depvar* is not missing are assumed selected, and those for which *depvar* is missing are assumed not selected.

`noconstant`, `offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` specifies that the first-step probit estimates of the selection equation be displayed before estimation.

`noskip` specifies that a full maximum-likelihood model with only a constant for the regression equation be fit. This model is not displayed but is used as the base model to compute a likelihood-ratio test for the model test statistic displayed in the estimation header. By default, the overall model test statistic is an asymptotically equivalent Wald test that all the parameters in the regression equation are zero (except the constant). For many models, this option can substantially increase estimation time.

`nshazard(`*newvar*`)` and `mills(`*newvar*`)` are synonyms; either will create a new variable containing the nonselection hazard—what Heckman (1979) referred to as the inverse of the Mills' ratio—from the selection equation. The nonselection hazard is computed from the estimated parameters of the selection equation.

`nocnsreport`; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with heckman but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Options for Heckman selection model (two-step)

Model

select(...) specifies the variables and options for the selection equation. It is an integral part of specifying a Heckman model and is required. The selection equation should contain at least one variable that is not in the outcome equation.

If $depvar_s$ is specified, it should be coded as 0 or 1, with 0 indicating an observation not selected and 1 indicating a selected observation. If $depvar_s$ is not specified, observations for which *depvar* is not missing are assumed selected, and those for which *depvar* is missing are assumed not selected.

twostep specifies that Heckman's (1979) two-step efficient estimates of the parameters, standard errors, and covariance matrix be produced.

noconstant; see [R] **estimation options**.

rhosigma, rhotrunc, rholimited, and rhoforce are rarely used options to specify how the two-step estimator (option twostep) handles unusual cases in which the two-step estimate of ρ is outside the admissible range for a correlation, $[-1, 1]$. When $\text{abs}(\rho) > 1$, the two-step estimate of the coefficient variance–covariance matrix may not be positive definite and thus may be unusable for testing. The default is rhosigma.

rhosigma specifies that ρ be truncated, as with the rhotrunc option, and that the estimate of σ be made consistent with $\widehat{\rho}$, the truncated estimate of ρ. So, $\widehat{\sigma} = \boldsymbol{\beta}_m\widehat{\rho}$; see *Methods and formulas* for the definition of $\boldsymbol{\beta}_m$. Both the truncated ρ and the new estimate of $\widehat{\sigma}$ are used in all computations to estimate the two-step covariance matrix.

rhotrunc specifies that ρ be truncated to lie in the range $[-1, 1]$. If the two-step estimate is less than -1, ρ is set to -1; if the two-step estimate is greater than 1, ρ is set to 1. This truncated value of ρ is used in all computations to estimate the two-step covariance matrix.

rholimited specifies that ρ be truncated only in computing the diagonal matrix $\mathbf{D}$ as it enters $\mathbf{V}_{\text{twostep}}$ and $\mathbf{Q}$; see *Methods and formulas*. In all other computations, the untruncated estimate of ρ is used.

rhoforce specifies that the two-step estimate of ρ be retained, even if it is outside the admissible range for a correlation. This option may, in rare cases, lead to a non–positive-definite covariance matrix.

These options have no effect when estimation is by maximum likelihood, the default. They also have no effect when the two-step estimate of ρ is in the range $[-1, 1]$.

SE

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(conventional)`, the default, uses the two-step variance estimator derived by Heckman.

Reporting

`level(#)`; see [R] **estimation options**.

`first` specifies that the first-step probit estimates of the selection equation be displayed before estimation.

`nshazard(`*newvar*`)` and `mills(`*newvar*`)` are synonyms; either will create a new variable containing the nonselection hazard—what Heckman (1979) referred to as the inverse of the Mills' ratio—from the selection equation. The nonselection hazard is computed from the estimated parameters of the selection equation.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `heckman` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

The Heckman selection model (Gronau 1974; Lewis 1974; Heckman 1976) assumes that there exists an underlying regression relationship,

$$y_j = \mathbf{x}_j\boldsymbol{\beta} + u_{1j} \qquad \textit{regression equation}$$

The dependent variable, however, is not always observed. Rather, the dependent variable for observation j is observed if

$$\mathbf{z}_j\boldsymbol{\gamma} + u_{2j} > 0 \qquad \textit{selection equation}$$

where

$$u_1 \sim N(0, \sigma)$$
$$u_2 \sim N(0, 1)$$
$$\text{corr}(u_1, u_2) = \rho$$

When $\rho \neq 0$, standard regression techniques applied to the first equation yield biased results. `heckman` provides consistent, asymptotically efficient estimates for all the parameters in such models.

In one classic example, the first equation describes the wages of women. Women choose whether to work, and thus, from our point of view as researchers, whether we observe their wages in our data. If women made this decision randomly, we could ignore that not all wages are observed and use ordinary regression to fit a wage model. Such an assumption of random participation, however, is unlikely to be true; women who would have low wages may be unlikely to choose to work, and thus the sample of observed wages is biased upward. In the jargon of economics, women choose not to work when their personal reservation wage is greater than the wage offered by employers. Thus

women who choose not to work might have even higher offer wages than those who do work—they may have high offer wages, but they have even higher reservation wages. We could tell a story that competency is related to wages, but competency is rewarded more at home than in the labor force.

In any case, in this problem—which is the paradigm for most such problems—a solution can be found if there are some variables that strongly affect the chances for observation (the reservation wage) but not the outcome under study (the offer wage). Such a variable might be the number of children in the home. (Theoretically, we do not need such identifying variables, but without them, we depend on functional form to identify the model. It would be difficult for anyone to take such results seriously because the functional-form assumptions have no firm basis in theory.)

▷ Example 1

In the syntax for `heckman`, *depvar* and *indepvars* are the dependent variable and regressors for the underlying regression model to be fit ($\mathbf{y} = \mathbf{X}\beta$), and $varlist_s$ are the variables ($\mathbf{Z}$) thought to determine whether *depvar* is observed or unobserved (selected or not selected). In our female wage example, the number of children at home would be included in the second list. By default, `heckman` assumes that missing values (see [U] **12.2.1 Missing values**) of *depvar* imply that the dependent variable is unobserved (not selected). With some datasets, it is more convenient to specify a binary variable ($depvar_s$) that identifies the observations for which the dependent is observed/selected ($depvar_s \neq 0$) or not observed ($depvar_s = 0$); `heckman` will accommodate either type of data.

We have a (fictional) dataset on 2,000 women, 1,343 of whom work:

```
. use http://www.stata-press.com/data/r12/womenwk
. summarize age educ married children wage
```

Variable	Obs	Mean	Std. Dev.	Min	Max
age	2000	36.208	8.28656	20	59
education	2000	13.084	3.045912	10	20
married	2000	.6705	.4701492	0	1
children	2000	1.6445	1.398963	0	5
wage	1343	23.69217	6.305374	5.88497	45.80979

We will assume that the hourly wage is a function of education and age, whereas the likelihood of working (the likelihood of the wage being observed) is a function of marital status, the number of children at home, and (implicitly) the wage (via the inclusion of age and education, which we think determine the wage):

```
. heckman wage educ age, select(married children educ age)
Iteration 0:   log likelihood = -5178.7009
Iteration 1:   log likelihood = -5178.3049
Iteration 2:   log likelihood = -5178.3045
Heckman selection model                         Number of obs      =      2000
(regression model with sample selection)        Censored obs       =       657
                                                Uncensored obs     =      1343
                                                Wald chi2(2)       =    508.44
Log likelihood = -5178.304                      Prob > chi2        =    0.0000
```

wage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
wage						
education	.9899537	.0532565	18.59	0.000	.8855729	1.094334
age	.2131294	.0206031	10.34	0.000	.1727481	.2535108
_cons	.4857752	1.077037	0.45	0.652	-1.625179	2.59673
select						
married	.4451721	.0673954	6.61	0.000	.3130794	.5772647
children	.4387068	.0277828	15.79	0.000	.3842534	.4931601
education	.0557318	.0107349	5.19	0.000	.0346917	.0767718
age	.0365098	.0041533	8.79	0.000	.0283694	.0446502
_cons	-2.491015	.1893402	-13.16	0.000	-2.862115	-2.119915
/athrho	.8742086	.1014225	8.62	0.000	.6754241	1.072993
/lnsigma	1.792559	.027598	64.95	0.000	1.738468	1.84665
rho	.7035061	.0512264			.5885365	.7905862
sigma	6.004797	.1657202			5.68862	6.338548
lambda	4.224412	.3992265			3.441942	5.006881

```
LR test of indep. eqns. (rho = 0):   chi2(1) =    61.20   Prob > chi2 = 0.0000
```

`heckman` assumes that `wage` is the dependent variable and that the first variable list (`educ` and `age`) are the determinants of `wage`. The variables specified in the `select()` option (`married`, `children`, `educ`, and `age`) are assumed to determine whether the dependent variable is observed (the selection equation). Thus we fit the model

$$\texttt{wage} = \beta_0 + \beta_1\texttt{educ} + \beta_2\texttt{age} + u_1$$

and we assumed that `wage` is observed if

$$\gamma_0 + \gamma_1\texttt{married} + \gamma_2\texttt{children} + \gamma_3\texttt{educ} + \gamma_4\texttt{age} + u_2 > 0$$

where u_1 and u_2 have correlation ρ.

The reported results for the wage equation are interpreted exactly as though we observed wage data for all women in the sample; the coefficients on age and education level represent the estimated marginal effects of the regressors in the underlying regression equation. The results for the two ancillary parameters require some explanation. `heckman` does not directly estimate ρ; to constrain ρ within its valid limits, and for numerical stability during optimization, it estimates the inverse hyperbolic tangent of ρ:

$$\operatorname{atanh}\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

This estimate is reported as /athrho. In the bottom panel of the output, heckman undoes this transformation for you: the estimated value of ρ is 0.7035061. The standard error for ρ is computed using the delta method, and its confidence intervals are the transformed intervals of /athrho.

Similarly, σ, the standard error of the residual in the wage equation, is not directly estimated; for numerical stability, heckman instead estimates $\ln\sigma$. The untransformed sigma is reported at the end of the output: 6.004797.

Finally, some researchers—especially economists—are used to the selectivity effect summarized not by ρ but by $\lambda = \rho\sigma$. heckman reports this, too, along with an estimate of the standard error and confidence interval.

◁

❑ Technical note

If each of the equations in the model had contained many regressors, the heckman command could have become long. An alternate way of specifying our wage model would be to use Stata's global macros. The following lines are an equivalent way of specifying our model:

```
. global wageeq "wage educ age"
. global seleq "married children educ age"
. heckman $wageeq, select($seleq)
```
(*output omitted*)

❑

❑ Technical note

The reported model χ^2 test is a Wald test that all coefficients in the regression model (except the constant) are 0. heckman is an estimation command, so you can use test, testnl, or lrtest to perform tests against whatever nested alternate model you choose; see [R] **test**, [R] **testnl**, and [R] **lrtest**.

The estimation of ρ and σ in the forms $\operatorname{atanh}\rho$ and $\ln\sigma$ extends the range of these parameters to infinity in both directions, thus avoiding boundary problems during the maximization. Tests of ρ must be made in the transformed units. However, because $\operatorname{atanh}(0) = 0$, the reported test for $\operatorname{atanh}\rho = 0$ is equivalent to the test for $\rho = 0$.

The likelihood-ratio test reported at the bottom of the output is an equivalent test for $\rho = 0$ and is computationally the comparison of the joint likelihood of an independent probit model for the selection equation and a regression model on the observed wage data against the Heckman model likelihood. Because $\chi^2 = 61.20$, this clearly justifies the Heckman selection equation with these data.

❑

▷ Example 2

heckman supports the Huber/White/sandwich estimator of variance under the vce(robust) and vce(cluster *clustvar*) options or when pweights are used for population-weighted data; see [U] **20.20 Obtaining robust variance estimates**. We can obtain robust standard errors for our wage model by specifying clustering on county of residence (the county variable).

```
. heckman wage educ age, select(married children educ age) vce(cluster county)
Iteration 0:   log pseudolikelihood = -5178.7009
Iteration 1:   log pseudolikelihood = -5178.3049
Iteration 2:   log pseudolikelihood = -5178.3045
Heckman selection model                         Number of obs      =      2000
(regression model with sample selection)        Censored obs       =       657
                                                Uncensored obs     =      1343
                                                Wald chi2(1)       =         .
Log pseudolikelihood = -5178.304                Prob > chi2        =         .
                                (Std. Err. adjusted for 10 clusters in county)
------------------------------------------------------------------------------
             |               Robust
        wage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
wage         |
   education |   .9899537   .0600061    16.50   0.000     .8723438    1.107564
         age |   .2131294    .020995    10.15   0.000       .17198    .2542789
       _cons |   .4857752   1.302103     0.37   0.709    -2.066299     3.03785
-------------+----------------------------------------------------------------
select       |
     married |   .4451721   .0731472     6.09   0.000     .3018062    .5885379
    children |   .4387068   .0312386    14.04   0.000     .3774802    .4999333
   education |   .0557318   .0110039     5.06   0.000     .0341645    .0772991
         age |   .0365098    .004038     9.04   0.000     .0285954    .0444242
       _cons |  -2.491015   .1153305   -21.60   0.000    -2.717059   -2.264972
-------------+----------------------------------------------------------------
     /athrho |   .8742086   .1403337     6.23   0.000     .5991596    1.149258
   /lnsigma  |   1.792559   .0258458    69.36   0.000     1.741902    1.843216
-------------+----------------------------------------------------------------
         rho |   .7035061   .0708796                      .5364513     .817508
       sigma |   6.004797    .155199                      5.708189    6.316818
      lambda |   4.224412   .5186709                      3.207835    5.240988
------------------------------------------------------------------------------
Wald test of indep. eqns. (rho = 0): chi2(1) =    38.81   Prob > chi2 = 0.0000
```

The robust standard errors tend to be a bit larger, but we notice no systematic differences. This finding is not surprising because the data were not constructed to have any county-specific correlations or any other characteristics that would deviate from the assumptions of the Heckman model.

◁

▷ Example 3

Stata also produces Heckman's (1979) two-step efficient estimator of the model with the `twostep` option. Maximum likelihood estimation of the parameters can be time consuming with large datasets, and the two-step estimates may provide a good alternative in such cases. Continuing with the women's wage model, we can obtain the two-step estimates with Heckman's consistent covariance estimates by typing

```
. heckman wage educ age, select(married children educ age) twostep
Heckman selection model -- two-step estimates   Number of obs      =      2000
(regression model with sample selection)        Censored obs       =       657
                                                Uncensored obs     =      1343
                                                Wald chi2(2)       =    442.54
                                                Prob > chi2        =    0.0000
```

wage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
wage						
education	.9825259	.0538821	18.23	0.000	.8769189	1.088133
age	.2118695	.0220511	9.61	0.000	.1686502	.2550888
_cons	.7340391	1.248331	0.59	0.557	-1.712645	3.180723
select						
married	.4308575	.074208	5.81	0.000	.2854125	.5763025
children	.4473249	.0287417	15.56	0.000	.3909922	.5036576
education	.0583645	.0109742	5.32	0.000	.0368555	.0798735
age	.0347211	.0042293	8.21	0.000	.0264318	.0430105
_cons	-2.467365	.1925635	-12.81	0.000	-2.844782	-2.089948
mills						
lambda	4.001615	.6065388	6.60	0.000	2.812821	5.19041
rho	0.67284					
sigma	5.9473529					

◁

❑ Technical note

The Heckman selection model depends strongly on the model being correct, much more so than ordinary regression. Running a separate probit or logit for sample inclusion followed by a regression, referred to in the literature as the two-part model (Manning, Duan, and Rogers 1987)—not to be confused with Heckman's two-step procedure—is an especially attractive alternative if the regression part of the model arose because of taking a logarithm of zero values. When the goal is to analyze an underlying regression model or to predict the value of the dependent variable that would be observed in the absence of selection, however, the Heckman model is more appropriate. When the goal is to predict an actual response, the two-part model is usually the better choice.

The Heckman selection model can be unstable when the model is not properly specified or if a specific dataset simply does not support the model's assumptions. For example, let's examine the solution to another simulated problem.

```
. use http://www.stata-press.com/data/r12/twopart
. heckman yt x1 x2 x3, select(z1 z2) nonrtol
Iteration 0:   log likelihood = -111.94996
Iteration 1:   log likelihood = -110.82258
Iteration 2:   log likelihood = -110.17707
Iteration 3:   log likelihood = -107.70663  (not concave)
Iteration 4:   log likelihood = -107.07729  (not concave)
  (output omitted)
Iteration 33:  log likelihood =  -104.0825  (not concave)
Iteration 34:  log likelihood =  -104.0825
Heckman selection model                         Number of obs      =       150
(regression model with sample selection)        Censored obs       =        87
                                                Uncensored obs     =        63
                                                Wald chi2(3)       =  8.64e+08
Log likelihood = -104.0825                      Prob > chi2        =    0.0000
------------------------------------------------------------------------------
          yt |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
yt           |
          x1 |   .8974192   .0002247  3994.69   0.000     .8969789    .8978595
          x2 |  -2.525303   .0001472 -1.7e+04   0.000    -2.525591   -2.525014
          x3 |   2.855786   .0004181  6829.86   0.000     2.854966    2.856605
       _cons |   .6975442   .0920515     7.58   0.000     .5171265    .8779619
-------------+----------------------------------------------------------------
select       |
          z1 |  -.6825988   .0900159    -7.58   0.000    -.8590267   -.5061709
          z2 |   1.003605    .132347     7.58   0.000     .7442097       1.263
       _cons |  -.3604652   .1232778    -2.92   0.003    -.6020852   -.1188452
-------------+----------------------------------------------------------------
     /athrho |   16.19193   280.9822     0.06   0.954     -534.523    566.9069
   /lnsigma  |  -.5396153   .1318714    -4.09   0.000    -.7980786   -.2811521
-------------+----------------------------------------------------------------
         rho |          1   9.73e-12                          -1           1
       sigma |   .5829725   .0768774                     .4501931    .7549135
      lambda |   .5829725   .0768774                     .4322955    .7336494
------------------------------------------------------------------------------
LR test of indep. eqns. (rho = 0):   chi2(1) =    25.67   Prob > chi2 = 0.0000
```

The model has converged to a value of ρ that is 1.0—within machine-rounding tolerances. Given the form of the likelihood for the Heckman selection model, this implies a division by zero, and it is surprising that the model solution turns out as well as it does. Reparameterizing ρ has allowed the estimation to converge, but we clearly have problems with the estimates. Moreover, if this had occurred in a large dataset, waiting for convergence might take considerable time.

This dataset was not intentionally developed to cause problems. It is actually generated by a "Heckman process" and when generated starting from different random values can be easily estimated. The luck of the draw here merely led to data that, despite the source, did not support the assumptions of the Heckman model.

The two-step model is generally more stable when the data are problematic. It even tolerates estimates of ρ less than -1 and greater than 1. For these reasons, the two-step model may be preferred when exploring a large dataset. Still, if the maximum likelihood estimates cannot converge, or converge to a value of ρ that is at the boundary of acceptable values, there is scant support for fitting a Heckman selection model on the data. Heckman (1979) discusses the implications of ρ being exactly 1 or 0, together with the implications of other possible covariance relationships among the model's determinants.

❑

James Joseph Heckman was born in Chicago in 1944 and studied mathematics at Colorado College and economics at Princeton. He has taught economics at Columbia and (since 1973) at the University of Chicago. He has worked on developing a scientific basis for economic policy evaluation, with emphasis on models of individuals or disaggregated groups and the problems and possibilities created by heterogeneity, diversity, and unobserved counterfactual states. In 2000, he shared the Nobel Prize in Economics with Daniel L. McFadden.

Saved results

`heckman` (maximum likelihood) saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_cens)`	number of censored observations
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_aux)`	number of auxiliary parameters
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(lambda)`	λ
`e(selambda)`	standard error of λ
`e(sigma)`	sigma
`e(chi2)`	χ^2
`e(chi2_c)`	χ^2 for comparison test
`e(p_c)`	p-value for comparison test
`e(p)`	significance of comparison test
`e(rho)`	ρ
`e(rank)`	rank of `e(V)`
`e(rank0)`	rank of `e(V)` for constant-only model
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	heckman
e(cmdline)	command as typed
e(depvar)	names of dependent variables
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(title2)	secondary title in estimation output
e(clustvar)	name of cluster variable
e(offset1)	offset for regression equation
e(offset2)	offset for selection equation
e(mills)	variable containing nonselection hazard (inverse of Mills')
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(method)	ml
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

heckman (two-step) saves the following in e():

Scalars

e(N)	number of observations
e(N_cens)	number of censored observations
e(df_m)	model degrees of freedom
e(lambda)	λ
e(selambda)	standard error of λ
e(sigma)	sigma
e(chi2)	χ^2
e(p)	significance of comparison test
e(rho)	ρ
e(rank)	rank of e(V)

Macros

e(cmd)	heckman
e(cmdline)	command as typed
e(depvar)	names of dependent variables
e(title)	title in estimation output
e(title2)	secondary title in estimation output
e(mills)	variable containing nonselection hazard (inverse of Mills')
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(rhometh)	rhosigma, rhotrunc, rholimited, or rhoforce
e(method)	twostep
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

heckman is implemented as an ado-file. Cameron and Trivedi (2010, 556–562) and Greene (2012, 873–880) provide good introductions to the Heckman selection model. Adkins and Hill (2008, 395–400) describe the two-step estimator with an application using Stata. Jones (2007, 35–40) illustrates Heckman estimation with an application to health economics.

Regression estimates using the nonselection hazard (Heckman 1979) provide starting values for maximum likelihood estimation.

The regression equation is

$$y_j = \mathbf{x}_j\boldsymbol{\beta} + u_{1j}$$

The selection equation is

$$\mathbf{z}_j\boldsymbol{\gamma} + u_{2j} > 0$$

where

$$u_1 \sim N(0, \sigma)$$
$$u_2 \sim N(0, 1)$$
$$\text{corr}(u_1, u_2) = \rho$$

The log likelihood for observation j, $\ln L_j = l_j$, is

$$l_j = \begin{cases} w_j \ln\Phi\left\{\dfrac{\mathbf{z}_j\boldsymbol{\gamma} + (y_j - \mathbf{x}_j\boldsymbol{\beta})\rho/\sigma}{\sqrt{1-\rho^2}}\right\} - \dfrac{w_j}{2}\left(\dfrac{y_j - \mathbf{x}_j\boldsymbol{\beta}}{\sigma}\right)^2 - w_j \ln(\sqrt{2\pi}\sigma) & y_j \text{ observed} \\ w_j \ln \Phi(-\mathbf{z}_j\boldsymbol{\gamma}) & y_j \text{ not observed} \end{cases}$$

where $\Phi(\cdot)$ is the standard cumulative normal and w_j is an optional weight for observation j.

In the maximum likelihood estimation, σ and ρ are not directly estimated. Directly estimated are $\ln\sigma$ and atanh ρ:

$$\text{atanh}\,\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

The standard error of $\lambda = \rho\sigma$ is approximated through the propagation of error (delta) method; that is,

$$\text{Var}(\lambda) \approx \mathbf{D}\,\text{Var}\{(\text{atanh}\,\rho \;\; \ln\sigma)\}\,\mathbf{D}'$$

where $\mathbf{D}$ is the Jacobian of λ with respect to atanh ρ and $\ln\sigma$.

With maximum likelihood estimation, this command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

The maximum likelihood version of heckman also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

The two-step estimates are computed using Heckman's (1979) procedure.

Probit estimates of the selection equation

$$\Pr(y_j \text{ observed} \mid \mathbf{z}_j) = \Phi(\mathbf{z}_j\boldsymbol{\gamma})$$

are obtained. From these estimates, the nonselection hazard—what Heckman (1979) referred to as the inverse of the Mills' ratio, m_j—for each observation j is computed as

$$m_j = \frac{\phi(\mathbf{z}_j\widehat{\boldsymbol{\gamma}})}{\Phi(\mathbf{z}_j\widehat{\boldsymbol{\gamma}})}$$

where ϕ is the normal density. We also define

$$\delta_j = m_j(m_j + \widehat{\boldsymbol{\gamma}}\mathbf{z}_j)$$

Following Heckman, the two-step parameter estimates of $\boldsymbol{\beta}$ are obtained by augmenting the regression equation with the nonselection hazard $\mathbf{m}$. Thus the regressors become $[\,\mathbf{X}\;\mathbf{m}\,]$, and we obtain the additional parameter estimate $\boldsymbol{\beta}_m$ on the variable containing the nonselection hazard.

A consistent estimate of the regression disturbance variance is obtained using the residuals from the augmented regression and the parameter estimate on the nonselection hazard,

$$\widehat{\sigma}^2 = \frac{\mathbf{e}'\mathbf{e} + \boldsymbol{\beta}_m^2 \sum_{j=1}^{N} \delta_j}{N}$$

The two-step estimate of ρ is then

$$\widehat{\rho} = \frac{\boldsymbol{\beta}_m}{\widehat{\sigma}}$$

Heckman derived consistent estimates of the coefficient covariance matrix on the basis of the augmented regression.

Let $\mathbf{W} = [\,\mathbf{X}\ \mathbf{m}\,]$ and $\mathbf{R}$ be a square, diagonal matrix of dimension N, with $(1 - \widehat{\rho}^2\delta_j)$ as the diagonal elements. The conventional VCE is

$$\mathbf{V}_{\text{twostep}} = \widehat{\sigma}^2(\mathbf{W}'\mathbf{W})^{-1}(\mathbf{W}'\mathbf{R}\mathbf{W} + \mathbf{Q})(\mathbf{W}'\mathbf{W})^{-1}$$

where

$$\mathbf{Q} = \widehat{\rho}^2(\mathbf{W}'\mathbf{D}\mathbf{Z})\mathbf{V}_{\mathbf{p}}(\mathbf{Z}'\mathbf{D}\mathbf{W})$$

where $\mathbf{D}$ is the square, diagonal matrix of dimension N with δ_j as the diagonal elements; $\mathbf{Z}$ is the data matrix of selection equation covariates; and $\mathbf{V}_p$ is the variance–covariance estimate from the probit estimation of the selection equation.

References

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Also see

[R] **heckman postestimation** — Postestimation tools for heckman

[R] **heckprob** — Probit model with sample selection

[R] **regress** — Linear regression

[R] **tobit** — Tobit regression

[R] **treatreg** — Treatment-effects model

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

heckman postestimation — Postestimation tools for heckman

Description

The following postestimation commands are available after `heckman`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`[1]	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[2]	likelihood-ratio test; not available with two-step estimator
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`[1]	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `estat ic` and `suest` are not appropriate after `heckman, twostep`.

[2] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

After ML or twostep

```
predict [type] newvar [if] [in] [, statistic nooffset]
```

After ML

```
predict [type] { stub* | newvar_reg newvar_sel newvar_athrho newvar_lnsigma }
    [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`xbsel`	linear prediction for selection equation
`stdpsel`	standard error of the linear prediction for selection equation
`pr(`a`,`b`)`	$\Pr(y_j \mid a < y_j < b)$
`e(`a`,`b`)`	$E(y_j \mid a < y_j < b)$
`ystar(`a`,`b`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$
`ycond`	$E(y_j \mid y_j$ observed$)$
`yexpected`	$E(y_j^*)$, y_j taken to be 0 where unobserved
`nshazard` or `mills`	nonselection hazard (also called the inverse of Mills' ratio)
`psel`	$\Pr(y_j$ observed$)$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

where a and b may be numbers or variables; a missing ($a \geq .$) means $-\infty$, and b missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction $\mathbf{x}_j\mathbf{b}$.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`xbsel` calculates the linear prediction for the selection equation.

`stdpsel` calculates the standard error of the linear prediction for the selection equation.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_1 < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names; `pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b}+u_1 < 30)$; `pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b}+u_1 < ub)$; and `pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_1 < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$; `pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$ and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$; `pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$ and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_1 \mid a < \mathbf{x}_j\mathbf{b} + u_1 < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated.
a and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b}+u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`ycond` calculates the expected value of the dependent variable conditional on the dependent variable being observed, that is, selected; $E(y_j \mid y_j \text{ observed})$.

`yexpected` calculates the expected value of the dependent variable (y_j^*), where that value is taken to be 0 when it is expected to be unobserved; $y_j^* = \Pr(y_j \text{ observed})E(y_j \mid y_j \text{ observed})$.

The assumption of 0 is valid for many cases where nonselection implies nonparticipation (for example, unobserved wage levels, insurance claims from those who are uninsured) but may be inappropriate for some problems (for example, unobserved disease incidence).

`nshazard` and `mills` are synonyms; both calculate the nonselection hazard—what Heckman (1979) referred to as the inverse of the Mills' ratio—from the selection equation.

`psel` calculates the probability of selection (or being observed): $\Pr(y_j \text{ observed}) = \Pr(\mathbf{z}_j\boldsymbol{\gamma} + u_{2j} > 0)$.

`nooffset` is relevant when you specify `offset(`*varname*`)` for `heckman`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores`, not available with `twostep`, calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\mathbf{z}_j\boldsymbol{\gamma})$.

The third new variable will contain $\partial \ln L/\partial(\operatorname{atanh}\rho)$.

The fourth new variable will contain $\partial \ln L/\partial(\ln\sigma)$.

Remarks

▷ Example 1

The default statistic produced by `predict` after `heckman` is the expected value of the dependent variable from the underlying distribution of the regression model. In the wage model of [R] **heckman**, this is the expected wage rate among all women, regardless of whether they were observed to participate in the labor force:

```
. use http://www.stata-press.com/data/r12/womenwk
. heckman wage educ age, select(married children educ age) vce(cluster county)
  (output omitted)
. predict heckwage
(option xb assumed; fitted values)
```

It is instructive to compare these predicted wage values from the Heckman model with an ordinary regression model—a model without the selection adjustment:

```
. regress wage educ age
      Source |       SS       df       MS              Number of obs =    1343
-------------+------------------------------           F(  2,  1340) =  227.49
       Model |  13524.0337     2  6762.01687            Prob > F      =  0.0000
    Residual |  39830.8609  1340  29.7245231            R-squared     =  0.2535
-------------+------------------------------           Adj R-squared =  0.2524
       Total |  53354.8946  1342  39.7577456            Root MSE      =   5.452

------------------------------------------------------------------------------
        wage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   education |   .8965829   .0498061    18.00   0.000     .7988765    .9942893
         age |   .1465739   .0187135     7.83   0.000      .109863    .1832848
       _cons |   6.084875   .8896182     6.84   0.000     4.339679    7.830071
------------------------------------------------------------------------------

. predict regwage
(option xb assumed; fitted values)
. summarize heckwage regwage
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
    heckwage |      2000    21.15532     3.83965    14.6479   32.85949
     regwage |      2000    23.12291    3.241911   17.98218   32.66439
```

Since this dataset was concocted, we know the true coefficients of the wage regression equation to be 1, 0.2, and 1, respectively. We can compute the true mean wage for our sample.

```
. generate truewage = 1 + .2*age + 1*educ
. summarize truewage
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
    truewage |      2000     21.3256    3.797904         15       32.8
```

Whereas the mean of the predictions from `heckman` is within 18 cents of the true mean wage, ordinary regression yields predictions that are on average about $1.80 per hour too high because of the selection effect. The regression predictions also show somewhat less variation than the true wages.

The coefficients from `heckman` are so close to the true values that they are not worth testing. Conversely, the regression equation is significantly off but seems to give the right sense. Would we be led far astray if we relied on the OLS coefficients? The effect of age is off by more than 5 cents per year of age, and the coefficient on education level is off by about 10%. We can test the OLS coefficient on education level against the true value by using `test`.

```
. test educ = 1
 ( 1)  education = 1
       F(  1,  1340) =    4.31
            Prob > F =    0.0380
```

Not only is the OLS coefficient on education substantially lower than the true parameter, but the difference from the true parameter is also statistically significant beyond the 5% level. We can perform a similar test for the OLS age coefficient:

```
. test age = .2
 ( 1)  age = .2
       F(  1,  1340) =    8.15
            Prob > F =    0.0044
```

We find even stronger evidence that the OLS regression results are biased away from the true parameters.

◁

▷ Example 2

Several other interesting aspects of the Heckman model can be explored with `predict`. Continuing with our wage model, we can obtain the expected wages for women conditional on participating in the labor force with the `ycond` option. Let's get these predictions and compare them with actual wages for women participating in the labor force.

```
. use http://www.stata-press.com/data/r12/womenwk, clear
. heckman wage educ age, select(married children educ age)
  (output omitted)
. predict hcndwage, ycond
. summarize wage hcndwage if wage != .
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
        wage |      1343    23.69217    6.305374    5.88497   45.80979
    hcndwage |      1343    23.68239    3.335087   16.18337    33.7567
```

We see that the average predictions from `heckman` are close to the observed levels but do not have the same mean. These conditional wage predictions are available for all observations in the dataset but can be directly compared only with observed wages, where individuals are participating in the labor force.

What if we were interested in making predictions about mean wages for all women? Here the expected wage is 0 for those who are not expected to participate in the labor force, with expected participation determined by the selection equation. These values can be obtained with the `yexpected` option of `predict`. For comparison, a variable can be generated where the wage is set to 0 for nonparticipants.

```
. predict hexpwage, yexpected
. generate wage0 = wage
(657 missing values generated)
. replace wage0 = 0 if wage == .
(657 real changes made)
```

```
. summarize hexpwage wage0
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
    hexpwage |       2000    15.92511    5.979336   2.492469   32.45858
       wage0 |       2000    15.90929    12.27081          0   45.80979
```

Again we note that the predictions from `heckman` are close to the observed mean hourly wage rate for all women. Why aren't the predictions using `ycond` and `yexpected` equal to their observed sample equivalents? For the Heckman model, unlike linear regression, the sample moments implied by the optimal solution to the model likelihood do not require that these predictions match observed data. Properly accounting for the additional variation from the selection equation requires that the model use more information than just the sample moments of the observed wages.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Reference

Heckman, J. 1979. Sample selection bias as a specification error. *Econometrica* 47: 153–161.

Also see

[R] **heckman** — Heckman selection model

[U] **20 Estimation and postestimation commands**

Title

heckprob — Probit model with sample selection

Syntax

```
heckprob depvar indepvars [if] [in] [weight],
    select([depvar_s =] varlist_s [, offset(varname) noconstant]) [options]
```

options	Description
Model	
* `select()`	specify selection equation: dependent and independent variables; whether to have constant term and offset variable
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`first`	report first-step probit estimates
`noskip`	perform likelihood-ratio test
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

* `select()` is required.

The full specification is `select(`[*depvar*$_s$ `=`] *varlist*$_s$ [`, offset(`*varname*`) noconstant`]`)`.

indepvars and *varlist*$_s$ may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *depvar*$_s$, and *varlist*$_s$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()`, `first`, `noskip`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`pweights`, `fweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Sample-selection models > Probit model with selection

Description

`heckprob` fits maximum-likelihood probit models with sample selection.

Options

Model

`select(...)` specifies the variables and options for the selection equation. It is an integral part of specifying a selection model and is required. The selection equation should contain at least one variable that is not in the outcome equation.

If $depvar_s$ is specified, it should be coded as 0 or 1, 0 indicating an observation not selected and 1 indicating a selected observation. If $depvar_s$ is not specified, observations for which *depvar* is not missing are assumed selected, and those for which *depvar* is missing are assumed not selected.

`noconstant`, `offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` specifies that the first-step probit estimates of the selection equation be displayed before estimation.

`noskip` specifies that a full maximum-likelihood model with only a constant for the regression equation be fit. This model is not displayed but is used as the base model to compute a likelihood-ratio test for the model test statistic displayed in the estimation header. By default, the overall model test statistic is an asymptotically equivalent Wald test that all the parameters in the regression equation are zero (except the constant). For many models, this option can substantially increase estimation time.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with heckprob but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

The probit model with sample selection (Van de Ven and Van Pragg 1981) assumes that there exists an underlying relationship

$$y_j^* = \mathbf{x}_j\boldsymbol{\beta} + u_{1j} \qquad \textit{latent equation}$$

such that we observe only the binary outcome

$$y_j^{\text{probit}} = (y_j^* > 0) \qquad \textit{probit equation}$$

The dependent variable, however, is not always observed. Rather, the dependent variable for observation j is observed if

$$y_j^{\text{select}} = (\mathbf{z}_j\boldsymbol{\gamma} + u_{2j} > 0) \qquad \textit{selection equation}$$

where

$$u_1 \sim N(0,1)$$
$$u_2 \sim N(0,1)$$
$$\text{corr}(u_1, u_2) = \rho$$

When $\rho \neq 0$, standard probit techniques applied to the first equation yield biased results. heckprob provides consistent, asymptotically efficient estimates for all the parameters in such models.

For the model to be well identified, the selection equation should have at least one variable that is not in the probit equation. Otherwise, the model is identified only by functional form, and the coefficients have no structural interpretation.

▷ Example 1

We use the data from Pindyck and Rubinfeld (1998). In this dataset, the variables are whether children attend private school (private), number of years the family has been at the present residence (years), log of property tax (logptax), log of income (loginc), and whether one voted for an increase in property taxes (vote).

In this example, we alter the meaning of the data. Here we assume that we observe whether children attend private school only if the family votes for increasing the property taxes. This assumption is not true in the dataset, and we make it only to illustrate the use of this command.

We observe whether children attend private school only if the head of household voted for an increase in property taxes. We assume that the vote is affected by the number of years in residence, the current property taxes paid, and the household income. We wish to model whether children are sent to private school on the basis of the number of years spent in the current residence and the current property taxes paid.

```
. use http://www.stata-press.com/data/r12/school
. heckprob private years logptax, select(vote=years loginc logptax)
Fitting probit model:
Iteration 0:   log likelihood = -17.122381
Iteration 1:   log likelihood = -16.243974
  (output omitted)
Iteration 5:   log likelihood = -15.883655
Fitting selection model:
Iteration 0:   log likelihood = -63.036914
Iteration 1:   log likelihood = -58.534843
Iteration 2:   log likelihood = -58.497292
Iteration 3:   log likelihood = -58.497288
Comparison:    log likelihood = -74.380943
Fitting starting values:
Iteration 0:   log likelihood = -40.895684
Iteration 1:   log likelihood = -16.654497
  (output omitted)
Iteration 6:   log likelihood = -15.753765
Fitting full model:
Iteration 0:   log likelihood = -75.010619  (not concave)
Iteration 1:   log likelihood = -74.287786
Iteration 2:   log likelihood = -74.250137
Iteration 3:   log likelihood = -74.245088
Iteration 4:   log likelihood = -74.244973
Iteration 5:   log likelihood = -74.244973
Probit model with sample selection              Number of obs      =        95
                                                Censored obs       =        36
                                                Uncensored obs     =        59
                                                Wald chi2(2)       =      1.04
Log likelihood = -74.24497                      Prob > chi2        =    0.5935
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
private      |
       years |  -.1142597   .1461717    -0.78   0.434     -.400751    .1722317
     logptax |   .3516098   1.016485     0.35   0.729    -1.640665    2.343884
       _cons |  -2.780665   6.905838    -0.40   0.687    -16.31586    10.75453
-------------+----------------------------------------------------------------
vote         |
       years |  -.0167511   .0147735    -1.13   0.257    -.0457067    .0122045
      loginc |   .9923024   .4430009     2.24   0.025     .1240366    1.860568
     logptax |  -1.278783   .5717545    -2.24   0.025    -2.399401   -.1581647
       _cons |   -.545821   4.070418    -0.13   0.893    -8.523694    7.432052
-------------+----------------------------------------------------------------
     /athrho |  -.8663156   1.450028    -0.60   0.550    -3.708318    1.975687
-------------+----------------------------------------------------------------
         rho |  -.6994973   .7405343                    -.9987984     .962269
------------------------------------------------------------------------------
LR test of indep. eqns. (rho = 0):   chi2(1) =     0.27   Prob > chi2 = 0.6020
```

The output shows several iteration logs. The first iteration log corresponds to running the probit model for those observations in the sample where we have observed the outcome. The second iteration log corresponds to running the selection probit model, which models whether we observe our outcome of interest. If $\rho = 0$, the sum of the log likelihoods from these two models will equal the log likelihood of the probit model with sample selection; this sum is printed in the iteration log as the comparison log likelihood. The third iteration log shows starting values for the iterations.

The final iteration log is for fitting the full probit model with sample selection. A likelihood-ratio test of the log likelihood for this model and the comparison log likelihood is presented at the end of the output. If we had specified the `vce(robust)` option, this test would be presented as a Wald test instead of as a likelihood-ratio test.

◁

▷ Example 2

In example 1, we could have obtained robust standard errors by specifying the `vce(robust)` option. We do this here and also eliminate the iteration logs by using the `nolog` option:

```
. heckprob private years logptax, sel(vote=years loginc logptax) vce(robust) nolog
Probit model with sample selection              Number of obs      =        95
                                                Censored obs       =        36
                                                Uncensored obs     =        59
                                                Wald chi2(2)       =      2.55
Log pseudolikelihood = -74.24497                Prob > chi2        =    0.2798
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
private						
years	-.1142597	.1113977	-1.03	0.305	-.3325951	.1040758
logptax	.3516098	.7358265	0.48	0.633	-1.090584	1.793803
_cons	-2.780665	4.786678	-0.58	0.561	-12.16238	6.601051
vote						
years	-.0167511	.0173344	-0.97	0.334	-.0507259	.0172237
loginc	.9923024	.4228044	2.35	0.019	.1636209	1.820984
logptax	-1.278783	.5095156	-2.51	0.012	-2.277415	-.2801508
_cons	-.545821	4.543892	-0.12	0.904	-9.451686	8.360044
/athrho	-.8663156	1.630643	-0.53	0.595	-4.062318	2.329687
rho	-.6994973	.8327753			-.9994079	.981233

```
Wald test of indep. eqns. (rho = 0): chi2(1) =     0.28   Prob > chi2 = 0.5952
```

Regardless of whether we specify the `vce(robust)` option, the outcome is not significantly different from the outcome obtained by fitting the probit and selection models separately. This result is not surprising because the selection mechanism estimated was invented for the example rather than borne from any economic theory.

◁

Saved results

heckprob saves the following in e():

Scalars

e(N)	number of observations
e(N_cens)	number of censored observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_aux)	number of auxiliary parameters
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(ll_c)	log likelihood, comparison model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(chi2_c)	χ^2 for comparison test
e(p_c)	p-value for comparison test
e(p)	significance of comparison test
e(rho)	ρ
e(rank)	rank of e(V)
e(rank0)	rank of e(V) for constant-only model
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	heckprob
e(cmdline)	command as typed
e(depvar)	names of dependent variables
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset1)	offset for regression equation
e(offset2)	offset for selection equation
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	type of comparison χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`heckprob` is implemented as an ado-file. Van de Ven and Van Pragg (1981) provide an introduction and an explanation of this model.

The probit equation is

$$y_j = (\mathbf{x}_j\boldsymbol{\beta} + u_{1j} > 0)$$

The selection equation is

$$\mathbf{z}_j\boldsymbol{\gamma} + u_{2j} > 0$$

where

$$u_1 \sim N(0,1)$$
$$u_2 \sim N(0,1)$$
$$\text{corr}(u_1, u_2) = \rho$$

The log likelihood is

$$\begin{aligned}\ln L = &\sum_{\substack{j\in S\\ y_j\neq 0}} w_j \ln\left\{\Phi_2\left(x_j\beta + \text{offset}_j^{\beta}, z_j\gamma + \text{offset}_j^{\gamma}, \rho\right)\right\}\\ &+ \sum_{\substack{j\in S\\ y_j=0}} w_j \ln\left\{\Phi_2\left(-x_j\beta + \text{offset}_j^{\beta}, z_j\gamma + \text{offset}_j^{\gamma}, -\rho\right)\right\}\\ &+ \sum_{j\notin S} w_j \ln\left\{1 - \Phi\left(z_j\gamma + \text{offset}_j^{\gamma}\right)\right\}\end{aligned}$$

where S is the set of observations for which y_j is observed, $\Phi_2(\cdot)$ is the cumulative bivariate normal distribution function (with mean $[\,0\ \ 0\,]'$), $\Phi(\cdot)$ is the standard cumulative normal, and w_j is an optional weight for observation j.

In the maximum likelihood estimation, ρ is not directly estimated. Directly estimated is atanh ρ:

$$\text{atanh}\,\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

From the form of the likelihood, it is clear that if $\rho = 0$, the log likelihood for the probit model with sample selection is equal to the sum of the probit model for the outcome y and the selection model. We can perform a likelihood-ratio test by comparing the likelihood of the full model with the sum of the log likelihoods for the probit and selection models.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`heckprob` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **heckprob postestimation** — Postestimation tools for heckprob

[R] **heckman** — Heckman selection model

[R] **probit** — Probit regression

[R] **treatreg** — Treatment-effects model

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

heckprob postestimation — Postestimation tools for heckprob

Description

The following postestimation commands are available after `heckprob`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_sel newvar_athrho} [if] [in], scores
```

statistic	Description
Main	
pmargin	$\Phi(\mathbf{x}_j\mathbf{b})$, success probability; the default
p11	$\Phi_2(\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, \rho)$, predicted probability $\Pr(y_j^{\text{probit}} = 1, y_j^{\text{select}} = 1)$
p10	$\Phi_2(\mathbf{x}_j\mathbf{b}, -\mathbf{z}_j\mathbf{g}, -\rho)$, predicted probability $\Pr(y_j^{\text{probit}} = 1, y_j^{\text{select}} = 0)$
p01	$\Phi_2(-\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, -\rho)$, predicted probability $\Pr(y_j^{\text{probit}} = 0, y_j^{\text{select}} = 1)$
p00	$\Phi_2(-\mathbf{x}_j\mathbf{b}, -\mathbf{z}_j\mathbf{g}, \rho)$, predicted probability $\Pr(y_j^{\text{probit}} = 0, y_j^{\text{select}} = 0)$
psel	$\Phi(\mathbf{z}_j\mathbf{g})$, selection probability
pcond	$\Phi_2(\mathbf{x}_j\mathbf{b}, \mathbf{z}_j\mathbf{g}, \rho)/\Phi(\mathbf{z}_j\mathbf{g})$, probability of success conditional on selection
xb	linear prediction
stdp	standard error of the linear prediction
xbsel	linear prediction for selection equation
stdpsel	standard error of the linear prediction for selection equation

where $\Phi(\cdot)$ is the standard normal distribution function and $\Phi_2(\cdot)$ is the bivariate normal distribution function.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pmargin`, the default, calculates the univariate (marginal) predicted probability of success $\Pr(y_j^{\text{probit}} = 1)$.

`p11` calculates the bivariate predicted probability $\Pr(y_j^{\text{probit}} = 1, y_j^{\text{select}} = 1)$.

`p10` calculates the bivariate predicted probability $\Pr(y_j^{\text{probit}} = 1, y_j^{\text{select}} = 0)$.

`p01` calculates the bivariate predicted probability $\Pr(y_j^{\text{probit}} = 0, y_j^{\text{select}} = 1)$.

`p00` calculates the bivariate predicted probability $\Pr(y_j^{\text{probit}} = 0, y_j^{\text{select}} = 0)$.

`psel` calculates the univariate (marginal) predicted probability of selection $\Pr(y_j^{\text{select}} = 1)$.

`pcond` calculates the conditional (on selection) predicted probability of success $\Pr(y_j^{\text{probit}} = 1, y_j^{\text{select}} = 1)/\Pr(y_j^{\text{select}} = 1)$.

`xb` calculates the probit linear prediction $\mathbf{x}_j\mathbf{b}$.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`xbsel` calculates the linear prediction for the selection equation.

`stdpsel` calculates the standard error of the linear prediction for the selection equation.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `heckprob`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\mathbf{z}_j\boldsymbol{\gamma})$.

The third new variable will contain $\partial \ln L/\partial(\text{atanh}\,\rho)$.

Remarks

▷ Example 1

It is instructive to compare the marginal predicted probabilities with the predicted probabilities that we would obtain by ignoring the selection mechanism. To compare the two approaches, we will synthesize data so that we know the "true" predicted probabilities.

First, we need to generate correlated error terms, which we can do using a standard Cholesky decomposition approach. For our example, we will clear any data from memory and then generate errors that have a correlation of 0.5 by using the following commands. We set the seed so that interested readers can type in these same commands and obtain the same results.

```
. set seed 12309
. set obs 5000
obs was 0, now 5000
. gen c1 = rnormal()
. gen c2 = rnormal()
. matrix P = (1,.5\.5,1)
. matrix A = cholesky(P)
. local fac1 = A[2,1]
. local fac2 = A[2,2]
. gen u1 = c1
. gen u2 = `fac1'*c1 + `fac2'*c2
```

We can check that the errors have the correct correlation by using the `correlate` command. We will also normalize the errors so that they have a standard deviation of one, so we can generate a bivariate probit model with known coefficients. We do that with the following commands:

```
. correlate u1 u2
(obs=5000)
             |       u1       u2
-------------+------------------
          u1 |   1.0000
          u2 |   0.5020   1.0000

. summarize u1
  (output omitted)
. replace u1 = u1/r(sd)
(5000 real changes made)
. summarize u2
  (output omitted)
. replace u2 = u2/r(sd)
(5000 real changes made)
. drop c1 c2
. gen x1 = runiform()-.5
. gen x2 = runiform()+1/3
. gen y1s = 0.5 + 4*x1 + u1
. gen y2s = 3 - 3*x2 + .5*x1 + u2
. gen y1 = (y1s>0)
. gen y2 = (y2s>0)
```

We have now created two dependent variables, `y1` and `y2`, which are defined by our specified coefficients. We also included error terms for each equation, and the error terms are correlated. We run `heckprob` to verify that the data have been correctly generated according to the model

$$y_1 = .5 + 4x_1 + u_1$$
$$y_2 = 3 + .5x_1 - 3x_2 + u_2$$

where we assume that y_1 is observed only if $y_2 = 1$.

```
. heckprob y1 x1, sel(y2 = x1 x2) nolog
Probit model with sample selection              Number of obs      =      5000
                                                Censored obs       =      1762
                                                Uncensored obs     =      3238

                                                Wald chi2(1)       =    953.71
Log likelihood =   -3679.5                      Prob > chi2        =    0.0000

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
y1           |
          x1 |   3.784705   .1225532    30.88   0.000     3.544505    4.024905
       _cons |   .4630922   .0453952    10.20   0.000     .3741192    .5520653
-------------+----------------------------------------------------------------
y2           |
          x1 |   .3693052   .0721694     5.12   0.000     .2278558    .5107547
          x2 |  -3.05069    .0832424   -36.65   0.000    -3.213842   -2.887538
       _cons |   3.037696   .0777733    39.06   0.000     2.885263    3.190128
-------------+----------------------------------------------------------------
     /athrho |   .5186232    .083546     6.21   0.000      .354876    .6823705
-------------+----------------------------------------------------------------
         rho |   .4766367   .0645658                      .3406927    .5930583
------------------------------------------------------------------------------
LR test of indep. eqns. (rho = 0):   chi2(1) =    40.43   Prob > chi2 = 0.0000
```

Now that we have verified that we have generated data according to a known model, we can obtain and then compare predicted probabilities from the probit model with sample selection and a (usual) probit model.

```
. predict pmarg
(option pmargin assumed; Pr(y1=1))
. probit y1 x1 if y2==1
  (output omitted)
. predict phat
(option pr assumed; Pr(y1))
```

Using the (marginal) predicted probabilities from the probit model with sample selection (`pmarg`) and the predicted probabilities from the (usual) probit model (`phat`), we can also generate the "true" predicted probabilities from the synthesized `y1s` variable and then compare the predicted probabilities:

```
. gen ptrue = normal(y1s)
. summarize pmarg ptrue phat
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       pmarg |       5000    .6071226    .3147861   .0766334   .9907113
       ptrue |       5000    .5974195     .348396   5.53e-06   .9999999
        phat |       5000    .6568175    .3025085   .1059824   .9954919
```

Here we see that ignoring the selection mechanism (comparing the `phat` variable with the true `ptrue` variable) results in predicted probabilities that are much higher than the true values. Looking at the marginal predicted probabilities from the model with sample selection, however, results in more accurate predictions.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **heckprob** — Probit model with sample selection

[U] **20 Estimation and postestimation commands**

Title

help — Display online help

Syntax

Display help information in Viewer

help [*command_or_topic_name*] [, nonew name(*viewername*) marker(*markername*)]

Display help information in Results window

chelp [*command_or_topic_name*]

Menu

Help > Stata Command...

Description

The help command displays help information about the specified command or topic.

Stata for Mac, Stata for Unix(GUI), and Stata for Windows:
help launches a new Viewer to display help for the specified command or topic. If help is not followed by a command or a topic name, Stata launches the Viewer and displays help contents, the table of contents for the online help.

Help may be accessed either by selecting **Help > Stata Command...** and filling in the desired command name or by typing help followed by a command or topic name.

chelp will display help in the Results window.

Stata for Unix(console):
Typing help followed by a command name or a topic name will display help on the console.

If help is not followed by a command or a topic name, a description of how to use the help system is displayed.

Stata for Unix(both GUI and console):
man is a synonym for chelp.

Options

nonew specifies that a new Viewer window not be opened for the help topic if a Viewer window is already open. The default is for a new Viewer window to be opened each time help is typed so that multiple help files may be viewed at once. nonew causes the help file to be displayed in the topmost open Viewer.

name(*viewername*) specifies that help be displayed in a Viewer window named *viewername*. If the named window already exists, its contents will be replaced. If the named window does not exist, it will be created.

`marker(`*markername*`)` specifies that the help file be opened to the position of *markername* within the help file.

Remarks

To obtain help for any Stata command, type `help` *command* or select **Help > Stata Command...** and fill in *command*.

`help` is best explained by examples.

To obtain help for . . .	type
`regress`	`help regress`
postestimation tools for `regress`	`help regress postestimation` or `help regress post`
graph option `xlabel()`	`help graph xlabel()`
Stata function `strpos()`	`help strpos()`
Mata function `optimize()`	`help mata optimize()`

Tips:

- `help` displays a subject table of contents for the online help.
- `help guide` displays a table of contents for basic Stata concepts.
- `help estimation commands` displays an alphabetical listing of all Stata estimation commands.
- `help functions` displays help on Stata functions by category.
- `help mata functions` displays a subject table of contents for Mata's functions.
- `help ts glossary` displays the glossary for the time-series manual, and similarly for the other Stata specialty manuals.

See [U] **4 Stata's help and search facilities** for a complete description of how to use `help`.

❑ Technical note

When you type `help` *topic*, Stata first looks along the adopath for *topic*`.sthlp`; see [U] **17.5 Where does Stata look for ado-files?**. ❑

Also see

[R] **hsearch** — Search help files

[R] **search** — Search Stata documentation

[R] **net search** — Search the Internet for installable packages

[GSM] **4 Getting help**

[GSW] **4 Getting help**

[GSU] **4 Getting help**

[U] **4 Stata's help and search facilities**

Title

hetprob — Heteroskedastic probit model

Syntax

```
hetprob depvar [indepvars] [if] [in] [weight] ,
    het(varlist[ , offset(varname)]) [options]
```

options	Description
Model	
*`het(varlist[...])`	independent variables to model the variance and possible offset variable
`noconstant`	suppress constant term
`offset(varname)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables
`constraints(constraints)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(vcetype)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noskip`	perform likelihood-ratio test
`nolrtest`	perform Wald test on variance
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

*`het()` is required. The full specification is `het(`*varlist*` [ , offset(`*varname*`) ])`.

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()`, `noskip`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Binary outcomes > Heteroskedastic probit regression

Description

`hetprob` fits a maximum-likelihood heteroskedastic probit model.

See [R] **logistic** for a list of related estimation commands.

Options

Model

`het(`*varlist* [`, offset(`*varname*`)`]`)` specifies the independent variables and the offset variable, if there is one, in the variance function. `het()` is required.

`noconstant`, `offset(`*varname*`)`; see [R] **estimation options**.

`asis` forces the retention of perfect predictor variables and their associated perfectly predicted observations and may produce instabilities in maximization; see [R] **probit**.

`constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`noskip` requests fitting of the constant-only model and calculation of the corresponding likelihood-ratio χ^2 statistic for testing significance of the full model. By default, a Wald χ^2 statistic is computed for testing the significance of the full model.

`nolrtest` specifies that a Wald test of whether `lnsigma2` $= 0$ be performed instead of the LR test.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, [`no`]`log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `hetprob` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Robust standard errors

Introduction

`hetprob` fits a maximum-likelihood heteroskedastic probit model, which is a generalization of the probit model. Let $y_j, j = 1, \ldots, N$, be a binary outcome variable taking on the value 0 (failure) or 1 (success). In the probit model, the probability that y_j takes on the value 1 is modeled as a nonlinear function of a linear combination of the k independent variables $\mathbf{x}_j = (x_{1j}, x_{2j}, \ldots, x_{kj})$,

$$\Pr(y_j = 1) = \Phi(\mathbf{x}_j\mathbf{b})$$

in which $\Phi()$ is the cumulative distribution function (CDF) of a standard normal random variable, that is, a normally distributed (Gaussian) random variable with mean 0 and variance 1. The linear combination of the independent variables, $\mathbf{x}_j\mathbf{b}$, is commonly called the *index function*, or *index*. Heteroskedastic probit generalizes the probit model by generalizing $\Phi()$ to a normal CDF with a variance that is no longer fixed at 1 but can vary as a function of the independent variables. `hetprob` models the variance as a multiplicative function of these m variables $\mathbf{z}_j = (z_{1j}, z_{2j}, \ldots, z_{mj})$, following Harvey (1976):

$$\sigma_j^2 = \{\exp(\mathbf{z}_j\boldsymbol{\gamma})\}^2$$

Thus the probability of success as a function of all the independent variables is

$$\Pr(y_j = 1) = \Phi\Big\{\mathbf{x}_j\mathbf{b}/\exp(\mathbf{z}_j\boldsymbol{\gamma})\Big\}$$

From this expression, it is clear that, unlike the index $\mathbf{x}_j\mathbf{b}$, no constant term can be present in $\mathbf{z}_j\boldsymbol{\gamma}$ if the model is to be identifiable.

Suppose that the binary outcomes y_j are generated by thresholding an unobserved random variable, w, which is normally distributed with mean $\mathbf{x}_j\mathbf{b}$ and variance 1 such that

$$y_j = \begin{cases} 1 & \text{if } w_j > 0 \\ 0 & \text{if } w_j \leq 0 \end{cases}$$

This process gives the probit model:

$$\Pr(y_j = 1) = \Pr(w_j > 0) = \Phi(\mathbf{x}_j\mathbf{b})$$

Now suppose that the unobserved w_j are heteroskedastic with variance

$$\sigma_j^2 = \{\exp(\mathbf{z}_j\boldsymbol{\gamma})\}^2$$

Relaxing the homoskedastic assumption of the probit model in this manner yields our multiplicative heteroskedastic probit model:

$$\Pr(y_j = 1) = \Phi\Big\{\mathbf{x}_j\mathbf{b}/\exp(\mathbf{z}_j\boldsymbol{\gamma})\Big\}$$

Example 1

For this example, we generate simulated data for a simple heteroskedastic probit model and then estimate the coefficients with `hetprob`:

```
. set obs 1000
obs was 0, now 1000
. set seed 1234567
. gen x = 1-2*runiform()
. gen xhet = runiform()
. gen sigma = exp(1.5*xhet)
. gen p = normal((0.3+2*x)/sigma)
. gen y = cond(runiform()<=p,1,0)
. hetprob y x, het(xhet)
Fitting probit model:
Iteration 0:   log likelihood = -688.53208
Iteration 1:   log likelihood = -591.59895
Iteration 2:   log likelihood = -591.50674
Iteration 3:   log likelihood = -591.50674
Fitting full model:
Iteration 0:   log likelihood = -591.50674
Iteration 1:   log likelihood = -572.12219
Iteration 2:   log likelihood =  -570.7742
Iteration 3:   log likelihood = -569.48921
Iteration 4:   log likelihood = -569.47828
Iteration 5:   log likelihood = -569.47827
Heteroskedastic probit model                    Number of obs     =       1000
                                                Zero outcomes     =        452
                                                Nonzero outcomes  =        548
                                                Wald chi2(1)      =      78.66
Log likelihood = -569.4783                      Prob > chi2       =     0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
y						
x	2.228031	.2512073	8.87	0.000	1.735673	2.720388
_cons	.2493822	.0862833	2.89	0.004	.08027	.4184943
lnsigma2						
xhet	1.602537	.2640131	6.07	0.000	1.085081	2.119993

```
Likelihood-ratio test of lnsigma2=0: chi2(1) =    44.06   Prob > chi2 = 0.0000
```

Above we created two variables, `x` and `xhet`, and then simulated the model

$$\Pr(\mathtt{y}=1) = F\left\{(\beta_0+\beta_1\mathtt{x})/\exp(\gamma_1\mathtt{xhet})\right\}$$

for $\beta_0 = 0.3$, $\beta_1 = 2$, and $\gamma_1 = 1.5$. According to `hetprob`'s output, all coefficients are significant, and, as we would expect, the Wald test of the full model versus the constant-only model—for example, the index consisting of $\beta_0+\beta_1\mathtt{x}$ versus that of just β_0—is significant with $\chi^2(1) = 79$. Likewise, the likelihood-ratio test of heteroskedasticity, which tests the full model with heteroskedasticity against the full model without, is significant with $\chi^2(1) = 44$. See [R] **maximize** for more explanation of the output. For this simple model, `hetprob` took five iterations to converge. As stated elsewhere (Greene 2012, 714), this is a difficult model to fit, and it is not uncommon for it to require many iterations or for the optimizer to print out warnings and informative messages during the optimization. Slow convergence is especially common for models in which one or more of the independent variables appear in both the index and variance functions. ◁

❑ Technical note

Stata interprets a value of 0 as a negative outcome (failure) and treats all other values (except missing) as positive outcomes (successes). Thus if your dependent variable takes on the values 0 and 1, then 0 is interpreted as failure and 1 as success. If your dependent variable takes on the values 0, 1, and 2, then 0 is still interpreted as failure, but both 1 and 2 are treated as successes.

❑

Robust standard errors

If you specify the `vce(robust)` option, `hetprob` reports robust standard errors as described in [U] **20.20 Obtaining robust variance estimates**. To illustrate the effect of this option, we will reestimate our coefficients by using the same model and data in our example, this time adding `vce(robust)` to our `hetprob` command.

▷ Example 2

```
. hetprob y x, het(xhet) vce(robust) nolog
Heteroskedastic probit model                      Number of obs     =       1000
                                                  Zero outcomes     =        452
                                                  Nonzero outcomes  =        548
                                                  Wald chi2(1)      =      65.23
Log pseudolikelihood = -569.4783                  Prob > chi2       =     0.0000
```

y	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
y						
x	2.22803	.2758597	8.08	0.000	1.687355	2.768705
_cons	.2493821	.0843367	2.96	0.003	.0840853	.4146789
lnsigma2						
xhet	1.602537	.2671326	6.00	0.000	1.078967	2.126107

```
Wald test of lnsigma2=0:              chi2(1) =    35.99   Prob > chi2 = 0.0000
```

The `vce(robust)` standard errors for two of the three parameters are larger than the previously reported conventional standard errors. This is to be expected, even though (by construction) we have perfect model specification because this option trades off efficient estimation of the coefficient variance–covariance matrix for robustness against misspecification.

◁

Specifying the `vce(cluster` *clustvar*`)` option relaxes the usual assumption of independence between observations to the weaker assumption of independence just between clusters; that is, `hetprob, vce(cluster` *clustvar*`)` is robust with respect to within-cluster correlation. This option is less efficient than the `xtgee` population-averaged models because `hetprob` inefficiently sums within cluster for the standard-error calculation rather than attempting to exploit what might be assumed about the within-cluster correlation.

Saved results

hetprob saves the following in e():

Scalars

e(N)	number of observations
e(N_f)	number of zero outcomes
e(N_s)	number of nonzero outcomes
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(ll_c)	log likelihood, comparison model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(chi2_c)	χ^2 for heteroskedasticity LR test
e(p_c)	p-value for heteroskedasticity LR test
e(df_m_c)	degrees of freedom for heteroskedasticity LR test
e(p)	significance
e(rank)	rank of e(V)
e(rank0)	rank of e(V) for constant-only model
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	hetprob
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset1)	offset for probit equation
e(offset2)	offset for variance equation
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(method)	requested estimation method
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`hetprob` is implemented as an ado-file.

The heteroskedastic probit model is a generalization of the probit model because it allows the scale of the inverse link function to vary from observation to observation as a function of the independent variables.

The log-likelihood function for the heteroskedastic probit model is

$$\ln L = \sum_{j \in S} w_j \ln \Phi\{\mathbf{x}_j\boldsymbol{\beta}/\exp(\mathbf{z}\boldsymbol{\gamma})\} + \sum_{j \notin S} w_j \ln\left[1 - \Phi\{\mathbf{x}_j\boldsymbol{\beta}/\exp(\mathbf{z}\boldsymbol{\gamma})\}\right]$$

where S is the set of all observations j such that $y_j \neq 0$ and w_j denotes the optional weights. $\ln L$ is maximized as described in [R] **maximize**.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`hetprob` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

Harvey, A. C. 1976. Estimating regression models with multiplicative heteroscedasticity. *Econometrica* 44: 461–465.

Also see

[R] **hetprob postestimation** — Postestimation tools for hetprob

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **probit** — Probit regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtprobit** — Random-effects and population-averaged probit models

[U] **20 Estimation and postestimation commands**

Title

hetprob postestimation — Postestimation tools for hetprob

Description

The following postestimation commands are available after `hetprob`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat (svy)`.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic* `nooffset`]

`predict` [*type*] { *stub*`*` | *newvar*$_{\text{reg}}$ *newvar*$_{\text{lnsigma2}}$ } [*if*] [*in*] `,` `scores`

statistic	Description
Main	
`pr`	probability of a positive outcome; the default
`xb`	linear prediction
`sigma`	standard deviation of the error term

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of a positive outcome.

`xb` calculates the linear prediction.

`sigma` calculates the standard deviation of the error term.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `hetprob`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\mathbf{z}_j\boldsymbol{\gamma})$.

Remarks

Once you have fit a model, you can use the `predict` command to obtain the predicted probabilities for both the estimation sample and other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**. `predict` without arguments calculates the predicted probability of a positive outcome. With the `xb` option, `predict` calculates the index function combination, $\mathbf{x}_j\mathbf{b}$, where $\mathbf{x}_j$ are the independent variables in the jth observation and $\mathbf{b}$ is the estimated parameter vector. With the `sigma` option, `predict` calculates the predicted standard deviation, $\sigma_j = \exp(\mathbf{z}_j\boldsymbol{\gamma})$.

▷ Example 1

We use `predict` to compute the predicted probabilities and standard deviations based on the model in example 2 in [R] **hetprob** to compare these with the actual values:

```
. predict phat
(option pr assumed; Pr(y))
. gen diff_p = phat - p
. summarize diff_p
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
      diff_p |      1000   -.0107081    .0131869  -.0466331    .010482
. predict sigmahat, sigma
. gen diff_s = sigmahat - sigma
. summarize diff_s
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
      diff_s |      1000    .1558881    .1363698   .0000417   .4819107
```

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **hetprob** — Heteroskedastic probit model

[U] **20 Estimation and postestimation commands**

Title

histogram — Histograms for continuous and categorical variables

Syntax

`histogram` *varname* [*if*] [*in*] [*weight*] [, [*continuous_opts* | *discrete_opts*] *options*]

continuous_opts	Description
Main	
`bin(#)`	set number of bins to #
`width(#)`	set width of bins to #
`start(#)`	set lower limit of first bin to #

discrete_opts	Description
Main	
`discrete`	specify that data are discrete
`width(#)`	set width of bins to #
`start(#)`	set theoretical minimum value to #

options	Description
Main	
`density`	draw as density; the default
`fraction`	draw as fractions
`frequency`	draw as frequencies
`percent`	draw as percentages
bar_options	rendition of bars
`addlabels`	add height labels to bars
`addlabopts(`*marker_label_options*`)`	affect rendition of labels
Density plots	
`normal`	add a normal density to the graph
`normopts(`*line_options*`)`	affect rendition of normal density
`kdensity`	add a kernel density estimate to the graph
`kdenopts(`*kdensity_options*`)`	affect rendition of kernel density
Add plots	
`addplot(`*plot*`)`	add other plots to the histogram
Y axis, X axis, Titles, Legend, Overall, By	
twoway_options	any options documented in [G-3] ***twoway_options***

`fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Graphics > Histogram

Description

`histogram` draws histograms of *varname*, which is assumed to be the name of a continuous variable unless the `discrete` option is specified.

Options for use in the continuous case

Main

`bin(#)` and `width(#)` are alternatives. They specify how the data are to be aggregated into bins: `bin()` by specifying the number of bins (from which the width can be derived) and `width()` by specifying the bin width (from which the number of bins can be derived).

If neither option is specified, results are the same as if `bin(`*k*`)` had been specified, where

$$k = \min\left\{\text{sqrt}(N), 10\ln(N)/\ln(10)\right\}$$

and where N is the (weighted) number of observations.

`start(#)` specifies the theoretical minimum of *varname*. The default is `start(`*m*`)`, where *m* is the observed minimum value of *varname*.

Specify `start()` when you are concerned about sparse data, for instance, if you know that *varname* can have a value of 0, but you are concerned that 0 may not be observed.

`start(#)`, if specified, must be less than or equal to *m*, or else an error will be issued.

Options for use in the discrete case

Main

`discrete` specifies that *varname* is discrete and that you want each unique value of *varname* to have its own bin (bar of histogram).

`width(#)` is rarely specified in the discrete case; it specifies the width of the bins. The default is `width(`*d*`)`, where *d* is the observed minimum difference between the unique values of *varname*.

Specify `width()` if you are concerned that your data are sparse. For example, in theory *varname* could take on the values, say, 1, 2, 3, ..., 9, but because of the sparseness, perhaps only the values 2, 4, 7, and 8 are observed. Here the default width calculation would produce `width(2)`, and you would want to specify `width(1)`.

`start(#)` is also rarely specified in the discrete case; it specifies the theoretical minimum value of *varname*. The default is `start(`*m*`)`, where *m* is the observed minimum value.

As with `width()`, specify `start(#)` if you are concerned that your data are sparse. In the previous example, you might also want to specify `start(1)`. `start()` does nothing more than add white space to the left side of the graph.

The value of # in `start()` must be less than or equal to *m*, or an error will be issued.

Options for use in both the continuous and discrete cases

Main

`density`, `fraction`, `frequency`, and `percent` specify whether you want the histogram scaled to density units, fractional units, frequencies, or percentages. `density` is the default.

`density` scales the height of the bars so that the sum of their areas equals 1.

`fraction` scales the height of the bars so that the sum of their heights equals 1.

`frequency` scales the height of the bars so that each bar's height is equal to the number of observations in the category. Thus the sum of the heights is equal to the total number of observations.

`percent` scales the height of the bars so that the sum of their heights equals 100.

bar_options are any of the options allowed by `graph twoway bar`; see [G-2] **graph twoway bar**.

One of the most useful *bar_options* is `barwidth(#)`, which specifies the width of the bars in *varname* units. By default, `histogram` draws the bars so that adjacent bars just touch. If you want gaps between the bars, do not specify `histogram`'s `width()` option—which would change how the histogram is calculated—but specify the *bar_option* `barwidth()` or the `histogram` option `gap`, both of which affect only how the bar is rendered.

The *bar_option* `horizontal` cannot be used with the `addlabels` option.

`addlabels` specifies that the top of each bar be labeled with the density, fraction, or frequency, as determined by the `density`, `fraction`, and `frequency` options.

`addlabopts(`*marker_label_options*`)` specifies how to render the labels atop the bars. See [G-3] ***marker_label_options***. Do not specify the *marker_label_option* `mlabel(`*varname*`)`, which specifies the variable to be used; this is specified for you by `histogram`.

`addlabopts()` will accept more options than those documented in [G-3] ***marker_label_options***. All options allowed by `twoway scatter` are also allowed by `addlabopts()`; see [G-2] **graph twoway scatter**. One particularly useful option is `yvarformat()`; see [G-3] ***advanced_options***.

Density plots

`normal` specifies that the histogram be overlaid with an appropriately scaled normal density. The normal will have the same mean and standard deviation as the data.

`normopts(`*line_options*`)` specifies details about the rendition of the normal curve, such as the color and style of line used. See [G-2] **graph twoway line**.

`kdensity` specifies that the histogram be overlaid with an appropriately scaled kernel density estimate of the density. By default, the estimate will be produced using the Epanechnikov kernel with an "optimal" half-width. This default corresponds to the default of `kdensity`; see [R] **kdensity**. How the estimate is produced can be controlled using the `kdenopts()` option described below.

`kdenopts(`*kdensity_options*`)` specifies details about how the kernel density estimate is to be produced along with details about the rendition of the resulting curve, such as the color and style of line used. The kernel density estimate is described in [G-2] **graph twoway kdensity**. As an example, if you wanted to produce kernel density estimates by using the Gaussian kernel with optimal half-width, you would specify `kdenopts(gauss)` and if you also wanted a half-width of 5, you would specify `kdenopts(gauss width(5))`.

Add plots

`addplot(`*plot*`)` allows adding more `graph twoway` plots to the graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall, By

twoway_options are any of the options documented in [G-3] ***twoway_options***. This includes, most importantly, options for titling the graph (see [G-3] ***title_options***), options for saving the graph to disk (see [G-3] ***saving_option***), and the `by()` option, which will allow you to simultaneously graph histograms for different subsets of the data (see [G-3] ***by_option***).

Remarks

Remarks are presented under the following headings:

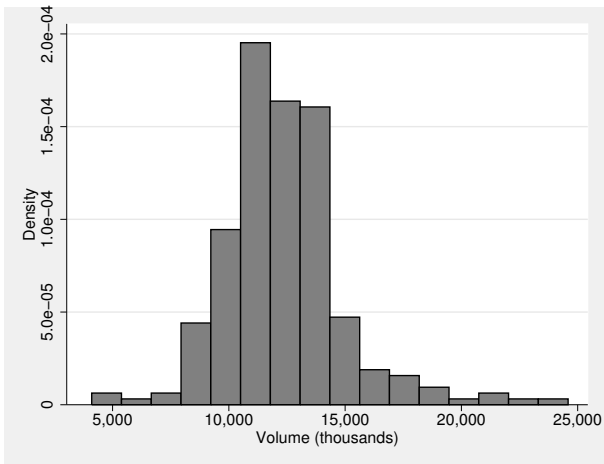
Histograms of continuous variables
Overlaying normal and kernel density estimates
Histograms of discrete variables
Use with by()

For an example of editing a histogram with the Graph Editor, see Pollock (2011, 29–31).

Histograms of continuous variables

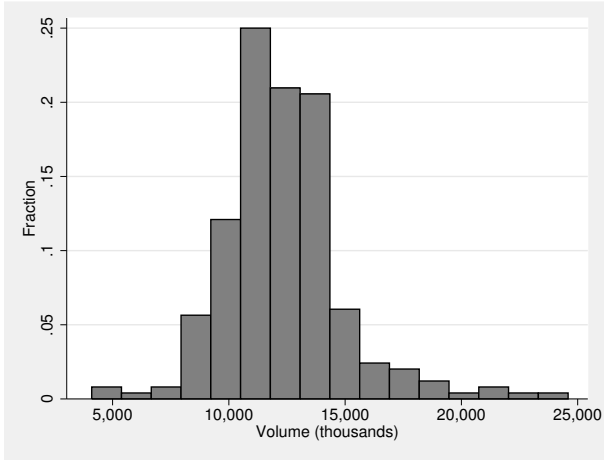
`histogram` assumes that the variable is continuous, so you need type only `histogram` followed by the variable name:

```
. use http://www.stata-press.com/data/r12/sp500
(S&P 500)
. histogram volume
(bin=15, start=4103, width=1280.3533)
```



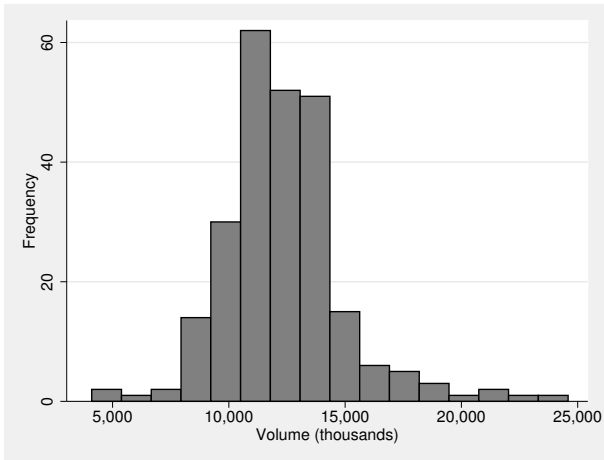
The small values reported for density on the y axis are correct; if you added up the area of the bars, you would get 1. Nevertheless, many people are used to seeing histograms scaled so that the bar heights sum to 1,

```
. histogram volume, fraction
(bin=15, start=4103, width=1280.3533)
```



and others are used to seeing histograms so that the bar height reflects the number of observations,

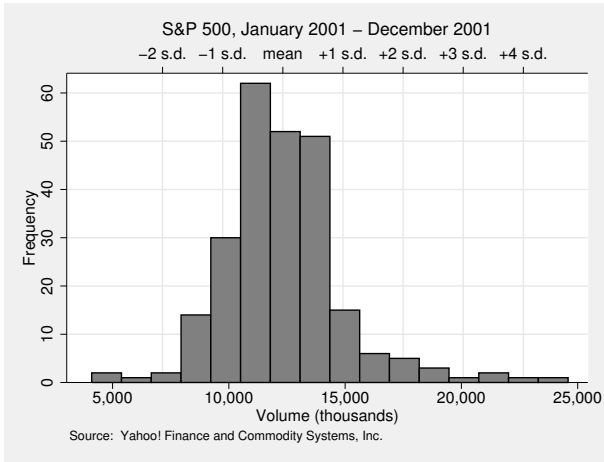
```
. histogram volume, frequency
(bin=15, start=4103, width=1280.3533)
```



Regardless of the scale you prefer, you can specify other options to make the graph look more impressive:

```
. summarize volume
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      volume |        248    12320.68    2585.929      4103    23308.3

. histogram volume, freq
>         xaxis(1 2)
>         ylabel(0(10)60, grid)
>         xlabel(12321 "mean"
>                9735 "-1 s.d."
>               14907 "+1 s.d."
>                7149 "-2 s.d."
>               17493 "+2 s.d."
>               20078 "+3 s.d."
>               22664 "+4 s.d."
>                                , axis(2) grid gmax)
>         xtitle("", axis(2))
>         subtitle("S&P 500, January 2001 - December 2001")
>         note("Source:  Yahoo! Finance and Commodity Systems, Inc.")
(bin=15, start=4103, width=1280.3533)
```



For an explanation of the `xaxis()` option—it created the upper and lower x axis—see [G-3] ***axis_choice_options***. For an explanation of the `ylabel()` and `xlabel()` options, see [G-3] ***axis_label_options***. For an explanation of the `subtitle()` and `note()` options, see [G-3] ***title_options***.

Overlaying normal and kernel density estimates

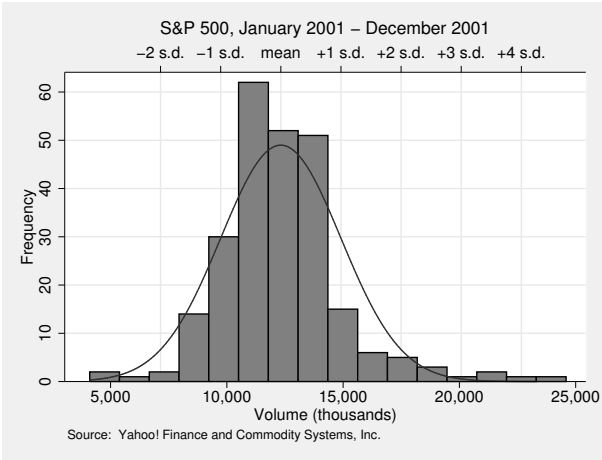
Specifying `normal` will overlay a normal density over the histogram. It would be enough to type

```
. histogram volume, normal
```

but we will add the option to our more impressive rendition:

```
. summarize volume
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      volume |        248    12320.68    2585.929      4103    23308.3
```

```
. histogram volume, freq normal
>         xaxis(1 2)
>         ylabel(0(10)60, grid)
>         xlabel(12321 "mean"
>                9735 "-1 s.d."
>               14907 "+1 s.d."
>                7149 "-2 s.d."
>               17493 "+2 s.d."
>               20078 "+3 s.d."
>               22664 "+4 s.d."
>                                , axis(2) grid gmax)
>         xtitle("", axis(2))
>         subtitle("S&P 500, January 2001 - December 2001")
>         note("Source:  Yahoo! Finance and Commodity Systems, Inc.")
(bin=15, start=4103, width=1280.3533)
```



If we instead wanted to overlay a kernel density estimate, we could specify `kdensity` in place of `normal`.

Histograms of discrete variables

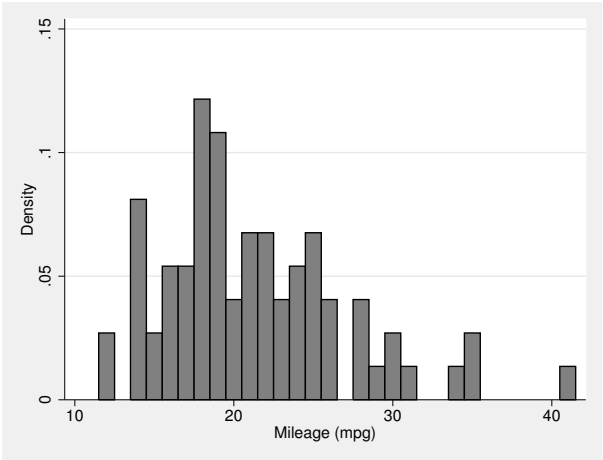
Specify `histogram`'s discrete option when you wish to treat the data as discrete—when you wish each unique value of the variable to be assigned its own bin. For instance, in the automobile data, `mpg` is a continuous variable, but the mileage ratings have been measured to integer precision. If we were to type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. histogram mpg
(bin=8, start=12, width=3.625)
```

`mpg` would be treated as continuous and categorized into eight bins by the default number-of-bins calculation, which is based on the number of observations, 74.

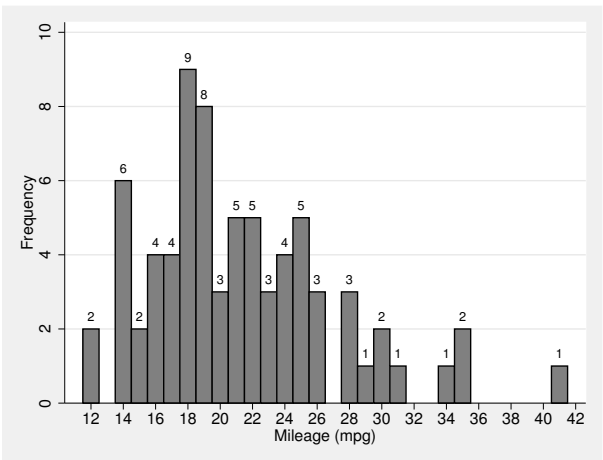
Adding the `discrete` option makes a histogram with a bin for each of the 21 unique values.

```
. histogram mpg, discrete
(start=12, width=1)
```



Just as in the continuous case, the y axis was reported in density, and we could specify the `fraction` or `frequency` options if we wanted it to be reported differently. Below we specify `frequency`, we specify `addlabels` to add a report of frequencies printed above the bars, we specify `ylabel(,grid)` to add horizontal grid lines, and we specify `xlabel(12(2)42)` to label the values 12, 14, ..., 42 on the x axis:

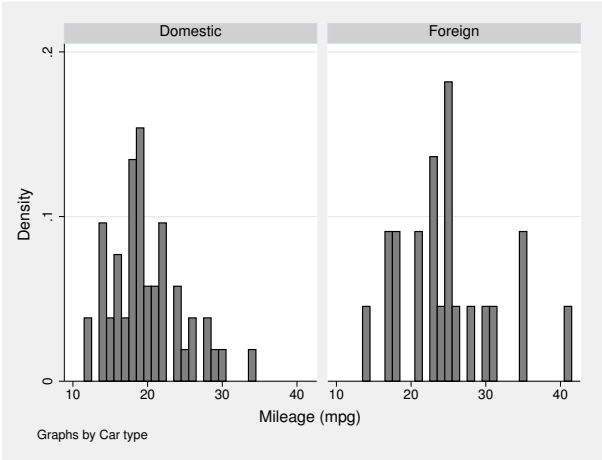
```
. histogram mpg, discrete freq addlabels ylabel(,grid) xlabel(12(2)42)
(start=12, width=1)
```



Use with by()

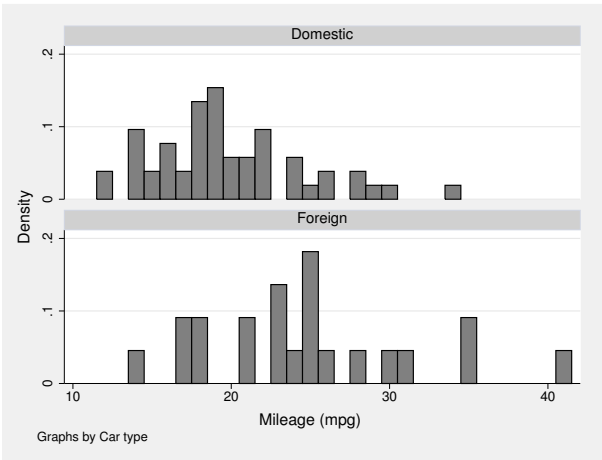
`histogram` may be used with `graph twoway`'s `by()`; for example,

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. histogram mpg, discrete by(foreign)
```



Here results would be easier to compare if the graphs were presented in one column:

```
. histogram mpg, discrete by(foreign, col(1))
```



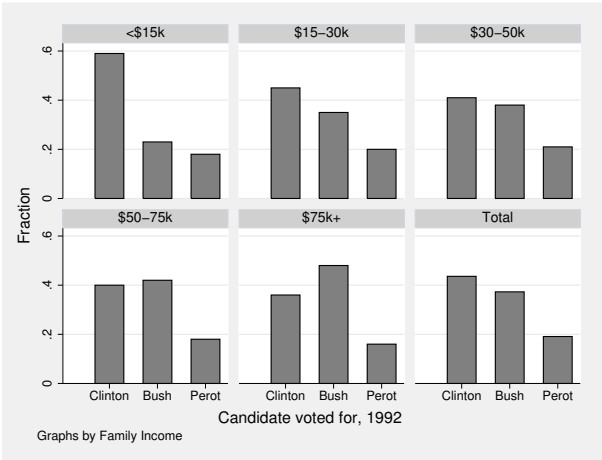
`col(1)` is a `by()` suboption—see [G-3] ***by_option***—and there are other useful suboptions, such as `total`, which will add an overall total histogram. `total` is a suboption of `by()`, not an option of `histogram`, so you would type

```
. histogram mpg, discrete by(foreign, total)
```

and not `histogram mpg, discrete by(foreign) total`.

As another example, Lipset (1993) reprinted data from the *New York Times* (November 5, 1992) collected by the Voter Research and Surveys based on questionnaires completed by 15,490 U.S. presidential voters from 300 polling places on election day in 1992.

```
. use http://www.stata-press.com/data/r12/voter
. histogram candi [freq=pop], discrete fraction by(inc, total)
> gap(40) xlabel(2 3 4, valuelabel)
```



We specified `gap(40)` to reduce the width of the bars by 40%. We also used `xlabel()`'s `valuelabel` suboption, which caused our bars to be labeled "Clinton", "Bush", and "Perot", rather than 2, 3, and 4; see [G-3] ***axis_label_options***.

Methods and formulas

`histogram` is implemented as an ado-file.

References

Cox, N. J. 2004. Speaking Stata: Graphing distributions. *Stata Journal* 4: 66–88.

——. 2005. Speaking Stata: Density probability plots. *Stata Journal* 5: 259–273.

Harrison, D. A. 2005. Stata tip 20: Generating histogram bin variables. *Stata Journal* 5: 280–281.

Lipset, S. M. 1993. The significance of the 1992 election. *PS: Political Science and Politics* 26: 7–16.

Pollock, P. H., III. 2011. *A Stata Companion to Political Analysis*. 2nd ed. Washington, DC: CQ Press.

Also see

[R] **kdensity** — Univariate kernel density estimation

[R] **spikeplot** — Spike plots and rootograms

[G-2] **graph twoway histogram** — Histogram plots

Title

hsearch — Search help files

Syntax

`hsearch` *word*(*s*)

`hsearch` *word*(*s*)`, build`

`hsearch, build`

Description

`hsearch` *word*(*s*) searches the help files for *word*(*s*) and presents a clickable list in the Viewer.

`hsearch` *word*(*s*)`, build` does the same thing but builds a new index first.

`hsearch, build` rebuilds the index but performs no search.

Option

`build` forces the index that `hsearch` uses to be built or rebuilt.

The index is automatically built the first time you use `hsearch`, and it is automatically rebuilt if you have recently installed an ado-file update by using `update`; see [R] **update**. Thus the `build` option is rarely specified.

You should specify `build` if you have recently installed user-written ado-files by using `net install` (see [R] **net**) or `ssc` (see [R] **ssc**), or if you have recently updated any of your own help files.

Remarks

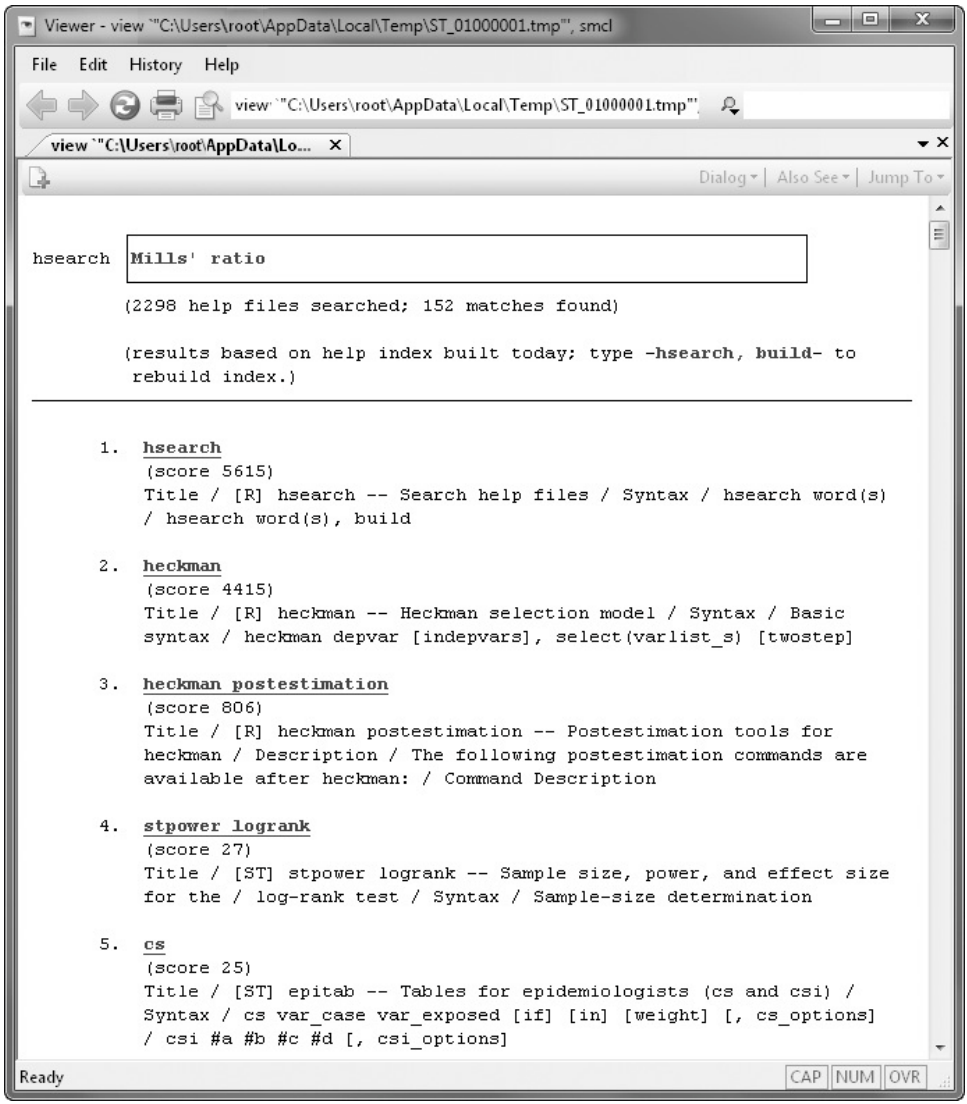
Remarks are presented under the following headings:

Using hsearch
Alternatives to hsearch
Recommendations
How hsearch works

Using hsearch

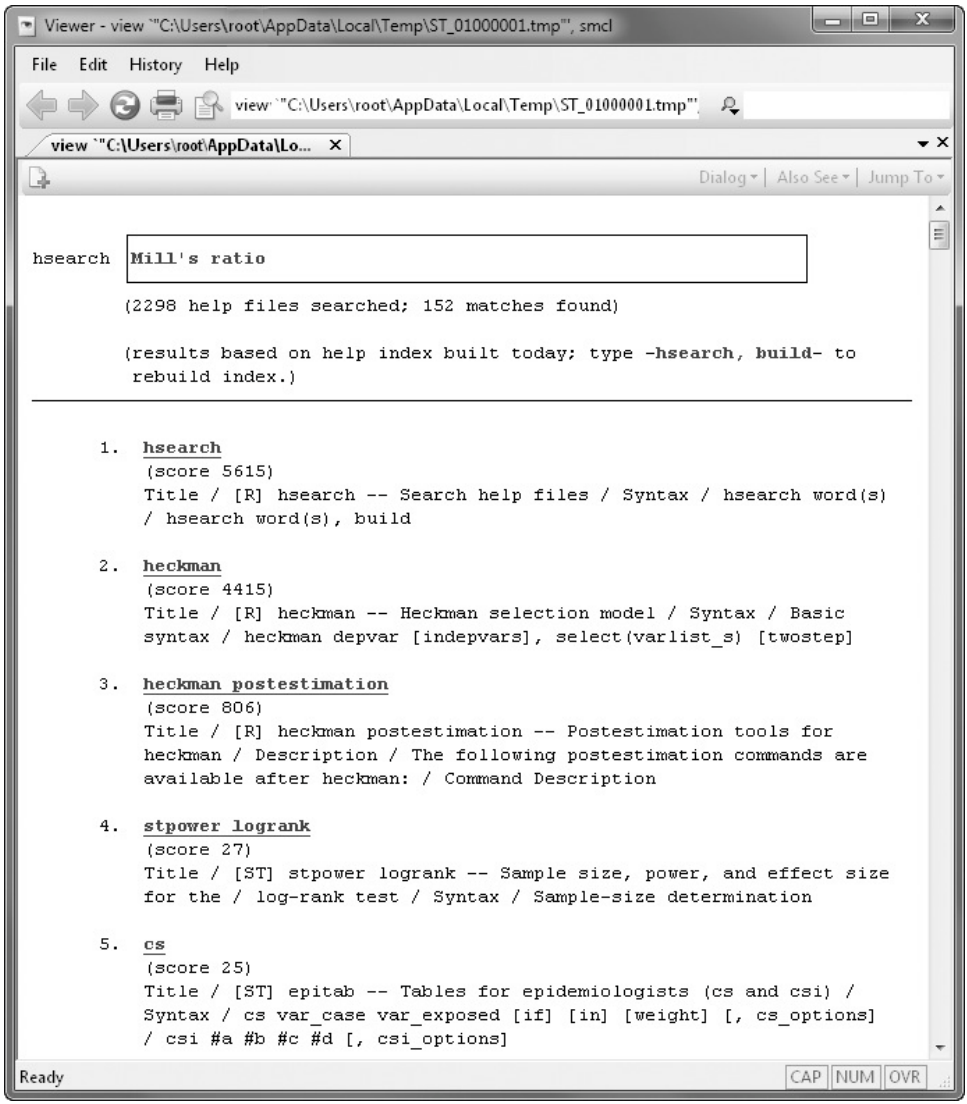
You use `hsearch` to find help for commands and features installed on your computer. If you wanted to find commands related to Mills' ratio, you would type

```
. hsearch Mills' ratio
```



You could just as well type

```
. hsearch Mill's ratio
```



or type any of

```
. hsearch Mills ratio
. hsearch mills ratio
```

or even

```
. hsearch ratio mills
```

because word order, capitalization, and punctuation do not matter.

Alternatives to hsearch

Alternatives to hsearch are search and findit:

```
. search mills ratio
. findit mills ratio
```

search, like hsearch, searches commands already installed on your computer. search searches the keywords; hsearch searches the help files themselves. Hence, hsearch usually finds everything that search finds and more. The fewer things that search finds should be more relevant.

findit searches keywords just as search does, but findit searches the web as well as your computer and so may find commands that you might wish to install.

Recommendations

- In general, hsearch is better than search. hsearch finds more and better organizes the list of what it finds.
- When you know that Stata can do what you are looking for but you cannot remember the command name or when you know that you installed a relevant user-written package, use hsearch.
- When you are unsure whether Stata can do a certain task, use hsearch first and then use findit.

How hsearch works

hsearch searches the .sthlp files.

Finding all those files and then looking through them would take a long time if hsearch did that every time you used it. Instead, hsearch builds an index of the .sthlp files and then searches that.

That file is called sthlpindex.idx and is stored in your PERSONAL directory.

Every so often, hsearch automatically rebuilds the index so that it accurately reflects what is installed on your computer. You can force hsearch to rebuild the index at any time by typing

```
. hsearch, build
```

Methods and formulas

hsearch is implemented as an ado-file.

Also see

[R] **net search** — Search the Internet for installable packages

[R] **search** — Search Stata documentation

Title

inequality — Inequality measures

Remarks

Stata does not have commands for inequality measures, except `roctab` has an option to report Gini and Pietra indices; see [R] **roctab**. Stata users, however, have developed an excellent suite of commands, many of which have been published in the *Stata Journal* (SJ) and in the *Stata Technical Bulletin* (STB).

Issue	Insert	Author(s)	Command	Description
STB-48	gr35	N. J. Cox	`psm`, `qsm`, `pdagum`, `qdagum`	Diagnostic plots for assessing Singh–Maddala and Dagum distributions fit by MLE
STB-23	sg31	R. Goldstein	`rspread`	Measures of diversity: Absolute and relative
STB-48	sg104	S. P. Jenkins	`sumdist`, `xfrac`, `ineqdeco`, `geivars`, `ineqfac`, `povdeco`	Analysis of income distributions
STB-48	sg106	S. P. Jenkins	`smfit`, `dagumfit`	Fitting Singh–Maddala and Dagum distributions by maximum likelihood
STB-48	sg107	S. P. Jenkins, P. Van Kerm	`glcurve`	Generalized Lorenz curves and related graphs
STB-49	sg107.1	S. P. Jenkins, P. Van Kerm	`glcurve`	update of sg107
SJ-1-1	gr0001	S. P. Jenkins, P. Van Kerm	`glcurve7`	update for Stata 7 of sg107.1
SJ-7-2	gr0001_3	S. P. Van Kerm, P. Jenkins	`glcurve`	update for Stata 8 of gr0001; *install this version*
STB-48	sg108	P. Van Kerm	`poverty`	Computing poverty indices
STB-51	sg115	D. Jolliffe, B. Krushelnytskyy	`ineqerr`	Bootstrap standard errors for indices of inequality
STB-51	sg117	D. Jolliffe, A. Semykina	`sepov`	Robust standard errors for the Foster–Greer–Thorbecke class of poverty indices
SJ-8-4	st0100_1	A. López-Feldman	`descogini`	Decomposing inequality and obtaining marginal effects
SJ-6-4	snp15_7	R. Newson	`somersd`	Gini coefficient is a special case of Somers' D
STB-23	sg30	E. Whitehouse	`lorenz`, `inequal`, `atkinson`, `relsgini`	Measures of inequality in Stata

More commands may be available; enter Stata and type `search inequality measure, all`.

Max Otto Lorenz (1876–1959) was born in Iowa and studied at the Universities of Iowa and Wisconsin. He proposed what is now known as the Lorenz curve in 1905. Lorenz worked for the Interstate Commerce Commission between 1911 and 1944, mainly with transportation data. His hobbies included calendar reform and Interlingua, a proposed international language.

To download and install the Jenkins and Van Kerm `glcurve` command from the Internet, for instance, you could

1. Select **Help > SJ and User-written Programs**.
2. Click on *Stata Journal*.
3. Click on *sj4-4*.
4. Click on *gr0001_1*.
5. Click on *click here to install*.

or you could instead do the following:

1. Navigate to the appropriate SJ issue:
   a. Type `net from http://www.stata-journal.com/software`
      Type `net cd sj4-4`
   or
   b. Type `net from http://www.stata-journal.com/software/sj4-4`
2. Type `net describe gr0001_1`
3. Type `net install gr0001_1`

To download and install the Jenkins `sumdist` command from the Internet, for instance, you could

1. Select **Help > SJ and User-written Programs**.
2. Click on *STB*.
3. Click on *stb48*.
4. Click on *sg104*.
5. Click on *click here to install*.

or you could instead do the following:

1. Navigate to the appropriate STB issue:
   a. Type `net from http://www.stata.com`
      Type `net cd stb`
      Type `net cd stb48`
   or
   b. Type `net from http://www.stata.com/stb/stb48`
2. Type `net describe sg104`
3. Type `net install sg104`

References

Cox, N. J. 1999. gr35: Diagnostic plots for assessing Singh–Maddala and Dagum distributions fitted by MLE. *Stata Technical Bulletin* 48: 2–4. Reprinted in *Stata Technical Bulletin Reprints*, vol. 8, pp. 72–74. College Station, TX: Stata Press.

Goldstein, R. 1995. sg31: Measures of diversity: Absolute and relative. *Stata Technical Bulletin* 23: 23–26. Reprinted in *Stata Technical Bulletin Reprints*, vol. 4, pp. 150–154. College Station, TX: Stata Press.

Haughton, J., and S. R. Khandker. 2009. *Handbook on Poverty + Inequality*. Washington, DC: World Bank.

Jenkins, S. P. 1999a. sg104: Analysis of income distributions. *Stata Technical Bulletin* 48: 4–18. Reprinted in *Stata Technical Bulletin Reprints*, vol. 8, pp. 243–260. College Station, TX: Stata Press.

——. 1999b. sg106: Fitting Singh–Maddala and Dagum distributions by maximum likelihood. *Stata Technical Bulletin* 48: 19–25. Reprinted in *Stata Technical Bulletin Reprints*, vol. 8, pp. 261–268. College Station, TX: Stata Press.

Jenkins, S. P., and P. Van Kerm. 1999a. sg107: Generalized Lorenz curves and related graphs. *Stata Technical Bulletin* 48: 25–29. Reprinted in *Stata Technical Bulletin Reprints*, vol. 8, pp. 269–274. College Station, TX: Stata Press.

——. 1999b. sg107.1: Generalized Lorenz curves and related graphs. *Stata Technical Bulletin* 49: 23. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, p. 171. College Station, TX: Stata Press.

——. 2001. Generalized Lorenz curves and related graphs: An update for Stata 7. *Stata Journal* 1: 107–112.

——. 2004. gr0001_1: Software Updates: Generalized Lorenz curves and related graphs. *Stata Journal* 4: 490.

——. 2006. gr0001_2: Software Updates: Generalized Lorenz curves and related graphs. *Stata Journal* 6: 597.

——. 2007. gr0001_3: Software Updates: Generalized Lorenz curves and related graphs. *Stata Journal* 7: 280.

Jolliffe, D., and B. Krushelnytskyy. 1999. sg115: Bootstrap standard errors for indices of inequality. *Stata Technical Bulletin* 51: 28–32. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 191–196. College Station, TX: Stata Press.

Jolliffe, D., and A. Semykina. 1999. sg117: Robust standard errors for the Foster–Greer–Thorbecke class of poverty indices. *Stata Technical Bulletin* 51: 34–36. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 200–203. College Station, TX: Stata Press.

Kleiber, C., and S. Kotz. 2003. *Statistical Size Distributions in Economics and Actuarial Sciences*. Hoboken, NJ: Wiley.

López-Feldman, A. 2006. Decomposing inequality and obtaining marginal effects. *Stata Journal* 6: 106–111.

——. 2008. Software Updates: Decomposing inequality and obtaining marginal effects. *Stata Journal* 8: 594.

Lorenz, M. O. 1905. Methods of measuring the concentration of wealth. *American Statistical Association* 9: 209–219.

Newson, R. 2006. Confidence intervals for rank statistics: Percentile slopes, differences, and ratios. *Stata Journal* 6: 497–520.

Van Kerm, P. 1999. sg108: Computing poverty indices. *Stata Technical Bulletin* 48: 29–33. Reprinted in *Stata Technical Bulletin Reprints*, vol. 8, pp. 274–278. College Station, TX: Stata Press.

Whitehouse, E. 1995. sg30: Measures of inequality in Stata. *Stata Technical Bulletin* 23: 20–23. Reprinted in *Stata Technical Bulletin Reprints*, vol. 4, pp. 146–150. College Station, TX: Stata Press.

Title

intreg — Interval regression

Syntax

```
intreg depvar1 depvar2 [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
het(*varlist*[, noconstant])	independent variables to model the variance; use noconstant to suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

$depvar_1$, $depvar_2$, *indepvars*, and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, fracpoly, jackknife, mfp, nestreg, rolling, statsby, stepwise, and svy are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

aweights are not allowed with the jackknife prefix; see [R] **jackknife**.

vce() and weights are not allowed with the svy prefix; see [SVY] **svy**.

aweights, fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

coeflegend does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Censored regression > Interval regression

Description

`intreg` fits a model of $y = [\, depvar_1,\ depvar_2 \,]$ on *indepvars*, where y for each observation is point data, interval data, left-censored data, or right-censored data.

$depvar_1$ and $depvar_2$ should have the following form:

Type of data		$depvar_1$	$depvar_2$
point data	$a = [\, a, a \,]$	a	a
interval data	$[\, a, b \,]$	a	b
left-censored data	$(-\infty, b \,]$	.	b
right-censored data	$[\, a, +\infty)$	a	.

Options

Model

`noconstant`; see [R] **estimation options**.

`het(`*varlist* [`, noconstant`]`)` specifies that *varlist* be included in the specification of the conditional variance. This *varlist* enters the variance specification collectively as multiplicative heteroskedasticity.

`offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, [`no`]`log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `intreg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

`intreg` is a generalization of the models fit by `tobit`. Cameron and Trivedi (2010, 548–550) discuss the differences among censored, truncated, and interval data. If you know that the value for the jth individual is somewhere in the interval $[\,y_{1j},\ y_{2j}\,]$, then the likelihood contribution from this individual is simply $\Pr(y_{1j} \leq Y_j \leq y_{2j})$. For censored data, their likelihoods contain terms of the form $\Pr(Y_j \leq y_j)$ for left-censored data and $\Pr(Y_j \geq y_j)$ for right-censored data, where y_j is the observed censoring value and Y_j denotes the random variable representing the dependent variable in the model.

Hence, `intreg` can fit models for data where each observation represents interval data, left-censored data, right-censored data, or point data. Regardless of the type of observation, the data should be stored in the dataset as interval data; that is, two dependent variables, *depvar*$_1$ and *depvar*$_2$, are used to hold the endpoints of the interval. If the data are left-censored, the lower endpoint is $-\infty$ and is represented by a missing value, '`.`', or an extended missing value, '`.a`, `.b`, ..., `.z`', in *depvar*$_1$. If the data are right-censored, the upper endpoint is $+\infty$ and is represented by a missing value, '`.`' (or an extended missing value), in *depvar*$_2$. Point data are represented by the two endpoints being equal.

Type of data		*depvar*$_1$	*depvar*$_2$
point data	$a = [\,a, a\,]$	a	a
interval data	$[\,a, b\,]$	a	b
left-censored data	$(\,-\infty, b\,]$	.	b
right-censored data	$[\,a, +\infty\,)$	a	.

Truly missing values of the dependent variable must be represented by missing values in both *depvar*$_1$ and *depvar*$_2$.

Interval data arise naturally in many contexts, such as wage data. Often you know only that, for example, a person's salary is between $30,000 and $40,000. Below we give an example for wage data and show how to set up *depvar*$_1$ and *depvar*$_2$.

▷ Example 1

We have a dataset that contains the yearly wages of working women. Women were asked via a questionnaire to indicate a category for their yearly income from employment. The categories were less than 5,000, 5,001–10,000, ..., 25,001–30,000, 30,001–40,000, 40,001–50,000, and more than 50,000. The wage categories are stored in the `wagecat` variable.

```
. use http://www.stata-press.com/data/r12/womenwage
(Wages of women)
. tab wagecat
```

Wage category ($1000s)	Freq.	Percent	Cum.
5	14	2.87	2.87
10	83	17.01	19.88
15	158	32.38	52.25
20	107	21.93	74.18
25	57	11.68	85.86
30	30	6.15	92.01
40	19	3.89	95.90
50	14	2.87	98.77
51	6	1.23	100.00
Total	488	100.00	

A value of 5 for `wagecat` represents the category less than 5,000, a value of 10 represents 5,001 – 10,000, . . . , and a value of 51 represents greater than 50,000.

To use `intreg`, we must create two variables, `wage1` and `wage2`, containing the lower and upper endpoints of the wage categories. Here is one way to do it. We first create a dataset containing the nine wage categories, lag the wage categories into `wage1`, and match-merge this dataset with nine observations back into the main one.

```
. by wagecat: keep if _n==1
(479 observations deleted)
. generate wage1 = wagecat[_n-1]
(1 missing value generated)
. keep wagecat wage1
. save lagwage
file lagwage.dta saved
. use http://www.stata-press.com/data/r12/womenwage
(Wages of women)
. merge m:1 wagecat using lagwage
    Result                           # of obs.
    -----------------------------------------
    not matched                             0
    matched                               488  (_merge==3)
    -----------------------------------------
```

Now we create the upper endpoint and list the new variables:

```
. generate wage2 = wagecat
. replace wage2 = . if wagecat == 51
(6 real changes made, 6 to missing)
. sort age, stable
```

```
. list wage1 wage2 in 1/10
```

	wage1	wage2
1.	.	5
2.	5	10
3.	5	10
4.	10	15
5.	.	5
6.	.	5
7.	.	5
8.	5	10
9.	5	10
10.	5	10

We can now run `intreg`:

```
. intreg wage1 wage2 age c.age#c.age nev_mar rural school tenure
Fitting constant-only model:
Iteration 0:   log likelihood = -967.24956
Iteration 1:   log likelihood =  -967.1368
Iteration 2:   log likelihood =  -967.1368
Fitting full model:
Iteration 0:   log likelihood = -856.65324
Iteration 1:   log likelihood = -856.33294
Iteration 2:   log likelihood = -856.33293
Interval regression                               Number of obs   =        488
                                                  LR chi2(6)      =     221.61
Log likelihood = -856.33293                       Prob > chi2     =     0.0000
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.7914438	.4433604	1.79	0.074	-.0775265	1.660414
c.age#c.age	-.0132624	.0073028	-1.82	0.069	-.0275757	.0010509
nev_mar	-.2075022	.8119581	-0.26	0.798	-1.798911	1.383906
rural	-3.043044	.7757324	-3.92	0.000	-4.563452	-1.522637
school	1.334721	.1357873	9.83	0.000	1.068583	1.600859
tenure	.8000664	.1045077	7.66	0.000	.5952351	1.004898
_cons	-12.70238	6.367117	-1.99	0.046	-25.1817	-.2230583
/lnsigma	1.987823	.0346543	57.36	0.000	1.919902	2.055744
sigma	7.299626	.2529634			6.82029	7.81265

```
  Observation summary:        14  left-censored observations
                               0     uncensored observations
                               6 right-censored observations
                             468       interval observations
```

We could also model these data by using an ordered probit model with `oprobit` (see [R] **oprobit**):

```
. oprobit wagecat age c.age#c.age nev_mar rural school tenure
Iteration 0:   log likelihood =  -881.1491
Iteration 1:   log likelihood = -764.31729
Iteration 2:   log likelihood = -763.31191
Iteration 3:   log likelihood = -763.31049
Iteration 4:   log likelihood = -763.31049
Ordered probit regression                       Number of obs   =        488
                                                LR chi2(6)      =     235.68
                                                Prob > chi2     =     0.0000
Log likelihood = -763.31049                     Pseudo R2       =     0.1337
```

wagecat	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.1674519	.0620333	2.70	0.007	.0458689	.289035
c.age#c.age	-.0027983	.0010214	-2.74	0.006	-.0048001	-.0007964
nev_mar	-.0046417	.1126737	-0.04	0.967	-.225478	.2161946
rural	-.5270036	.1100449	-4.79	0.000	-.7426875	-.3113196
school	.2010587	.0201189	9.99	0.000	.1616263	.2404911
tenure	.0989916	.0147887	6.69	0.000	.0700063	.127977
/cut1	2.650637	.8957245			.8950495	4.406225
/cut2	3.941018	.8979167			2.181134	5.700903
/cut3	5.085205	.9056582			3.310148	6.860263
/cut4	5.875534	.9120933			4.087864	7.663204
/cut5	6.468723	.918117			4.669247	8.268199
/cut6	6.922726	.9215455			5.11653	8.728922
/cut7	7.34471	.9237628			5.534168	9.155252
/cut8	7.963441	.9338881			6.133054	9.793828

We can directly compare the log likelihoods for the `intreg` and `oprobit` models because both likelihoods are discrete. If we had point data in our `intreg` estimation, the likelihood would be a mixture of discrete and continuous terms, and we could not compare it directly with the `oprobit` likelihood.

Here the `oprobit` log likelihood is significantly larger (that is, less negative), so it fits better than the `intreg` model. The `intreg` model assumes normality, but the distribution of wages is skewed and definitely nonnormal. Normality is more closely approximated if we model the log of wages.

```
. generate logwage1 = log(wage1)
(14 missing values generated)
. generate logwage2 = log(wage2)
(6 missing values generated)
. intreg logwage1 logwage2 age c.age#c.age nev_mar rural school tenure
Fitting constant-only model:
Iteration 0:   log likelihood = -889.23647
Iteration 1:   log likelihood = -889.06346
Iteration 2:   log likelihood = -889.06346
Fitting full model:
Iteration 0:   log likelihood = -773.81968
Iteration 1:   log likelihood = -773.36566
Iteration 2:   log likelihood = -773.36563
Interval regression                             Number of obs   =        488
                                                LR chi2(6)      =     231.40
Log likelihood = -773.36563                     Prob > chi2     =     0.0000
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.0645589	.0249954	2.58	0.010	.0155689	.1135489
c.age#c.age	-.0010812	.0004115	-2.63	0.009	-.0018878	-.0002746
nev_mar	-.0058151	.0454867	-0.13	0.898	-.0949674	.0833371
rural	-.2098361	.0439454	-4.77	0.000	-.2959675	-.1237047
school	.0804832	.0076783	10.48	0.000	.0654341	.0955323
tenure	.0397144	.0058001	6.85	0.000	.0283464	.0510825
_cons	.7084023	.3593193	1.97	0.049	.0041495	1.412655
/lnsigma	-.906989	.0356265	-25.46	0.000	-.9768157	-.8371623
sigma	.4037381	.0143838			.3765081	.4329373

```
  Observation summary:        14  left-censored observations
                               0     uncensored observations
                               6 right-censored observations
                             468       interval observations
```

The log likelihood of this `intreg` model is close to the `oprobit` log likelihood, and the z statistics for both models are similar. ◁

❑ Technical note

`intreg` has two parameterizations for the log-likelihood function: the transformed parameterization $(\beta/\sigma,\ 1/\sigma)$ and the untransformed parameterization $(\beta,\ \ln(\sigma))$. By default, the log likelihood for `intreg` is parameterized in the transformed parameter space. This parameterization tends to be more convergent, but it requires that any starting values and constraints have the same parameterization, and it prevents the estimation with multiplicative heteroskedasticity. Therefore, when the `het()` option is specified, `intreg` switches to the untransformed log likelihood for the fit of the conditional-variance model. Similarly, specifying `from()` or `constraints()` causes the optimization in the untransformed parameter space to allow constraints on (and starting values for) the coefficients on the covariates without reference to σ.

The estimation results are all saved in the $(\beta,\ \ln(\sigma))$ metric. ❑

Saved results

intreg saves the following in e():

Scalars

e(N)	number of observations
e(N_unc)	number of uncensored observations
e(N_lc)	number of left-censored observations
e(N_rc)	number of right-censored observations
e(N_int)	number of interval observations
e(k)	number of parameters
e(k_aux)	number of auxiliary parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(ll_c)	log likelihood, comparison model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	p-value for model χ^2 test
e(sigma)	sigma
e(se_sigma)	standard error of sigma
e(rank)	rank of e(V)
e(rank0)	rank of e(V) for constant-only model
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	intreg
e(cmdline)	command as typed
e(depvar)	names of dependent variables
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(het)	heteroskedasticity, if het() specified
e(ml_score)	program used to implement scores
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(footnote)	program and arguments to display footnote
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`intreg` is implemented as an ado-file.

See Wooldridge (2009, sec. 17.4) or Davidson and MacKinnon (2004, sec. 11.6) for an introduction to censored and truncated regression models.

The likelihood for `intreg` subsumes that of the `tobit` models.

Let $\mathbf{y} = \mathbf{X}\boldsymbol{\beta}+\boldsymbol{\epsilon}$ be the model. $\mathbf{y}$ represents continuous outcomes—either observed or not observed. Our model assumes $\boldsymbol{\epsilon} \sim N(\mathbf{0}, \sigma^2\mathbf{I})$.

For observations $j \in \mathcal{C}$, we observe y_j, that is, point data. Observations $j \in \mathcal{L}$ are left-censored; we know only that the unobserved y_j is less than or equal to $y_{\mathcal{L}j}$, a censoring value that we do know. Similarly, observations $j \in \mathcal{R}$ are right-censored; we know only that the unobserved y_j is greater than or equal to $y_{\mathcal{R}j}$. Observations $j \in \mathcal{I}$ are intervals; we know only that the unobserved y_j is in the interval $[\, y_{1j},\, y_{2j} \,]$.

The log likelihood is

$$
\begin{aligned}
\ln L = &-\frac{1}{2}\sum_{j\in\mathcal{C}} w_j \left\{ \left(\frac{y_j - \mathbf{x}\boldsymbol{\beta}}{\sigma} \right)^2 + \log 2\pi\sigma^2 \right\} \\
&+ \sum_{j\in\mathcal{L}} w_j \log \Phi\left(\frac{y_{\mathcal{L}j} - \mathbf{x}\boldsymbol{\beta}}{\sigma} \right) \\
&+ \sum_{j\in\mathcal{R}} w_j \log \left\{ 1 - \Phi\left(\frac{y_{\mathcal{R}j} - \mathbf{x}\boldsymbol{\beta}}{\sigma} \right) \right\} \\
&+ \sum_{j\in\mathcal{I}} w_j \log \left\{ \Phi\left(\frac{y_{2j} - \mathbf{x}\boldsymbol{\beta}}{\sigma} \right) - \Phi\left(\frac{y_{1j} - \mathbf{x}\boldsymbol{\beta}}{\sigma} \right) \right\}
\end{aligned}
$$

where $\Phi()$ is the standard cumulative normal and w_j is the weight for the jth observation. If no weights are specified, $w_j = 1$. If `aweights` are specified, $w_j = 1$, and σ is replaced by $\sigma/\sqrt{a_j}$ in the above, where a_j are the `aweights` normalized to sum to N.

Maximization is as described in [R] **maximize**; the estimate reported as `_sigma` is $\widehat{\sigma}$.

See Amemiya (1973) for a generalization of the tobit model to variable, but known, cutoffs.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`intreg` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **intreg postestimation** — Postestimation tools for intreg

[R] **tobit** — Tobit regression

[R] **regress** — Linear regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtintreg** — Random-effects interval-data regression models

[XT] **xttobit** — Random-effects tobit models

[U] **20 Estimation and postestimation commands**

Title

intreg postestimation — Postestimation tools for intreg

Description

The following postestimation commands are available after `intreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_lnsigma} [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`pr(`*a*`,`*b*`)`	$\Pr(a < y_j < b)$
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` postestimation results.

where a and b may be numbers or variables; a missing ($a \geq .$) means $-\infty$, and b missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \mid a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated.
a and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`nooffset` is relevant only if you specified `offset(`*varname*`)`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial \ln\sigma$.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **intreg** — Interval regression

[U] **20 Estimation and postestimation commands**

Title

ivprobit — Probit model with continuous endogenous regressors

Syntax

Maximum likelihood estimator

```
ivprobit depvar [varlist1] (varlist2 = varlistiv) [if] [in] [weight] [, mle_options]
```

Two-step estimator

```
ivprobit depvar [varlist1] (varlist2 = varlistiv) [if] [in] [weight], twostep
    [tse_options]
```

mle_options	Description
Model	
`mle`	use conditional maximum-likelihood estimator; the default
`asis`	retain perfect predictor variables
`constraints(`*constraints*`)`	apply specified linear constraints
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`first`	report first-stage regression
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process
`coeflegend`	display legend instead of statistics

tse_options	Description
Model	
* twostep	use Newey's two-step estimator; the default is mle
asis	retain perfect predictor variables
SE	
vce(*vcetype*)	*vcetype* may be twostep, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
first	report first-stage regression
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
coeflegend	display legend instead of statistics

*twostep is required.

varlist$_1$ and *varlist*$_{\text{iv}}$ may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar, *varlist*$_1$, *varlist*$_2$, and *varlist*$_{\text{iv}}$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
bootstrap, by, jackknife, rolling, statsby, and svy are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
vce(), first, twostep, and weights are not allowed with the svy prefix; see [SVY] **svy**.
fweights, iweights, and pweights are allowed with the maximum likelihood estimator. fweights are allowed with Newey's two-step estimator. See [U] **11.1.6 weight**.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Endogenous covariates > Probit model with endogenous covariates

Description

ivprobit fits probit models where one or more of the regressors are endogenously determined. By default, ivprobit uses maximum likelihood estimation. Alternatively, Newey's (1987) minimum chi-squared estimator can be invoked with the twostep option. Both estimators assume that the endogenous regressors are continuous and are not appropriate for use with discrete endogenous regressors. See [R] **ivtobit** for tobit estimation with endogenous regressors and [R] **probit** for probit estimation when the model contains no endogenous regressors.

Options for ML estimator

Model

mle requests that the conditional maximum-likelihood estimator be used. This is the default.

asis requests that all specified variables and observations be retained in the maximization process. This option is typically not used and may introduce numerical instability. Normally, ivprobit drops any endogenous or exogenous variables that perfectly predict success or failure in the dependent variable. The associated observations are also dropped. For more information, see *Model identification* in [R] **probit**.

`constraints(`*constraints*`)`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` requests that the parameters for the reduced-form equations showing the relationships between the endogenous variables and instruments be displayed. For the two-step estimator, `first` shows the first-stage regressions. For the maximum likelihood estimator, these parameters are estimated jointly with the parameters of the probit equation. The default is not to show these parameter estimates.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. This model's likelihood function can be difficult to maximize, especially with multiple endogenous variables. The `difficult` and `technique(bfgs)` options may be helpful in achieving convergence.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `ivprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Options for two-step estimator

Model

`twostep` is required and requests that Newey's (1987) efficient two-step estimator be used to obtain the coefficient estimates.

`asis` requests that all specified variables and observations be retained in the maximization process. This option is typically not used and may introduce numerical instability. Normally, `ivprobit` drops any endogenous or exogenous variables that perfectly predict success or failure in the dependent variable. The associated observations are also dropped. For more information, see *Model identification* in [R] **probit**.

SE

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` requests that the parameters for the reduced-form equations showing the relationships between the endogenous variables and instruments be displayed. For the two-step estimator, `first` shows the first-stage regressions. For the maximum likelihood estimator, these parameters are estimated jointly with the parameters of the probit equation. The default is not to show these parameter estimates.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `ivprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Model setup
Model identification

Model setup

`ivprobit` fits models with dichotomous dependent variables and endogenous regressors. You can use it to fit a probit model when you suspect that one or more of the regressors are correlated with the error term. `ivprobit` is to probit modeling what `ivregress` is to linear regression analysis; see [R] **ivregress** for more information.

Formally, the model is

$$y_{1i}^* = \boldsymbol{y}_{2i}\boldsymbol{\beta} + \boldsymbol{x}_{1i}\boldsymbol{\gamma} + u_i$$
$$\boldsymbol{y}_{2i} = \boldsymbol{x}_{1i}\boldsymbol{\Pi}_1 + \boldsymbol{x}_{2i}\boldsymbol{\Pi}_2 + \boldsymbol{v}_i$$

where $i = 1, \ldots, N$, $\boldsymbol{y}_{2i}$ is a $1 \times p$ vector of endogenous variables, $\boldsymbol{x}_{1i}$ is a $1 \times k_1$ vector of exogenous variables, $\boldsymbol{x}_{2i}$ is a $1 \times k_2$ vector of additional instruments, and the equation for $\boldsymbol{y}_{2i}$ is written in reduced form. By assumption, $(u_i, \boldsymbol{v}_i) \sim \mathrm{N}(\mathbf{0}, \boldsymbol{\Sigma})$, where σ_{11} is normalized to one to identify the model. $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ are vectors of structural parameters, and $\boldsymbol{\Pi}_1$ and $\boldsymbol{\Pi}_2$ are matrices of reduced-form parameters. This is a recursive model: $\mathbf{y}_{2i}$ appears in the equation for y_{1i}^*, but y_{1i}^* does not appear in the equation for $\mathbf{y}_{2i}$. We do not observe y_{1i}^*; instead, we observe

$$y_{1i} = \begin{cases} 0 & y_{1i}^* < 0 \\ 1 & y_{1i}^* \geq 0 \end{cases}$$

The order condition for identification of the structural parameters requires that $k_2 \geq p$. Presumably, $\boldsymbol{\Sigma}$ is not block diagonal between u_i and $\boldsymbol{v}_i$; otherwise, $\boldsymbol{y}_{2i}$ would not be endogenous.

❑ Technical note

This model is derived under the assumption that $(u_i, \boldsymbol{v}_i)$ is independent and identically distributed multivariate normal for all i. The `vce(cluster` *clustvar*`)` option can be used to control for a lack of independence. As with most probit models, if u_i is heteroskedastic, point estimates will be inconsistent. ❑

Example 1

We have hypothetical data on 500 two-parent households, and we wish to model whether the woman is employed. We have a variable, `fem_work`, that is equal to one if she has a job and zero otherwise. Her decision to work is a function of the number of children at home (`kids`), number of years of schooling completed (`fem_educ`), and other household income measured in thousands of dollars (`other_inc`). We suspect that unobservable shocks affecting the woman's decision to hold a job also affect the household's other income. Therefore, we treat `other_inc` as endogenous. As an instrument, we use the number of years of schooling completed by the man (`male_educ`).

The syntax for specifying the exogenous, endogenous, and instrumental variables is identical to that used in `ivregress`; see [R] **ivregress** for details.

```
. use http://www.stata-press.com/data/r12/laborsup
. ivprobit fem_work fem_educ kids (other_inc = male_educ)
Fitting exogenous probit model
Iteration 0:   log likelihood = -344.63508
Iteration 1:   log likelihood = -255.36855
Iteration 2:   log likelihood = -255.31444
Iteration 3:   log likelihood = -255.31444
Fitting full model
Iteration 0:   log likelihood = -2371.4753
Iteration 1:   log likelihood = -2369.3178
Iteration 2:   log likelihood = -2368.2198
Iteration 3:   log likelihood = -2368.2062
Iteration 4:   log likelihood = -2368.2062
Probit model with endogenous regressors           Number of obs   =        500
                                                  Wald chi2(3)    =     163.88
Log likelihood = -2368.2062                       Prob > chi2     =     0.0000
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
other_inc	-.0542756	.0060854	-8.92	0.000	-.0662027	-.0423485
fem_educ	.211111	.0268648	7.86	0.000	.1584569	.2637651
kids	-.1820929	.0478267	-3.81	0.000	-.2758316	-.0883543
_cons	.3672083	.4480724	0.82	0.412	-.5109975	1.245414
/athrho	.3907858	.1509443	2.59	0.010	.0949403	.6866313
/lnsigma	2.813383	.0316228	88.97	0.000	2.751404	2.875363
rho	.3720374	.1300519			.0946561	.5958135
sigma	16.66621	.5270318			15.66461	17.73186

```
Instrumented:  other_inc
Instruments:   fem_educ kids male_educ
Wald test of exogeneity (/athrho = 0): chi2(1) =     6.70 Prob > chi2 = 0.0096
```

Because we did not specify `mle` or `twostep`, `ivprobit` used the maximum likelihood estimator by default. At the top of the output, we see the iteration log. `ivprobit` fits a probit model ignoring endogeneity to obtain starting values for the endogenous model. The header of the output contains the sample size as well as a Wald statistic and p-value for the test of the hypothesis that all the slope coefficients are jointly zero. Below the table of coefficients, Stata reminds us that the endogenous variable is `other_inc` and that `fem_educ`, `kids`, and `male_educ` were used as instruments.

At the bottom of the output is a Wald test of the exogeneity of the instrumented variables. If the test statistic is not significant, there is not sufficient information in the sample to reject the null that there is no endogeneity. Then a regular probit regression may be appropriate; the point estimates

from `ivprobit` are consistent, though those from `probit` (see [R] **probit**) are likely to have smaller standard errors.

◁

Various two-step estimators have also been proposed for the endogenous probit model, and Newey's (1987) minimum chi-squared estimator is available with the `twostep` option.

▷ Example 2

Refitting our labor-supply model with the two-step estimator yields

```
. ivprobit fem_work fem_educ kids (other_inc = male_educ), twostep
Checking reduced-form model...
Two-step probit with endogenous regressors        Number of obs   =        500
                                                  Wald chi2(3)    =      93.97
                                                  Prob > chi2     =     0.0000
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   other_inc |   -.058473   .0093364    -6.26   0.000    -.0767719    -.040174
    fem_educ |    .227437   .0281628     8.08   0.000     .1722389     .282635
        kids |  -.1961748   .0496323    -3.95   0.000    -.2934522   -.0988973
       _cons |   .3956061   .4982649     0.79   0.427    -.5809752    1.372187
------------------------------------------------------------------------------
Instrumented:  other_inc
Instruments:   fem_educ kids male_educ
------------------------------------------------------------------------------
Wald test of exogeneity:     chi2(1) =     6.50           Prob > chi2 = 0.0108
```

All the coefficients have the same signs as their counterparts in the maximum likelihood model. The Wald test at the bottom of the output confirms our earlier finding of endogeneity.

◁

❑ Technical note

In a standard probit model, the error term is assumed to have a variance of one. In the probit model with endogenous regressors, we assume that $(u_i, \boldsymbol{v}_i)$ is multivariate normal with covariance matrix

$$\mathrm{Var}(u_i, \boldsymbol{v}_i) = \boldsymbol{\Sigma} = \begin{bmatrix} 1 & \boldsymbol{\Sigma}_{21}' \\ \boldsymbol{\Sigma}_{21} & \boldsymbol{\Sigma}_{22} \end{bmatrix}$$

With the properties of the multivariate normal distribution, $\mathrm{Var}(u_i|\boldsymbol{v}_i) = 1 - \boldsymbol{\Sigma}_{21}'\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}$. As a result, Newey's estimator and other two-step probit estimators do not yield estimates of $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ but rather $\boldsymbol{\beta}/\sigma$ and $\boldsymbol{\gamma}/\sigma$, where σ is the square root of $\mathrm{Var}(u_i|\boldsymbol{v}_i)$. Hence, we cannot directly compare the estimates obtained from Newey's estimator with those obtained via maximum likelihood or with those obtained from `probit`. See Wooldridge (2010, 585–594) for a discussion of Rivers and Vuong's (1988) two-step estimator. The issues raised pertaining to the interpretation of the coefficients of that estimator are identical to those that arise with Newey's estimator. Wooldridge also discusses ways to obtain marginal effects from two-step estimators.

❑

Despite the coefficients not being directly comparable to their maximum likelihood counterparts, the two-step estimator is nevertheless useful. The maximum likelihood estimator may have difficulty

converging, especially with multiple endogenous variables. The two-step estimator, consisting of nothing more complicated than a probit regression, will almost certainly converge. Moreover, although the coefficients from the two models are not directly comparable, the two-step estimates can still be used to test for statistically significant relationships.

Model identification

As in the linear simultaneous-equation model, the order condition for identification requires that the number of excluded exogenous variables (that is, the additional instruments) be at least as great as the number of included endogenous variables. `ivprobit` checks this for you and issues an error message if the order condition is not met.

Like `probit`, `logit`, and `logistic`, `ivprobit` checks the exogenous and endogenous variables to see if any of them predict the outcome variable perfectly. It will then drop offending variables and observations and fit the model on the remaining data. Instruments that are perfect predictors do not affect estimation, so they are not checked. See *Model identification* in [R] **probit** for more information.

`ivprobit` will also occasionally display messages such as

```
Note: 4 failures and 0 successes completely determined.
```

For an explanation of this message, see [R] **logit**.

Saved results

`ivprobit, mle` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_cds)`	number of completely determined successes
`e(N_cdf)`	number of completely determined failures
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_aux)`	number of auxiliary parameters
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(N_clust)`	number of clusters
`e(endog_ct)`	number of endogenous regressors
`e(p)`	model Wald p-value
`e(p_exog)`	exogeneity test Wald p-value
`e(chi2)`	model Wald χ^2
`e(chi2_exog)`	Wald χ^2 test of exogeneity
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	1 if converged, 0 otherwise

Macros

e(cmd)	ivprobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(instd)	instrumented variables
e(insts)	instruments
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(chi2type)	Wald; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(asis)	asis, if specified
e(method)	ml
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(footnote)	program used to implement the footnote display
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(rules)	information about perfect predictors
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(Sigma)	$\widehat{\mathbf{\Sigma}}$
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

`ivprobit, twostep` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_cds)`	number of completely determined successes
`e(N_cdf)`	number of completely determined failures
`e(df_m)`	model degrees of freedom
`e(df_exog)`	degrees of freedom for χ^2 test of exogeneity
`e(p)`	model Wald p-value
`e(p_exog)`	exogeneity test Wald p-value
`e(chi2)`	model Wald χ^2
`e(chi2_exog)`	Wald χ^2 test of exogeneity
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`ivprobit`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(instd)`	instrumented variables
`e(insts)`	instruments
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(chi2type)`	`Wald`; type of model χ^2 test
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(asis)`	`asis`, if specified
`e(method)`	`twostep`
`e(properties)`	`b V`
`e(estat_cmd)`	program used to implement `estat`
`e(predict)`	program used to implement `predict`
`e(footnote)`	program used to implement the footnote display
`e(marginsok)`	predictions allowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(Cns)`	constraints matrix
`e(rules)`	information about perfect predictors
`e(V)`	variance–covariance matrix of the estimators

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`ivprobit` is implemented as an ado-file.

Fitting limited-dependent variable models with endogenous regressors has received considerable attention in the econometrics literature. Building on the results of Amemiya (1978, 1979), Newey (1987) developed an efficient method of estimation that encompasses both Rivers and Vuong's (1988) simultaneous-equations probit model and Smith and Blundell's (1986) simultaneous-equations tobit model. With modern computers, maximum likelihood estimation is feasible as well. For compactness, we write the model as

$$y_{1i}^{*} = \boldsymbol{z}_i\boldsymbol{\delta} + u_i \tag{1a}$$

$$\boldsymbol{y}_{2i} = \boldsymbol{x}_i\boldsymbol{\Pi} + \boldsymbol{v}_i \tag{1b}$$

where $\boldsymbol{z}_i = (\boldsymbol{y}_{2i}, \boldsymbol{x}_{1i})$, $\boldsymbol{x}_i = (\boldsymbol{x}_{1i}, \boldsymbol{x}_{2i})$, $\boldsymbol{\delta} = (\boldsymbol{\beta}', \boldsymbol{\gamma}')'$, and $\boldsymbol{\Pi} = (\boldsymbol{\Pi}_1', \boldsymbol{\Pi}_2')'$.

Deriving the likelihood function is straightforward because we can write the joint density $f\left(y_{1i}, \boldsymbol{y}_{2i}|\boldsymbol{x}_i\right)$ as $f\left(y_{1i}|\boldsymbol{y}_{2i}, \boldsymbol{x}_i\right) f\left(\boldsymbol{y}_{2i}|\boldsymbol{x}_i\right)$. When there is an endogenous regressor, the log likelihood for observation i is

$$\ln L_i = w_i \left[y_{1i} \ln\Phi\left(m_i\right) + \left(1 - y_{1i}\right) \ln\left\{1 - \Phi\left(m_i\right)\right\} + \ln\phi\left(\frac{y_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi}}{\sigma}\right) - \ln\sigma \right]$$

where

$$m_i = \frac{\boldsymbol{z}_i\boldsymbol{\delta} + \rho\left(y_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi}\right)/\sigma}{\left(1 - \rho^2\right)^{\frac{1}{2}}}$$

$\Phi(\cdot)$ and $\phi(\cdot)$ are the standard normal distribution and density functions, respectively; σ is the standard deviation of v_i; ρ is the correlation coefficient between u_i and v_i; and w_i is the weight for observation i or one if no weights were specified. Instead of estimating σ and ρ, we estimate $\ln\sigma$ and $\operatorname{atanh}\rho$, where

$$\operatorname{atanh}\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

For multiple endogenous regressors, let

$$\operatorname{Var}(u_i, \boldsymbol{v}_i) = \boldsymbol{\Sigma} = \begin{bmatrix} 1 & \boldsymbol{\Sigma}_{21}' \\ \boldsymbol{\Sigma}_{21} & \boldsymbol{\Sigma}_{22} \end{bmatrix}$$

As in any probit model, we have imposed the normalization $\operatorname{Var}(u_i) = 1$ to identify the model. The log likelihood for observation i is

$$\ln L_i = w_i \left[y_{1i} \ln\Phi\left(m_i\right) + \left(1 - y_{1i}\right) \ln\left\{1 - \Phi\left(m_i\right)\right\} + \ln f(\boldsymbol{y}_{2i}|\boldsymbol{x}_i) \right]$$

where

$$\ln f(\boldsymbol{y}_{2i}|\boldsymbol{x}_i) = -\frac{p}{2}\ln 2\pi - \frac{1}{2}\ln\left|\boldsymbol{\Sigma}_{22}\right| - \frac{1}{2}\left(\boldsymbol{y}_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi}\right)\boldsymbol{\Sigma}_{22}^{-1}\left(\boldsymbol{y}_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi}\right)'$$

and

$$m_i = \left(1 - \boldsymbol{\Sigma}_{21}'\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}\right)^{-\frac{1}{2}}\left\{\boldsymbol{z}_i\boldsymbol{\delta} + \left(\boldsymbol{y}_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi}\right)\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}\right\}$$

Instead of maximizing the log-likelihood function with respect to $\boldsymbol{\Sigma}$, we maximize with respect to the Cholesky decomposition $\boldsymbol{S}$ of $\boldsymbol{\Sigma}$; that is, there exists a lower triangular matrix, $\boldsymbol{S}$, such that $\boldsymbol{S}\boldsymbol{S}' = \boldsymbol{\Sigma}$. This maximization ensures that $\boldsymbol{\Sigma}$ is positive definite, as a covariance matrix must be. Let

$$\boldsymbol{S} = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ s_{21} & s_{22} & 0 & \dots & 0 \\ s_{31} & s_{32} & s_{33} & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ s_{p+1,1} & s_{p+1,2} & s_{p+1,3} & \dots & s_{p+1,p+1} \end{bmatrix}$$

With maximum likelihood estimation, this command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

The maximum likelihood version of `heckman` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

The two-step estimates are obtained using Newey's (1987) minimum chi-squared estimator. The reduced-form equation for y_{1i}^* is

$$\begin{aligned} y_{1i}^* &= (\boldsymbol{x}_i\boldsymbol{\Pi} + \boldsymbol{v}_i)\boldsymbol{\beta} + \boldsymbol{x}_{1i}\boldsymbol{\gamma} + u_i \\ &= \boldsymbol{x}_i\boldsymbol{\alpha} + \boldsymbol{v}_i\boldsymbol{\beta} + u_i \\ &= \boldsymbol{x}_i\boldsymbol{\alpha} + \nu_i \end{aligned}$$

where $\nu_i = \boldsymbol{v}_i\boldsymbol{\beta} + u_i$. Because u_i and $\boldsymbol{v}_i$ are jointly normal, ν_i is also normal. Note that

$$\boldsymbol{\alpha} = \begin{bmatrix} \boldsymbol{\Pi}_1 \\ \boldsymbol{\Pi}_2 \end{bmatrix} \boldsymbol{\beta} + \begin{bmatrix} \boldsymbol{I} \\ \boldsymbol{0} \end{bmatrix} \boldsymbol{\gamma} = D(\boldsymbol{\Pi})\boldsymbol{\delta}$$

where $D(\boldsymbol{\Pi}) = (\boldsymbol{\Pi}, \boldsymbol{I}_1)$ and $\boldsymbol{I}_1$ is defined such that $\boldsymbol{x}_i\boldsymbol{I}_1 = \boldsymbol{x}_{1i}$. Letting $\widehat{\boldsymbol{z}}_i = (\boldsymbol{x}_i\widehat{\boldsymbol{\Pi}}, \boldsymbol{x}_{1i})$, $\widehat{\boldsymbol{z}}_i\boldsymbol{\delta} = \boldsymbol{x}_i D(\widehat{\boldsymbol{\Pi}})\boldsymbol{\delta}$, where $D(\widehat{\boldsymbol{\Pi}}) = (\widehat{\boldsymbol{\Pi}}, \boldsymbol{I}_1)$. Thus one estimator of $\boldsymbol{\alpha}$ is $D(\widehat{\boldsymbol{\Pi}})\boldsymbol{\delta}$; denote this estimator by $\widehat{\boldsymbol{D}}\boldsymbol{\delta}$.

$\boldsymbol{\alpha}$ could also be estimated directly as the solution to

$$\max_{\boldsymbol{\alpha},\boldsymbol{\lambda}} \sum_{i=1}^{N} l(y_{1i}, \boldsymbol{x}_i\boldsymbol{\alpha} + \widehat{\boldsymbol{v}}_i\boldsymbol{\lambda}) \tag{2}$$

where $l(\cdot)$ is the log likelihood for probit. Denote this estimator by $\widetilde{\boldsymbol{\alpha}}$. The inclusion of the $\widehat{\boldsymbol{v}}_i\boldsymbol{\lambda}$ term follows because the multivariate normality of $(u_i, \boldsymbol{v}_i)$ implies that, conditional on $\boldsymbol{y}_{2i}$, the expected value of u_i is nonzero. Because $\boldsymbol{v}_i$ is unobservable, the least-squares residuals from fitting (1*b*) are used.

Amemiya (1978) shows that the estimator of $\boldsymbol{\delta}$ defined by

$$\max_{\boldsymbol{\delta}} \ (\widetilde{\boldsymbol{\alpha}} - \widehat{\boldsymbol{D}}\boldsymbol{\delta})' \widehat{\boldsymbol{\Omega}}^{-1} (\widetilde{\boldsymbol{\alpha}} - \widehat{\boldsymbol{D}}\boldsymbol{\delta})$$

where $\widehat{\boldsymbol{\Omega}}$ is a consistent estimator of the covariance of $\sqrt{N}(\widetilde{\boldsymbol{\alpha}} - \widehat{\boldsymbol{D}}\boldsymbol{\delta})$, is asymptotically efficient relative to all other estimators that minimize the distance between $\widetilde{\boldsymbol{\alpha}}$ and $D(\widehat{\boldsymbol{\Pi}})\boldsymbol{\delta}$. Thus an efficient estimator of $\boldsymbol{\delta}$ is

$$\widehat{\boldsymbol{\delta}} = (\widehat{\boldsymbol{D}}' \widehat{\boldsymbol{\Omega}}^{-1} \widehat{\boldsymbol{D}})^{-1} \widehat{\boldsymbol{D}}' \widehat{\boldsymbol{\Omega}}^{-1} \widetilde{\boldsymbol{\alpha}} \tag{3}$$

and

$$\mathrm{Var}(\widehat{\boldsymbol{\delta}}) = (\widehat{\boldsymbol{D}}' \widehat{\boldsymbol{\Omega}}^{-1} \widehat{\boldsymbol{D}})^{-1} \tag{4}$$

To implement this estimator, we need $\widehat{\boldsymbol{\Omega}}^{-1}$.

Consider the two-step maximum likelihood estimator that results from first fitting (1*b*) by OLS and computing the residuals $\widehat{\boldsymbol{v}}_i = \boldsymbol{y}_{2i} - \boldsymbol{x}_i\widehat{\boldsymbol{\Pi}}$. The estimator is then obtained by solving

$$\max_{\boldsymbol{\delta},\boldsymbol{\lambda}} \sum_{i=1}^{N} l(y_{1i}, \boldsymbol{z}_i\boldsymbol{\delta} + \widehat{\boldsymbol{v}}_i\boldsymbol{\lambda})$$

This is the two-step instrumental variables (2SIV) estimator proposed by Rivers and Vuong (1988), and its role will become apparent shortly.

From Proposition 5 of Newey (1987), $\sqrt{N}(\widetilde{\boldsymbol{\alpha}} - \widehat{\boldsymbol{D}}\boldsymbol{\delta}) \xrightarrow{d} \mathrm{N}(\mathbf{0}, \boldsymbol{\Omega})$, where

$$\boldsymbol{\Omega} = \boldsymbol{J}_{\alpha\alpha}^{-1} + (\boldsymbol{\lambda} - \boldsymbol{\beta})' \boldsymbol{\Sigma}_{22} (\boldsymbol{\lambda} - \boldsymbol{\beta}) \boldsymbol{Q}^{-1}$$

and $\boldsymbol{\Sigma}_{22} = E\{\boldsymbol{v}_i' \boldsymbol{v}_i\}$. $\boldsymbol{J}_{\alpha\alpha}^{-1}$ is simply the covariance matrix of $\widetilde{\boldsymbol{\alpha}}$, ignoring that $\widehat{\boldsymbol{\Pi}}$ is an estimated parameter matrix. Moreover, Newey shows that the covariance matrix from an OLS regression of $\boldsymbol{y}_{2i}(\widehat{\boldsymbol{\lambda}} - \widehat{\boldsymbol{\beta}})$ on $\boldsymbol{x}_i$ is a consistent estimator of the second term. $\widehat{\boldsymbol{\lambda}}$ can be obtained from solving (2), and the 2SIV estimator yields a consistent estimate, $\widehat{\boldsymbol{\beta}}$.

Mechanically, estimation proceeds in several steps.

1. Each of the endogenous right-hand-side variables is regressed on all the exogenous variables, and the fitted values and residuals are calculated. The matrix $\widehat{D} = D(\widehat{\boldsymbol{\Pi}})$ is assembled from the estimated coefficients.
2. `probit` is used to solve (2) and obtain $\widetilde{\boldsymbol{\alpha}}$ and $\widehat{\boldsymbol{\lambda}}$. The portion of the covariance matrix corresponding to $\boldsymbol{\alpha}$, $\boldsymbol{J}_{\alpha\alpha}^{-1}$, is also saved.
3. The 2SIV estimator is evaluated, and the parameters $\widehat{\boldsymbol{\beta}}$ corresponding to $\boldsymbol{y}_{2i}$ are collected.
4. $\boldsymbol{y}_{2i}(\widehat{\boldsymbol{\lambda}} - \widehat{\boldsymbol{\beta}})$ is regressed on $\boldsymbol{x}_i$. The covariance matrix of the parameters from this regression is added to $\boldsymbol{J}_{\alpha\alpha}^{-1}$, yielding $\widehat{\boldsymbol{\Omega}}$.
5. Evaluating (3) and (4) yields the estimates $\widehat{\boldsymbol{\delta}}$ and $\mathrm{Var}(\widehat{\boldsymbol{\delta}})$.
6. A Wald test of the null hypothesis $H_0 : \boldsymbol{\lambda} = \mathbf{0}$, using the 2SIV estimates, serves as our test of exogeneity.

The two-step estimates are not directly comparable to those obtained from the maximum likelihood estimator or from `probit`. The argument is the same for Newey's efficient estimator as for Rivers and Vuong's (1988) 2SIV estimator, so we consider the simpler 2SIV estimator. From the properties of the normal distribution,

$$E(u_i|\boldsymbol{v}_i) = \boldsymbol{v}_i \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21} \qquad \text{and} \qquad \mathrm{Var}(u_i|\boldsymbol{v}_i) = 1 - \boldsymbol{\Sigma}_{21}' \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21}$$

We write u_i as $u_i = \boldsymbol{v}_i \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21} + e_i = \boldsymbol{v}_i \boldsymbol{\lambda} + e_i$, where $e_i \sim \mathrm{N}(0, 1 - \rho^2)$, $\rho^2 = \boldsymbol{\Sigma}_{21}' \boldsymbol{\Sigma}_{22}^{-1} \boldsymbol{\Sigma}_{21}$, and e_i is independent of $\boldsymbol{v}_i$. In the second stage of 2SIV, we use a probit regression to estimate the parameters of

$$y_{1i} = \boldsymbol{z}_i \boldsymbol{\delta} + \boldsymbol{v}_i \boldsymbol{\lambda} + e_i$$

Because $\boldsymbol{v}_i$ is unobservable, we use the sample residuals from the first-stage regressions.

$$\Pr(y_{1i} = 1|\boldsymbol{z}_i, \boldsymbol{v}_i) = \Pr(\boldsymbol{z}_i \boldsymbol{\delta} + \boldsymbol{v}_i \boldsymbol{\lambda} + e_i > 0|\boldsymbol{z}_i, \boldsymbol{v}_i) = \Phi\left\{(1 - \rho^2)^{-\frac{1}{2}} (\boldsymbol{z}_i \boldsymbol{\delta} + \boldsymbol{v}_i \boldsymbol{\lambda})\right\}$$

Hence, as mentioned previously, 2SIV and Newey's estimator do not estimate $\boldsymbol{\delta}$ and $\boldsymbol{\lambda}$ but rather

$$\boldsymbol{\delta}_\rho = \frac{1}{(1 - \rho^2)^{\frac{1}{2}}} \boldsymbol{\delta} \qquad \text{and} \qquad \boldsymbol{\lambda}_\rho = \frac{1}{(1 - \rho^2)^{\frac{1}{2}}} \boldsymbol{\lambda}$$

Acknowledgments

The two-step estimator is based on the `probitiv` command written by Jonah Gelbach, Department of Economics, Yale University, and the `ivprob` command written by Joe Harkness, Institute of Policy Studies, Johns Hopkins University.

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Also see

[R] **ivprobit postestimation** — Postestimation tools for ivprobit

[R] **gmm** — Generalized method of moments estimation

[R] **ivregress** — Single-equation instrumental-variables regression

[R] **ivtobit** — Tobit model with continuous endogenous regressors

[R] **probit** — Probit regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtprobit** — Random-effects and population-averaged probit models

[U] **20 Estimation and postestimation commands**

Title

ivprobit postestimation — Postestimation tools for ivprobit

Description

The following postestimation commands are of special interest after `ivprobit`:

Command	Description
`estat classification`	report various summary statistics, including the classification table
`lroc`	compute area under ROC curve and graph the curve
`lsens`	graph sensitivity and specificity versus probability cutoff

These commands are not appropriate after the two-step estimator or the `svy` prefix.

For information about these commands, see [R] **logistic postestimation**.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`[1]	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[2]	likelihood-ratio test; not available with two-step estimator
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`[1]	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `estat ic` and `suest` are not appropriate after `ivprobit, twostep`.

[2] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat (svy)`.

Syntax for predict

After ML or twostep

```
predict [type] newvar [if] [in] [, statistic rules asif]
```

After ML

```
predict [type] {stub* | newvarlist} [if] [in], scores
```

statistic	Description
Main	
xb	linear prediction; the default
stdp	standard error of the linear prediction
pr	probability of a positive outcome; not available with two-step estimator

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`pr` calculates the probability of a positive outcome. `pr` is not available with the two-step estimator.

`rules` requests that Stata use any rules that were used to identify the model when making the prediction. By default, Stata calculates missing for excluded observations. `rules` is not available with the two-step estimator.

`asif` requests that Stata ignore the rules and the exclusion criteria and calculate predictions for all observations possible using the estimated parameters from the model. `asif` is not available with the two-step estimator.

`scores`, not available with `twostep`, calculates equation-level score variables.

For models with one endogenous regressor, four new variables are created.

The first new variable will contain $\partial \ln L/\partial(\boldsymbol{z}_i\boldsymbol{\delta})$.

The second new variable will contain $\partial \ln L/\partial(\boldsymbol{x}_i\boldsymbol{\Pi})$.

The third new variable will contain $\partial \ln L/\partial \operatorname{atanh} \rho$.

The fourth new variable will contain $\partial \ln L/\partial \ln\sigma$.

For models with p endogenous regressors, $p + \{(p+1)(p+2)\}/2$ new variables are created.

The first new variable will contain $\partial \ln L/\partial(\boldsymbol{z}_i\boldsymbol{\delta})$.

The second through $(p+1)$th new variables will contain $\partial \ln L/\partial(\boldsymbol{x}_i\boldsymbol{\Pi}_k)$, $k = 1, \ldots, p$, where $\boldsymbol{\Pi}_k$ is the kth column of $\boldsymbol{\Pi}$.

The remaining score variables will contain the partial derivatives of $\ln L$ with respect to s_{21}, s_{31}, ..., $s_{p+1,1}$, s_{22}, ..., $s_{p+1,2}$, ..., $s_{p+1,p+1}$, where $s_{m,n}$ denotes the (m,n) element of the Cholesky decomposition of the error covariance matrix.

Remarks

Remarks are presented under the following headings:

Marginal effects
Obtaining predicted values

Marginal effects

▷ Example 1

We can obtain marginal effects by using the `margins` command after `ivprobit`. We will calculate average marginal effects by using the labor-supply model of example 1 in [R] **ivprobit**.

```
. use http://www.stata-press.com/data/r12/laborsup
. ivprobit fem_work fem_educ kids (other_inc = male_educ)
  (output omitted)
. margins, dydx(*) predict(pr)
Average marginal effects                        Number of obs   =        500
Model VCE    : OIM
Expression   : Probability of positive outcome, predict(pr)
dy/dx w.r.t. : other_inc fem_educ kids male_educ
```

	dy/dx	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
other_inc	-.014015	.0009836	-14.25	0.000	-.0159428	-.0120872
fem_educ	.0545129	.0066007	8.26	0.000	.0415758	.06745
kids	-.0470199	.0123397	-3.81	0.000	-.0712052	-.0228346
male_educ	0	(omitted)				

Here we see that a \$1,000 increase in `other_inc` leads to an average decrease of 0.014 in the probability that the woman has a job. `male_edu` has no effect because it appears only as an instrument. ◁

Obtaining predicted values

After fitting your model with `ivprobit`, you can obtain the linear prediction and its standard error for both the estimation sample and other samples by using the `predict` command; see [U] **20 Estimation and postestimation commands** and [R] **predict**. If you had used the maximum likelihood estimator, you could also obtain the probability of a positive outcome.

`predict`'s `pr` option calculates the probability of a positive outcome, remembering any rules used to identify the model, and calculates missing for excluded observations. `predict`'s `rules` option uses the rules in predicting probabilities, whereas `predict`'s `asif` option ignores both the rules and the exclusion criteria and calculates probabilities for all possible observations by using the estimated parameters from the model. See *Obtaining predicted values* in [R] **probit postestimation** for an example.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

The linear prediction is calculated as $\boldsymbol{z}_i\widehat{\boldsymbol{\delta}}$, where $\widehat{\boldsymbol{\delta}}$ is the estimated value of $\boldsymbol{\delta}$, and $\boldsymbol{z}_i$ and $\boldsymbol{\delta}$ are defined in (1*a*) of [R] **ivprobit**. The probability of a positive outcome is $\Phi(\boldsymbol{z}_i\widehat{\boldsymbol{\delta}})$, where $\Phi(\cdot)$ is the standard normal distribution function.

Also see

[R] **ivprobit** — Probit model with continuous endogenous regressors

[U] **20 Estimation and postestimation commands**

Title

ivregress — Single-equation instrumental-variables regression

Syntax

```
ivregress estimator depvar [varlist1] (varlist2 = varlistiv) [if] [in] [weight]
    [, options]
```

estimator	Description
`2sls`	two-stage least squares (2SLS)
`liml`	limited-information maximum likelihood (LIML)
`gmm`	generalized method of moments (GMM)

options	Description
Model	
`noconstant`	suppress constant term
`hascons`	has user-supplied constant
GMM[1]	
`wmatrix(`*wmtype*`)`	*wmtype* may be `robust`, `cluster` *clustvar*, `hac` *kernel*, or `unadjusted`
`center`	center moments in weight matrix computation
`igmm`	use iterative instead of two-step GMM estimator
`eps(#)`[2]	specify # for parameter convergence criterion; default is `eps(1e-6)`
`weps(#)`[2]	specify # for weight matrix convergence criterion; default is `weps(1e-6)`
optimization_options[2]	control the optimization process; seldom used
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `unadjusted`, `robust`, `cluster` *clustvar*, `bootstrap`, `jackknife`, or `hac` *kernel*
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`first`	report first-stage regression
`small`	make degrees-of-freedom adjustments and report small-sample statistics
`noheader`	display only the coefficient table
`depname(`*depname*`)`	substitute dependent variable name
`eform(`*string*`)`	report exponentiated coefficients and use *string* to label them
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`perfect`	do not check for collinearity between endogenous regressors and excluded instruments
`coeflegend`	display legend instead of statistics

[1]These options may be specified only when gmm is specified.

[2]These options may be specified only when igmm is specified.

varlist$_1$ and *varlist*$_{\text{iv}}$ may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *varlist*$_1$, *varlist*$_2$, and *varlist*$_{\text{iv}}$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, jackknife, rolling, statsby, and svy are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

aweights are not allowed with the jackknife prefix; see [R] **jackknife**.

hascons, vce(), noheader, depname(), and weights are not allowed with the svy prefix; see [SVY] **svy**.

aweights, fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

perfect and coeflegend do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Endogenous covariates > Single-equation instrumental-variables regression

Description

ivregress fits a linear regression of *depvar* on *varlist*$_1$ and *varlist*$_2$, using *varlist*$_{\text{iv}}$ (along with *varlist*$_1$) as instruments for *varlist*$_2$. ivregress supports estimation via two-stage least squares (2SLS), limited-information maximum likelihood (LIML), and generalized method of moments (GMM).

In the language of instrumental variables, *varlist*$_1$ and *varlist*$_{\text{iv}}$ are the exogenous variables, and *varlist*$_2$ are the endogenous variables.

Options

Model

noconstant; see [R] **estimation options**.

hascons indicates that a user-defined constant or its equivalent is specified among the independent variables.

GMM

wmatrix(*wmtype*) specifies the type of weighting matrix to be used in conjunction with the GMM estimator.

Specifying wmatrix(robust) requests a weighting matrix that is optimal when the error term is heteroskedastic. wmatrix(robust) is the default.

Specifying wmatrix(cluster *clustvar*) requests a weighting matrix that accounts for arbitrary correlation among observations within clusters identified by *clustvar*.

Specifying wmatrix(hac *kernel #*) requests a heteroskedasticity- and autocorrelation-consistent (HAC) weighting matrix using the specified kernel (see below) with # lags. The bandwidth of a kernel is equal to $\#+1$.

Specifying wmatrix(hac *kernel* opt) requests an HAC weighting matrix using the specified kernel, and the lag order is selected using Newey and West's (1994) optimal lag-selection algorithm.

Specifying wmatrix(hac *kernel*) requests an HAC weighting matrix using the specified kernel and $N-2$ lags, where N is the sample size.

There are three kernels available for HAC weighting matrices, and you may request each one by using the name used by statisticians or the name perhaps more familiar to economists:

bartlett or nwest requests the Bartlett (Newey–West) kernel;

parzen or gallant requests the Parzen (Gallant 1987) kernel; and

quadraticspectral or andrews requests the quadratic spectral (Andrews 1991) kernel.

Specifying wmatrix(unadjusted) requests a weighting matrix that is suitable when the errors are homoskedastic. The GMM estimator with this weighting matrix is equivalent to the 2SLS estimator.

center requests that the sample moments be centered (demeaned) when computing GMM weight matrices. By default, centering is not done.

igmm requests that the iterative GMM estimator be used instead of the default two-step GMM estimator. Convergence is declared when the relative change in the parameter vector from one iteration to the next is less than eps() or the relative change in the weight matrix is less than weps().

eps(#) specifies the convergence criterion for successive parameter estimates when the iterative GMM estimator is used. The default is eps(1e-6). Convergence is declared when the relative difference between successive parameter estimates is less than eps() and the relative difference between successive estimates of the weighting matrix is less than weps().

weps(#) specifies the convergence criterion for successive estimates of the weighting matrix when the iterative GMM estimator is used. The default is weps(1e-6). Convergence is declared when the relative difference between successive parameter estimates is less than eps() and the relative difference between successive estimates of the weighting matrix is less than weps().

optimization_options: iterate(#), [no]log. iterate() specifies the maximum number of iterations to perform in conjunction with the iterative GMM estimator. The default is 16,000 or the number set using set maxiter (see [R] **maximize**). log/nolog specifies whether to show the iteration log. These options are seldom used.

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

vce(unadjusted), the default for 2sls and liml, specifies that an unadjusted (nonrobust) VCE matrix be used. The default for gmm is based on the *wmtype* specified in the wmatrix() option; see wmatrix(*wmtype*) above. If wmatrix() is specified with gmm but vce() is not, then *vcetype* is set equal to *wmtype*. To override this behavior and obtain an unadjusted (nonrobust) VCE matrix, specify vce(unadjusted).

ivregress also allows the following:

vce(hac *kernel* [#|opt]) specifies that an HAC covariance matrix be used. The syntax used with vce(hac *kernel* ...) is identical to that used with wmatrix(hac *kernel* ...); see wmatrix(*wmtype*) above.

Reporting

level(#); see [R] **estimation options**.

first requests that the first-stage regression results be displayed.

`small` requests that the degrees-of-freedom adjustment $N/(N-k)$ be made to the variance–covariance matrix of parameters and that small-sample F and t statistics be reported, where N is the sample size and k is the number of parameters estimated. By default, no degrees-of-freedom adjustment is made, and Wald and z statistics are reported. Even with this option, no degrees-of-freedom adjustment is made to the weighting matrix when the GMM estimator is used.

`noheader` suppresses the display of the summary statistics at the top of the output, displaying only the coefficient table.

`depname(`*depname*`)` is used only in programs and ado-files that use `ivregress` to fit models other than instrumental-variables regression. `depname()` may be specified only at estimation time. *depname* is recorded as the identity of the dependent variable, even though the estimates are calculated using *depvar*. This method affects the labeling of the output—not the results calculated—but could affect later calculations made by `predict`, where the residual would be calculated as deviations from *depname* rather than *depvar*. `depname()` is most typically used when *depvar* is a temporary variable (see [P] **macro**) used as a proxy for *depname*.

`eform(`*string*`)` is used only in programs and ado-files that use `ivregress` to fit models other than instrumental-variables regression. `eform()` specifies that the coefficient table be displayed in "exponentiated form", as defined in [R] **maximize**, and that *string* be used to label the exponentiated coefficients in the table.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following options are available with `ivregress` but are not shown in the dialog box:

`perfect` requests that `ivregress` not check for collinearity between the endogenous regressors and excluded instruments, allowing one to specify "perfect" instruments. This option cannot be used with the LIML estimator. This option may be required when using `ivregress` to implement other estimators.

`coeflegend`; see [R] **estimation options**.

Remarks

`ivregress` performs instrumental-variables regression and weighted instrumental-variables regression. For a general discussion of instrumental variables, see Baum (2006), Cameron and Trivedi (2005; 2010, chap. 6) Davidson and MacKinnon (1993, 2004), Greene (2012, chap. 8), and Wooldridge (2009, 2010). See Hall (2005) for a lucid presentation of GMM estimation. Angrist and Pischke (2009, chap. 4) offer a casual yet thorough introduction to instrumental-variables estimators, including their use in estimating treatment effects. Some of the earliest work on simultaneous systems can be found in Cowles Commission monographs—Koopmans and Marschak (1950) and Koopmans and Hood (1953)—with the first developments of 2SLS appearing in Theil (1953) and Basmann (1957). However, Stock and Watson (2011, 422–424) present an example of the method of instrumental variables that was first published in 1928 by Philip Wright.

The syntax for `ivregress` assumes that you want to fit one equation from a system of equations or an equation for which you do not want to specify the functional form for the remaining equations of the system. To fit a full system of equations, using either 2SLS equation-by-equation or three-stage least squares, see [R] **reg3**. An advantage of `ivregress` is that you can fit one equation of a multiple-equation system without specifying the functional form of the remaining equations.

Formally, the model fit by `ivregress` is

$$y_i = \mathbf{y}_i\beta_1 + \mathbf{x}_{1i}\beta_2 + u_i \tag{1}$$

$$\mathbf{y}_i = \mathbf{x}_{1i}\boldsymbol{\Pi}_1 + \mathbf{x}_{2i}\boldsymbol{\Pi}_2 + \mathbf{v}_i \tag{2}$$

Here y_i is the dependent variable for the ith observation, $\mathbf{y}_i$ represents the endogenous regressors (*varlist*$_2$ in the syntax diagram), $\mathbf{x}_{1i}$ represents the included exogenous regressors (*varlist*$_1$ in the syntax diagram), and $\mathbf{x}_{2i}$ represents the excluded exogenous regressors (*varlist*$_{\text{iv}}$ in the syntax diagram). $\mathbf{x}_{1i}$ and $\mathbf{x}_{2i}$ are collectively called the instruments. u_i and $\mathbf{v}_i$ are zero-mean error terms, and the correlations between u_i and the elements of $\mathbf{v}_i$ are presumably nonzero.

The rest of the discussion is presented under the following headings:

2SLS and LIML estimators
GMM estimator

2SLS and LIML estimators

The most common instrumental-variables estimator is 2SLS.

▷ Example 1: 2SLS estimator

We have state data from the 1980 census on the median dollar value of owner-occupied housing (`hsngval`) and the median monthly gross rent (`rent`). We want to model `rent` as a function of `hsngval` and the percentage of the population living in urban areas (`pcturban`):

$$\texttt{rent}_i = \beta_0 + \beta_1 \texttt{hsngval}_i + \beta_2 \texttt{pcturban}_i + u_i$$

where i indexes states and u_i is an error term.

Because random shocks that affect rental rates in a state probably also affect housing values, we treat `hsngval` as endogenous. We believe that the correlation between `hsngval` and u is not equal to zero. On the other hand, we have no reason to believe that the correlation between `pcturban` and u is nonzero, so we assume that `pcturban` is exogenous.

Because we are treating `hsngval` as an endogenous regressor, we must have one or more additional variables available that are correlated with `hsngval` but uncorrelated with u. Moreover, these excluded exogenous variables must not affect `rent` directly, because if they do then they should be included in the regression equation we specified above. In our dataset, we have a variable for family income (`faminc`) and for region of the country (`region`) that we believe are correlated with `hsngval` but not the error term. Together, `pcturban`, `faminc`, and factor variables `2.region`, `3.region`, and `4.region` constitute our set of instruments.

To fit the equation in Stata, we specify the dependent variable and the list of included exogenous variables. In parentheses, we specify the endogenous regressors, an equal sign, and the excluded exogenous variables. Only the additional exogenous variables must be specified to the right of the equal sign; the exogenous variables that appear in the regression equation are automatically included as instruments.

Here we fit our model with the 2SLS estimator:

```
. use http://www.stata-press.com/data/r12/hsng
(1980 Census housing data)
. ivregress 2sls rent pcturban (hsngval = faminc i.region)
Instrumental variables (2SLS) regression          Number of obs =      50
                                                  Wald chi2(2)  =   90.76
                                                  Prob > chi2   =  0.0000
                                                  R-squared     =  0.5989
                                                  Root MSE      =  22.166
------------------------------------------------------------------------------
        rent |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     hsngval |   .0022398   .0003284     6.82   0.000     .0015961    .0028836
    pcturban |    .081516   .2987652     0.27   0.785     -.504053     .667085
       _cons |   120.7065   15.22839     7.93   0.000     90.85942    150.5536
------------------------------------------------------------------------------
Instrumented:  hsngval
Instruments:   pcturban faminc 2.region 3.region 4.region
```

As we would expect, states with higher housing values have higher rental rates. The proportion of a state's population that is urban does not have a significant effect on rents.

◁

❑ Technical note

In a simultaneous-equations framework, we could write the model we just fit as

$$\texttt{hsngval}_i = \pi_0 + \pi_1\texttt{faminc}_i + \pi_2\texttt{2.region}_i + \pi_3\texttt{3.region}_i + \pi_4\texttt{4.region}_i + v_i$$
$$\texttt{rent}_i = \beta_0 + \beta_1\texttt{hsngval}_i + \beta_2\texttt{pcturban}_i + u_i$$

which here happens to be recursive (triangular), because `hsngval` appears in the equation for `rent` but `rent` does not appear in the equation for `hsngval`. In general, however, systems of simultaneous equations are not recursive. Because this system is recursive, we could fit the two equations individually via OLS if we were willing to assume that u and v were independent. For a more detailed discussion of triangular systems, see Kmenta (1997, 719–720).

Historically, instrumental-variables estimation and systems of simultaneous equations were taught concurrently, and older textbooks describe instrumental-variables estimation solely in the context of simultaneous equations. However, in recent decades, the treatment of endogeneity and instrumental-variables estimation has taken on a much broader scope, while interest in the specification of complete systems of simultaneous equations has waned. Most recent textbooks, such as Cameron and Trivedi (2005), Davidson and MacKinnon (1993, 2004), and Wooldridge (2009, 2010), treat instrumental-variables estimation as an integral part of the modern economists' toolkit and introduce it long before shorter discussions on simultaneous equations.

❑

In addition to the 2SLS member of the κ-class estimators, `ivregress` implements the LIML estimator. Both theoretical and Monte Carlo exercises indicate that the LIML estimator may yield less bias and confidence intervals with better coverage rates than the 2SLS estimator. See Poi (2006) and Stock, Wright, and Yogo (2002) (and the papers cited therein) for Monte Carlo evidence.

▷ Example 2: LIML estimator

Here we refit our model with the LIML estimator:

```
. ivregress liml rent pcturban (hsngval = faminc i.region)
Instrumental variables (LIML) regression              Number of obs =      50
                                                      Wald chi2(2)  =   75.71
                                                      Prob > chi2   =  0.0000
                                                      R-squared     =  0.4901
                                                      Root MSE      =  24.992
------------------------------------------------------------------------------
        rent |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     hsngval |   .0026686   .0004173     6.39   0.000     .0018507    .0034865
    pcturban |  -.1827391   .3571132    -0.51   0.609    -.8826681    .5171899
       _cons |   117.6087   17.22625     6.83   0.000     83.84587    151.3715
------------------------------------------------------------------------------
Instrumented:  hsngval
Instruments:   pcturban faminc 2.region 3.region 4.region
```

These results are qualitatively similar to the 2SLS results, although the coefficient on **hsngval** is about 19% higher.

◁

GMM estimator

Since the celebrated paper of Hansen (1982), the GMM has been a popular method of estimation in economics and finance, and it lends itself well to instrumental-variables estimation. The basic principle is that we have some *moment* or *orthogonality* conditions of the form

$$E(\mathbf{z}_i u_i) = \mathbf{0} \tag{3}$$

From (1), we have $u_i = y_i - \mathbf{y}_i\boldsymbol{\beta}_1 - \mathbf{x}_{1i}\boldsymbol{\beta}_2$. What are the elements of the instrument vector $\mathbf{z}_i$? By assumption, $\mathbf{x}_{1i}$ is uncorrelated with u_i, as are the excluded exogenous variables $\mathbf{x}_{2i}$, and so we use $\mathbf{z}_i = [\mathbf{x}_{1i}\ \mathbf{x}_{2i}]$. The moment conditions are simply the mathematical representation of the assumption that the instruments are exogenous—that is, the instruments are orthogonal to (uncorrelated with) u_i.

If the number of elements in $\mathbf{z}_i$ is just equal to the number of unknown parameters, then we can apply the analogy principle to (3) and solve

$$\frac{1}{N}\sum_i \mathbf{z}_i u_i = \frac{1}{N}\sum_i \mathbf{z}_i\left(y_i - \mathbf{y}_i\boldsymbol{\beta}_1 - \mathbf{x}_{1i}\boldsymbol{\beta}_2\right) = \mathbf{0} \tag{4}$$

This equation is known as the method of moments estimator. Here where the number of instruments equals the number of parameters, the method of moments estimator coincides with the 2SLS estimator, which also coincides with what has historically been called the indirect least-squares estimator (Judge et al. 1985, 595).

The "generalized" in GMM addresses the case in which the number of instruments (columns of $\mathbf{z}_i$) exceeds the number of parameters to be estimated. Here there is no unique solution to the population moment conditions defined in (3), so we cannot use (4). Instead, we define the objective function

$$Q(\boldsymbol{\beta}_1, \boldsymbol{\beta}_2) = \left(\frac{1}{N}\sum_i \mathbf{z}_i u_i\right)' \mathbf{W} \left(\frac{1}{N}\sum_i \mathbf{z}_i u_i\right) \tag{5}$$

where $\mathbf{W}$ is a positive-definite matrix with the same number of rows and columns as the number of columns of $\mathbf{z}_i$. $\mathbf{W}$ is known as the weighting matrix, and we specify its structure with the `wmatrix()` option. The GMM estimator of (β_1, β_2) minimizes $Q(\beta_1, \beta_2)$; that is, the GMM estimator chooses β_1 and β_2 to make the moment conditions as close to zero as possible for a given $\mathbf{W}$. For a more general GMM estimator, see [R] **gmm**. `gmm` does not restrict you to fitting a single linear equation, though the syntax is more complex.

A well-known result is that if we define the matrix $\mathbf{S}_0$ to be the covariance of $\mathbf{z}_i u_i$ and set $\mathbf{W} = \mathbf{S}_0^{-1}$, then we obtain the optimal two-step GMM estimator, where by optimal estimator we mean the one that results in the smallest variance given the moment conditions defined in (3).

Suppose that the errors u_i are heteroskedastic but independent among observations. Then

$$\mathbf{S}_0 = E(\mathbf{z}_i u_i u_i \mathbf{z}_i') = E(u_i^2 \mathbf{z}_i \mathbf{z}_i')$$

and the sample analogue is

$$\widehat{\mathbf{S}} = \frac{1}{N} \sum_i \widehat{u}_i^2 \mathbf{z}_i \mathbf{z}_i' \tag{6}$$

To implement this estimator, we need estimates of the sample residuals $\widehat{u}_i$. `ivregress gmm` obtains the residuals by estimating β_1 and β_2 by 2SLS and then evaluates (6) and sets $\mathbf{W} = \widehat{\mathbf{S}}^{-1}$. Equation (6) is the same as the center term of the "sandwich" robust covariance matrix available from most Stata estimation commands through the `vce(robust)` option.

▷ Example 3: GMM estimator

Here we refit our model of rents by using the GMM estimator, allowing for heteroskedasticity in u_i:

```
. ivregress gmm rent pcturban (hsngval = faminc i.region), wmatrix(robust)
Instrumental variables (GMM) regression               Number of obs =      50
                                                      Wald chi2(2)  =  112.09
                                                      Prob > chi2   =  0.0000
                                                      R-squared     =  0.6616
GMM weight matrix: Robust                             Root MSE      =  20.358

------------------------------------------------------------------------------
             |               Robust
        rent |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     hsngval |   .0014643   .0004473     3.27   0.001     .0005877    .002341
    pcturban |   .7615482   .2895105     2.63   0.009     .1941181    1.328978
       _cons |   112.1227   10.80234    10.38   0.000     90.95052    133.2949
------------------------------------------------------------------------------
Instrumented:  hsngval
Instruments:   pcturban faminc 2.region 3.region 4.region
```

Because we requested that a heteroskedasticity-consistent weighting matrix be used during estimation but did not specify the `vce()` option, `ivregress` reported standard errors that are robust to heteroskedasticity. Had we specified `vce(unadjusted)`, we would have obtained standard errors that would be correct only if the weighting matrix $\mathbf{W}$ does in fact converge to $\mathbf{S}_0^{-1}$.

◁

❑ Technical note

Many software packages that implement GMM estimation use the same heteroskedasticity-consistent weighting matrix we used in the previous example to obtain the optimal two-step estimates but do not use a heteroskedasticity-consistent VCE, even though they may label the standard errors as being "robust". To replicate results obtained from other packages, you may have to use the `vce(unadjusted)` option. See *Methods and formulas* below for a discussion of robust covariance matrix estimation in the GMM framework.

❑

By changing our definition of $\mathbf{S}_0$, we can obtain GMM estimators suitable for use with other types of data that violate the assumption that the errors are independent and identically distributed. For example, you may have a dataset that consists of multiple observations for each person in a sample. The observations that correspond to the same person are likely to be correlated, and the estimation technique should account for that lack of independence. Say that in your dataset, people are identified by the variable `personid` and you type

```
. ivregress gmm ..., wmatrix(cluster personid)
```

Here `ivregress` estimates $\mathbf{S}_0$ as

$$\widehat{\mathbf{S}} = \frac{1}{N}\sum_{c\in C}\mathbf{q}_c\mathbf{q}_c'$$

where C denotes the set of clusters and

$$\mathbf{q}_c = \sum_{i\in c_j}\widehat{u}_i\mathbf{z}_i$$

where c_j denotes the jth cluster. This weighting matrix accounts for the within-person correlation among observations, so the GMM estimator that uses this version of $\mathbf{S}_0$ will be more efficient than the estimator that ignores this correlation.

▷ Example 4: GMM estimator with clustering

We have data from the National Longitudinal Survey on young women's wages as reported in a series of interviews from 1968 through 1988, and we want to fit a model of wages as a function of each woman's age and age squared, job tenure, birth year, and level of education. We believe that random shocks that affect a woman's wage also affect her job tenure, so we treat tenure as endogenous. As additional instruments, we use her union status, number of weeks worked in the past year, and a dummy indicating whether she lives in a metropolitan area. Because we have several observations for each woman (corresponding to interviews done over several years), we want to control for clustering on each person.

```
. use http://www.stata-press.com/data/r12/nlswork
(National Longitudinal Survey.  Young Women 14-26 years of age in 1968)
. ivregress gmm ln_wage age c.age#c.age birth_yr grade
> (tenure = union wks_work msp), wmatrix(cluster idcode)
Instrumental variables (GMM) regression               Number of obs =   18625
                                                      Wald chi2(5)  = 1807.17
                                                      Prob > chi2   =  0.0000
                                                      R-squared     =       .
GMM weight matrix: Cluster (idcode)                   Root MSE      =  .46951
                             (Std. Err. adjusted for 4110 clusters in idcode)
------------------------------------------------------------------------------
             |               Robust
     ln_wage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      tenure |    .099221   .0037764    26.27   0.000     .0918194    .1066227
         age |   .0171146   .0066895     2.56   0.011     .0040034    .0302259
             |
 c.age#c.age |  -.0005191    .000111    -4.68   0.000    -.0007366   -.0003016
             |
    birth_yr |  -.0085994   .0021932    -3.92   0.000     -.012898   -.0043008
       grade |    .071574   .0029938    23.91   0.000     .0657062    .0774417
       _cons |   .8575071   .1616274     5.31   0.000     .5407231    1.174291
------------------------------------------------------------------------------
Instrumented:  tenure
Instruments:   age c.age#c.age birth_yr grade union wks_work msp
```

Both job tenure and years of schooling have significant positive effects on wages.

◁

Time-series data are often plagued by serial correlation. In these cases, we can construct a weighting matrix to account for the fact that the error in period t is probably correlated with the errors in periods $t-1$, $t-2$, etc. An HAC weighting matrix can be used to account for both serial correlation and potential heteroskedasticity.

To request an HAC weighting matrix, you specify the `wmatrix(hac` *kernel* $\left[\,\#\,|\,$`opt`$\,\right]$`)` option. *kernel* specifies which of three kernels to use: `bartlett`, `parzen`, or `quadraticspectral`. *kernel* determines the amount of weight given to lagged values when computing the HAC matrix, and # denotes the maximum number of lags to use. Many texts refer to the bandwidth of the kernel instead of the number of lags; the bandwidth is equal to the number of lags plus one. If neither `opt` nor # is specified, then $N-2$ lags are used, where N is the sample size.

If you specify `wmatrix(hac` *kernel* `opt)`, then `ivregress` uses Newey and West's (1994) algorithm for automatically selecting the number of lags to use. Although the authors' Monte Carlo simulations do show that the procedure may result in size distortions of hypothesis tests, the procedure is still useful when little other information is available to help choose the number of lags.

For more on GMM estimation, see Baum (2006); Baum, Schaffer, and Stillman (2003, 2007); Cameron and Trivedi (2005); Davidson and MacKinnon (1993, 2004); Hayashi (2000); or Wooldridge (2010). See Newey and West (1987) for an introduction to HAC covariance matrix estimation.

Saved results

ivregress saves the following in e():

Scalars

e(N)	number of observations
e(mss)	model sum of squares
e(df_m)	model degrees of freedom
e(rss)	residual sum of squares
e(df_r)	residual degrees of freedom
e(r2)	R^2
e(r2_a)	adjusted R^2
e(F)	F statistic
e(rmse)	root mean squared error
e(N_clust)	number of clusters
e(chi2)	χ^2
e(kappa)	κ used in LIML estimator
e(J)	value of GMM objective function
e(wlagopt)	lags used in HAC weight matrix (if Newey–West algorithm used)
e(vcelagopt)	lags used in HAC VCE matrix (if Newey–West algorithm used)
e(rank)	rank of e(V)
e(iterations)	number of GMM iterations (0 if not applicable)

Macros

e(cmd)	ivregress
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(instd)	instrumented variable
e(insts)	instruments
e(constant)	noconstant or hasconstant if specified
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(hac_kernel)	HAC kernel
e(hac_lag)	HAC lag
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(estimator)	2sls, liml, or gmm
e(exogr)	exogenous regressors
e(wmatrix)	*wmtype* specified in wmatrix()
e(moments)	centered if center specified
e(small)	small if small-sample statistics
e(depname)	*depname* if depname(*depname*) specified; otherwise same as e(depvar)
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(footnote)	program used to implement footnote display
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(W)	weight matrix used to compute GMM estimates
e(S)	moment covariance matrix used to compute GMM variance–covariance matrix
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

ivregress is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Notation
2SLS and LIML estimators
GMM estimator

Notation

Items printed in lowercase and italicized (for example, x) are scalars. Items printed in lowercase and boldfaced (for example, $\mathbf{x}$) are vectors. Items printed in uppercase and boldfaced (for example, $\mathbf{X}$) are matrices.

The model is

$$\mathbf{y} = \mathbf{Y}\boldsymbol{\beta}_1 + \mathbf{X}_1\boldsymbol{\beta}_2 + \mathbf{u} = \mathbf{X}\boldsymbol{\beta} + \mathbf{u}$$

$$\mathbf{Y} = \mathbf{X}_1\boldsymbol{\Pi}_1 + \mathbf{X}_2\boldsymbol{\Pi}_2 + \mathbf{v} = \mathbf{Z}\boldsymbol{\Pi} + \mathbf{V}$$

where $\mathbf{y}$ is an $N \times 1$ vector of the left-hand-side variable; N is the sample size; $\mathbf{Y}$ is an $N \times p$ matrix of p endogenous regressors; $\mathbf{X}_1$ is an $N \times k_1$ matrix of k_1 included exogenous regressors; $\mathbf{X}_2$ is an $N \times k_2$ matrix of k_2 excluded exogenous variables, $\mathbf{X} = [\mathbf{Y}\ \mathbf{X}_1]$, $\mathbf{Z} = [\mathbf{X}_1\ \mathbf{X}_2]$; $\mathbf{u}$ is an $N \times 1$ vector of errors; $\mathbf{V}$ is an $N \times p$ matrix of errors; $\boldsymbol{\beta} = [\boldsymbol{\beta}_1\ \boldsymbol{\beta}_2]$ is a $k = (p + k_1) \times 1$ vector of parameters; and $\boldsymbol{\Pi}$ is a $(k_1 + k_2) \times p$ vector of parameters. If a constant term is included in the model, then one column of $\mathbf{X}_1$ contains all ones.

Let $\mathbf{v}$ be a column vector of weights specified by the user. If no weights are specified, $\mathbf{v} = \mathbf{1}$. Let $\mathbf{w}$ be a column vector of normalized weights. If no weights are specified or if the user specified fweights or iweights, $\mathbf{w} = \mathbf{v}$; otherwise, $\mathbf{w} = \{\mathbf{v}/(\mathbf{1}'\mathbf{v})\}(\mathbf{1}'\mathbf{1})$. Let $\mathbf{D}$ denote the $N \times N$ matrix with $\mathbf{w}$ on the main diagonal and zeros elsewhere. If no weights are specified, $\mathbf{D}$ is the identity matrix.

The weighted number of observations n is defined as $\mathbf{1}'\mathbf{w}$. For iweights, this is truncated to an integer. The *sum of the weights* is $\mathbf{1}'\mathbf{v}$. Define $c = 1$ if there is a constant in the regression and zero otherwise.

The order condition for identification requires that $k_2 \geq p$: the number of excluded exogenous variables must be at least as great as the number of endogenous regressors.

In the following formulas, if weights are specified, $\mathbf{X}_1'\mathbf{X}_1$, $\mathbf{X}'\mathbf{X}$, $\mathbf{X}'\mathbf{y}$, $\mathbf{y}'\mathbf{y}$, $\mathbf{Z}'\mathbf{Z}$, $\mathbf{Z}'\mathbf{X}$, and $\mathbf{Z}'\mathbf{y}$ are replaced with $\mathbf{X}_1'\mathbf{D}\mathbf{X}_1$, $\mathbf{X}'\mathbf{D}\mathbf{X}$, $\mathbf{X}'\mathbf{D}\mathbf{y}$, $\mathbf{y}'\mathbf{D}\mathbf{y}$, $\mathbf{Z}'\mathbf{D}\mathbf{Z}$, $\mathbf{Z}'\mathbf{D}\mathbf{X}$, and $\mathbf{Z}'\mathbf{D}\mathbf{y}$, respectively. We suppress the $\mathbf{D}$ below to simplify the notation.

2SLS and LIML estimators

Define the κ-class estimator of β as

$$\mathbf{b} = \left\{\mathbf{X}'(\mathbf{I}-\kappa\mathbf{M}_\mathbf{Z})^{-1}\mathbf{X}\right\}^{-1}\mathbf{X}'(\mathbf{I}-\kappa\mathbf{M}_\mathbf{Z})^{-1}\mathbf{y}$$

where $\mathbf{M}_\mathbf{Z} = \mathbf{I} - \mathbf{Z}(\mathbf{Z}'\mathbf{Z})^{-1}\mathbf{Z}'$. The 2SLS estimator results from setting $\kappa = 1$. The LIML estimator results from selecting κ to be the minimum eigenvalue of $(\mathbf{Y}'\mathbf{M}_\mathbf{Z}\mathbf{Y})^{-1/2}\mathbf{Y}'\mathbf{M}_{\mathbf{X}_1}\mathbf{Y}(\mathbf{Y}'\mathbf{M}_\mathbf{Z}\mathbf{Y})^{-1/2}$, where $\mathbf{M}_{\mathbf{X}_1} = \mathbf{I} - \mathbf{X}_1(\mathbf{X}_1'\mathbf{X}_1)^{-1}\mathbf{X}_1'$.

The total sum of squares (TSS) equals $\mathbf{y}'\mathbf{y}$ if there is no intercept and $\mathbf{y}'\mathbf{y} - \left\{(\mathbf{1}'\mathbf{y})^2/n\right\}$ otherwise. The degrees of freedom are $n-c$. The error sum of squares (ESS) is defined as $\mathbf{y}'\mathbf{y} - 2\mathbf{b}\mathbf{X}'\mathbf{y} + \mathbf{b}'\mathbf{X}'\mathbf{X}\mathbf{b}$. The model sum of squares (MSS) equals TSS − ESS. The degrees of freedom are $k-c$.

The mean squared error, s^2, is defined as ESS$/(n-k)$ if `small` is specified and ESS$/n$ otherwise. The root mean squared error is s, its square root.

If $c = 1$ and `small` is not specified, a Wald statistic, W, of the joint significance of the $k-1$ parameters of β except the constant term is calculated; $W \sim \chi^2(k-1)$. If $c = 1$ and `small` is specified, then an F statistic is calculated as $F = W/(k-1)$; $F \sim F(k-1, n-k)$.

The R-squared is defined as $R^2 = 1 - \text{ESS}/\text{TSS}$.

The adjusted R-squared is $R^2_\text{a} = 1 - (1-R^2)(n-c)/(n-k)$.

If `robust` is not specified, then $\text{Var}(\mathbf{b}) = s^2\left\{\mathbf{X}'(\mathbf{I}-\kappa\mathbf{M}_\mathbf{Z})^{-1}\mathbf{X}\right\}^{-1}$. For a discussion of robust variance estimates in regression and regression with instrumental variables, see *Methods and formulas* in [R] **regress**. If `small` is not specified, then $k = 0$ in the formulas given there.

This command also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

GMM estimator

We obtain an initial consistent estimate of β by using the 2SLS estimator; see above. Using this estimate of β, we compute the weighting matrix $\mathbf{W}$ and calculate the GMM estimator

$$\mathbf{b}_\text{GMM} = \left\{\mathbf{X}'\mathbf{Z}\mathbf{W}\mathbf{Z}'\mathbf{X}\right\}^{-1}\mathbf{X}'\mathbf{Z}\mathbf{W}\mathbf{Z}'\mathbf{y}$$

The variance of $\mathbf{b}_\text{GMM}$ is

$$\text{Var}(\mathbf{b}_\text{GMM}) = n\left\{\mathbf{X}'\mathbf{Z}\mathbf{W}\mathbf{Z}'\mathbf{X}\right\}^{-1}\mathbf{X}'\mathbf{Z}\mathbf{W}\widehat{\mathbf{S}}\mathbf{W}\mathbf{Z}'\mathbf{X}\left\{\mathbf{X}'\mathbf{Z}\mathbf{W}\mathbf{Z}'\mathbf{X}\right\}^{-1}$$

$\text{Var}(\mathbf{b}_\text{GMM})$ is of the sandwich form $\mathbf{DMD}$; see [P] **_robust**. If the user specifies the `small` option, `ivregress` implements a small-sample adjustment by multiplying the VCE by $N/(N-k)$.

If `vce(unadjusted)` is specified, then we set $\widehat{\mathbf{S}} = \mathbf{W}^{-1}$ and the VCE reduces to the "optimal" GMM variance estimator

$$\text{Var}(\beta_\text{GMM}) = n\left\{\mathbf{X}'\mathbf{Z}\mathbf{W}\mathbf{Z}'\mathbf{X}\right\}^{-1}$$

However, if $\mathbf{W}^{-1}$ is not a good estimator of $E(\mathbf{z}_i u_i u_i \mathbf{z}_i')$, then the optimal GMM estimator is inefficient, and inference based on the optimal variance estimator could be misleading.

$\mathbf{W}$ is calculated using the residuals from the initial 2SLS estimates, whereas $\mathbf{S}$ is estimated using the residuals based on $\mathbf{b}_{\mathrm{GMM}}$. The `wmatrix()` option affects the form of $\mathbf{W}$, whereas the `vce()` option affects the form of $\mathbf{S}$. Except for different residuals being used, the formulas for $\mathbf{W}^{-1}$ and $\mathbf{S}$ are identical, so we focus on estimating $\mathbf{W}^{-1}$.

If `wmatrix(unadjusted)` is specified, then

$$\mathbf{W}^{-1} = \frac{s^2}{n}\sum_i \mathbf{z}_i\mathbf{z}_i'$$

where $s^2 = \sum_i u_i^2/n$. This weight matrix is appropriate if the errors are homoskedastic.

If `wmatrix(robust)` is specified, then

$$\mathbf{W}^{-1} = \frac{1}{n}\sum_i u_i^2\mathbf{z}_i\mathbf{z}_i'$$

which is appropriate if the errors are heteroskedastic.

If `wmatrix(cluster` *clustvar*`)` is specified, then

$$\mathbf{W}^{-1} = \frac{1}{n}\sum_c \mathbf{q}_c\mathbf{q}_c'$$

where c indexes clusters,

$$\mathbf{q}_c = \sum_{i\in c_j} u_i\mathbf{z}_i$$

and c_j denotes the jth cluster.

If `wmatrix(hac` *kernel* `[#])` is specified, then

$$\mathbf{W}^{-1} = \frac{1}{n}\sum_i u_i^2\mathbf{z}_i\mathbf{z}_i' + \frac{1}{n}\sum_{l=1}^{l=n-1}\sum_{i=l+1}^{i=n} K(l,m)u_iu_{i-l}\left(\mathbf{z}_i\mathbf{z}_{i-l}' + \mathbf{z}_{i-l}\mathbf{z}_i'\right)$$

where $m = \#$ if # is specified and $m = n-2$ otherwise. Define $z = l/(m+1)$. If *kernel* is `nwest`, then

$$K(l,m) = \begin{cases} 1-z & 0 \le z \le 1 \\ 0 & \text{otherwise} \end{cases}$$

If *kernel* is `gallant`, then

$$K(l,m) = \begin{cases} 1-6z^2+6z^3 & 0 \le z \le 0.5 \\ 2(1-z)^3 & 0.5 < z \le 1 \\ 0 & \text{otherwise} \end{cases}$$

If *kernel* is `quadraticspectral`, then

$$K(l,m) = \begin{cases} 1 & z = 0 \\ 3\left\{\sin(\theta)/\theta - \cos(\theta)\right\}/\theta^2 & \text{otherwise} \end{cases}$$

where $\theta = 6\pi z/5$.

If `wmatrix(hac` *kernel* `opt)` is specified, then `ivregress` uses Newey and West's (1994) automatic lag-selection algorithm, which proceeds as follows. Define $\mathbf{h}$ to be a $(k_1+k_2)\times 1$ vector containing ones in all rows except for the row corresponding to the constant term (if present); that row contains a zero. Define

$$f_i = (u_i \mathbf{z}_i)\mathbf{h}$$

$$\widehat{\sigma}_j = \frac{1}{n}\sum_{i=j+1}^{n} f_i f_{i-j} \qquad j = 0, \ldots, m^*$$

$$\widehat{s}^{(q)} = 2\sum_{j=1}^{m^*} \widehat{\sigma}_j j^q$$

$$\widehat{s}^{(0)} = \widehat{\sigma}_0 + 2\sum_{j=1}^{m^*} \widehat{\sigma}_j$$

$$\widehat{\gamma} = c_\gamma \left\{ \left(\frac{\widehat{s}^{(q)}}{\widehat{s}^{(0)}} \right)^2 \right\}^{1/2q+1}$$

$$m = \widehat{\gamma} n^{1/(2q+1)}$$

where q, m^*, and c_γ depend on the kernel specified:

Kernel	q	m^*	c_γ
Bartlett	1	int $\{20(T/100)^{2/9}\}$	1.1447
Parzen	2	int $\{20(T/100)^{4/25}\}$	2.6614
Quadratic spectral	2	int $\{20(T/100)^{2/25}\}$	1.3221

where int(x) denotes the integer obtained by truncating x toward zero. For the Bartlett and Parzen kernels, the optimal lag is min$\{$int$(m), m^*\}$. For the quadratic spectral, the optimal lag is min$\{m, m^*\}$.

If `center` is specified, when computing weighting matrices `ivregress` replaces the term $u_i z_i$ in the formulas above with $u_i \mathbf{z}_i - \overline{u\mathbf{z}}$, where $\overline{u\mathbf{z}} = \sum_i u_i \mathbf{z}_i / N$.

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Also see

[R] **ivregress postestimation** — Postestimation tools for ivregress

[R] **gmm** — Generalized method of moments estimation

[R] **ivprobit** — Probit model with continuous endogenous regressors

[R] **ivtobit** — Tobit model with continuous endogenous regressors

[R] **reg3** — Three-stage estimation for systems of simultaneous equations

[R] **regress** — Linear regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtivreg** — Instrumental variables and two-stage least squares for panel-data models

Stata Structural Equation Modeling Reference Manual

[U] **20 Estimation and postestimation commands**

Title

ivregress postestimation — Postestimation tools for ivregress

Description

The following postestimation commands are of special interest after `ivregress`:

Command	Description
`estat endogenous`	perform tests of endogeneity
`estat firststage`	report "first-stage" regression statistics
`estat overid`	perform tests of overidentifying restrictions

These commands are not appropriate after the `svy` prefix.

For information about these commands, see below.

The following postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	VCE and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Special-interest postestimation commands

`estat endogenous` performs tests to determine whether endogenous regressors in the model are in fact exogenous. After GMM estimation, the C (difference-in-Sargan) statistic is reported. After 2SLS estimation with an unadjusted VCE, the Durbin (1954) and Wu–Hausman (Wu 1974; Hausman 1978) statistics are reported. After 2SLS estimation with a robust VCE, Wooldridge's (1995) robust score test and a robust regression-based test are reported. In all cases, if the test statistic is significant, then the variables being tested must be treated as endogenous. `estat endogenous` is not available after LIML estimation.

`estat firststage` reports various statistics that measure the relevance of the excluded exogenous variables. By default, whether the equation has one or more than one endogenous regressor determines what statistics are reported.

`estat overid` performs tests of overidentifying restrictions. If the 2SLS estimator was used, Sargan's (1958) and Basmann's (1960) χ^2 tests are reported, as is Wooldridge's (1995) robust score test; if the LIML estimator was used, Anderson and Rubin's (1950) χ^2 test and Basmann's F test are reported; and if the GMM estimator was used, Hansen's (1982) J statistic χ^2 test is reported. A statistically significant test statistic always indicates that the instruments may not be valid.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic]

predict [type] {stub* | newvarlist} [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`residuals`	residuals
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`pr(a,b)`	$\Pr(a < y_j < b)$
`e(a,b)`	$E(y_j \mid a < y_j < b)$
`ystar(a,b)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

where a and b may be numbers or variables; a missing ($a \geq .$) means $-\infty$, and b missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`residuals` calculates the residuals, that is, $y_j - \mathbf{x}_j\mathbf{b}$. These are based on the estimated equation when the observed values of the endogenous variables are used—not the projections of the instruments onto the endogenous variables.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. This is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \mid a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated.
a and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`scores` calculates the scores for the model. A new score variable is created for each endogenous regressor, as well as an equation-level score that applies to all exogenous variables and constant term (if present).

Syntax for estat endogenous

```
estat endogenous [ varlist ] [ , lags(#) forceweights forcenonrobust ]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat endogenous

`lags(#)` specifies the number of lags to use for prewhitening when computing the heteroskedasticity- and autocorrelation-consistent (HAC) version of the score test of endogeneity. Specifying `lags(0)` requests no prewhitening. This option is valid only when the model was fit via 2SLS and an HAC covariance matrix was requested when the model was fit. The default is `lags(1)`.

`forceweights` requests that the tests of endogeneity be computed even though `aweights`, `pweights`, or `iweights` were used in the previous estimation. By default, these tests are conducted only after unweighted or frequency-weighted estimation. The reported critical values may be inappropriate for weighted data, so the user must determine whether the critical values are appropriate for a given application.

forcenonrobust requests that the Durbin and Wu–Hausman tests be performed after 2SLS estimation even though a robust VCE was used at estimation time. This option is available only if the model was fit by 2SLS.

Syntax for estat firststage

```
estat firststage [, all forcenonrobust]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat firststage

all requests that all first-stage goodness-of-fit statistics be reported regardless of whether the model contains one or more endogenous regressors. By default, if the model contains one endogenous regressor, then the first-stage R^2, adjusted R^2, partial R^2, and F statistics are reported, whereas if the model contains multiple endogenous regressors, then Shea's partial R^2 and adjusted partial R^2 are reported instead.

forcenonrobust requests that the minimum eigenvalue statistic and its critical values be reported even though a robust VCE was used at estimation time. The reported critical values assume that the errors are independent and identically distributed (i.i.d.) normal, so the user must determine whether the critical values are appropriate for a given application.

Syntax for estat overid

```
estat overid [, lags(#) forceweights forcenonrobust]
```

Menu

Statistics > Postestimation > Reports and statistics

Options for estat overid

lags(#) specifies the number of lags to use for prewhitening when computing the heteroskedasticity- and autocorrelation-consistent (HAC) version of the score test of overidentifying restrictions. Specifying lags(0) requests no prewhitening. This option is valid only when the model was fit via 2SLS and an HAC covariance matrix was requested when the model was fit. The default is lags(1).

forceweights requests that the tests of overidentifying restrictions be computed even though aweights, pweights, or iweights were used in the previous estimation. By default, these tests are conducted only after unweighted or frequency-weighted estimation. The reported critical values may be inappropriate for weighted data, so the user must determine whether the critical values are appropriate for a given application.

`forcenonrobust` requests that the Sargan and Basmann tests of overidentifying restrictions be performed after 2SLS or LIML estimation even though a robust VCE was used at estimation time. These tests assume that the errors are i.i.d. normal, so the user must determine whether the critical values are appropriate for a given application.

Remarks

Remarks are presented under the following headings:

estat endogenous
estat firststage
estat overid

estat endogenous

A natural question to ask is whether a variable presumed to be endogenous in the previously fit model could instead be treated as exogenous. If the endogenous regressors are in fact exogenous, then the OLS estimator is more efficient; and depending on the strength of the instruments and other factors, the sacrifice in efficiency by using an instrumental-variables estimator can be significant. Thus, unless an instrumental-variables estimator is really needed, OLS should be used instead. `estat endogenous` provides several tests of endogeneity after 2SLS and GMM estimation.

▷ Example 1

In example 1 of [R] **ivregress**, we fit a model of the average rental rate for housing in a state as a function of the percentage of the population living in urban areas and the average value of houses. We treated `hsngval` as endogenous because unanticipated shocks that affect rental rates probably affect house prices as well. We used family income and region dummies as additional instruments for `hsngval`. Here we test whether we could treat `hsngval` as exogenous.

```
. use http://www.stata-press.com/data/r12/hsng
(1980 Census housing data)
. ivregress 2sls rent pcturban (hsngval = faminc i.region)
  (output omitted)
. estat endogenous

  Tests of endogeneity
  Ho: variables are exogenous

  Durbin (score) chi2(1)          =  12.8473  (p = 0.0003)
  Wu-Hausman F(1,46)              =  15.9067  (p = 0.0002)
```

Because we did not specify any variable names after the `estat endogenous` command, Stata by default tested all the endogenous regressors (namely, `hsngval`) in our model. The null hypothesis of the Durbin and Wu–Hausman tests is that the variable under consideration can be treated as exogenous. Here both test statistics are highly significant, so we reject the null of exogeneity; we must continue to treat `hsngval` as endogenous.

◁

The difference between the Durbin and Wu–Hausman tests of endogeneity is that the former uses an estimate of the error term's variance based on the model assuming the variables being tested are exogenous, while the latter uses an estimate of the error variance based on the model assuming the variables being tested are endogenous. Under the null hypothesis that the variables being tested are exogenous, both estimates of the error variance are consistent. What we label the Wu–Hausman statistic is Wu's (1974) "T_2" statistic, which Hausman (1978) showed can be calculated very easily via linear regression. Baum, Schaffer, and Stillman (2003, 2007) provide a lucid discussion of these tests.

When you fit a model with multiple endogenous regressors, you can test the exogeneity of a subset of the regressors while continuing to treat the others as endogenous. For example, say you have three endogenous regressors, `y1`, `y2`, and `y3`, and you fit your model by typing

```
. ivregress depvar ... (y1 y2 y3 = ...)
```

Suppose you are confident that `y1` must be treated as endogenous, but you are undecided about `y2` and `y3`. To test whether `y2` and `y3` can be treated as exogenous, you would type

```
. estat endogenous y2 y3
```

The Durbin and Wu–Hausman tests assume that the error term is i.i.d. Therefore, if you requested a robust VCE at estimation time, `estat endogenous` will instead report Wooldridge's (1995) score test and a regression-based test of exogeneity. Both these tests can tolerate heteroskedastic and autocorrelated errors, while only the regression-based test is amenable to clustering.

▷ Example 2

We refit our housing model, requesting robust standard errors, and then test the exogeneity of `hsngval`:

```
. use http://www.stata-press.com/data/r12/hsng
(1980 Census housing data)
. ivregress 2sls rent pcturban (hsngval = faminc i.region), vce(robust)
  (output omitted)
. estat endogenous
  Tests of endogeneity
  Ho: variables are exogenous
  Robust score chi2(1)            =  2.10428  (p = 0.1469)
  Robust regression F(1,46)       =  4.31101  (p = 0.0435)
```

Wooldridge's score test does not reject the null hypothesis that `hsngval` is exogenous at conventional significance levels ($p = 0.1469$). However, the regression-based test does reject the null hypothesis at the 5% significance level ($p = 0.0435$). Typically, these two tests yield the same conclusion; the fact that our dataset has only 50 observations could be contributing to the discrepancy. Here we would be inclined to continue to treat `hsngval` as endogenous. Even if `hsngval` is exogenous, the 2SLS estimates are still consistent. On the other hand, if `hsngval` is in fact endogenous, the OLS estimates would not be consistent. Moreover, as we will see in our discussion of the `estat overid` command, our additional instruments may be invalid. To test whether an endogenous variable can be treated as exogenous, we must have a valid set of instruments to use to fit the model in the first place!

◁

Unlike the Durbin and Wu–Hausman tests, Wooldridge's score and the regression-based tests do not allow you to test a subset of the endogenous regressors in the model; you can test only whether all the endogenous regressors are in fact exogenous.

After GMM estimation, `estat endogenous` calculates what Hayashi (2000, 220) calls the C statistic, also known as the difference-in-Sargan statistic. The C statistic can be made robust to heteroskedasticity, autocorrelation, and clustering; and the version reported by `estat endogenous` is determined by the weight matrix requested via the `wmatrix()` option used when fitting the model with `ivregress`. Additionally, the test can be used to determine the exogeneity of a subset of the endogenous regressors, regardless of the type of weight matrix used.

If you fit your model using the LIML estimator, you can use the `hausman` command to carry out a traditional Hausman (1978) test between the OLS and LIML estimates.

estat firststage

For an excluded exogenous variable to be a valid instrument, it must be sufficiently correlated with the included endogenous regressors but uncorrelated with the error term. In recent decades, researchers have paid considerable attention to the issue of instruments that are only weakly correlated with the endogenous regressors. In such cases, the usual 2SLS, GMM, and LIML estimators are biased toward the OLS estimator, and inference based on the standard errors reported by, for example, `ivregress` can be severely misleading. For more information on the theory behind instrumental-variables estimation with weak instruments, see Nelson and Startz (1990); Staiger and Stock (1997); Hahn and Hausman (2003); the survey article by Stock, Wright, and Yogo (2002); and Angrist and Pischke (2009, chap. 4).

When the instruments are only weakly correlated with the endogenous regressors, some Monte Carlo evidence suggests that the LIML estimator performs better than the 2SLS and GMM estimators; see, for example, Poi (2006) and Stock, Wright, and Yogo (2002) (and the papers cited therein). On the other hand, the LIML estimator often results in confidence intervals that are somewhat larger than those from the 2SLS estimator.

Moreover, using more instruments is not a solution, because the biases of instrumental-variables estimators increase with the number of instruments. See Hahn and Hausman (2003).

`estat firststage` produces several statistics for judging the explanatory power of the instruments and is most easily explained with examples.

▷ Example 3

Again building on the model fit in example 1 of [R] **ivregress**, we now explore the degree of correlation between the additional instruments `faminc`, `2.region`, `3.region`, and `4.region` and the endogenous regressor `hsngval`:

```
. use http://www.stata-press.com/data/r12/hsng
(1980 Census housing data)
. ivregress 2sls rent pcturban (hsngval = faminc i.region)
  (output omitted)
. estat firststage
  First-stage regression summary statistics
```

Variable	R-sq.	Adjusted R-sq.	Partial R-sq.	F(4,44)	Prob > F
hsngval	0.6908	0.6557	0.5473	13.2978	0.0000

```
  Minimum eigenvalue statistic = 13.2978
```

Critical Values	# of endogenous regressors:	1
Ho: Instruments are weak	# of excluded instruments:	4

	5%	10%	20%	30%
2SLS relative bias	16.85	10.27	6.71	5.34

	10%	15%	20%	25%
2SLS Size of nominal 5% Wald test	24.58	13.96	10.26	8.31
LIML Size of nominal 5% Wald test	5.44	3.87	3.30	2.98

To understand these results, recall that the first-stage regression is

$$\texttt{hsngval}_i = \pi_0 + \pi_1\texttt{pcturban}_i + \pi_2\texttt{faminc} + \pi_3\texttt{2.region} + \pi_4\texttt{3.region} + \pi_5\texttt{4.region} + v_i$$

where v_i is an error term. The column marked "R-sq." is the simple R^2 from fitting the first-stage regression by OLS, and the column marked "Adjusted R-sq." is the adjusted R^2 from that regression. Higher values purportedly indicate stronger instruments, and instrumental-variables estimators exhibit less bias when the instruments are strongly correlated with the endogenous variable.

Looking at just the R^2 and adjusted R^2 can be misleading, however. If `hsngval` were strongly correlated with the included exogenous variable `pcturban` but only weakly correlated with the additional instruments, then these statistics could be large even though a weak-instrument problem is present.

The partial R^2 statistic measures the correlation between `hsngval` and the additional instruments after *partialling out* the effect of `pcturban`. Unlike the R^2 and adjusted R^2 statistics, the partial R^2 statistic will not be inflated because of strong correlation between `hsngval` and `pcturban`. Bound, Jaeger, and Baker (1995) and others have promoted using this statistic.

The column marked "F(4, 44)" is an F statistic for the joint significance of π_2, π_3, π_4, and π_5, the coefficients on the additional instruments. Its p-value is listed in the column marked "Prob > F". If the F statistic is not significant, then the additional instruments have no significant explanatory power for `hsngval` after controlling for the effect of `pcturban`. However, Hall, Rudebusch, and Wilcox (1996) used Monte Carlo simulation to show that simply having an F statistic that is significant at the typical 5% or 10% level is not sufficient. Stock, Wright, and Yogo (2002) suggest that the F statistic should exceed 10 for inference based on the 2SLS estimator to be reliable when there is one endogenous regressor.

`estat firststage` also presents the Cragg and Donald (1993) minimum eigenvalue statistic as a further test of weak instruments. Stock and Yogo (2005) discuss two characterizations of weak instruments: first, weak instruments cause instrumental-variables estimators to be biased; second, hypothesis tests of parameters estimated by instrumental-variables estimators may suffer from severe size distortions. The test statistic in our example is 13.30, which is identical to the F statistic just discussed because our model contains one endogenous regressor.

The null hypothesis of each of Stock and Yogo's tests is that the set of instruments is weak. To perform these tests, we must first choose either the largest relative bias of the 2SLS estimator we are willing to tolerate or the largest rejection rate of a nominal 5% Wald test we are willing to tolerate. If the test statistic exceeds the critical value, we can conclude that our instruments are not weak.

The row marked "2SLS relative bias" contains critical values for the test that the instruments are weak based on the bias of the 2SLS estimator *relative to* the bias of the OLS estimator. For example, from past experience we might know that the OLS estimate of a parameter β may be 50% too high. Saying that we are willing to tolerate a 10% relative bias means that we are willing to tolerate a bias of the 2SLS estimator no greater than 5% (that is, 10% of 50%). In our rental rate model, if we are willing to tolerate a 10% relative bias, then we can conclude that our instruments are not weak because the test statistic of 13.30 exceeds the critical value of 10.22. However, if we were willing to tolerate only a relative bias of 5%, we would conclude that our instruments are weak because $13.30 < 16.85$.

The rows marked "2SLS Size of nominal 5% Wald test" and "LIML Size of nominal 5% Wald test" contain critical values pertaining to Stock and Yogo's (2005) second characterization of weak instruments. This characterization defines a set of instruments to be weak if a Wald test at the 5% level can have an actual rejection rate of no more than 10%, 15%, 20%, or 25%. Using the current example, suppose that we are willing to accept a rejection rate of at most 10%. Because $13.30 < 24.58$, we cannot reject the null hypothesis of weak instruments. On the other hand, if we use the LIML estimator instead, then we can reject the null hypothesis because $13.30 > 5.44$.

◁

❑ Technical note

Stock and Yogo (2005) tabulated critical values for 2SLS relative biases of 5%, 10%, 20%, and 30% for models with 1, 2, or 3 endogenous regressors and between 3 and 30 excluded exogenous variables (instruments). They also provide critical values for worst-case rejection rates of 5%, 10%, 20%, and 25% for nominal 5% Wald tests of the endogenous regressors with 1 or 2 endogenous regressors and between 1 and 30 instruments. If the model previously fit by `ivregress` has more instruments or endogenous regressors than these limits, the critical values are not shown. Stock and Yogo did not consider GMM estimators.

❑

When the model being fit contains more than one endogenous regressor, the R^2 and F statistics described above can overstate the relevance of the excluded instruments. Suppose that there are two endogenous regressors, Y_1 and Y_2, and that there are two additional instruments, z_1 and z_2. Say that z_1 is highly correlated with both Y_1 and Y_2 but z_2 is not correlated with either Y_1 or Y_2. Then the first-stage regression of Y_1 on z_1 and z_2 (along with the included exogenous variables) will produce large R^2 and F statistics, as will the regression of Y_2 on z_1, z_2, and the included exogenous variables. Nevertheless, the lack of correlation between z_2 and Y_1 and Y_2 is problematic. Here, although the order condition indicates that the model is just identified (the number of excluded instruments equals the number of endogenous regressors), the irrelevance of z_2 implies that the model is in fact not identified. Even if the model is overidentified, including irrelevant instruments can adversely affect the properties of instrumental-variables estimators, because their biases increase as the number of instruments increases.

▷ Example 4

`estat firststage` presents different statistics when the model contains multiple endogenous regressors. For illustration, we refit our model of rental rates, assuming that both `hsngval` and `faminc` are endogenously determined. We use `i.region` along with `popden`, a measure of population density, as additional instruments.

```
. ivregress 2sls rent pcturban (hsngval faminc = i.region popden)
(output omitted)
. estat firststage
Shea's partial R-squared
```

Variable	Shea's Partial R-sq.	Shea's Adj. Partial R-sq.
hsngval	0.3477	0.2735
faminc	0.1893	0.0972

```
Minimum eigenvalue statistic = 2.51666
```

Critical Values Ho: Instruments are weak	# of endogenous regressors: 2 # of excluded instruments: 4			
	5%	10%	20%	30%
2SLS relative bias	11.04	7.56	5.57	4.73
	10%	15%	20%	25%
2SLS Size of nominal 5% Wald test	16.87	9.93	7.54	6.28
LIML Size of nominal 5% Wald test	4.72	3.39	2.99	2.79

Consider the endogenous regressor `hsngval`. Part of its variation is attributable to its correlation with the other regressors `pcturban` and `faminc`. The other component of `hsngval`'s variation is peculiar to it and orthogonal to the variation in the other regressors. Similarly, we can think of the instruments as predicting the variation in `hsngval` in two ways, one stemming from the fact that the predicted values of `hsngval` are correlated with the predicted values of the other regressors and one from the variation in the predicted values of `hsngval` that is orthogonal to the variation in the predicted values of the other regressors.

What really matters for instrumental-variables estimation is whether the component of `hsngval` that is orthogonal to the other regressors can be explained by the component of the predicted value of `hsngval` that is orthogonal to the predicted values of the other regressors in the model. Shea's (1997) partial R^2 statistic measures this correlation. Because the bias of instrumental-variables estimators increases as more instruments are used, Shea's adjusted partial R^2 statistic is often used instead, as it makes a degrees-of-freedom adjustment for the number of instruments, analogous to the adjusted R^2 measure used in OLS regression. Although what constitutes a "low" value for Shea's partial R^2 depends on the specifics of the model being fit and the data used, these results, taken in isolation, do not strike us as being a particular cause for concern.

However, with this specification the minimum eigenvalue statistic is low. We cannot reject the null hypothesis of weak instruments for either of the characterizations we have discussed.

◁

By default, `estat firststage` determines which statistics to present based on the number of endogenous regressors in the model previously fit. However, you can specify the `all` option to obtain all the statistics.

❑ Technical note

If the previous estimation was conducted using `aweights`, `pweights`, or `iweights`, then the first-stage regression summary statistics are computed using those weights. However, in these cases the minimum eigenvalue statistic and its critical values are not available.

If the previous estimation included a robust VCE, then the first-stage F statistic is based on a robust VCE as well; for example, if you fit your model with an HAC VCE using the Bartlett kernel and four lags, then the F statistic reported is based on regression results using an HAC VCE using the Bartlett kernel and four lags. By default, the minimum eigenvalue statistic and its critical values are not displayed. You can use the `forcenonrobust` option to obtain them in these cases; the minimum eigenvalue statistic is computed using the weights, though the critical values reported may not be appropriate.

❑

estat overid

In addition to the requirement that instrumental variables be correlated with the endogenous regressors, the instruments must also be uncorrelated with the structural error term. If the model is overidentified, meaning that the number of additional instruments exceeds the number of endogenous regressors, then we can test whether the instruments are uncorrelated with the error term. If the model is just identified, then we cannot perform a test of overidentifying restrictions.

The estimator you used to fit the model determines which tests of overidentifying restrictions `estat overid` reports. If you used the 2SLS estimator without a robust VCE, `estat overid` reports Sargan's (1958) and Basmann's (1960) χ^2 tests. If you used the 2SLS estimator and requested a robust

VCE, Wooldridge's robust score test of overidentifying restrictions is performed instead; without a robust VCE, Wooldridge's test statistic is identical to Sargan's test statistic. If you used the LIML estimator, `estat overid` reports the Anderson–Rubin (1950) likelihood-ratio test and Basmann's (1960) F test. `estat overid` reports Hansen's (1982) J statistic if you used the GMM estimator. Davidson and MacKinnon (1993, 235–236) give a particularly clear explanation of the intuition behind tests of overidentifying restrictions. Also see Judge et al. (1985, 614–616) for a summary of tests of overidentifying restrictions for the 2SLS and LIML estimators.

Tests of overidentifying restrictions actually test two different things simultaneously. One, as we have discussed, is whether the instruments are uncorrelated with the error term. The other is that the equation is misspecified and that one or more of the excluded exogenous variables should in fact be included in the structural equation. Thus a significant test statistic could represent either an invalid instrument or an incorrectly specified structural equation.

▷ Example 5

Here we refit the model that treated just `hsngval` as endogenous using 2SLS, and then we perform tests of overidentifying restrictions:

```
. ivregress 2sls rent pcturban (hsngval = faminc i.region)
(output omitted)
. estat overid
Tests of overidentifying restrictions:
Sargan (score) chi2(3) =  11.2877  (p = 0.0103)
Basmann chi2(3)        =  12.8294  (p = 0.0050)
```

Both test statistics are significant at the 5% test level, which means that either one or more of our instruments are invalid or that our structural model is specified incorrectly.

One possibility is that the error term in our structural model is heteroskedastic. Both Sargan's and Basmann's tests assume that the errors are i.i.d.; if the errors are not i.i.d., then these tests are not valid. Here we refit the model by requesting heteroskedasticity-robust standard errors, and then we use `estat overid` to obtain Wooldridge's score test of overidentifying restrictions, which is robust to heteroskedasticity.

```
. ivregress 2sls rent pcturban (hsngval = faminc i.region), vce(robust)
(output omitted)
. estat overid
Test of overidentifying restrictions:
Score chi2(3)          =   6.8364  (p = 0.0773)
```

Here we no longer reject the null hypothesis that our instruments are valid at the 5% significance level, though we do reject the null at the 10% level. You can verify that the robust standard error on the coefficient for `hsngval` is more than twice as large as its nonrobust counterpart and that the robust standard error for `pcturban` is nearly 50% larger.

◁

❑ Technical note

The test statistic for the test of overidentifying restrictions performed after GMM estimation is simply the sample size times the value of the objective function $Q(\beta_1, \beta_2)$ defined in (5) of [R] **ivregress**, evaluated at the GMM parameter estimates. If the weighting matrix $\mathbf{W}$ is optimal, meaning that $\mathbf{W} = \mathrm{Var}(\mathbf{z}_i u_i)$, then $Q(\beta_1, \beta_2) \overset{A}{\sim} \chi^2(q)$, where q is the number of overidentifying restrictions. However, if the estimated $\mathbf{W}$ is not optimal, then the test statistic will not have an asymptotic χ^2 distribution.

Like the Sargan and Basmann tests of overidentifying restrictions for the 2SLS estimator, the Anderson–Rubin and Basmann tests after LIML estimation are predicated on the errors' being i.i.d. If the previous LIML results were reported with robust standard errors, then `estat overid` by default issues an error message and refuses to report the Anderson–Rubin and Basmann test statistics. You can use the `forcenonrobust` option to override this behavior. You can also use `forcenonrobust` to obtain the Sargan and Basmann test statistics after 2SLS estimation with robust standard errors. ❑

By default, `estat overid` issues an error message if the previous estimation was conducted using `aweights`, `pweights`, or `iweights`. You can use the `forceweights` option to override this behavior, though the test statistics may no longer have the expected χ^2 distributions.

Saved results

After 2SLS estimation, `estat endogenous` saves the following in `r()`:

Scalars

`r(durbin)`	Durbin χ^2 statistic
`r(p_durbin)`	p-value for Durbin χ^2 statistic
`r(wu)`	Wu–Hausman F statistic
`r(p_wu)`	p-value for Wu–Hausman F statistic
`r(df)`	degrees of freedom
`r(wudf_r)`	denominator degrees of freedom for Wu–Hausman F
`r(r_score)`	robust score statistic
`r(p_r_score)`	p-value for robust score statistic
`r(hac_score)`	HAC score statistic
`r(p_hac_score)`	p-value for HAC score statistic
`r(lags)`	lags used in prewhitening
`r(regF)`	regression-based F statistic
`r(p_regF)`	p-value for regression-based F statistic
`r(regFdf_n)`	regression-based F numerator degrees of freedom
`r(regFdf_r)`	regression-based F denominator degrees of freedom

After GMM estimation, `estat endogenous` saves the following in `r()`:

Scalars

`r(C)`	C χ^2 statistic
`r(p_C)`	p-value for C χ^2 statistic
`r(df)`	degrees of freedom

`estat firststage` saves the following in `r()`:

Scalars

`r(mineig)`	minimum eigenvalue statistic

Matrices

`r(mineigcv)`	critical values for minimum eigenvalue statistic
`r(multiresults)`	Shea's partial R^2 statistics
`r(singleresults)`	first-stage R^2 and F statistics

After 2SLS estimation, `estat overid` saves the following in `r()`:

Scalars

`r(lags)`	lags used in prewhitening
`r(df)`	χ^2 degrees of freedom
`r(score)`	score χ^2 statistic
`r(p_score)`	p-value for score χ^2 statistic
`r(basmann)`	Basmann χ^2 statistic
`r(p_basmann)`	p-value for Basmann χ^2 statistic
`r(sargan)`	Sargan χ^2 statistic
`r(p_sargan)`	p-value for Sargan χ^2 statistic

After LIML estimation, `estat overid` saves the following in `r()`:

Scalars

`r(ar)`	Anderson–Rubin χ^2 statistic
`r(p_ar)`	p-value for Anderson–Rubin χ^2 statistic
`r(ar_df)`	χ^2 degrees of freedom
`r(basmann)`	Basmann F statistic
`r(p_basmann)`	p-value for Basmann F statistic
`r(basmann_df_n)`	F numerator degrees of freedom
`r(basmann_df_d)`	F denominator degrees of freedom

After GMM estimation, `estat overid` saves the following in `r()`:

Scalars

`r(HansenJ)`	Hansen's J χ^2 statistic
`r(p_HansenJ)`	p-value for Hansen's J χ^2 statistic
`r(J_df)`	χ^2 degrees of freedom

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Methods and formulas are presented under the following headings:

Notation
estat endogenous
estat firststage
estat overid

Notation

Recall from [R] **ivregress** that the model is

$$\mathbf{y} = \mathbf{Y}\boldsymbol{\beta}_1 + \mathbf{X}_1\boldsymbol{\beta}_2 + \mathbf{u} = \mathbf{X}\boldsymbol{\beta} + \mathbf{u}$$

$$\mathbf{Y} = \mathbf{X}_1\boldsymbol{\Pi}_1 + \mathbf{X}_2\boldsymbol{\Pi}_2 + \mathbf{V} = \mathbf{Z}\boldsymbol{\Pi} + \mathbf{V}$$

where $\mathbf{y}$ is an $N \times 1$ vector of the left-hand-side variable, N is the sample size, $\mathbf{Y}$ is an $N \times p$ matrix of p endogenous regressors, $\mathbf{X}_1$ is an $N \times k_1$ matrix of k_1 included exogenous regressors, $\mathbf{X}_2$ is an $N \times k_2$ matrix of k_2 excluded exogenous variables, $\mathbf{X} = [\mathbf{Y}\ \mathbf{X}_1]$, $\mathbf{Z} = [\mathbf{X}_1\ \mathbf{X}_2]$, $\mathbf{u}$ is an $N \times 1$ vector of errors, $\mathbf{V}$ is an $N \times p$ matrix of errors, $\boldsymbol{\beta} = [\boldsymbol{\beta}_1\ \boldsymbol{\beta}_2]$ is a $k = (p + k_1) \times 1$ vector of parameters, and $\boldsymbol{\Pi}$ is a $(k_1 + k_2) \times p$ vector of parameters. If a constant term is included in the model, then one column of $\mathbf{X}_1$ contains all ones.

estat endogenous

Partition $\mathbf{Y}$ as $\mathbf{Y} = [\mathbf{Y}_1\ \mathbf{Y}_2]$, where $\mathbf{Y}_1$ represents the p_1 endogenous regressors whose endogeneity is being tested and $\mathbf{Y}_2$ represents the p_2 endogenous regressors whose endogeneity is not being tested. If the endogeneity of all endogenous regressors is being tested, $\mathbf{Y} = \mathbf{Y_1}$ and $p_2 = 0$. After GMM estimation, `estat endogenous` refits the model treating $\mathbf{Y}_1$ as exogenous using the same type of weight matrix as requested at estimation time with the `wmatrix()` option; denote the Sargan statistic from this model by J_e and the estimated weight matrix by $\mathbf{W}_e$. Let $\mathbf{S}_e = \mathbf{W}_e^{-1}$. `estat endogenous` removes from $\mathbf{S}_e$ the rows and columns corresponding to the variables represented by $\mathbf{Y}_1$; denote the inverse of the resulting matrix by $\mathbf{W}_e'$. Next `estat endogenous` fits the model treating both $\mathbf{Y}_1$ and $\mathbf{Y}_2$ as endogenous, using the weight matrix $\mathbf{W}_e'$; denote the Sargan statistic from this model by J_c. Then $C = (J_e - J_c) \sim \chi^2(p_1)$. If one simply used the J statistic from the original model fit by `ivregress` in place of J_c, then in finite samples $J_e - J$ might be negative. The procedure used by `estat endogenous` is guaranteed to yield $C \geq 0$; see Hayashi (2000, 220).

Let $\widehat{\mathbf{u}}_c$ denote the residuals from the model treating both $\mathbf{Y}_1$ and $\mathbf{Y}_2$ as endogenous, and let $\widehat{\mathbf{u}}_e$ denote the residuals from the model treating only $\mathbf{Y}_2$ as endogenous. Then Durbin's (1954) statistic is

$$D = \frac{\widehat{\mathbf{u}}_e'\mathbf{P}_{ZY_1}\widehat{\mathbf{u}}_e - \widehat{\mathbf{u}}_c'\mathbf{P}_Z\widehat{\mathbf{u}}_c}{\widehat{\mathbf{u}}_e'\widehat{\mathbf{u}}_e/N}$$

where $\mathbf{P}_Z = \mathbf{Z}(\mathbf{Z}'\mathbf{Z})^{-1}\mathbf{Z}'$ and $\mathbf{P}_{ZY_1} = [\mathbf{Z}\ \mathbf{Y}_1]([\mathbf{Z}\ \mathbf{Y}_1]'[\mathbf{Z}\ \mathbf{Y}_1])^{-1}[\mathbf{Z}\ \mathbf{Y}_1]'$ $D \sim \chi^2(p_1)$. The Wu–Hausman (Wu 1974; Hausman 1978) statistic is

$$WH = \frac{(\widehat{\mathbf{u}}_e'\mathbf{P}_{ZY_1}\widehat{\mathbf{u}}_e - \widehat{\mathbf{u}}_c'\mathbf{P}_Z\widehat{\mathbf{u}}_c)/p_1}{\{\widehat{\mathbf{u}}_e'\widehat{\mathbf{u}}_e - (\widehat{\mathbf{u}}_e'\mathbf{P}_{ZY_1}\widehat{\mathbf{u}}_e - \widehat{\mathbf{u}}_c'\mathbf{P}_Z\widehat{\mathbf{u}}_c)\}/(N - k_1 - p - p_1)}$$

$WH \sim F(p_1, N - k_1 - p - p_1)$. Baum, Schaffer, and Stillman (2003, 2007) discuss these tests in more detail.

Next we describe Wooldridge's (1995) score test. The nonrobust version of Wooldridge's test is identical to Durbin's test. Suppose a robust covariance matrix was used at estimation time. Let $\widehat{\mathbf{e}}$ denote the sample residuals obtained by fitting the model via OLS, treating $\mathbf{Y}$ as exogenous. We then regress each variable represented in $\mathbf{Y}$ on $\mathbf{Z}$; call the residuals for the jth regression $\widehat{\mathbf{r}}_j$, $j = 1, \ldots, p$. Define $\widehat{k}_{ij} = \widehat{e}_i\widehat{r}_{ij}$, $i = 1, \ldots, N$. We then run the regression

$$\mathbf{1} = \theta_1\widehat{\mathbf{k}}_1 + \cdots + \theta_p\widehat{\mathbf{k}}_p + \epsilon$$

where $\mathbf{1}$ is an $N \times 1$ vector of ones and $\boldsymbol{\epsilon}$ is a regression error term. $N - \text{RSS} \sim \chi^2(p)$, where RSS is the residual sum of squares from the regression just described. If instead an HAC VCE was used at estimation time, then before running the final regression we prewhiten the $\widehat{\mathbf{k}}_j$ series by using a VAR(q) model, where q is the number of lags specified with the `lags()` option.

The regression-based test proceeds as follows. Following Hausman (1978, 1259), we regress $\mathbf{Y}$ on $\mathbf{Z}$ and obtain the residuals $\widehat{\mathbf{V}}$. Next we fit the augmented regression

$$\mathbf{y} = \mathbf{Y}\boldsymbol{\beta}_1 + \mathbf{X}_1\boldsymbol{\beta}_2 + \widehat{\mathbf{V}}\boldsymbol{\gamma} + \boldsymbol{\epsilon}$$

by OLS regression, where ϵ is a regression error term. A test of the exogeneity of $\mathbf{Y}$ is equivalent to a test of $\boldsymbol{\gamma} = \mathbf{0}$. As Cameron and Trivedi (2005, 276) suggest, this test can be made robust to heteroskedasticity, autocorrelation, or clustering by using the appropriate robust VCE when testing $\boldsymbol{\gamma} = \mathbf{0}$. When a nonrobust VCE is used, this test is equivalent to the Wu–Hausman test described earlier. One cannot simply fit this augmented regression via 2SLS to test the endogeneity of a subset of the endogenous regressors; Davidson and MacKinnon (1993, 229–231) discuss a test of $\boldsymbol{\gamma} = \mathbf{0}$ for the homoskedastic version of the augmented regression fit by 2SLS, but an appropriate robust test is not apparent.

estat firststage

When the structural equation includes one endogenous regressor, `estat firststage` fits the regression

$$\mathbf{Y} = \mathbf{X}_1\boldsymbol{\pi}_1 + \mathbf{X}_2\boldsymbol{\pi}_2 + \mathbf{v}$$

via OLS. The R^2 and adjusted R^2 from that regression are reported in the output, as well as the F statistic from the Wald test of H_0: $\boldsymbol{\pi}_2 = \mathbf{0}$. To obtain the partial R^2 statistic, `estat firststage` fits the regression

$$\mathbf{M}_{\mathbf{X}_1}\mathbf{y} = \mathbf{M}_{\mathbf{X}_1}\mathbf{X}_2\boldsymbol{\xi} + \boldsymbol{\epsilon}$$

by OLS, where $\boldsymbol{\epsilon}$ is a regression error term, $\boldsymbol{\xi}$ is a $k_2 \times 1$ parameter vector, and $\mathbf{M}_{\mathbf{X}_1} = \mathbf{I} - \mathbf{X}_1(\mathbf{X}_1'\mathbf{X}_1)^{-1}\mathbf{X}_1'$; that is, the partial R^2 is the R^2 between $\mathbf{y}$ and $\mathbf{X}_2$ after eliminating the effects of $\mathbf{X}_1$. If the model contains multiple endogenous regressors and the `all` option is specified, these statistics are calculated for each endogenous regressor in turn.

To calculate Shea's partial R^2, let $\mathbf{y}_1$ denote the endogenous regressor whose statistic is being calculated and $\mathbf{Y}_0$ denote the other endogenous regressors. Define $\widetilde{\mathbf{y}}_1$ as the residuals obtained from regressing $\mathbf{y}_1$ on $\mathbf{Y}_0$ and $\mathbf{X}_1$. Let $\widehat{\mathbf{y}}_1$ denote the fitted values obtained from regressing $\mathbf{y}_1$ on $\mathbf{X}_1$ and $\mathbf{X}_2$; that is, $\widehat{\mathbf{y}}_1$ are the fitted values from the first-stage regression for $\mathbf{y}_1$, and define the columns of $\widehat{\mathbf{Y}}_0$ analogously. Finally, let $\widetilde{\widehat{\mathbf{y}}}_1$ denote the residuals from regressing $\widehat{\mathbf{y}}_1$ on $\widehat{\mathbf{Y}}_0$ and $\mathbf{X}_1$. Shea's partial R^2 is the simple R^2 from the regression of $\widetilde{\mathbf{y}}_1$ on $\widetilde{\widehat{\mathbf{y}}}_1$; denote this as R^2_S. Shea's adjusted partial R^2 is equal to $1 - (1 - R^2_S)(N-1)/(N - k_Z + 1)$ if a constant term is included and $1 - (1 - R^2_S)(N-1)/(N - k_Z)$ if there is no constant term included in the model, where $k_Z = k_1 + k_2$. For one endogenous regressor, one instrument, no exogenous regressors, and a constant term, R^2_S equals the adjusted R^2_S.

The Stock and Yogo minimum eigenvalue statistic, first proposed by Cragg and Donald (1993) as a test for underidentification, is the minimum eigenvalue of the matrix

$$\mathbf{G} = \frac{1}{k_Z}\widehat{\boldsymbol{\Sigma}}_{\mathbf{VV}}^{-1/2}\mathbf{Y}'\mathbf{M}_{\mathbf{X}_1}'\mathbf{X}_2(\mathbf{X}_2'\mathbf{M}_{\mathbf{X}_1}\mathbf{X}_2)^{-1}\mathbf{X}_2'\mathbf{M}_{\mathbf{X}_1}\mathbf{Y}\widehat{\boldsymbol{\Sigma}}_{\mathbf{VV}}^{-1/2}$$

where

$$\widehat{\boldsymbol{\Sigma}}_{\mathbf{VV}} = \frac{1}{N - k_Z}\mathbf{Y}'\mathbf{M}_{\mathbf{Z}}\mathbf{Y}$$

$\mathbf{M}_{\mathbf{Z}} = \mathbf{I} - \mathbf{Z}(\mathbf{Z}'\mathbf{Z})^{-1}\mathbf{Z}'$, and $\mathbf{Z} = [\mathbf{X}_1\ \mathbf{X}_2]$. Critical values are obtained from the tables in Stock and Yogo (2005).

estat overid

The Sargan (1958) and Basmann (1960) χ^2 statistics are calculated by running the auxiliary regression

$$\widehat{\mathbf{u}} = \mathbf{Z}\boldsymbol{\delta} + \mathbf{e}$$

where $\widehat{\mathbf{u}}$ are the sample residuals from the model and $\mathbf{e}$ is an error term. Then Sargan's statistic is

$$S = N\left(1 - \frac{\widehat{\mathbf{e}}'\widehat{\mathbf{e}}}{\widehat{\mathbf{u}}'\widehat{\mathbf{u}}}\right)$$

where $\widehat{\mathbf{e}}$ are the residuals from that auxiliary regression. Basmann's statistic is calculated as

$$B = S\frac{N - k_Z}{N - S}$$

Both S and B are distributed $\chi^2(m)$, where m, the number of overidentifying restrictions, is equal to $k_Z - k$, where k is the number of endogenous regressors.

Wooldridge's (1995) score test of overidentifying restrictions is identical to Sargan's (1958) statistic under the assumption of i.i.d. and therefore is not recomputed unless a robust VCE was used at estimation time. If a heteroskedasticity-robust VCE was used, Wooldridge's test proceeds as follows. Let $\widehat{\mathbf{Y}}$ denote the $N \times k$ matrix of fitted values obtained by regressing the endogenous regressors on $\mathbf{X}_1$ and $\mathbf{X}_2$. Let $\mathbf{Q}$ denote an $N \times m$ matrix of excluded exogenous variables; the test statistic to be calculated is invariant to whichever m of the k_2 excluded exogenous variables is chosen. Define the ith element of $\widehat{\mathbf{k}}_j$, $i = 1, \ldots, N$, $j = 1, \ldots, m$, as

$$k_{ij} = \widehat{q}_{ij} u_i$$

where $\widehat{q}_{ij}$ is the ith element of $\widehat{\mathbf{q}}_j$, the fitted values from regressing the jth column of $\mathbf{Q}$ on $\widehat{\mathbf{Y}}$ and $\mathbf{X}_1$. Finally, fit the regression

$$\mathbf{1} = \theta_1 \widehat{\mathbf{k}}_1 + \cdots + \theta_m \widehat{\mathbf{k}}_m + \boldsymbol{\epsilon}$$

where $\mathbf{1}$ is an $N \times 1$ vector of ones and $\boldsymbol{\epsilon}$ is a regression error term, and calculate the residual sum of squares, RSS. Then the test statistic is $W = N - \text{RSS}$. $W \sim \chi^2(m)$. If an HAC VCE was used at estimation, then the $\widehat{\mathbf{k}}_j$ are prewhitened using a VAR(p) model, where p is specified using the `lags()` option.

The Anderson–Rubin (1950), AR, test of overidentifying restrictions for use after the LIML estimator is calculated as $\text{AR} = N(\kappa - 1)$, where κ is the minimal eigenvalue of a certain matrix defined in *Methods and formulas* of [R] **ivregress**. $\text{AR} \sim \chi^2(m)$. (Some texts define this statistic as $N \ln(\kappa)$ because $\ln(x) \approx (x - 1)$ for x near one.) Basmann's F statistic for use after the LIML estimator is calculated as $B_F = (\kappa - 1)(N - k_Z)/m$. $B_F \sim F(m, N - k_Z)$.

Hansen's J statistic is simply the sample size times the value of the GMM objective function defined in (5) of [R] **ivregress**, evaluated at the estimated parameter values. Under the null hypothesis that the overidentifying restrictions are valid, $J \sim \chi^2(m)$.

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Also see

[R] **ivregress** — Single-equation instrumental-variables regression

[U] **20 Estimation and postestimation commands**

Title

ivtobit — Tobit model with continuous endogenous regressors

Syntax

Maximum likelihood estimator

```
ivtobit depvar [varlist1] (varlist2 = varlistiv) [if] [in] [weight],
    ll[(#)] ul[(#)] [mle_options]
```

Two-step estimator

```
ivtobit depvar [varlist1] (varlist2 = varlistiv) [if] [in] [weight], twostep
    ll[(#)] ul[(#)] [tse_options]
```

mle_options	Description
Model	
*`ll[(#)]`	lower limit for left censoring
*`ul[(#)]`	upper limit for right censoring
`mle`	use conditional maximum-likelihood estimator; the default
`constraints(`*constraints*`)`	apply specified linear constraints
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`first`	report first-stage regression
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process
`coeflegend`	display legend instead of statistics

*You must specify at least one of `ll[(#)]` and `ul[(#)]`.

tse_options	Description
Model	
*twostep	use Newey's two-step estimator; the default is mle
*ll[(#)]	lower limit for left censoring
*ul[(#)]	upper limit for right censoring
SE	
vce(*vcetype*)	*vcetype* may be twostep, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
first	report first-stage regression
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
coeflegend	display legend instead of statistics

*twostep is required. You must specify at least one of ll[(#)] and ul[(#)].

varlist$_1$ and *varlist*$_{\text{iv}}$ may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar, *varlist*$_1$, *varlist*$_2$, and *varlist*$_{\text{iv}}$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
bootstrap, by, jackknife, rolling, statsby, and svy are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
vce(), first, twostep, and weights are not allowed with the svy prefix; see [SVY] **svy**.
fweights, iweights, and pweights are allowed with the maximum likelihood estimator. fweights are allowed with Newey's two-step estimator. See [U] **11.1.6 weight**.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Endogenous covariates > Tobit model with endogenous covariates

Description

ivtobit fits tobit models where one or more of the regressors is endogenously determined. By default, ivtobit uses maximum likelihood estimation. Alternatively, Newey's (1987) minimum chi-squared estimator can be invoked with the twostep option. Both estimators assume that the endogenous regressors are continuous and so are not appropriate for use with discrete endogenous regressors. See [R] **ivprobit** for probit estimation with endogenous regressors and [R] **tobit** for tobit estimation when the model contains no endogenous regressors.

Options for ML estimator

Model

ll(#) and ul(#) indicate the lower and upper limits for censoring, respectively. You may specify one or both. Observations with *depvar* $\leq$ ll() are left-censored; observations with *depvar* $\geq$ ul() are right-censored; and remaining observations are not censored. You do not have to specify the censoring values at all. It is enough to type ll, ul, or both. When you do not specify a censoring value, ivtobit assumes that the lower limit is the minimum observed in the data (if ll is specified) and that the upper limit is the maximum (if ul is specified).

`mle` requests that the conditional maximum-likelihood estimator be used. This is the default.

`constraints(`*constraints*`)`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` requests that the parameters for the reduced-form equations showing the relationships between the endogenous variables and instruments be displayed. For the two-step estimator, `first` shows the first-stage regressions. For the maximum likelihood estimator, these parameters are estimated jointly with the parameters of the tobit equation. The default is not to show these parameter estimates.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. This model's likelihood function can be difficult to maximize, especially with multiple endogenous variables. The `difficult` and `technique(bfgs)` options may be helpful in achieving convergence.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `ivtobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Options for two-step estimator

Model

`twostep` is required and requests that Newey's (1987) efficient two-step estimator be used to obtain the coefficient estimates.

`ll(#)` and `ul(#)` indicate the lower and upper limits for censoring, respectively. You may specify one or both. Observations with *depvar* $\leq$ `ll()` are left-censored; observations with *depvar* $\geq$ `ul()` are right-censored; and remaining observations are not censored. You do not have to specify the censoring values at all. It is enough to type `ll`, `ul`, or both. When you do not specify a censoring value, `ivtobit` assumes that the lower limit is the minimum observed in the data (if `ll` is specified) and that the upper limit is the maximum (if `ul` is specified).

SE

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` requests that the parameters for the reduced-form equations showing the relationships between the endogenous variables and instruments be displayed. For the two-step estimator, `first` shows the first-stage regressions. For the maximum likelihood estimator, these parameters are estimated jointly with the parameters of the tobit equation. The default is not to show these parameter estimates.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `ivtobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

`ivtobit` fits models with censored dependent variables and endogenous regressors. You can use it to fit a tobit model when you suspect that one or more of the regressors is correlated with the error term. `ivtobit` is to tobit what `ivregress` is to linear regression analysis; see [R] **ivregress** for more information.

Formally, the model is

$$y_{1i}^* = \boldsymbol{y}_{2i}\boldsymbol{\beta} + \boldsymbol{x}_{1i}\boldsymbol{\gamma} + u_i$$
$$\boldsymbol{y}_{2i} = \boldsymbol{x}_{1i}\boldsymbol{\Pi}_1 + \boldsymbol{x}_{2i}\boldsymbol{\Pi}_2 + \boldsymbol{v}_i$$

where $i = 1, \ldots, N$; $\boldsymbol{y}_{2i}$ is a $1 \times p$ vector of endogenous variables; $\boldsymbol{x}_{1i}$ is a $1 \times k_1$ vector of exogenous variables; $\boldsymbol{x}_{2i}$ is a $1 \times k_2$ vector of additional instruments; and the equation for $\boldsymbol{y}_{2i}$ is written in reduced form. By assumption $(u_i, \boldsymbol{v}_i) \sim \mathrm{N}(\boldsymbol{0})$. $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ are vectors of structural parameters, and $\boldsymbol{\Pi}_1$ and $\boldsymbol{\Pi}_2$ are matrices of reduced-form parameters. We do not observe y_{1i}^*; instead, we observe

$$y_{1i} = \begin{cases} a & y_{1i}^* < a \\ y_{1i}^* & a \le y_{1i}^* \le b \\ b & y_{1i}^* > b \end{cases}$$

The order condition for identification of the structural parameters is that $k_2 \ge p$. Presumably, $\boldsymbol{\Sigma}$ is not block diagonal between u_i and $\boldsymbol{v}_i$; otherwise, $\boldsymbol{y}_{2i}$ would not be endogenous.

❑ Technical note

This model is derived under the assumption that $(u_i, \boldsymbol{v}_i)$ is independent and identically distributed multivariate normal for all i. The `vce(cluster` *clustvar*`)` option can be used to control for a lack of independence. As with the standard tobit model without endogeneity, if u_i is heteroskedastic, point estimates will be inconsistent.

❑

Example 1

Using the same dataset as in [R] **ivprobit**, we now want to estimate women's incomes. In our hypothetical world, all women who choose not to work receive $10,000 in welfare and child-support payments. Therefore, we never observe incomes under $10,000: a woman offered a job with an annual wage less than that would not accept and instead would collect the welfare payment. We model income as a function of the number of years of schooling completed, the number of children at home, and other household income. We again believe that `other_inc` is endogenous, so we use `male_educ` as an instrument.

```
. use http://www.stata-press.com/data/r12/laborsup
. ivtobit fem_inc fem_educ kids (other_inc = male_educ), ll
Fitting exogenous tobit model
Fitting full model
Iteration 0:   log likelihood = -3228.4224
Iteration 1:   log likelihood = -3226.2882
Iteration 2:   log likelihood =  -3226.085
Iteration 3:   log likelihood = -3226.0845
Iteration 4:   log likelihood = -3226.0845
Tobit model with endogenous regressors            Number of obs   =        500
                                                  Wald chi2(3)    =     117.42
Log likelihood = -3226.0845                       Prob > chi2     =     0.0000
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
other_inc	-.9045399	.1329762	-6.80	0.000	-1.165168	-.6439114
fem_educ	3.272391	.3968708	8.25	0.000	2.494538	4.050243
kids	-3.312357	.7218628	-4.59	0.000	-4.727182	-1.897532
_cons	19.24735	7.372391	2.61	0.009	4.797725	33.69697
/alpha	.2907654	.1379965	2.11	0.035	.0202972	.5612336
/lns	2.874031	.0506672	56.72	0.000	2.774725	2.973337
/lnv	2.813383	.0316228	88.97	0.000	2.751404	2.875363
s	17.70826	.897228			16.03422	19.55707
v	16.66621	.5270318			15.66461	17.73186

```
Instrumented:  other_inc
Instruments:   fem_educ kids male_educ
Wald test of exogeneity (/alpha = 0): chi2(1) =     4.44  Prob > chi2 = 0.0351
  Obs. summary:        272  left-censored observations at fem_inc<=10
                       228     uncensored observations
                         0 right-censored observations
```

Because we did not specify `mle` or `twostep`, `ivtobit` used the maximum likelihood estimator by default. `ivtobit` fits a tobit model, ignoring endogeneity, to get starting values for the full model. The header of the output contains the maximized log likelihood, the number of observations, and a Wald statistic and p-value for the test of the hypothesis that all the slope coefficients are jointly zero. At the end of the output, we see a count of the censored and uncensored observations.

Near the bottom of the output is a Wald test of the exogeneity of the instrumented variables. If the test statistic is not significant, there is not sufficient information in the sample to reject the null hypothesis of no endogeneity. Then the point estimates from `ivtobit` are consistent, although those from `tobit` are likely to have smaller standard errors.

◁

Various two-step estimators have also been proposed for the endogenous tobit model, and Newey's (1987) minimum chi-squared estimator is available with the `twostep` option.

▷ Example 2

Refitting our labor-supply model with the two-step estimator yields

```
. ivtobit fem_inc fem_educ kids (other_inc = male_educ), ll twostep
Two-step tobit with endogenous regressors         Number of obs   =       500
                                                  Wald chi2(3)    =    117.38
                                                  Prob > chi2     =    0.0000
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
   other_inc |  -.9045397   .1330015    -6.80   0.000    -1.165218   -.6438616
    fem_educ |    3.27239   .3969399     8.24   0.000     2.494402    4.050378
        kids |  -3.312356   .7220066    -4.59   0.000    -4.727463   -1.897249
       _cons |   19.24735    7.37392     2.61   0.009     4.794728    33.69997
------------------------------------------------------------------------------
Instrumented:  other_inc
Instruments:   fem_educ kids male_educ
------------------------------------------------------------------------------
Wald test of exogeneity:     chi2(1) =     4.64           Prob > chi2 = 0.0312
  Obs. summary:        272  left-censored observations at fem_inc<=10
                       228     uncensored observations
                         0 right-censored observations
```

All the coefficients have the same signs as their counterparts in the maximum likelihood model. The Wald test at the bottom of the output confirms our earlier finding of endogeneity.

◁

❑ Technical note

In the tobit model with endogenous regressors, we assume that $(u_i, \boldsymbol{v}_i)$ is multivariate normal with covariance matrix

$$\mathrm{Var}(u_i, \boldsymbol{v}_i) = \boldsymbol{\Sigma} = \begin{bmatrix} \sigma_u^2 & \boldsymbol{\Sigma}_{21}' \\ \boldsymbol{\Sigma}_{21} & \boldsymbol{\Sigma}_{22} \end{bmatrix}$$

Using the properties of the multivariate normal distribution, $\mathrm{Var}(u_i|\boldsymbol{v}_i) \equiv \sigma^2_{u|v} = \sigma_u^2 - \boldsymbol{\Sigma}_{21}'\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}$. Calculating the marginal effects on the conditional expected values of the observed and latent dependent variables and on the probability of censoring requires an estimate of σ_u^2. The two-step estimator identifies only $\sigma^2_{u|v}$, not σ_u^2, so only the linear prediction and its standard error are available after you have used the `twostep` option. However, unlike the two-step probit estimator described in [R] **ivprobit**, the two-step tobit estimator does identify $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$. See Wooldridge (2010, 683–684) for more information.

❑

Saved results

`ivtobit, mle` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_unc)`	number of uncensored observations
`e(N_lc)`	number of left-censored observations
`e(N_rc)`	number of right-censored observations
`e(llopt)`	contents of `ll()`
`e(ulopt)`	contents of `ul()`
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_aux)`	number of auxiliary parameters
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(N_clust)`	number of clusters
`e(endog_ct)`	number of endogenous regressors
`e(p)`	model Wald p-value
`e(p_exog)`	exogeneity test Wald p-value
`e(chi2)`	model Wald χ^2
`e(chi2_exog)`	Wald χ^2 test of exogeneity
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

`e(cmd)`	`ivtobit`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(instd)`	instrumented variables
`e(insts)`	instruments
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(clustvar)`	name of cluster variable
`e(chi2type)`	`Wald`; type of model χ^2 test
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(method)`	`ml`
`e(opt)`	type of optimization
`e(which)`	`max` or `min`; whether optimizer is to perform maximization or minimization
`e(ml_method)`	type of `ml` method
`e(user)`	name of likelihood-evaluator program
`e(technique)`	maximization technique
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(footnote)`	program used to implement the footnote display
`e(marginsok)`	predictions allowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(Sigma)	$\widehat{\Sigma}$
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

ivtobit, twostep saves the following in e():

Scalars

e(N)	number of observations
e(N_unc)	number of uncensored observations
e(N_lc)	number of left-censored observations
e(N_rc)	number of right-censored observations
e(llopt)	contents of ll()
e(ulopt)	contents of ul()
e(df_m)	model degrees of freedom
e(df_exog)	degrees of freedom for χ^2 test of exogeneity
e(p)	model Wald p-value
e(p_exog)	exogeneity test Wald p-value
e(chi2)	model Wald χ^2
e(chi2_exog)	Wald χ^2 test of exogeneity
e(rank)	rank of e(V)

Macros

e(cmd)	ivtobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(instd)	instrumented variables
e(insts)	instruments
e(wtype)	weight type
e(wexp)	weight expression
e(chi2type)	Wald; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(method)	twostep
e(properties)	b V
e(predict)	program used to implement predict
e(footnote)	program used to implement the footnote display
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

ivtobit is implemented as an ado-file.

The estimation procedure used by ivtobit is similar to that used by ivprobit. For compactness, we write the model as

$$y_{1i}^* = \boldsymbol{z}_i\boldsymbol{\delta} + u_i \tag{1a}$$
$$\boldsymbol{y}_{2i} = \boldsymbol{x}_i\boldsymbol{\Pi} + \boldsymbol{v}_i \tag{1b}$$

where $\boldsymbol{z}_i = (\boldsymbol{y}_{2i}, \boldsymbol{x}_{1i})$, $\boldsymbol{x}_i = (\boldsymbol{x}_{1i}, \boldsymbol{x}_{2i})$, $\boldsymbol{\delta} = (\boldsymbol{\beta}', \boldsymbol{\gamma}')'$, and $\boldsymbol{\Pi} = (\boldsymbol{\Pi}_1', \boldsymbol{\Pi}_2')'$. We do not observe y_{1i}^*; instead, we observe

$$y_{1i} = \begin{cases} a & y_{1i}^* < a \\ y_{1i}^* & a \le y_{1i}^* \le b \\ b & y_{1i}^* > b \end{cases}$$

$(u_i, \boldsymbol{v}_i)$ is distributed multivariate normal with mean zero and covariance matrix

$$\boldsymbol{\Sigma} = \begin{bmatrix} \sigma_u^2 & \boldsymbol{\Sigma}_{21}' \\ \boldsymbol{\Sigma}_{21} & \boldsymbol{\Sigma}_{22} \end{bmatrix}$$

Using the properties of the multivariate normal distribution, we can write $u_i = \boldsymbol{v}_i'\boldsymbol{\alpha} + \epsilon_i$, where $\boldsymbol{\alpha} = \boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}$; $\epsilon_i \sim \mathrm{N}(0; \sigma_{u|v}^2)$, where $\sigma_{u|v}^2 = \sigma_u^2 - \boldsymbol{\Sigma}_{21}'\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}$; and ϵ_i is independent of $\boldsymbol{v}_i$, $\boldsymbol{z}_i$, and $\boldsymbol{x}_i$.

The likelihood function is straightforward to derive because we can write the joint density $f(y_{1i}, \boldsymbol{y}_{2i}|\boldsymbol{x}_i)$ as $f(y_{1i}|\boldsymbol{y}_{2i}, \boldsymbol{x}_i)\, f(\boldsymbol{y}_{2i}|\boldsymbol{x}_i)$. With one endogenous regressor,

$$\ln f(y_{2i}|\boldsymbol{x}_i) = -\frac{1}{2}\left\{ \ln 2\pi + \ln\sigma_v^2 + \frac{(y_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi})^2}{\sigma_v^2} \right\}$$

and

$$\ln f(y_{1i}|y_{2i}, \boldsymbol{x}_i) = \begin{cases} \ln\left\{1 - \Phi\left(\frac{m_i - a}{\sigma_{u|v}}\right)\right\} & y_{1i} = a \\ -\frac{1}{2}\left\{ \ln 2\pi + \ln\sigma_{u|v}^2 + \frac{(y_{1i} - m_i)^2}{\sigma_{u|v}^2} \right\} & a < y_{1i} < b \\ \ln\Phi\left(\frac{m_i - b}{\sigma_{u|v}}\right) & y_{1i} = b \end{cases}$$

where

$$m_i = \boldsymbol{z}_i\boldsymbol{\delta} + \alpha\,(y_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi})$$

and $\Phi(\cdot)$ is the normal distribution function so that the log likelihood for observation i is

$$\ln L_i = w_i\left\{ \ln f(y_{1i}|y_{2i}, \boldsymbol{x}_i) + \ln f(y_{2i}|\boldsymbol{x}_i) \right\}$$

where w_i is the weight for observation i or one if no weights were specified. Instead of estimating $\sigma_{u|v}$ and σ_v directly, we estimate $\ln\sigma_{u|v}$ and $\ln\sigma_v$.

For multiple endogenous regressors, we have

$$\ln f(\boldsymbol{y}_{2i}|\boldsymbol{x}_i) = -\frac{1}{2}\left(\ln 2\pi + \ln|\boldsymbol{\Sigma}_{22}| + \boldsymbol{v}_i'\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{v}_i \right)$$

and $\ln f(y_{1i}|\boldsymbol{y}_{2i}, \boldsymbol{x}_i)$ is the same as before, except that now

$$m_i = \boldsymbol{z}_i\boldsymbol{\delta} + (\boldsymbol{y}_{2i} - \boldsymbol{x}_i\boldsymbol{\Pi})\boldsymbol{\Sigma}_{22}^{-1}\boldsymbol{\Sigma}_{21}$$

Instead of maximizing the log-likelihood function with respect to $\boldsymbol{\Sigma}$, we maximize with respect to the Cholesky decomposition $\boldsymbol{S}$ of $\boldsymbol{\Sigma}$; that is, there exists a lower triangular matrix $\boldsymbol{S}$ such that $\boldsymbol{S}\boldsymbol{S}' = \boldsymbol{\Sigma}$. This maximization ensures that $\boldsymbol{\Sigma}$ is positive definite, as a covariance matrix must be. Let

$$\boldsymbol{S} = \begin{bmatrix} s_{11} & 0 & 0 & \dots & 0 \\ s_{21} & s_{22} & 0 & \dots & 0 \\ s_{31} & s_{32} & s_{33} & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ s_{p+1,1} & s_{p+1,2} & s_{p+1,3} & \dots & s_{p+1,p+1} \end{bmatrix}$$

With maximum likelihood estimation, this command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

The maximum likelihood version of `ivtobit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

The two-step estimates are obtained using Newey's (1987) minimum chi-squared estimator. The procedure is identical to the one described in [R] **ivprobit**, except that `tobit` is used instead of `probit`.

Acknowledgments

The two-step estimator is based on the `tobitiv` command written by Jonah Gelbach, Department of Economics, Yale University, and the `ivtobit` command written by Joe Harkness, Institute of Policy Studies, Johns Hopkins University.

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Also see

[R] **ivtobit postestimation** — Postestimation tools for ivtobit

[R] **gmm** — Generalized method of moments estimation

[R] **ivprobit** — Probit model with continuous endogenous regressors

[R] **ivregress** — Single-equation instrumental-variables regression

[R] **regress** — Linear regression

[R] **tobit** — Tobit regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtintreg** — Random-effects interval-data regression models

[XT] **xttobit** — Random-effects tobit models

[U] **20 Estimation and postestimation commands**

Title

ivtobit postestimation — Postestimation tools for ivtobit

Description

The following postestimation commands are available after `ivtobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`[1]	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[2]	likelihood-ratio test; not available with two-step estimator
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`[1]	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `estat ic` and `suest` are not appropriate after `ivtobit, twostep`.

[2] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat (svy)`.

Syntax for predict

After ML or twostep

```
predict [type] newvar [if] [in] [, statistic]
```

After ML

```
predict [type] {stub* | newvarlist} [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`stdf`	standard error of the forecast; not available with two-step estimator
`pr(`*a*`,`*b*`)`	$\Pr(a < y_j < b)$; not available with two-step estimator
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$; not available with two-step estimator
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j = \max\{a, \min(y_j, b)\}$; not available with two-step estimator

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

where *a* and *b* may be numbers or variables; *a* missing ($a \geq .$) means $-\infty$, and *b* missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction. It can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**. `stdf` is not available with the two-step estimator.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$; `pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which *lb* $\geq .$ and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$; `pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which *ub* $\geq .$ and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`pr(`*a*`,`*b*`)` is not available with the two-step estimator.

`e(`*a*`,`*b*`)` calculates $E(\boldsymbol{x}_j\boldsymbol{b} + u_j \mid a < \boldsymbol{x}_j\boldsymbol{b} + u_j < b)$, the expected value of $y_j|\boldsymbol{x}_j$ conditional on $y_j|\boldsymbol{x}_j$ being in the interval (a, b), meaning that $y_j|\boldsymbol{x}_j$ is truncated. a and b are specified as they are for `pr()`. `e(`*a*`,`*b*`)` is not available with the two-step estimator.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\boldsymbol{x}_j\boldsymbol{b} + u_j \leq a$, $y_j^* = b$ if $\boldsymbol{x}_j\boldsymbol{b} + u_j \geq b$, and $y_j^* = \boldsymbol{x}_j\boldsymbol{b} + u_j$ otherwise, meaning that y_j^* is censored. a and b are specified as they are for `pr()`. `ystar(`*a*`,`*b*`)` is not available with the two-step estimator.

`scores`, not available with `twostep`, calculates equation-level score variables.

For models with one endogenous regressor, five new variables are created.

The first new variable will contain $\partial \ln L/\partial(\boldsymbol{z}_i\boldsymbol{\delta})$.

The second new variable will contain $\partial \ln L/\partial(\boldsymbol{x}_i\boldsymbol{\Pi})$.

The third new variable will contain $\partial \ln L/\partial\alpha$.

The fourth new variable will contain $\partial \ln L/\partial \ln\sigma_{u|v}$.

The fifth new variable will contain $\partial \ln L/\partial \ln\sigma_v$.

For models with p endogenous regressors, $p + \{(p+1)(p+2)\}/2 + 1$ new variables are created.

The first new variable will contain $\partial \ln L/\partial(\boldsymbol{z}_i\boldsymbol{\delta})$.

The second through $(p+1)$th new score variables will contain $\partial \ln L/\partial(\boldsymbol{x}_i\boldsymbol{\Pi}_k)$, $k = 1, \ldots, p$, where $\boldsymbol{\Pi}_k$ is the kth column of $\boldsymbol{\Pi}$.

The remaining score variables will contain the partial derivatives of $\ln L$ with respect to s_{11}, s_{21}, …, $s_{p+1,1}$, s_{22}, …, $s_{p+1,2}$, …, $s_{p+1,p+1}$, where $s_{m,n}$ denotes the (m, n) element of the Cholesky decomposition of the error covariance matrix.

Remarks

Remarks are presented under the following headings:

Marginal effects
Obtaining predicted values

Marginal effects

▷ Example 1

We can obtain average marginal effects by using the `margins` command after `ivtobit`. For the labor-supply model of example 1 in [R] **ivtobit**, suppose that we wanted to know the average marginal effects on the woman's expected income, conditional on her income being greater than $10,000.

```
. use http://www.stata-press.com/data/r12/laborsup
. ivtobit fem_inc fem_educ kids (other_inc = male_educ), ll
  (output omitted)
. margins, dydx(*) predict(e(10, .))
Average marginal effects                        Number of obs   =        500
Model VCE    : OIM
Expression   : E(fem_inc|fem_inc>10), predict(e(10, .))
dy/dx w.r.t. : other_inc fem_educ kids male_educ
```

	Delta-method dy/dx	Std. Err.	z	P>|z|	[95% Conf.	Interval]
other_inc	-.3420189	.0553591	-6.18	0.000	-.4505208	-.233517
fem_educ	1.237336	.1534025	8.07	0.000	.9366723	1.537999
kids	-1.252447	.2725166	-4.60	0.000	-1.78657	-.7183246
male_educ	0	(omitted)				

In our sample, increasing the number of children in the family by one decreases the expected wage by \$1,252 on average (wages in our dataset are measured in thousands of dollars). `male_edu` has no effect because it appears only as an instrument.

◁

Obtaining predicted values

After fitting your model using `ivtobit`, you can obtain the linear prediction and its standard error for both the estimation sample and other samples using the `predict` command. If you used the maximum likelihood estimator, you can also obtain conditional expected values of the observed and latent dependent variables, the standard error of the forecast, and the probability of observing the dependent variable in a specified interval. See [U] **20 Estimation and postestimation commands** and [R] **predict**.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

The linear prediction is calculated as $\boldsymbol{z}_i\widehat{\boldsymbol{\delta}}$, where $\widehat{\boldsymbol{\delta}}$ is the estimated value of $\boldsymbol{\delta}$, and $\boldsymbol{z}_i$ and $\boldsymbol{\delta}$ are defined in (1a) of [R] **ivtobit**. Expected values and probabilities are calculated using the same formulas as those used by the standard exogenous tobit model.

Also see

[R] **ivtobit** — Tobit model with continuous endogenous regressors

[U] **20 Estimation and postestimation commands**

Title

jackknife — Jackknife estimation

Syntax

`jackknife` *exp_list* [`,` *options eform_option*] `:` *command*

options	Description
Main	
`eclass`	number of observations used is stored in `e(N)`
`rclass`	number of observations used is stored in `r(N)`
`n(`*exp*`)`	specify *exp* that evaluates to the number of observations used
Options	
`cluster(`*varlist*`)`	variables identifying sample clusters
`idcluster(`*newvar*`)`	create new cluster ID variable
`saving(`*filename*`, ...)`	save results to *filename*; save statistics in double precision; save results to *filename* every # replications
`keep`	keep pseudovalues
`mse`	use MSE formula for variance estimation
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`notable`	suppress table of results
`noheader`	suppress table header
`nolegend`	suppress table legend
`verbose`	display the full table legend
`nodots`	suppress replication dots
`noisily`	display any output from *command*
`trace`	trace *command*
`title(`*text*`)`	use *text* as title for jackknife results
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Advanced	
`nodrop`	do not drop observations
`reject(`*exp*`)`	identify invalid results
eform_option	display coefficient table in exponentiated form
`coeflegend`	display legend instead of statistics

`svy` is allowed; see [SVY] **svy jackknife**.

All weight types supported by *command* are allowed except `aweights`; see [U] **11.1.6 weight**.

eform_option and `coeflegend` do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

exp_list contains	(*name*: *elist*)
	elist
	eexp
elist contains	*newvar* = (*exp*)
	(*exp*)
eexp is	*specname*
	[*eqno*]*specname*
specname is	_b
	_b[]
	_se
	_se[]
eqno is	##
	name

exp is a standard Stata expression; see [U] **13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

Menu

Statistics > Resampling > Jackknife estimation

Description

`jackknife` performs jackknife estimation. Typing

```
. jackknife exp_list: command
```

executes *command* once for each observation in the dataset, leaving the associated observation out of the calculations that make up *exp_list*.

command defines the statistical command to be executed. Most Stata commands and user-written programs can be used with `jackknife`, as long as they follow standard Stata syntax and allow the `if` qualifier; see [U] **11 Language syntax**. The `by` prefix may not be part of *command*.

exp_list specifies the statistics to be collected from the execution of *command*. If *command* changes the contents in `e(b)`, *exp_list* is optional and defaults to `_b`.

Many estimation commands allow the `vce(jackknife)` option. For those commands, we recommend using `vce(jackknife)` over `jackknife` because the estimation command already handles clustering and other model-specific details for you. The `jackknife` prefix command is intended for use with nonestimation commands, such as `summarize`, user-written commands, or functions of coefficients.

`jknife` is a synonym for `jackknife`.

Options

Main

`eclass`, `rclass`, and `n(`*exp*`)` specify where *command* saves the number of observations on which it based the calculated results. We strongly advise you to specify one of these options.

`eclass` specifies that *command* save the number of observations in `e(N)`.

`rclass` specifies that *command* save the number of observations in `r(N)`.

`n(`*exp*`)` specifies an expression that evaluates to the number of observations used. Specifying `n(r(N))` is equivalent to specifying the `rclass` option. Specifying `n(e(N))` is equivalent to specifying the `eclass` option. If *command* saves the number of observations in `r(N1)`, specify `n(r(N1))`.

If you specify no options, `jackknife` will assume `eclass` or `rclass`, depending on which of `e(N)` and `r(N)` is not missing (in that order). If both `e(N)` and `r(N)` are missing, `jackknife` assumes that all observations in the dataset contribute to the calculated result. If that assumption is incorrect, the reported standard errors will be incorrect. For instance, say that you specify

```
. jackknife coef=_b[x2]: myreg y x1 x2 x3
```

where `myreg` uses `e(n)` instead of `e(N)` to identify the number of observations used in calculations. Further assume that observation 42 in the dataset has `x3` equal to missing. The 42nd observation plays no role in obtaining the estimates, but `jackknife` has no way of knowing that and will use the wrong N. If, on the other hand, you specify

```
. jackknife coef=_b[x2], n(e(n)): myreg y x1 x2 x3
```

`jackknife` will notice that observation 42 plays no role. The `n(e(n))` option is specified because `myreg` is an estimation command but it saves the number of observations used in `e(n)` (instead of the standard `e(N)`). When `jackknife` runs the regression omitting the 42nd observation, `jackknife` will observe that `e(n)` has the same value as when `jackknife` previously ran the regression using all the observations. Thus `jackknife` will know that `myreg` did not use the observation.

Options

`cluster(`*varlist*`)` specifies the variables identifying sample clusters. If `cluster()` is specified, one cluster is left out of each call to *command*, instead of 1 observation.

`idcluster(`*newvar*`)` creates a new variable containing a unique integer identifier for each resampled cluster, starting at `1` and leading up to the number of clusters. This option may be specified only when the `cluster()` option is specified. `idcluster()` helps identify the cluster to which a pseudovalue belongs.

`saving(`*filename*`[ , `*suboptions*`])` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

`double` specifies that the results for each replication be stored as `double`s, meaning 8-byte reals. By default, they are stored as `float`s, meaning 4-byte reals. This option may be used without the `saving()` option to compute the variance estimates by using double precision.

`every(#)` specifies that results be written to disk every #th replication. `every()` should be specified only in conjunction with `saving()` when *command* takes a long time for each replication. This option will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

`replace` specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

`keep` specifies that new variables be added to the dataset containing the pseudovalues of the requested statistics. For instance, if you typed

```
. jackknife coef=_b[x2], eclass keep: regress y x1 x2 x3
```

new variable `coef` would be added to the dataset containing the pseudovalues for `_b[x2]`. Let b be the value of `_b[x2]` when all observations are used to fit the model, and let $b(j)$ be the value when the jth observation is omitted. The pseudovalues are defined as

$$\text{pseudovalue}_j = N\{b - b(j)\} + b(j)$$

where N is the number of observations used to produce b.

When the `cluster()` option is specified, each cluster is given at most one nonmissing pseudovalue. The `keep` option implies the `nodrop` option.

`mse` specifies that `jackknife` compute the variance by using deviations of the replicates from the observed value of the statistics based on the entire dataset. By default, `jackknife` computes the variance by using deviations of the pseudovalues from their mean.

Reporting

`level(#)`; see [R] **estimation options**.

`notable` suppresses the display of the table of results.

`noheader` suppresses the display of the table header. This option implies `nolegend`.

`nolegend` suppresses the display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

`verbose` specifies that the full table legend be displayed. By default, coefficients and standard errors are not displayed.

`nodots` suppresses display of the replication dots. By default, one dot character is displayed for each successful replication. A red 'x' is displayed if *command* returns an error or if one of the values in *exp_list* is missing.

`noisily` specifies that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`title(`*text*`)` specifies a title to be displayed above the table of jackknife results; the default title is `Jackknife results` or what is produced in `e(title)` by an estimation command.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Advanced

`nodrop` prevents observations outside `e(sample)` and the `if` and `in` qualifiers from being dropped before the data are resampled.

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

The following options are available with `jackknife` but are not shown in the dialog box:

eform_option causes the coefficient table to be displayed in exponentiated form; see [R] ***eform_option***. *command* determines which *eform_option* is allowed (`eform(`*string*`)` and `eform` are always allowed).

command determines which of the following are allowed (`eform(`*string*`)` and `eform` are always allowed):

eform_option	Description
`eform(`*string*`)`	use *string* for the column title
`eform`	exponentiated coefficient, *string* is `exp(b)`
`hr`	hazard ratio, *string* is `Haz. Ratio`
`shr`	subhazard ratio, *string* is `SHR`
`irr`	incidence-rate ratio, *string* is `IRR`
`or`	odds ratio, *string* is `Odds Ratio`
`rrr`	relative-risk ratio, *string* is `RRR`

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Jackknifed standard deviation
Collecting multiple statistics
Collecting coefficients

Introduction

Although the jackknife—developed in the late 1940s and early 1950s—is of largely historical interest today, it is still useful in searching for overly influential observations. This feature is often forgotten. In any case, the jackknife is

- an alternative, first-order unbiased estimator for a statistic;
- a data-dependent way to calculate the standard error of the statistic and to obtain significance levels and confidence intervals; and
- a way of producing measures called pseudovalues for each observation, reflecting the observation's influence on the overall statistic.

The idea behind the simplest form of the jackknife—the one implemented here—is to repeatedly calculate the statistic in question, each time omitting just one of the dataset's observations. Assume that our statistic of interest is the sample mean. Let y_j be the jth observation of our data on some measurement y, where $j = 1, \ldots, N$ and N is the sample size. If $\overline{y}$ is the sample mean of y using the entire dataset and $\overline{y}_{(j)}$ is the mean when the jth observation is omitted, then

$$\overline{y} = \frac{(N-1)\,\overline{y}_{(j)} + y_j}{N}$$

Solving for y_j, we obtain

$$y_j = N\,\overline{y} - (N-1)\,\overline{y}_{(j)}$$

These are the pseudovalues that `jackknife` calculates. To move this discussion beyond the sample mean, let $\widehat{\theta}$ be the value of our statistic (not necessarily the sample mean) using the entire dataset, and let $\widehat{\theta}_{(j)}$ be the computed value of our statistic with the jth observation omitted. The pseudovalue for the jth observation is

$$\widehat{\theta}^{*}_{j} = N\,\widehat{\theta} - (N-1)\,\widehat{\theta}_{(j)}$$

The mean of the pseudovalues is the alternative, first-order unbiased estimator mentioned above, and the standard error of the mean of the pseudovalues is an estimator for the standard error of $\widehat{\theta}$ (Tukey 1958).

When the `cluster()` option is given, clusters are omitted instead of observations, and N is the number of clusters instead of the sample size.

The jackknife estimate of variance has been largely replaced by the bootstrap estimate (see [R] **bootstrap**), which is widely viewed as more efficient and robust. The use of jackknife pseudovalues to detect outliers is too often forgotten and is something the bootstrap does not provide. See Mosteller and Tukey (1977, 133–163) and Mooney and Duval (1993, 22–27) for more information.

▷ Example 1

As our first example, we will show that the jackknife standard error of the sample mean is equivalent to the standard error of the sample mean computed using the classical formula in the `ci` command. We use the `double` option to compute the standard errors with the same precision as the `ci` command.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. jackknife r(mean), double: summarize mpg
Jackknife replications (74)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
........................
Jackknife results                               Number of obs      =        74
                                                Replications       =        74

      command:  summarize mpg, mean
        _jk_1:  r(mean)
          n():  r(N)

------------------------------------------------------------------------------
             |              Jackknife
             |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _jk_1 |     21.2973   .6725511    31.67   0.000      19.9569     22.63769
------------------------------------------------------------------------------

. ci mpg
    Variable |        Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+---------------------------------------------------------------
         mpg |         74     21.2973    .6725511        19.9569     22.63769
```

◁

Jackknifed standard deviation

▷ Example 2

Mosteller and Tukey (1977, 139–140) request a 95% confidence interval for the standard deviation of the 11 values:

0.1, 0.1, 0.1, 0.4, 0.5, 1.0, 1.1, 1.3, 1.9, 1.9, 4.7

Stata's `summarize` command calculates the mean and standard deviation and saves them as `r(mean)` and `r(sd)`. To obtain the jackknifed standard deviation of the 11 values and save the pseudovalues as a new variable, `sd`, we would type

```
. clear
. input x
            x
  1. 0.1
  2. 0.1
  3. 0.1
  4. 0.4
  5. 0.5
  6. 1.0
  7. 1.1
  8. 1.3
  9. 1.9
 10. 1.9
 11. 4.7
 12. end
. jackknife sd=r(sd), rclass keep: summarize x
(running summarize on estimation sample)
Jackknife replications (11)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
...........
Jackknife results                               Number of obs      =        11
                                                Replications       =        11

      command:  summarize x
           sd:  r(sd)
         n():  r(N)

------------------------------------------------------------------------------
             |             Jackknife
             |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          sd |    1.343469    .624405     2.15   0.057    -.047792     2.73473
------------------------------------------------------------------------------
```

Interpreting the output, the standard deviation reported by `summarize mpg` is 1.34. The jackknife standard error is 0.62. The 95% confidence interval for the standard deviation is -0.048 to 2.73.

By specifying `keep`, `jackknife` creates in our dataset a new variable, `sd`, for the pseudovalues.

```
. list, sep(4)
```

	x	sd
1.	.1	1.139977
2.	.1	1.139977
3.	.1	1.139977
4.	.4	.8893147
5.	.5	.824267
6.	1	.632489
7.	1.1	.6203189
8.	1.3	.6218889
9.	1.9	.835419
10.	1.9	.835419
11.	4.7	7.703949

The jackknife estimate is the average of the `sd` variable, so `sd` contains the individual values of our statistic. We can see that the last observation is substantially larger than the others. The last observation is certainly an outlier, but whether that reflects the considerable information it contains or indicates that it should be excluded from analysis depends on the context of the problem. Here Mosteller

and Tukey created the dataset by sampling from an exponential distribution, so the observation is informative.

◁

▷ Example 3

Let's repeat the example above using the automobile dataset, obtaining the standard error of the standard deviation of mpg.

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. jackknife sd=r(sd), rclass keep: summarize mpg
(running summarize on estimation sample)
Jackknife replications (74)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
........................
Jackknife results                                 Number of obs      =        74
                                                  Replications       =        74

      command:  summarize mpg
           sd:  r(sd)
         n():  r(N)
```

	Coef.	Jackknife Std. Err.	t	P>|t|	[95% Conf.	Interval]
sd	5.785503	.6072509	9.53	0.000	4.575254	6.995753

Let's look at sd more carefully:

```
. summarize sd, detail
                    pseudovalues: r(sd)
-------------------------------------------------------------
      Percentiles      Smallest
 1%     2.870471       2.870471
 5%     2.870471       2.870471
10%     2.906255       2.870471       Obs                  74
25%     3.328489       2.870471       Sum of Wgt.          74

50%     3.948335                      Mean           5.817374
                       Largest        Std. Dev.       5.22377
75%     6.844418       17.34316
90%     9.597018        19.7617       Variance       27.28777
95%     17.34316        19.7617       Skewness        4.07202
99%     38.60905       38.60905       Kurtosis       23.37823
. list make mpg sd if sd > 30
```

	make	mpg	sd
71.	VW Diesel	41	38.60905

Here the VW Diesel is the only diesel car in our dataset.

◁

Collecting multiple statistics

▷ Example 4

`jackknife` is not limited to collecting just one statistic. For instance, we can use `summarize, detail` and then obtain the jackknife estimate of the standard deviation and skewness. `summarize, detail` saves the standard deviation in `r(sd)` and the skewness in `r(skewness)`, so we might type

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. jackknife sd=r(sd) skew=r(skewness), rclass: summarize mpg, detail
(running summarize on estimation sample)
Jackknife replications (74)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
........................
Jackknife results                                 Number of obs      =        74
                                                  Replications       =        74
      command:  summarize mpg, detail
           sd:  r(sd)
         skew:  r(skewness)
         n():  r(N)
------------------------------------------------------------------------------
             |             Jackknife
             |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          sd |    5.785503   .6072509     9.53   0.000     4.575254    6.995753
        skew |     .9487176   .3367242     2.82   0.006     .2776272    1.619808
------------------------------------------------------------------------------
```

◁

Collecting coefficients

▷ Example 5

`jackknife` can also collect coefficients from estimation commands. For instance, using `auto.dta`, we might wish to obtain the jackknife standard errors of the coefficients from a regression in which we model the mileage of a car by its weight and trunk space. To do this, we could refer to the coefficients as `_b[weight]`, `_b[trunk]`, `_se[weight]`, and `_se[trunk]` in the *exp_list*, or we could simply use the extended expressions `_b`. In fact, `jackknife` assumes `_b` by default when used with estimation commands.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. jackknife: regress mpg weight trunk
(running regress on estimation sample)
Jackknife replications (74)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
........................
Linear regression                               Number of obs      =        74
                                                Replications       =        74
                                                F(   2,     73)    =     78.10
                                                Prob > F           =    0.0000
                                                R-squared          =    0.6543
                                                Adj R-squared      =    0.6446
                                                Root MSE           =    3.4492

------------------------------------------------------------------------------
             |             Jackknife
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0056527   .0010216    -5.53   0.000    -.0076887   -.0036167
       trunk |   -.096229   .1486236    -0.65   0.519    -.3924354    .1999773
       _cons |   39.68913   1.873324    21.19   0.000      35.9556    43.42266
------------------------------------------------------------------------------
```

If you are going to use `jackknife` to estimate standard errors of model coefficients, we recommend using the `vce(jackknife)` option when it is allowed with the estimation command; see [R] ***vce_option***.

```
. regress mpg weight trunk, vce(jackknife, nodots)
Linear regression                               Number of obs      =        74
                                                Replications       =        74
                                                F(   2,     73)    =     78.10
                                                Prob > F           =    0.0000
                                                R-squared          =    0.6543
                                                Adj R-squared      =    0.6446
                                                Root MSE           =    3.4492

------------------------------------------------------------------------------
             |             Jackknife
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0056527   .0010216    -5.53   0.000    -.0076887   -.0036167
       trunk |   -.096229   .1486236    -0.65   0.519    -.3924354    .1999773
       _cons |   39.68913   1.873324    21.19   0.000      35.9556    43.42266
------------------------------------------------------------------------------
```

◁

John Wilder Tukey (1915–2000) was born in Massachusetts. He studied chemistry at Brown and mathematics at Princeton and afterward worked at both Princeton and Bell Labs, as well as being involved in a great many government projects, consultancies, and committees. He made outstanding contributions to several areas of statistics, including time series, multiple comparisons, robust statistics, and exploratory data analysis. Tukey was extraordinarily energetic and inventive, not least in his use of terminology: he is credited with inventing the terms bit and software, in addition to ANOVA, boxplot, data analysis, hat matrix, jackknife, stem-and-leaf plot, trimming, and winsorizing, among many others. Tukey's direct and indirect impacts mark him as one of the greatest statisticians of all time.

Saved results

jknife saves the following in e():

Scalars

e(N)	sample size
e(N_reps)	number of complete replications
e(N_misreps)	number of incomplete replications
e(N_clust)	number of clusters
e(k_eq)	number of equations in e(b)
e(k_extra)	number of extra equations
e(k_exp)	number of expressions
e(k_eexp)	number of extended expressions (_b or _se)
e(df_r)	degrees of freedom

Macros

e(cmdname)	command name from *command*
e(cmd)	same as e(cmdname) or jackknife
e(command)	*command*
e(cmdline)	command as typed
e(prefix)	jackknife
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(cluster)	cluster variables
e(pseudo)	new variables containing pseudovalues
e(nfunction)	e(N), r(N), n() option, or empty
e(exp#)	expression for the #th statistic
e(mse)	from mse option
e(vce)	jackknife
e(vcetype)	title used to label Std. Err.
e(properties)	b V

Matrices

e(b)	observed statistics
e(b_jk)	jackknife estimates
e(V)	jackknife variance–covariance matrix
e(V_modelbased)	model-based variance

When *exp_list* is _b, jackknife will also carry forward most of the results already in e() from *command*.

Methods and formulas

jackknife is implemented as an ado-file.

Let $\widehat{\theta}$ be the observed value of the statistic, that is, the value of the statistic calculated using the original dataset. Let $\widehat{\theta}_{(j)}$ be the value of the statistic computed by leaving out the *j*th observation (or cluster); thus $j = 1, 2, \ldots, N$ identifies an individual observation (or cluster), and N is the total number of observations (or clusters). The *j*th pseudovalue is given by

$$\widehat{\theta}^*_j = \widehat{\theta}_{(j)} + N\{\widehat{\theta} - \widehat{\theta}_{(j)}\}$$

When the mse option is specified, the standard error is estimated as

$$\widehat{\mathrm{se}} = \left\{ \frac{N-1}{N} \sum_{j=1}^{N} (\widehat{\theta}_{(j)} - \widehat{\theta})^2 \right\}^{1/2}$$

and the jackknife estimate is

$$\bar{\theta}_{(.)} = \frac{1}{N}\sum_{j=1}^{N}\widehat{\theta}_{(j)}$$

Otherwise, the standard error is estimated as

$$\widehat{\mathrm{se}} = \left\{\frac{1}{N(N-1)}\sum_{j=1}^{N}(\widehat{\theta}^{*}_{j} - \bar{\theta}^{*})^{2}\right\}^{1/2} \qquad \bar{\theta}^{*} = \frac{1}{N}\sum_{j=1}^{N}\widehat{\theta}^{*}_{j}$$

where $\bar{\theta}^{*}$ is the jackknife estimate. The variance–covariance matrix is similarly computed.

References

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Mooney, C. Z., and R. D. Duval. 1993. *Bootstrapping: A Nonparametric Approach to Statistical Inference*. Newbury Park, CA: Sage.

Mosteller, F., and J. W. Tukey. 1977. *Data Analysis and Regression: A Second Course in Statistics*. Reading, MA: Addison–Wesley.

Tukey, J. W. 1958. Bias and confidence in not-quite large samples. Abstract in *Annals of Mathematical Statistics* 29: 614.

Also see

[R] **jackknife postestimation** — Postestimation tools for jackknife

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **permute** — Monte Carlo permutation tests

[R] **simulate** — Monte Carlo simulations

[SVY] **svy jackknife** — Jackknife estimation for survey data

[U] **13.5 Accessing coefficients and standard errors**

[U] **13.6 Accessing results from Stata commands**

[U] **20 Estimation and postestimation commands**

Title

jackknife postestimation — Postestimation tools for jackknife

Description

The following postestimation commands are available after `jackknife`:

Command	Description
*`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
*`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
*`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
*`predict`	predictions, residuals, influence statistics, and other diagnostic measures
*`predictnl`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
*`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

*This postestimation command is allowed only if it may be used after *command*.

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

The syntax of `predict` (and whether `predict` is even allowed) following `jackknife` depends on the *command* used with `jackknife`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **jackknife** — Jackknife estimation

[U] **20 Estimation and postestimation commands**

Title

kappa — Interrater agreement

Syntax

Interrater agreement, two unique raters

`kap` *varname*$_1$ *varname*$_2$ [*if*] [*in*] [*weight*] [`,` *options*]

Weights for weighting disagreements

`kapwgt` *wgtid* [`1` `\` `#` `1` [`\` `#` `#` `1` ...]]

Interrater agreement, nonunique raters, variables record ratings for each rater

`kap` *varname*$_1$ *varname*$_2$ *varname*$_3$ [...] [*if*] [*in*] [*weight*]

Interrater agreement, nonunique raters, variables record frequency of ratings

`kappa` *varlist* [*if*] [*in*]

options	Description
Main	
`tab`	display table of assessments
`wgt(`*wgtid*`)`	specify how to weight disagreements; see *Options* for alternatives
`absolute`	treat rating categories as absolute

`fweights` are allowed; see [U] **11.1.6 weight**.

Menu

kap: two unique raters

Statistics > Epidemiology and related > Other > Interrater agreement, two unique raters

kapwgt

Statistics > Epidemiology and related > Other > Define weights for the above (kap)

kap: nonunique raters

Statistics > Epidemiology and related > Other > Interrater agreement, nonunique raters

kappa

Statistics > Epidemiology and related > Other > Interrater agreement, nonunique raters with frequencies

Description

kap (first syntax) calculates the kappa-statistic measure of interrater agreement when there are two unique raters and two or more ratings.

kapwgt defines weights for use by kap in measuring the importance of disagreements.

kap (second syntax) and kappa calculate the kappa-statistic measure when there are two or more (nonunique) raters and two outcomes, more than two outcomes when the number of raters is fixed, and more than two outcomes when the number of raters varies. kap (second syntax) and kappa produce the same results; they merely differ in how they expect the data to be organized.

kap assumes that each observation is a subject. *varname*$_1$ contains the ratings by the first rater, *varname*$_2$ by the second rater, and so on.

kappa also assumes that each observation is a subject. The variables, however, record the frequencies with which ratings were assigned. The first variable records the number of times the first rating was assigned, the second variable records the number of times the second rating was assigned, and so on.

Options

Main

tab displays a tabulation of the assessments by the two raters.

wgt(*wgtid*) specifies that *wgtid* be used to weight disagreements. You can define your own weights by using kapwgt; wgt() then specifies the name of the user-defined matrix. For instance, you might define

```
. kapwgt mine 1 \ .8 1 \ 0 .8 1 \ 0 0 .8 1
```

and then

```
. kap rata ratb, wgt(mine)
```

Also, two prerecorded weights are available.

wgt(w) specifies weights $1 - |i - j|/(k - 1)$, where i and j index the rows and columns of the ratings by the two raters and k is the maximum number of possible ratings.

wgt(w2) specifies weights $1 - \{(i - j)/(k - 1)\}^2$.

absolute is relevant only if wgt() is also specified. The absolute option modifies how i, j, and k are defined and how corresponding entries are found in a user-defined weighting matrix. When absolute is not specified, i and j refer to the row and column index, not to the ratings themselves. Say that the ratings are recorded as $\{0, 1, 1.5, 2\}$. There are four ratings; $k = 4$, and i and j are still 1, 2, 3, and 4 in the formulas above. Index 3, for instance, corresponds to rating $= 1.5$. This system is convenient but can, with some data, lead to difficulties.

When absolute is specified, all ratings must be integers, and they must be coded from the set $\{1, 2, 3, \ldots\}$. Not all values need be used; integer values that do not occur are simply assumed to be unobserved.

Remarks

Remarks are presented under the following headings:

Two raters
More than two raters

The kappa-statistic measure of agreement is scaled to be 0 when the amount of agreement is what would be expected to be observed by chance and 1 when there is perfect agreement. For intermediate values, Landis and Koch (1977a, 165) suggest the following interpretations:

below 0.0	Poor
0.00–0.20	Slight
0.21–0.40	Fair
0.41–0.60	Moderate
0.61–0.80	Substantial
0.81–1.00	Almost perfect

Two raters

▷ Example 1

Consider the classification by two radiologists of 85 xeromammograms as normal, benign disease, suspicion of cancer, or cancer (a subset of the data from Boyd et al. [1982] and discussed in the context of kappa in Altman [1991, 403–405]).

```
. use http://www.stata-press.com/data/r12/rate2
(Altman p. 403)
. tabulate rada radb
```

Radiologist A's assessment	Radiologist B's assessment				
	normal	benign	suspect	cancer	Total
normal	21	12	0	0	33
benign	4	17	1	0	22
suspect	3	9	15	2	29
cancer	0	0	0	1	1
Total	28	38	16	3	85

Our dataset contains two variables: `rada`, radiologist A's assessment, and `radb`, radiologist B's assessment. Each observation is a patient.

We can obtain the kappa measure of interrater agreement by typing

```
. kap rada radb
```

Agreement	Expected Agreement	Kappa	Std. Err.	Z	Prob>Z
63.53%	30.82%	0.4728	0.0694	6.81	0.0000

If each radiologist had made his determination randomly (but with probabilities equal to the overall proportions), we would expect the two radiologists to agree on 30.8% of the patients. In fact, they agreed on 63.5% of the patients, or 47.3% of the way between random agreement and perfect agreement. The amount of agreement indicates that we can reject the hypothesis that they are making their determinations randomly.

◁

▷ Example 2: Weighted kappa, prerecorded weight w

There is a difference between two radiologists disagreeing about whether a xeromammogram indicates cancer or the suspicion of cancer and disagreeing about whether it indicates cancer or is normal. The weighted kappa attempts to deal with this. `kap` provides two "prerecorded" weights, `w` and `w2`:

```
. kap rada radb, wgt(w)
Ratings weighted by:
   1.0000   0.6667   0.3333   0.0000
   0.6667   1.0000   0.6667   0.3333
   0.3333   0.6667   1.0000   0.6667
   0.0000   0.3333   0.6667   1.0000
            Expected
Agreement   Agreement     Kappa   Std. Err.         Z      Prob>Z
------------------------------------------------------------------
  86.67%      69.11%     0.5684      0.0788       7.22       0.0000
```

The `w` weights are given by $1 - |i-j|/(k-1)$, where i and j index the rows of columns of the ratings by the two raters and k is the maximum number of possible ratings. The weighting matrix is printed above the table. Here the rows and columns of the 4×4 matrix correspond to the ratings normal, benign, suspicious, and cancerous.

A weight of 1 indicates that an observation should count as perfect agreement. The matrix has 1s down the diagonals—when both radiologists make the same assessment, they are in agreement. A weight of, say, 0.6667 means that they are in two-thirds agreement. In our matrix, they get that score if they are "one apart"—one radiologist assesses cancer and the other is merely suspicious, or one is suspicious and the other says benign, and so on. An entry of 0.3333 means that they are in one-third agreement, or, if you prefer, two-thirds disagreement. That is the score attached when they are "two apart". Finally, they are in complete disagreement when the weight is zero, which happens only when they are three apart—one says cancer and the other says normal. ◁

▷ Example 3: Weighted kappa, prerecorded weight w2

The other prerecorded weight is `w2`, where the weights are given by $1 - \{(i-j)/(k-1)\}^2$:

```
. kap rada radb, wgt(w2)
Ratings weighted by:
   1.0000   0.8889   0.5556   0.0000
   0.8889   1.0000   0.8889   0.5556
   0.5556   0.8889   1.0000   0.8889
   0.0000   0.5556   0.8889   1.0000
            Expected
Agreement   Agreement     Kappa   Std. Err.         Z      Prob>Z
------------------------------------------------------------------
  94.77%      84.09%     0.6714      0.1079       6.22       0.0000
```

The `w2` weight makes the categories even more alike and is probably inappropriate here. ◁

▷ Example 4: Weighted kappa, user-defined weights

In addition to using prerecorded weights, we can define our own weights with the `kapwgt` command. For instance, we might feel that suspicious and cancerous are reasonably similar, that benign and normal are reasonably similar, but that the suspicious/cancerous group is nothing like the benign/normal group:

```
. kapwgt xm 1 \ .8 1 \ 0 0 1 \ 0 0 .8 1
. kapwgt xm
 1.0000
 0.8000 1.0000
 0.0000 0.0000 1.0000
 0.0000 0.0000 0.8000 1.0000
```

We name the weights `xm`, and after the weight name, we enter the lower triangle of the weighting matrix, using `\` to separate rows. We have four outcomes, so we continued entering numbers until we had defined the fourth row of the weighting matrix. If we type `kapwgt` followed by a name and nothing else, it shows us the weights recorded under that name. Satisfied that we have entered them correctly, we now use the weights to recalculate kappa:

```
. kap rada radb, wgt(xm)
Ratings weighted by:
   1.0000   0.8000   0.0000   0.0000
   0.8000   1.0000   0.0000   0.0000
   0.0000   0.0000   1.0000   0.8000
   0.0000   0.0000   0.8000   1.0000

            Expected
Agreement   Agreement      Kappa   Std. Err.         Z      Prob>Z
------------------------------------------------------------------
  80.47%      52.67%     0.5874      0.0865      6.79      0.0000
```

◁

❑ Technical note

In addition to using weights for weighting the differences in categories, you can specify Stata's traditional weights for weighting the data. In the examples above, we have 85 observations in our dataset—one for each patient. If we only knew the table of outcomes—that there were 21 patients rated normal by both radiologists, etc.—it would be easier to enter the table into Stata and work from it. The easiest way to enter the data is with `tabi`; see [R] **tabulate twoway**.

```
. tabi 21 12 0 0 \ 4 17 1 0 \ 3 9 15 2 \ 0 0 0 1, replace
```

row	col 1	2	3	4	Total
1	21	12	0	0	33
2	4	17	1	0	22
3	3	9	15	2	29
4	0	0	0	1	1
Total	28	38	16	3	85

Pearson chi2(9) = 77.8111 Pr = 0.000

`tabi` reported the Pearson χ^2 for this table, but we do not care about it. The important thing is that, with the `replace` option, `tabi` left the table in memory:

```
. list in 1/5
```

	row	col	pop
1.	1	1	21
2.	1	2	12
3.	1	3	0
4.	1	4	0
5.	2	1	4

The variable `row` is radiologist A's assessment, `col` is radiologist B's assessment, and `pop` is the number so assessed by both. Thus

```
. kap row col [freq=pop]
```

Agreement	Expected Agreement	Kappa	Std. Err.	Z	Prob>Z
63.53%	30.82%	0.4728	0.0694	6.81	0.0000

If we are going to keep these data, the names `row` and `col` are not indicative of what the data reflect. We could type (see [U] **12.6 Dataset, variable, and value labels**)

```
. rename row rada
. rename col radb
. label var rada "Radiologist A's assessment"
. label var radb "Radiologist B's assessment"
. label define assess 1 normal 2 benign 3 suspect 4 cancer
. label values rada assess
. label values radb assess
. label data "Altman p. 403"
```

`kap`'s `tab` option, which can be used with or without weighted data, shows the table of assessments:

```
. kap rada radb [freq=pop], tab
```

Radiologist A's assessment	Radiologist B's assessment: normal	benign	suspect	cancer	Total
normal	21	12	0	0	33
benign	4	17	1	0	22
suspect	3	9	15	2	29
cancer	0	0	0	1	1
Total	28	38	16	3	85

Agreement	Expected Agreement	Kappa	Std. Err.	Z	Prob>Z
63.53%	30.82%	0.4728	0.0694	6.81	0.0000

❑

❑ Technical note

You have data on individual patients. There are two raters, and the possible ratings are 1, 2, 3, and 4, but neither rater ever used rating 3:

```
. use http://www.stata-press.com/data/r12/rate2no3, clear
. tabulate ratera raterb
```

ratera	raterb 1	2	4	Total
1	6	4	3	13
2	5	3	3	11
4	1	1	26	28
Total	12	8	32	52

Here `kap` would determine that the ratings are from the set $\{1, 2, 4\}$ because those were the only values observed. `kap` would expect a user-defined weighting matrix to be 3×3, and if it were not, `kap` would issue an error message. In the formula-based weights, the calculation would be based on $i, j = 1, 2, 3$ corresponding to the three observed ratings $\{1, 2, 4\}$.

Specifying the `absolute` option would clarify that the ratings are 1, 2, 3, and 4; it just so happens that rating 3 was never assigned. If a user-defined weighting matrix were also specified, `kap` would expect it to be 4×4 or larger (larger because we can think of the ratings being 1, 2, 3, 4, 5, ... and it just so happens that ratings 5, 6, ... were never observed, just as rating 3 was not observed). In the formula-based weights, the calculation would be based on $i, j = 1, 2, 4$.

```
. kap ratera raterb, wgt(w)
Ratings weighted by:
   1.0000   0.5000   0.0000
   0.5000   1.0000   0.5000
   0.0000   0.5000   1.0000
             Expected
Agreement    Agreement      Kappa    Std. Err.          Z       Prob>Z
------------------------------------------------------------------------
  79.81%       57.17%      0.5285      0.1169        4.52       0.0000
. kap ratera raterb, wgt(w) absolute
Ratings weighted by:
   1.0000   0.6667   0.0000
   0.6667   1.0000   0.3333
   0.0000   0.3333   1.0000
             Expected
Agreement    Agreement      Kappa    Std. Err.          Z       Prob>Z
------------------------------------------------------------------------
  81.41%       55.08%      0.5862      0.1209        4.85       0.0000
```

If all conceivable ratings are observed in the data, specifying `absolute` makes no difference. For instance, if rater A assigns ratings $\{1, 2, 4\}$ and rater B assigns $\{1, 2, 3, 4\}$, the complete set of assigned ratings is $\{1, 2, 3, 4\}$, the same that `absolute` would specify. Without `absolute`, it makes no difference whether the ratings are coded $\{1, 2, 3, 4\}$, $\{0, 1, 2, 3\}$, $\{1, 7, 9, 100\}$, $\{0, 1, 1.5, 2.0\}$, or otherwise.

❑

More than two raters

For more than two raters, the mathematics are such that the two raters are not considered unique. For instance, if there are three raters, there is no assumption that the three raters who rate the first subject are the same as the three raters who rate the second. Although we call this the "more than two raters" case, it can be used with two raters when the raters' identities vary.

The nonunique rater case can be usefully broken down into three subcases: 1) there are two possible ratings, which we will call positive and negative; 2) there are more than two possible ratings, but the number of raters per subject is the same for all subjects; and 3) there are more than two possible ratings, and the number of raters per subject varies. `kappa` handles all these cases. To emphasize that there is no assumption of constant identity of raters across subjects, the variables specified contain counts of the number of raters rating the subject into a particular category.

Jacob Cohen (1923–1998) was born in New York City. After studying psychology at City College of New York and New York University, he worked as a medical psychologist until 1959 when he became a full professor in the Department of Psychology at New York University. He made many contributions to research methods, including the kappa measure. He persistently emphasized the value of multiple regression and the importance of power and of measuring effects rather than testing significance.

▷ Example 5: Two ratings

Fleiss, Levin, and Paik (2003, 612) offers the following hypothetical ratings by different sets of raters on 25 subjects:

Subject	No. of raters	No. of pos. ratings	Subject	No. of raters	No. of pos. ratings
1	2	2	14	4	3
2	2	0	15	2	0
3	3	2	16	2	2
4	4	3	17	3	1
5	3	3	18	2	1
6	4	1	19	4	1
7	3	0	20	5	4
8	5	0	21	3	2
9	2	0	22	4	0
10	4	4	23	3	0
11	5	5	24	3	3
12	3	3	25	2	2
13	4	4			

We have entered these data into Stata, and the variables are called `subject`, `raters`, and `pos`. `kappa`, however, requires that we specify variables containing the number of positive ratings and negative ratings, that is, `pos` and `raters-pos`:

```
. use http://www.stata-press.com/data/r12/p612
. gen neg = raters-pos
. kappa pos neg
Two-outcomes, multiple raters:
        Kappa        Z        Prob>Z
-------------------------------------
       0.5415     5.28       0.0000
```

We would have obtained the same results if we had typed `kappa neg pos`.

◁

▷ Example 6: More than two ratings, constant number of raters, kappa

Each of 10 subjects is rated into one of three categories by five raters (Fleiss, Levin, and Paik 2003, 615):

```
. use http://www.stata-press.com/data/r12/p615, clear
. list
```

	subject	cat1	cat2	cat3
1.	1	1	4	0
2.	2	2	0	3
3.	3	0	0	5
4.	4	4	0	1
5.	5	3	0	2
6.	6	1	4	0
7.	7	5	0	0
8.	8	0	4	1
9.	9	1	0	4
10.	10	3	0	2

We obtain the kappa statistic:

```
. kappa cat1-cat3
```

Outcome	Kappa	Z	Prob>Z
cat1	0.2917	2.92	0.0018
cat2	0.6711	6.71	0.0000
cat3	0.3490	3.49	0.0002
combined	0.4179	5.83	0.0000

The first part of the output shows the results of calculating kappa for each of the categories separately against an amalgam of the remaining categories. For instance, the `cat1` line is the two-rating kappa, where positive is `cat1` and negative is `cat2` or `cat3`. The test statistic, however, is calculated differently (see *Methods and formulas*). The combined kappa is the appropriately weighted average of the individual kappas. There is considerably less agreement about the rating of subjects into the first category than there is for the second.

◁

▷ Example 7: More than two ratings, constant number of raters, kap

Now suppose that we have the same data as in the previous example but that the data are organized differently:

```
. use http://www.stata-press.com/data/r12/p615b
. list
```

	subject	rater1	rater2	rater3	rater4	rater5
1.	1	1	2	2	2	2
2.	2	1	1	3	3	3
3.	3	3	3	3	3	3
4.	4	1	1	1	1	3
5.	5	1	1	1	3	3
6.	6	1	2	2	2	2
7.	7	1	1	1	1	1
8.	8	2	2	2	2	3
9.	9	1	3	3	3	3
10.	10	1	1	1	3	3

Here we would use `kap` rather than `kappa` because the variables record ratings for each rater.

```
. kap rater1 rater2 rater3 rater4 rater5
There are 5 raters per subject:
```

Outcome	Kappa	Z	Prob>Z
1	0.2917	2.92	0.0018
2	0.6711	6.71	0.0000
3	0.3490	3.49	0.0002
combined	0.4179	5.83	0.0000

It does not matter which rater is which when there are more than two raters.

◁

▷ Example 8: More than two ratings, varying number of raters, kappa

In this unfortunate case, kappa can be calculated, but there is no test statistic for testing against $\kappa > 0$. We do nothing differently—`kappa` calculates the total number of raters for each subject, and, if it is not a constant, `kappa` suppresses the calculation of test statistics.

```
. use http://www.stata-press.com/data/r12/rvary
. list
```

	subject	cat1	cat2	cat3
1.	1	1	3	0
2.	2	2	0	3
3.	3	0	0	5
4.	4	4	0	1
5.	5	3	0	2
6.	6	1	4	0
7.	7	5	0	0
8.	8	0	4	1
9.	9	1	0	2
10.	10	3	0	2

```
. kappa cat1-cat3
```

Outcome	Kappa	Z	Prob>Z
cat1	0.2685	.	.
cat2	0.6457	.	.
cat3	0.2938	.	.
combined	0.3816	.	.

```
Note:  number of ratings per subject vary; cannot calculate test
       statistics.
```

◁

▷ Example 9: More than two ratings, varying number of raters, kap

This case is similar to the previous example, but the data are organized differently:

```
. use http://www.stata-press.com/data/r12/rvary2
. list
```

	subject	rater1	rater2	rater3	rater4	rater5
1.	1	1	2	2	.	2
2.	2	1	1	3	3	3
3.	3	3	3	3	3	3
4.	4	1	1	1	1	3
5.	5	1	1	1	3	3
6.	6	1	2	2	2	2
7.	7	1	1	1	1	1
8.	8	2	2	2	2	3
9.	9	1	3	.	.	3
10.	10	1	1	1	3	3

Here we specify `kap` instead of `kappa` because the variables record ratings for each rater.

```
. kap rater1-rater5
There are between 3 and 5 (median = 5.00) raters per subject:
```

Outcome	Kappa	Z	Prob>Z
1	0.2685	.	.
2	0.6457	.	.
3	0.2938	.	.
combined	0.3816	.	.

```
Note:  number of ratings per subject vary; cannot calculate test
       statistics.
```

◁

Saved results

kap and kappa save the following in r():

Scalars

r(N)	number of subjects (kap only)	r(kappa)	kappa
r(prop_o)	observed proportion of agreement (kap only)	r(z)	z statistic
r(prop_e)	expected proportion of agreement (kap only)	r(se)	standard error for kappa statistic

Methods and formulas

kap, kapwgt, and kappa are implemented as ado-files.

The kappa statistic was first proposed by Cohen (1960). The generalization for weights reflecting the relative seriousness of each possible disagreement is due to Cohen (1968). The analysis-of-variance approach for $k = 2$ and $m \geq 2$ is due to Landis and Koch (1977b). See Altman (1991, 403–409) or Dunn (2000, chap. 2) for an introductory treatment and Fleiss, Levin, and Paik (2003, chap. 18) for a more detailed treatment. All formulas below are as presented in Fleiss, Levin, and Paik (2003). Let m be the number of raters, and let k be the number of rating outcomes.

Methods and formulas are presented under the following headings:

kap: $m = 2$
kappa: $m > 2$, $k = 2$
kappa: $m > 2$, $k > 2$

kap: m = 2

Define w_{ij} ($i = 1, \ldots, k$ and $j = 1, \ldots, k$) as the weights for agreement and disagreement (wgt()), or, if the data are not weighted, define $w_{ii} = 1$ and $w_{ij} = 0$ for $i \neq j$. If wgt(w) is specified, $w_{ij} = 1 - |i - j|/(k - 1)$. If wgt(w2) is specified, $w_{ij} = 1 - \{(i - j)/(k - 1)\}^2$.

The observed proportion of agreement is

$$p_o = \sum_{i=1}^{k} \sum_{j=1}^{k} w_{ij} p_{ij}$$

where p_{ij} is the fraction of ratings i by the first rater and j by the second. The expected proportion of agreement is

$$p_e = \sum_{i=1}^{k} \sum_{j=1}^{k} w_{ij} p_{i\cdot} p_{\cdot j}$$

where $p_{i\cdot} = \sum_j p_{ij}$ and $p_{\cdot j} = \sum_i p_{ij}$.

Kappa is given by $\widehat{\kappa} = (p_o - p_e)/(1 - p_e)$.

The standard error of $\widehat{\kappa}$ for testing against 0 is

$$\widehat{s}_0 = \frac{1}{(1 - p_e)\sqrt{n}} \left(\left[\sum_i \sum_j p_{i\cdot} p_{\cdot j} \{ w_{ij} - (\overline{w}_{i\cdot} + \overline{w}_{\cdot j}) \}^2 \right] - p_e^2 \right)^{1/2}$$

where n is the number of subjects being rated, $\overline{w}_{i\cdot} = \sum_j p_{\cdot j} w_{ij}$, and $\overline{w}_{\cdot j} = \sum_i p_{i\cdot} w_{ij}$. The test statistic $Z = \widehat{\kappa}/\widehat{s}_0$ is assumed to be distributed $N(0, 1)$.

kappa: m > 2, k = 2

Each subject i, $i = 1, \ldots, n$, is found by x_i of m_i raters to be positive (the choice as to what is labeled positive is arbitrary).

The overall proportion of positive ratings is $\overline{p} = \sum_i x_i/(n\overline{m})$, where $\overline{m} = \sum_i m_i/n$. The between-subjects mean square is (approximately)

$$B = \frac{1}{n}\sum_i \frac{(x_i - m_i\overline{p})^2}{m_i}$$

and the within-subject mean square is

$$W = \frac{1}{n(\overline{m}-1)}\sum_i \frac{x_i(m_i - x_i)}{m_i}$$

Kappa is then defined as

$$\widehat{\kappa} = \frac{B - W}{B + (\overline{m}-1)W}$$

The standard error for testing against 0 (Fleiss and Cuzick 1979) is approximately equal to and is calculated as

$$\widehat{s}_0 = \frac{1}{(\overline{m}-1)\sqrt{n\overline{m}_H}}\left\{2(\overline{m}_H - 1) + \frac{(\overline{m} - \overline{m}_H)(1 - 4\overline{pq})}{\overline{m}\overline{p}\overline{q}}\right\}^{1/2}$$

where $\overline{m}_H$ is the harmonic mean of m_i and $\overline{q} = 1 - \overline{p}$.

The test statistic $Z = \widehat{\kappa}/\widehat{s}_0$ is assumed to be distributed $N(0, 1)$.

kappa: m > 2, k > 2

Let x_{ij} be the number of ratings on subject i, $i = 1, \ldots, n$, into category j, $j = 1, \ldots, k$. Define $\overline{p}_j$ as the overall proportion of ratings in category j, $\overline{q}_j = 1 - \overline{p}_j$, and let $\widehat{\kappa}_j$ be the kappa statistic given above for $k = 2$ when category j is compared with the amalgam of all other categories. Kappa is

$$\overline{\kappa} = \frac{\sum_j \overline{p}_j\overline{q}_j\widehat{\kappa}_j}{\sum_j \overline{p}_j\overline{q}_j}$$

(Landis and Koch 1977b). In the case where the number of raters per subject, $\sum_j x_{ij}$, is a constant m for all i, Fleiss, Nee, and Landis (1979) derived the following formulas for the approximate standard errors. The standard error for testing $\widehat{\kappa}_j$ against 0 is

$$\widehat{s}_j = \left\{\frac{2}{nm(m-1)}\right\}^{1/2}$$

and the standard error for testing $\overline{\kappa}$ is

$$\overline{s} = \frac{\sqrt{2}}{\sum_j \overline{p}_j \overline{q}_j \sqrt{nm(m-1)}} \left\{ \left(\sum_j \overline{p}_j \overline{q}_j \right)^2 - \sum_j \overline{p}_j \overline{q}_j (\overline{q}_j - \overline{p}_j) \right\}^{1/2}$$

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Title

kdensity — Univariate kernel density estimation

Syntax

`kdensity` *varname* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`kernel(`*kernel*`)`	specify kernel function; default is `kernel(epanechnikov)`
`bwidth(#)`	half-width of kernel
`generate(`*newvar*$_x$ *newvar*$_d$`)`	store the estimation points in *newvar*$_x$ and the density estimate in *newvar*$_d$
`n(#)`	estimate density using # points; default is min(N, 50)
`at(`*var*$_x$`)`	estimate density using the values specified by *var*$_x$
`nograph`	suppress graph
Kernel plot	
cline_options	affect rendition of the plotted kernel density estimate
Density plots	
`normal`	add normal density to the graph
`normopts(`*cline_options*`)`	affect rendition of normal density
`student(#)`	add Student's t density with # degrees of freedom to the graph
`stopts(`*cline_options*`)`	affect rendition of the Student's t density
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

kernel	Description
`epanechnikov`	Epanechnikov kernel function; the default
`epan2`	alternative Epanechnikov kernel function
`biweight`	biweight kernel function
`cosine`	cosine trace kernel function
`gaussian`	Gaussian kernel function
`parzen`	Parzen kernel function
`rectangle`	rectangle kernel function
`triangle`	triangle kernel function

`fweights`, `aweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Nonparametric analysis > Kernel density estimation

Description

`kdensity` produces kernel density estimates and graphs the result.

Options

Main

`kernel(`*kernel*`)` specifies the kernel function for use in calculating the kernel density estimate. The default kernel is the Epanechnikov kernel (`epanechnikov`).

`bwidth(#)` specifies the half-width of the kernel, the width of the density window around each point. If `bwidth()` is not specified, the "optimal" width is calculated and used. The optimal width is the width that would minimize the mean integrated squared error if the data were Gaussian and a Gaussian kernel were used, so it is not optimal in any global sense. In fact, for multimodal and highly skewed densities, this width is usually too wide and oversmooths the density (Silverman 1992).

`generate(`*newvar*$_x$ *newvar*$_d$`)` stores the results of the estimation. *newvar*$_x$ will contain the points at which the density is estimated. *newvar*$_d$ will contain the density estimate.

`n(#)` specifies the number of points at which the density estimate is to be evaluated. The default is $\min(N, 50)$, where N is the number of observations in memory.

`at(`*var*$_x$`)` specifies a variable that contains the values at which the density should be estimated. This option allows you to more easily obtain density estimates for different variables or different subsamples of a variable and then overlay the estimated densities for comparison.

`nograph` suppresses the graph. This option is often used with the `generate()` option.

Kernel plot

cline_options affect the rendition of the plotted kernel density estimate. See [G-3] ***cline_options***.

Density plots

`normal` requests that a normal density be overlaid on the density estimate for comparison.

`normopts(`*cline_options*`)` specifies details about the rendition of the normal curve, such as the color and style of line used. See [G-3] ***cline_options***.

`student(#)` specifies that a Student's t density with # degrees of freedom be overlaid on the density estimate for comparison.

`stopts(`*cline_options*`)` affects the rendition of the Student's t density. See [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Kernel density estimators approximate the density $f(x)$ from observations on x. Histograms do this, too, and the histogram itself is a kind of kernel density estimate. The data are divided into nonoverlapping intervals, and counts are made of the number of data points within each interval. Histograms are bar graphs that depict these frequency counts—the bar is centered at the midpoint of each interval—and its height reflects the average number of data points in the interval.

In more general kernel density estimates, the range is still divided into intervals, and estimates of the density at the center of intervals are produced. One difference is that the intervals are allowed to overlap. We can think of sliding the interval—called a window—along the range of the data and collecting the center-point density estimates. The second difference is that, rather than merely counting the number of observations in a window, a kernel density estimator assigns a weight between 0 and 1—based on the distance from the center of the window—and sums the weighted values. The function that determines these weights is called the kernel.

Kernel density estimates have the advantages of being smooth and of being independent of the choice of origin (corresponding to the location of the bins in a histogram).

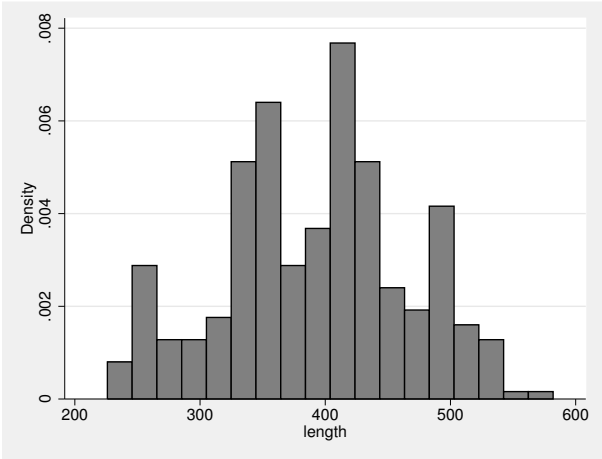
See Salgado-Ugarte, Shimizu, and Taniuchi (1993) and Fox (1990) for discussions of kernel density estimators that stress their use as exploratory data-analysis tools.

Cox (2007) gives a lucid introductory tutorial on kernel density estimation with several Stata produced examples. He provides tips and tricks for working with skewed or bounded distributions and applying the same techniques to estimate the intensity function of a point process.

▷ Example 1: Histogram and kernel density estimate

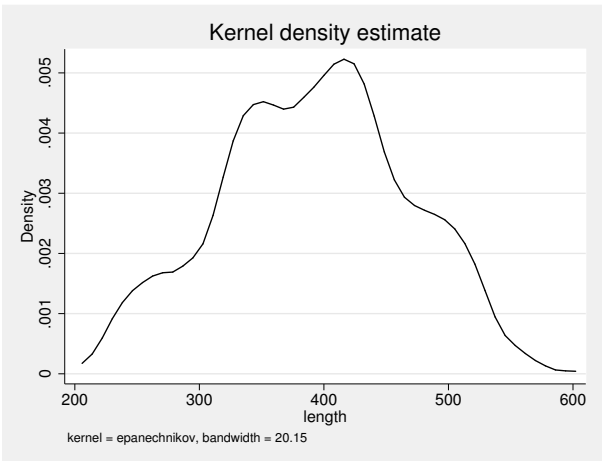
Goeden (1978) reports data consisting of 316 length observations of coral trout. We wish to investigate the underlying density of the lengths. To begin on familiar ground, we might draw a histogram. In [R] **histogram**, we suggest setting the bins to $\min(\sqrt{n}, 10 \cdot \log_{10} n)$, which for $n = 316$ is roughly 18:

```
. use http://www.stata-press.com/data/r12/trocolen
. histogram length, bin(18)
(bin=18, start=226, width=19.777778)
```



The kernel density estimate, on the other hand, is smooth.

```
. kdensity length
```



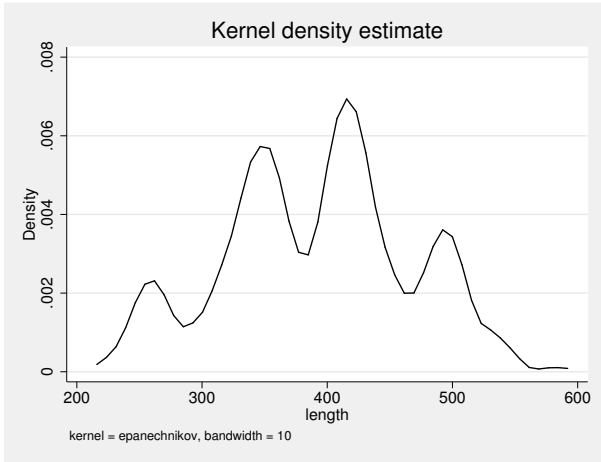
Kernel density estimators are, however, sensitive to an assumption, just as are histograms. In histograms, we specify a number of bins. For kernel density estimators, we specify a width. In the graph above, we used the default width. `kdensity` is smarter than `twoway histogram` in that its default width is not a fixed constant. Even so, the default width is not necessarily best.

`kdensity` saves the width in the returned scalar `bwidth`, so typing `display r(bwidth)` reveals it. Doing this, we discover that the width is approximately 20.

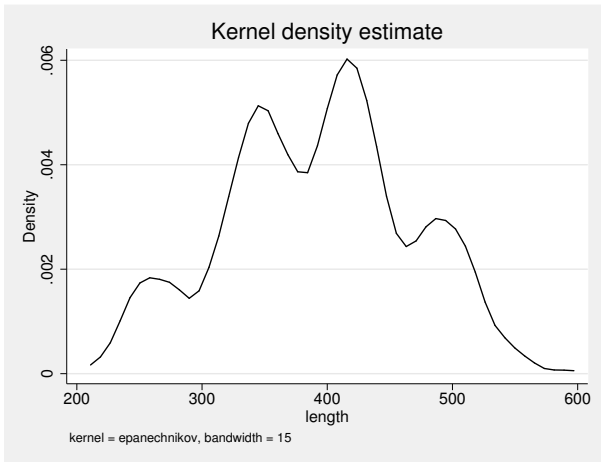
Widths are similar to the inverse of the number of bins in a histogram in that smaller widths provide more detail. The units of the width are the units of x, the variable being analyzed. The width is specified as a half-width, meaning that the kernel density estimator with half-width 20 corresponds to sliding a window of size 40 across the data.

We can specify half-widths for ourselves by using the `bwidth()` option. Smaller widths do not smooth the density as much:

```
. kdensity length, bwidth(10)
```




```
. kdensity length, bwidth(15)
```



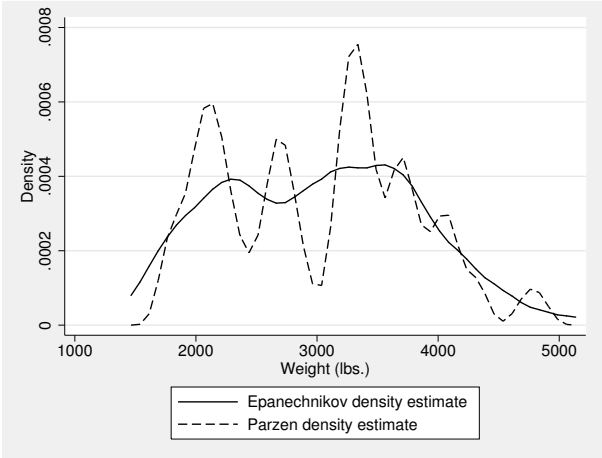
◁

▷ Example 2: Different kernels can produce different results

When widths are held constant, different kernels can produce surprisingly different results. This is really an attribute of the kernel and width combination; for a given width, some kernels are more sensitive than others at identifying peaks in the density estimate.

We can see this when using a dataset with lots of peaks. In the automobile dataset, we characterize the density of `weight`, the weight of the vehicles. Below we compare the Epanechnikov and Parzen kernels.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. kdensity weight, kernel(epanechnikov) nograph generate(x epan)
. kdensity weight, kernel(parzen) nograph generate(x2 parzen)
. label var epan "Epanechnikov density estimate"
. label var parzen "Parzen density estimate"
. line epan parzen x, sort ytitle(Density) legend(cols(1))
```

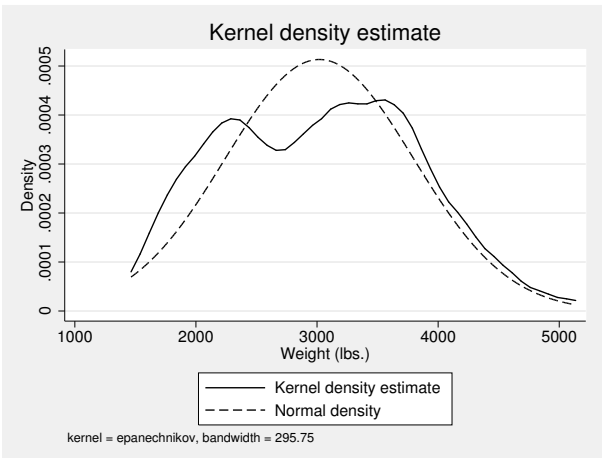


We did not specify a width, so we obtained the default width. That width is not a function of the selected kernel, but of the data. See *Methods and formulas* for the calculation of the optimal width.

Example 3: Density with overlaid normal density

In examining the density estimates, we may wish to overlay a normal density or a Student's t density for comparison. Using automobile weights, we can get an idea of the distance from normality by using the `normal` option.

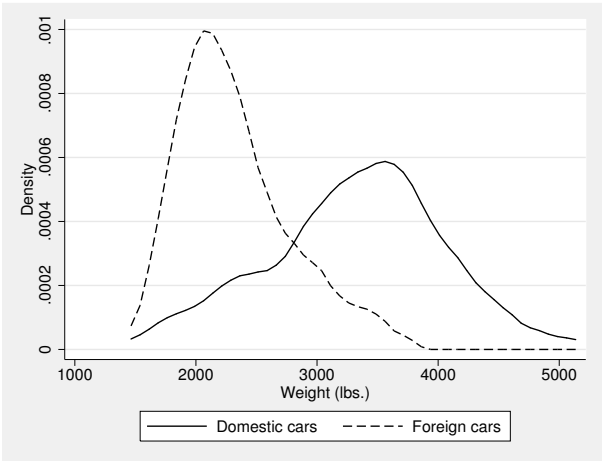
```
. kdensity weight, kernel(epanechnikov) normal
```



▷ Example 4: Compare two densities

We also may want to compare two or more densities. In this example, we will compare the density estimates of the weights for the foreign and domestic cars.

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. kdensity weight, nograph generate(x fx)
. kdensity weight if foreign==0, nograph generate(fx0) at(x)
. kdensity weight if foreign==1, nograph generate(fx1) at(x)
. label var fx0 "Domestic cars"
. label var fx1 "Foreign cars"
. line fx0 fx1 x, sort ytitle(Density)
```



◁

❑ Technical note

Although all the examples we included had densities of less than 1, the density may exceed 1.

The probability density $f(x)$ of a continuous variable, x, has the units and dimensions of the reciprocal of x. If x is measured in meters, $f(x)$ has units $1/$meter. Thus the density is not measured on a probability scale, so it is possible for $f(x)$ to exceed 1.

To see this, think of a uniform density on the interval 0 to 1. The area under the density curve is 1: this is the product of the density, which is constant at 1, and the range, which is 1. If the variable is then transformed by doubling, the area under the curve remains 1 and is the product of the density, constant at 0.5, and the range, which is 2. Conversely, if the variable is transformed by halving, the area under the curve also remains at 1 and is the product of the density, constant at 2, and the range, which is 0.5. (Strictly, the range is measured in certain units, and the density is measured in the reciprocal of those units, so the units cancel on multiplication.)

❑

Saved results

kdensity saves the following in r():

Scalars
- r(bwidth) kernel bandwidth
- r(n) number of points at which the estimate was evaluated
- r(scale) density bin width

Macros
- r(kernel) name of kernel

Methods and formulas

kdensity is implemented as an ado-file.

A kernel density estimate is formed by summing the weighted values calculated with the kernel function K, as in

$$\widehat{f}_K = \frac{1}{qh}\sum_{i=1}^{n} w_i K\left(\frac{x - X_i}{h}\right)$$

where $q = \sum_i w_i$ if weights are frequency weights (fweight) or analytic weights (aweight), and $q = 1$ if weights are importance weights (iweights). Analytic weights are rescaled so that $\sum_i w_i = n$ (see [U] **11 Language syntax**). If weights are not used, then $w_i = 1$, for $i = 1, \ldots, n$. kdensity includes seven different kernel functions. The Epanechnikov is the default function if no other kernel is specified and is the most efficient in minimizing the mean integrated squared error.

Kernel	Formula	
Biweight	$K[z] = \begin{cases} \frac{15}{16}(1-z^2)^2 \\ 0 \end{cases}$	if $\lvert z\rvert < 1$ otherwise
Cosine	$K[z] = \begin{cases} 1+\cos(2\pi z) \\ 0 \end{cases}$	if $\lvert z\rvert < 1/2$ otherwise
Epanechnikov	$K[z] = \begin{cases} \frac{3}{4}(1-\frac{1}{5}z^2)/\sqrt{5} \\ 0 \end{cases}$	if $\lvert z\rvert < \sqrt{5}$ otherwise
Epan2	$K[z] = \begin{cases} \frac{3}{4}(1-z^2) \\ 0 \end{cases}$	if $\lvert z\rvert < 1$ otherwise
Gaussian	$K[z] = \frac{1}{\sqrt{2\pi}}e^{-z^2/2}$	
Parzen	$K[z] = \begin{cases} \frac{4}{3} - 8z^2 + 8\lvert z\rvert^3 \\ 8(1-\lvert z\rvert)^3/3 \\ 0 \end{cases}$	if $\lvert z\rvert \le 1/2$ if $1/2 < \lvert z\rvert \le 1$ otherwise
Rectangular	$K[z] = \begin{cases} 1/2 \\ 0 \end{cases}$	if $\lvert z\rvert < 1$ otherwise
Triangular	$K[z] = \begin{cases} 1-\lvert z\rvert \\ 0 \end{cases}$	if $\lvert z\rvert < 1$ otherwise

From the definitions given in the table, we can see that the choice of h will drive how many values are included in estimating the density at each point. This value is called the *window width* or *bandwidth*. If the window width is not specified, it is determined as

$$m = \min\left(\sqrt{\text{variance}_x},\ \frac{\text{interquartile range}_x}{1.349}\right)$$
$$h = \frac{0.9m}{n^{1/5}}$$

where x is the variable for which we wish to estimate the kernel and n is the number of observations.

Most researchers agree that the choice of kernel is not as important as the choice of bandwidth. There is a great deal of literature on choosing bandwidths under various conditions; see, for example, Parzen (1962) or Tapia and Thompson (1978). Also see Newton (1988) for a comparison with sample spectral density estimation in time-series applications.

Acknowledgments

We gratefully acknowledge the previous work by Isaías H. Salgado-Ugarte of Universidad Nacional Autónoma de México, and Makoto Shimizu and Toru Taniuchi of the University of Tokyo; see Salgado-Ugarte, Shimizu, and Taniuchi (1993). Their article provides a good overview of the subject of univariate kernel density estimation and presents arguments for its use in exploratory data analysis.

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Also see

[R] **histogram** — Histograms for continuous and categorical variables

Title

ksmirnov — Kolmogorov–Smirnov equality-of-distributions test

Syntax

One-sample Kolmogorov–Smirnov test

```
ksmirnov varname = exp [if] [in]
```

Two-sample Kolmogorov–Smirnov test

```
ksmirnov varname [if] [in], by(groupvar) [ exact ]
```

Menu

one-sample

Statistics > Nonparametric analysis > Tests of hypotheses > One-sample Kolmogorov-Smirnov test

two-sample

Statistics > Nonparametric analysis > Tests of hypotheses > Two-sample Kolmogorov-Smirnov test

Description

`ksmirnov` performs one- and two-sample Kolmogorov–Smirnov tests of the equality of distributions. In the first syntax, *varname* is the variable whose distribution is being tested, and *exp* must evaluate to the corresponding (theoretical) cumulative. In the second syntax, *groupvar* must take on two distinct values. The distribution of *varname* for the first value of *groupvar* is compared with that of the second value.

When testing for normality, please see [R] **sktest** and [R] **swilk**.

Options for two-sample test

Main

`by(`*groupvar*`)` is required. It specifies a binary variable that identifies the two groups.

`exact` specifies that the exact p-value be computed. This may take a long time if $n > 50$.

Remarks

▷ Example 1: Two-sample test

Say that we have data on `x` that resulted from two different experiments, labeled as `group==1` and `group==2`. Our data contain

```
. use http://www.stata-press.com/data/r12/ksxmpl
. list
```

	group	x
1.	2	2
2.	1	0
3.	2	3
4.	1	4
5.	1	5
6.	2	8
7.	2	10

We wish to use the two-sample Kolmogorov–Smirnov test to determine if there are any differences in the distribution of `x` for these two groups:

```
. ksmirnov x, by(group)
Two-sample Kolmogorov-Smirnov test for equality of distribution functions
 Smaller group       D       P-value  Corrected
 ------------------------------------------------
 1:                   0.5000    0.424
 2:                  -0.1667    0.909
 Combined K-S:        0.5000    0.785      0.735
```

The first line tests the hypothesis that `x` for group 1 contains *smaller* values than for group 2. The largest difference between the distribution functions is 0.5. The approximate p-value for this is 0.424, which is not significant.

The second line tests the hypothesis that `x` for group 1 contains *larger* values than for group 2. The largest difference between the distribution functions in this direction is 0.1667. The approximate p-value for this small difference is 0.909.

Finally, the approximate p-value for the combined test is 0.785, corrected to 0.735. The p-values `ksmirnov` calculates are based on the asymptotic distributions derived by Smirnov (1933). These approximations are not good for small samples ($n < 50$). They are too conservative—real p-values tend to be substantially smaller. We have also included a less conservative approximation for the nondirectional hypothesis based on an empirical continuity correction—the 0.735 reported in the third column.

That number, too, is only an approximation. An exact value can be calculated using the `exact` option:

```
. ksmirnov x, by(group) exact
Two-sample Kolmogorov-Smirnov test for equality of distribution functions
 Smaller group       D       P-value      Exact
 ------------------------------------------------
 1:                   0.5000    0.424
 2:                  -0.1667    0.909
 Combined K-S:        0.5000    0.785      0.657
```

◁

▷ Example 2: One-sample test

Let's now test whether `x` in the example above is distributed normally. Kolmogorov–Smirnov is not a particularly powerful test in testing for normality, and we do not endorse such use of it; see [R] **sktest** and [R] **swilk** for better tests.

In any case, we will test against a normal distribution with the same mean and standard deviation:

```
. summarize x
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
           x |          7    4.571429    3.457222           0         10

. ksmirnov x = normal((x-4.571429)/3.457222)

One-sample Kolmogorov-Smirnov test against theoretical distribution
           normal((x-4.571429)/3.457222)
 Smaller group       D       P-value  Corrected
 ------------------------------------------------
 x:                  0.1650    0.683
 Cumulative:        -0.1250    0.803
 Combined K-S:       0.1650    0.991      0.978
```

Because Stata has no way of knowing that we based this calculation on the calculated mean and standard deviation of `x`, the test statistics will be slightly conservative in addition to being approximations. Nevertheless, they clearly indicate that the data cannot be distinguished from normally distributed data.

◁

Saved results

`ksmirnov` saves the following in `r()`:

Scalars

`r(D_1)`	D from line 1	`r(D)`	combined D
`r(p_1)`	p-value from line 1	`r(p)`	combined p-value
`r(D_2)`	D from line 2	`r(p_cor)`	corrected combined p-value
`r(p_2)`	p-value from line 2	`r(p_exact)`	exact combined p-value

Macros

`r(group1)`	name of group from line 1	`r(group2)`	name of group from line 2

Methods and formulas

`ksmirnov` is implemented as an ado-file.

In general, the Kolmogorov–Smirnov test (Kolmogorov 1933; Smirnov 1933; also see Conover [1999], 428–465) is not very powerful against differences in the tails of distributions. In return for this, it is fairly powerful for alternative hypotheses that involve lumpiness or clustering in the data.

The directional hypotheses are evaluated with the statistics

$$D^+ = \max_x \Big\{ F(x) - G(x) \Big\}$$
$$D^- = \min_x \Big\{ F(x) - G(x) \Big\}$$

where $F(x)$ and $G(x)$ are the empirical distribution functions for the sample being compared. The combined statistic is

$$D = \max\Big(|D^+|\,,\, |D^-| \Big)$$

The p-value for this statistic may be obtained by evaluating the asymptotic limiting distribution. Let m be the sample size for the first sample, and let n be the sample size for the second sample. Smirnov (1933) shows that

$$\lim_{m,n\to\infty} \Pr\left\{\sqrt{mn/(m+n)}D_{m,n} \le z\right\} = 1 - 2\sum_{i=1}^{\infty}(-1)^{i-1}\exp\left(-2i^2z^2\right)$$

The first five terms form the approximation P_a used by Stata. The exact p-value is calculated by a counting algorithm; see Gibbons and Chakraborti (2011, 236–238). A corrected p-value was obtained by modifying the asymptotic p-value by using a numerical approximation technique:

$$Z = \Phi^{-1}(P_a) + 1.04/\min(m,n) + 2.09/\max(m,n) - 1.35/\sqrt{mn/(m+n)}$$
$$p\text{-value} = \Phi(Z)$$

where $\Phi(\cdot)$ is the cumulative normal distribution.

Andrei Nikolayevich Kolmogorov (1903–1987), of Russia, was one of the great mathematicians of the twentieth century, making outstanding contributions in many different branches, including set theory, measure theory, probability and statistics, approximation theory, functional analysis, classical dynamics, and theory of turbulence. He was a faculty member at Moscow State University for more than 60 years.

Nikolai Vasilyevich Smirnov (1900–1966) was a Russian statistician whose work included contributions in nonparametric statistics, order statistics, and goodness of fit. After army service and the study of philosophy and philology, he turned to mathematics and eventually rose to be head of mathematical statistics at the Steklov Mathematical Institute in Moscow.

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Also see

[R] **runtest** — Test for random order

[R] **sktest** — Skewness and kurtosis test for normality

[R] **swilk** — Shapiro–Wilk and Shapiro–Francia tests for normality

Title

kwallis — Kruskal–Wallis equality-of-populations rank test

Syntax

`kwallis` *varname* [*if*] [*in*] , `by(`*groupvar*`)`

Menu

Statistics > Nonparametric analysis > Tests of hypotheses > Kruskal-Wallis rank test

Description

`kwallis` tests the hypothesis that several samples are from the same population. In the syntax diagram above, *varname* refers to the variable recording the outcome, and *groupvar* refers to the variable denoting the population. `by()` is required.

Option

`by(`*groupvar*`)` is required. It specifies a variable that identifies the groups.

Remarks

▷ Example 1

We have data on the 50 states. The data contain the median age of the population, `medage`, and the region of the country, `region`, for each state. We wish to test for the equality of the median age distribution across all four regions simultaneously:

```
. use http://www.stata-press.com/data/r12/census
(1980 Census data by state)
. kwallis medage, by(region)
Kruskal-Wallis equality-of-populations rank test
```

region	Obs	Rank Sum
NE	9	376.50
N Cntrl	12	294.00
South	16	398.00
West	13	206.50

```
chi-squared =    17.041 with 3 d.f.
probability =     0.0007
chi-squared with ties =    17.062 with 3 d.f.
probability =     0.0007
```

From the output, we see that we can reject the hypothesis that the populations are the same at any level below 0.07%. ◁

Saved results

`kwallis` saves the following in `r()`:

Scalars

`r(df)`	degrees of freedom
`r(chi2)`	χ^2
`r(chi2_adj)`	χ^2 adjusted for ties

Methods and formulas

`kwallis` is implemented as an ado-file.

The Kruskal–Wallis test (Kruskal and Wallis 1952, 1953; also see Altman [1991, 213–215]; Conover [1999, 288–297]; and Riffenburgh [2005, 287–291]) is a multiple-sample generalization of the two-sample Wilcoxon (also called Mann–Whitney) rank sum test (Wilcoxon 1945; Mann and Whitney 1947). Samples of sizes n_j, $j = 1, \ldots, m$, are combined and ranked in ascending order of magnitude. Tied values are assigned the average ranks. Let n denote the overall sample size, and let $R_j = \sum_{i=1}^{n_j} R(X_{ji})$ denote the sum of the ranks for the jth sample. The Kruskal–Wallis one-way analysis-of-variance test, H, is defined as

$$H = \frac{1}{S^2}\left\{\sum_{j=1}^{m}\frac{R_j^2}{n_j} - \frac{n(n+1)^2}{4}\right\}$$

where

$$S^2 = \frac{1}{n-1}\left\{\sum_{\text{all ranks}} R(X_{ji})^2 - \frac{n(n+1)^2}{4}\right\}$$

If there are no ties, this equation simplifies to

$$H = \frac{12}{n(n+1)}\sum_{j=1}^{m}\frac{R_j^2}{n_j} - 3(n+1)$$

The sampling distribution of H is approximately χ^2 with $m-1$ degrees of freedom.

William Henry Kruskal (1919–2005) was born in New York City. He studied mathematics and statistics at Antioch College, Harvard, and Columbia, and joined the University of Chicago in 1951. He made many outstanding contributions to linear models, nonparametric statistics, government statistics, and the history and methodology of statistics.

Wilson Allen Wallis (1912–1998) was born in Philadelphia. He studied psychology and economics at the Universities of Minnesota and Chicago and at Columbia. He taught at Yale, Stanford, and Chicago, before moving as president (later chancellor) to the University of Rochester in 1962. He also served in several Republican administrations. Wallis served as editor of the *Journal of the American Statistical Association*, coauthored a popular introduction to statistics, and contributed to nonparametric statistics.

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Also see

[R] **nptrend** — Test for trend across ordered groups

[R] **oneway** — One-way analysis of variance

[R] **sdtest** — Variance-comparison tests

[R] **signrank** — Equality tests on matched data

Title

ladder — Ladder of powers

Syntax

Ladder of powers

```
ladder varname [if] [in] [ , generate(newvar) noadjust ]
```

Ladder-of-powers histograms

```
gladder varname [if] [in] [ , histogram_options combine_options ]
```

Ladder-of-powers quantile–normal plots

```
qladder varname [if] [in] [ , qnorm_options combine_options ]
```

`by` is allowed with `ladder`; see [D] **by**.

Menu

ladder

Statistics > Summaries, tables, and tests > Distributional plots and tests > Ladder of powers

gladder

Statistics > Summaries, tables, and tests > Distributional plots and tests > Ladder-of-powers histograms

qladder

Statistics > Summaries, tables, and tests > Distributional plots and tests > Ladder-of-powers quantile-normal plots

Description

`ladder` searches a subset of the ladder of powers (Tukey 1977) for a transform that converts *varname* into a normally distributed variable. `sktest` tests for normality; see [R] **sktest**. Also see [R] **boxcox**.

`gladder` displays nine histograms of transforms of *varname* according to the ladder of powers. `gladder` is useful pedagogically, but we do not advise looking at histograms for research work; `ladder` or `qnorm` (see [R] **diagnostic plots**) is preferred.

`qladder` displays the quantiles of transforms of *varname* according to the ladder of powers against the quantiles of a normal distribution.

Options for ladder

Main

`generate(`*newvar*`)` saves the transformed values corresponding to the minimum chi-squared value from the table. We do not recommend using `generate()` because it is literal in interpreting the minimum, thus ignoring nearly equal but perhaps more interpretable transforms.

`noadjust` is the `noadjust` option to `sktest`; see [R] **sktest**.

Options for gladder

histogram_options affect the rendition of the histograms across all relevant transformations; see [R] **histogram**. Here the `normal` option is assumed, so you must supply the `nonormal` option to suppress the overlaid normal density. Also, `gladder` does not allow the `width(#)` option of `histogram`.

combine_options are any of the options documented in [G-2] **graph combine**. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Options for qladder

qnorm_options affect the rendition of the quantile–normal plots across all relevant transformations. See [R] **diagnostic plots**.

combine_options are any of the options documented in [G-2] **graph combine**. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

▷ Example 1: ladder

We have data on the mileage rating of 74 automobiles and wish to find a transform that makes the variable normally distributed:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ladder mpg
```

Transformation	formula	chi2(2)	P(chi2)
cubic	mpg^3	43.59	0.000
square	mpg^2	27.03	0.000
identity	mpg	10.95	0.004
square root	sqrt(mpg)	4.94	0.084
log	log(mpg)	0.87	0.647
1/(square root)	1/sqrt(mpg)	0.20	0.905
inverse	1/mpg	2.36	0.307
1/square	1/(mpg^2)	11.99	0.002
1/cubic	1/(mpg^3)	24.30	0.000

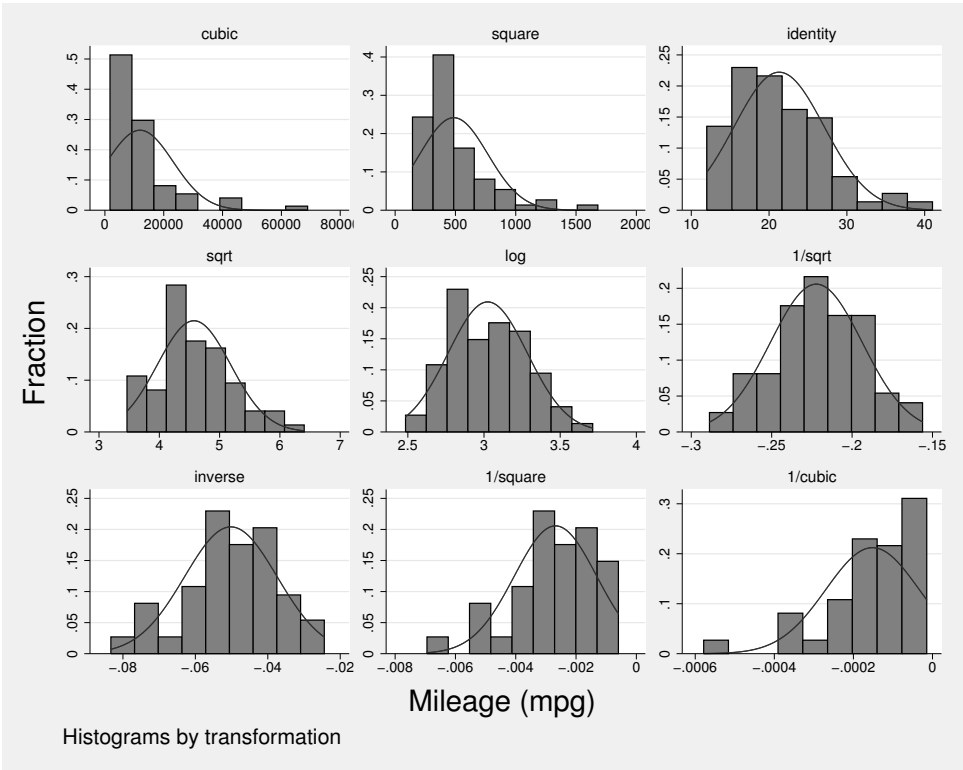
If we had typed `ladder mpg, gen(mpgx)`, the variable `mpgx` containing $1/\sqrt{\texttt{mpg}}$ would have been automatically generated for us. This is the perfect example of why you should not, in general, specify the `generate()` option. We also cannot reject the hypothesis that the inverse of `mpg` is normally distributed and that $1/\texttt{mpg}$—gallons per mile—has a better interpretation. It is a measure of energy consumption.

◁

▷ Example 2: gladder

`gladder` explores the same transforms as `ladder` but presents results graphically:

```
. gladder mpg, fraction
```



◁

❑ Technical note

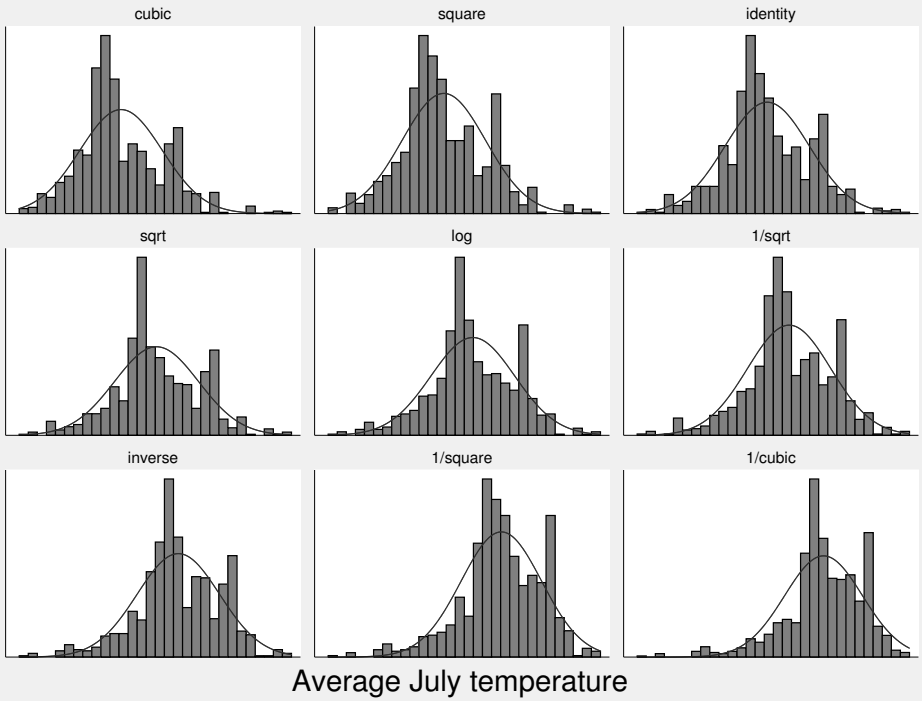
`gladder` is useful pedagogically, but be careful when using it for research work, especially with many observations. For instance, consider the following data on the average July temperature in degrees Fahrenheit for 954 U.S. cities:

```
. use http://www.stata-press.com/data/r12/citytemp
(City Temperature Data)
. ladder tempjuly
Transformation          formula                chi2(2)       P(chi2)
-----------------------------------------------------------------------
cubic                   tempjuly^3               47.49         0.000
square                  tempjuly^2               19.70         0.000
identity                tempjuly                  3.83         0.147
square root             sqrt(tempjuly)            1.83         0.400
log                     log(tempjuly)             5.40         0.067
1/(square root)         1/sqrt(tempjuly)         13.72         0.001
inverse                 1/tempjuly               26.36         0.000
1/square                1/(tempjuly^2)           64.43         0.000
1/cubic                 1/(tempjuly^3)               .         0.000
```

The period in the last line indicates that the χ^2 is very large; see [R] **sktest**.

From the table, we see that there is certainly a difference in normality between the square and square-root transform. If, however, you can see the difference between the transforms in the diagram below, you have better eyes than we do:

```
. gladder tempjuly, l1title("") ylabel(none) xlabel(none)
```

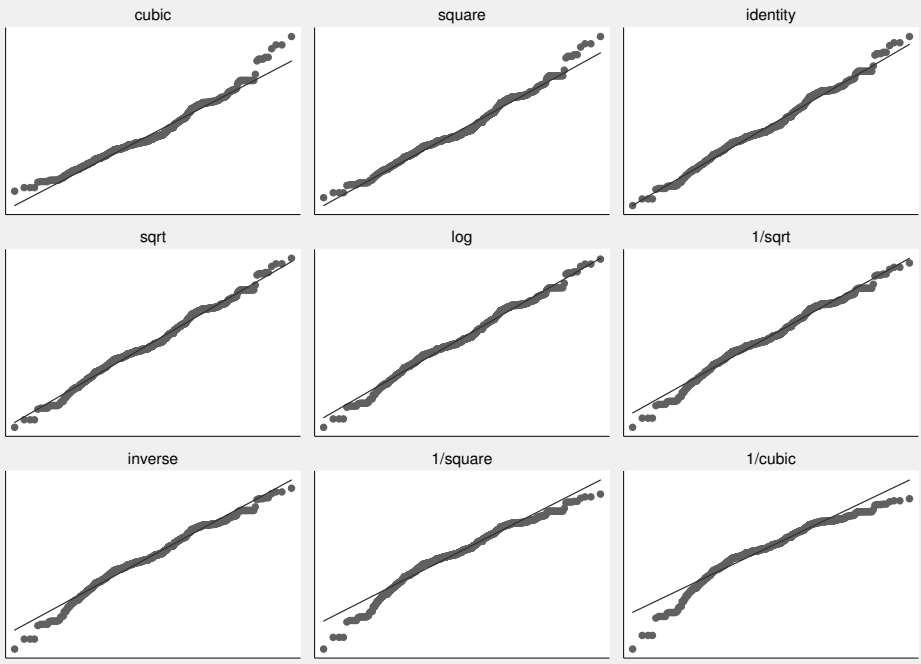


❑

▷ Example 3: qladder

A better graph for seeing normality is the quantile–normal graph, which can be produced by `qladder`.

```
. qladder tempjuly, ylabel(none) xlabel(none)
```



Quantile–Normal plots by transformation

This graph shows that for the square transform, the upper tail—and only the upper tail—diverges from what would be expected. This divergence is detected by `sktest` (see [R] **sktest**) as a problem with skewness, as we would learn from using `sktest` to examine `tempjuly` squared and square rooted.

◁

Saved results

`ladder` saves the following in `r()`:

Scalars

`r(N)`	number of observations
`r(invcube)`	χ^2 for inverse-cubic transformation
`r(P_invcube)`	significance level for inverse-cubic transformation
`r(invsq)`	χ^2 for inverse-square transformation
`r(P_invsq)`	significance level for inverse-square transformation
`r(inv)`	χ^2 for inverse transformation
`r(P_inv)`	significance level for inverse transformation
`r(invsqrt)`	χ^2 for inverse-root transformation
`r(P_invsqrt)`	significance level for inverse-root transformation
`r(log)`	χ^2 for log transformation
`r(P_log)`	significance level for log transformation
`r(sqrt)`	χ^2 for square-root transformation
`r(P_sqrt)`	significance level for square-root transformation
`r(ident)`	χ^2 for untransformed data
`r(P_ident)`	significance level for untransformed data
`r(square)`	χ^2 for square transformation
`r(P_square)`	significance level for square transformation
`r(cube)`	χ^2 for cubic transformation
`r(P_cube)`	significance level for cubic transformation

Methods and formulas

`ladder`, `gladder`, and `qladder` are implemented as ado-files.

For `ladder`, results are as reported by `sktest`; see [R] **sktest**. If `generate()` is specified, the transform with the minimum χ^2 value is chosen.

`gladder` sets the number of bins to $\min(\sqrt{n}, 10\log_{10} n)$, rounded to the closest integer, where n is the number of unique values of *varname*. See [R] **histogram** for a discussion of the optimal number of bins.

Also see Findley (1990) for a ladder-of-powers variable transformation program that produces one-way graphs with overlaid box plots, in addition to histograms with overlaid normals. Buchner and Findley (1990) discuss ladder-of-powers transformations as one aspect of preliminary data analysis. Also see Hamilton (1992, 18–23) and Hamilton (2009, 142–144).

Acknowledgment

`qladder` was written by Jeroen Weesie, Utrecht University, Utrecht, The Netherlands.

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Also see

[R] **diagnostic plots** — Distributional diagnostic plots

[R] **lnskew0** — Find zero-skewness log or Box–Cox transform

[R] **lv** — Letter-value displays

[R] **sktest** — Skewness and kurtosis test for normality

Title

level — Set default confidence level

Syntax

```
set level # [, permanently]
```

Description

`set level` specifies the default confidence level for confidence intervals for all commands that report confidence intervals. The initial value is 95, meaning 95% confidence intervals. # may be between 10.00 and 99.99, and # can have at most two digits after the decimal point.

Option

`permanently` specifies that, in addition to making the change right now, the `level` setting be remembered and become the default setting when you invoke Stata.

Remarks

To change the level of confidence intervals reported by a particular command, you need not reset the default confidence level. All commands that report confidence intervals have a `level(#)` option. When you do not specify the option, the confidence intervals are calculated for the default level set by `set level`, or for 95% if you have not reset `set level`.

▷ Example 1

We use the `ci` command to obtain the confidence interval for the mean of `mpg`:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ci mpg
    Variable |       Obs        Mean    Std. Err.       [95% Conf. Interval]
-------------+--------------------------------------------------------------
         mpg |        74      21.2973    .6725511         19.9569    22.63769
```

To obtain 90% confidence intervals, we would type

```
. ci mpg, level(90)
    Variable |       Obs        Mean    Std. Err.       [90% Conf. Interval]
-------------+--------------------------------------------------------------
         mpg |        74      21.2973    .6725511        20.17683    22.41776
```

or

```
. set level 90
. ci mpg
    Variable |       Obs        Mean    Std. Err.       [90% Conf. Interval]
-------------+--------------------------------------------------------------
         mpg |        74      21.2973    .6725511        20.17683    22.41776
```

If we opt for the second alternative, the next time that we fit a model (say, with `regress`), 90% confidence intervals will be reported. If we wanted 95% confidence intervals, we could specify `level(95)` on the estimation command, or we could reset the default by typing `set level 95`.

The current setting of `level()` is stored as the c-class value `c(level)`; see [P] **creturn**.

◁

Also see

[R] **query** — Display system parameters

[P] **creturn** — Return c-class values

[U] **20 Estimation and postestimation commands**

[U] **20.7 Specifying the width of confidence intervals**

Title

lincom — Linear combinations of estimators

Syntax

`lincom` *exp* [, *options*]

options	Description
`eform`	generic label; `exp(b)`
`or`	odds ratio
`hr`	hazard ratio
`shr`	subhazard ratio
`irr`	incidence-rate ratio
`rrr`	relative-risk ratio
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats

where *exp* is any linear combination of coefficients that is a valid syntax for `test`; see [R] **test**. *exp* must not contain an equal sign.

Menu

Statistics > Postestimation > Linear combinations of estimates

Description

`lincom` computes point estimates, standard errors, t or z statistics, p-values, and confidence intervals for linear combinations of coefficients after any estimation command. Results can optionally be displayed as odds ratios, hazard ratios, incidence-rate ratios, or relative-risk ratios.

`lincom` can be used with `svy` estimation results; see [SVY] **svy postestimation**.

Options

`eform`, `or`, `hr`, `shr`, `irr`, and `rrr` all report coefficient estimates as $\exp(\widehat{\beta})$ rather than $\widehat{\beta}$. Standard errors and confidence intervals are similarly transformed. `or` is the default after `logistic`. The only difference in these options is how the output is labeled.

Option	Label	Explanation	Example commands
`eform`	`exp(b)`	Generic label	`cloglog`
`or`	`Odds Ratio`	Odds ratio	`logistic`, `logit`
`hr`	`Haz. Ratio`	Hazard ratio	`stcox`, `streg`
`shr`	`SHR`	Subhazard ratio	`stcrreg`
`irr`	`IRR`	Incidence-rate ratio	`poisson`
`rrr`	`RRR`	Relative-risk ratio	`mlogit`

exp may not contain any additive constants when you use the `eform`, `or`, `hr`, `irr`, or `rrr` option.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, and `sformat(%`*fmt*`)`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Using lincom
Odds ratios and incidence-rate ratios
Multiple-equation models

Using lincom

After fitting a model and obtaining estimates for coefficients $\beta_1, \beta_2, \ldots, \beta_k$, you may want to view estimates for linear combinations of the β_i, such as $\beta_1 - \beta_2$. `lincom` can display estimates for any linear combination of the form $c_0 + c_1\beta_1 + c_2\beta_2 + \cdots + c_k\beta_k$.

`lincom` works after any estimation command for which `test` works. Any valid expression for `test` syntax 1 (see [R] **test**) is a valid expression for `lincom`.

`lincom` is useful for viewing odds ratios, hazard ratios, etc., for one group (that is, one set of covariates) relative to another group (that is, another set of covariates). See the examples below.

▷ Example 1

We perform a linear regression:

```
. use http://www.stata-press.com/data/r12/regress
. regress y x1 x2 x3
```

Source	SS	df	MS	Number of obs =	148
				F(3, 144) =	96.12
Model	3259.3561	3	1086.45203	Prob > F =	0.0000
Residual	1627.56282	144	11.3025196	R-squared =	0.6670
				Adj R-squared =	0.6600
Total	4886.91892	147	33.2443464	Root MSE =	3.3619

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
x1	1.457113	1.07461	1.36	0.177	-.666934	3.581161
x2	2.221682	.8610358	2.58	0.011	.5197797	3.923583
x3	-.006139	.0005543	-11.08	0.000	-.0072345	-.0050435
_cons	36.10135	4.382693	8.24	0.000	27.43863	44.76407

To see the difference of the coefficients of `x2` and `x1`, we type

```
. lincom x2 - x1
 ( 1)  - x1 + x2 = 0
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	.7645682	.9950282	0.77	0.444	-1.20218	2.731316

The expression can be any linear combination.

```
. lincom 3*x1 + 500*x3
 ( 1)  3*x1 + 500*x3 = 0
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	1.301825	3.396624	0.38	0.702	-5.411858	8.015507

Nonlinear expressions are not allowed.

```
. lincom x2/x1
not possible with test
r(131);
```

For information about estimating nonlinear expressions, see [R] **nlcom**. ◁

❑ Technical note

`lincom` uses the same shorthands for coefficients as does `test` (see [R] **test**). When you type `x1`, for instance, `lincom` knows that you mean the coefficient of `x1`. The formal syntax for referencing this coefficient is actually `_b[x1]`, or alternatively, `_coef[x1]`. So, more formally, in the last example we could have typed

```
. lincom 3*_b[x1] + 500*_b[x3]
```
(*output omitted*)

❑

Odds ratios and incidence-rate ratios

After logistic regression, the `or` option can be specified with `lincom` to display odds ratios for any effect. Incidence-rate ratios after commands such as `poisson` can be similarly obtained by specifying the `irr` option.

▷ Example 2

Consider the low birthweight dataset from Hosmer and Lemeshow (2000, 25). We fit a logistic regression model of low birthweight (variable `low`) on the following variables:

Variable	Description	Coding
`age`	age in years	
`race`	race	1 if white, 2 if black, 3 if other
`smoke`	smoking status	1 if smoker, 0 if nonsmoker
`ht`	history of hypertension	1 if yes, 0 if no
`ui`	uterine irritability	1 if yes, 0 if no
`lwd`	maternal weight before pregnancy	1 if weight $<$ 110 lb., 0 otherwise
`ptd`	history of premature labor	1 if yes, 0 if no
`c.age##lwd`	`age` main effects, `lwd` main effects, and their interaction	
`smoke##lwd`	`smoke` main effects, `lwd` main effects, and their interaction	

We first fit a model without the interaction terms by using `logit`.

```
. use http://www.stata-press.com/data/r12/lbw3
(Hosmer & Lemeshow data)
. logit low age lwd i.race smoke ptd ht ui
Iteration 0:   log likelihood =   -117.336
Iteration 1:   log likelihood =   -99.3982
Iteration 2:   log likelihood = -98.780418
Iteration 3:   log likelihood = -98.777998
Iteration 4:   log likelihood = -98.777998
Logistic regression                               Number of obs   =        189
                                                  LR chi2(8)      =      37.12
                                                  Prob > chi2     =     0.0000
Log likelihood = -98.777998                       Pseudo R2       =     0.1582
```

low	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.0464796	.0373888	-1.24	0.214	-.1197603	.0268011
lwd	.8420615	.4055338	2.08	0.038	.0472299	1.636893
race						
2	1.073456	.5150753	2.08	0.037	.0639273	2.082985
3	.815367	.4452979	1.83	0.067	-.0574008	1.688135
smoke	.8071996	.404446	2.00	0.046	.0145001	1.599899
ptd	1.281678	.4621157	2.77	0.006	.3759478	2.187408
ht	1.435227	.6482699	2.21	0.027	.1646414	2.705813
ui	.6576256	.4666192	1.41	0.159	-.2569313	1.572182
_cons	-1.216781	.9556797	-1.27	0.203	-3.089878	.656317

To get the odds ratio for black smokers relative to white nonsmokers (the reference group), we type

```
. lincom 2.race + smoke, or
 ( 1)  [low]2.race + [low]smoke = 0
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	6.557805	4.744692	2.60	0.009	1.588176	27.07811

`lincom` computed $\exp(\beta_{\texttt{2.race}} + \beta_{\texttt{smoke}}) = 6.56$. To see the odds ratio for white smokers relative to black nonsmokers, we type

```
. lincom smoke - 2.race, or
 ( 1)  - [low]2.race + [low]smoke = 0
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.7662425	.4430176	-0.46	0.645	.2467334	2.379603

Now let's add the interaction terms to the model (Hosmer and Lemeshow 1989, table 4.10). This time, we will use `logistic` rather than `logit`. By default, `logistic` displays odds ratios.

```
. logistic low i.race ht ui ptd c.age##lwd smoke##lwd
Logistic regression                               Number of obs   =        189
                                                  LR chi2(10)     =      42.66
                                                  Prob > chi2     =     0.0000
Log likelihood =  -96.00616                       Pseudo R2       =     0.1818
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
race						
2	2.95383	1.532789	2.09	0.037	1.068277	8.167465
3	2.137589	.9919138	1.64	0.102	.8608708	5.307752
ht	3.893141	2.575201	2.05	0.040	1.064768	14.2346
ui	2.071284	.9931388	1.52	0.129	.8092926	5.301192
ptd	3.426633	1.615282	2.61	0.009	1.360252	8.632089
age	.9194513	.041896	-1.84	0.065	.8408967	1.005344
1.lwd	.1772934	.3312384	-0.93	0.354	.0045539	6.902367
lwd#c.age						
1	1.15883	.09602	1.78	0.075	.9851215	1.36317
1.smoke	3.168096	1.452378	2.52	0.012	1.289956	7.78076
smoke#lwd						
1 1	.2447849	.2003996	-1.72	0.086	.0491956	1.217988
_cons	.599443	.6519163	-0.47	0.638	.0711271	5.051971

Hosmer and Lemeshow (1989, table 4.13) consider the effects of smoking (`smoke` = 1) and low maternal weight before pregnancy (`lwd` = 1). The effect of smoking among non–low-weight mothers (`lwd` = 0) is given by the odds ratio 3.17 for `smoke` in the `logistic` output. The effect of smoking among low-weight mothers is given by

```
. lincom 1.smoke + 1.smoke#1.lwd
 ( 1)  [low]1.smoke + [low]1.smoke#1.lwd = 0
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.7755022	.574951	-0.34	0.732	.1813465	3.316323

We did not have to specify the `or` option. After `logistic`, `lincom` assumes `or` by default.

The effect of low weight (`lwd` = 1) is more complicated because we fit an `age` × `lwd` interaction. We must specify the age of mothers for the effect. The effect among 30-year-old nonsmokers is given by

```
. lincom 1.lwd + 30*1.lwd#c.age
 ( 1)  [low]1.lwd + 30*[low]1.lwd#c.age = 0
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	14.7669	13.5669	2.93	0.003	2.439264	89.39633

`lincom` computed $\exp(\beta_{\texttt{1.lwd}} + 30\beta_{\texttt{age\#1.lwd}}) = 14.8$. It may seem odd that we entered it as `1.lwd + 30*1.lwd#c.age`, but remember that these terms are just `lincom`'s (and `test`'s) shorthands for `_b[1.lwd]` and `_b[1.lwd#c.age]`. We could have typed

```
. lincom _b[1.lwd] + 30*_b[1.lwd#c.age]
 ( 1)  [low]1.lwd + 30*[low]1.lwd#c.age = 0
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	14.7669	13.5669	2.93	0.003	2.439264	89.39633

Multiple-equation models

`lincom` also works with multiple-equation models. The only difference is how you refer to the coefficients. Recall that for multiple-equation models, coefficients are referenced using the syntax

[*eqno*]*varname*

where *eqno* is the equation number or equation name and *varname* is the corresponding variable name for the coefficient; see [U] **13.5 Accessing coefficients and standard errors** and [R] **test** for details.

Example 3

Let's consider example 4 from [R] **mlogit** (Tarlov et al. 1989; Wells et al. 1989).

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. mlogit insure age male nonwhite i.site, nolog
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(10)     =      42.99
                                                Prob > chi2     =     0.0000
Log likelihood = -534.36165                     Pseudo R2       =     0.0387
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.011745	.0061946	-1.90	0.058	-.0238862	.0003962
male	.5616934	.2027465	2.77	0.006	.1643175	.9590693
nonwhite	.9747768	.2363213	4.12	0.000	.5115955	1.437958
site						
2	.1130359	.2101903	0.54	0.591	-.2989296	.5250013
3	-.5879879	.2279351	-2.58	0.010	-1.034733	-.1412433
_cons	.2697127	.3284422	0.82	0.412	-.3740222	.9134476
Uninsure						
age	-.0077961	.0114418	-0.68	0.496	-.0302217	.0146294
male	.4518496	.3674867	1.23	0.219	-.268411	1.17211
nonwhite	.2170589	.4256361	0.51	0.610	-.6171725	1.05129
site						
2	-1.211563	.4705127	-2.57	0.010	-2.133751	-.2893747
3	-.2078123	.3662926	-0.57	0.570	-.9257327	.510108
_cons	-1.286943	.5923219	-2.17	0.030	-2.447872	-.1260134

To see the estimate of the sum of the coefficient of `male` and the coefficient of `nonwhite` for the `Prepaid` outcome, we type

```
. lincom [Prepaid]male + [Prepaid]nonwhite
 ( 1)  [Prepaid]male + [Prepaid]nonwhite = 0
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	1.53647	.3272489	4.70	0.000	.8950741	2.177866

To view the estimate as a ratio of relative risks (see [R] **mlogit** for the definition and interpretation), we specify the `rrr` option.

```
. lincom [Prepaid]male + [Prepaid]nonwhite, rrr
 ( 1)  [Prepaid]male + [Prepaid]nonwhite = 0
```

insure	RRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	4.648154	1.521103	4.70	0.000	2.447517	8.827451

◁

Saved results

`lincom` saves the following in `r()`:

Scalars

`r(estimate)`	point estimate
`r(se)`	estimate of standard error
`r(df)`	degrees of freedom

Methods and formulas

`lincom` is implemented as an ado-file.

References

Hosmer, D. W., Jr., and S. Lemeshow. 1989. *Applied Logistic Regression*. New York: Wiley.

——. 2000. *Applied Logistic Regression*. 2nd ed. New York: Wiley.

Tarlov, A. R., J. E. Ware, Jr., S. Greenfield, E. C. Nelson, E. Perrin, and M. Zubkoff. 1989. The medical outcomes study. An application of methods for monitoring the results of medical care. *Journal of the American Medical Association* 262: 925–930.

Wells, K. B., R. D. Hays, M. A. Burnam, W. H. Rogers, S. Greenfield, and J. E. Ware, Jr. 1989. Detection of depressive disorder for patients receiving prepaid or fee-for-service care. Results from the Medical Outcomes Survey. *Journal of the American Medical Association* 262: 3298–3302.

Also see

[R] **nlcom** — Nonlinear combinations of estimators

[R] **test** — Test linear hypotheses after estimation

[R] **testnl** — Test nonlinear hypotheses after estimation

[U] **13.5 Accessing coefficients and standard errors**

[U] **20 Estimation and postestimation commands**

Title

linktest — Specification link test for single-equation models

Syntax

`linktest` [*if*] [*in*] [, *cmd_options*]

When `if` and `in` are not specified, the link test is performed on the same sample as the previous estimation.

Menu

Statistics > Postestimation > Tests > Specification link test for single-equation models

Description

`linktest` performs a link test for model specification after any single-equation estimation command, such as `logistic`, `regress`, `stcox`, etc.

Option

Main

cmd_options must be the same options specified with the underlying estimation command, except the *display_options* may differ.

Remarks

The form of the link test implemented here is based on an idea of Tukey (1949), which was further described by Pregibon (1980), elaborating on work in his unpublished thesis (Pregibon 1979). See *Methods and formulas* below for more details.

▷ Example 1

We want to explain the mileage ratings of cars in our automobile dataset by using the weight, engine displacement, and whether the car is manufactured outside the United States:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displ foreign
```

Source	SS	df	MS
Model	1619.71935	3	539.906448
Residual	823.740114	70	11.7677159
Total	2443.45946	73	33.4720474

Number of obs	74
F(3, 70)	45.88
Prob > F	0.0000
R-squared	0.6629
Adj R-squared	0.6484
Root MSE	3.4304

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0067745	.0011665	-5.81	0.000	-.0091011	-.0044479
displacement	.0019286	.0100701	0.19	0.849	-.0181556	.0220129
foreign	-1.600631	1.113648	-1.44	0.155	-3.821732	.6204699
_cons	41.84795	2.350704	17.80	0.000	37.15962	46.53628

On the basis of the R^2, we are reasonably pleased with this model.

If our model really is specified correctly, then if we were to regress `mpg` on the prediction and the prediction squared, the prediction squared would have no explanatory power. This is what `linktest` does:

```
. linktest
```

Source	SS	df	MS		
				Number of obs	= 74
				F(2, 71)	= 76.75
Model	1670.71514	2	835.357572	Prob > F	= 0.0000
Residual	772.744316	71	10.8837228	R-squared	= 0.6837
				Adj R-squared	= 0.6748
Total	2443.45946	73	33.4720474	Root MSE	= 3.299

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
_hat	-.4127198	.6577736	-0.63	0.532	-1.724283	.8988434
_hatsq	.0338198	.015624	2.16	0.034	.0026664	.0649732
_cons	14.00705	6.713276	2.09	0.041	.6211539	27.39294

We find that the prediction squared does have explanatory power, so our specification is not as good as we thought.

Although `linktest` is formally a test of the specification of the dependent variable, it is often interpreted as a test that, conditional on the specification, the independent variables are specified incorrectly. We will follow that interpretation and now include weight squared in our model:

```
. regress mpg weight c.weight#c.weight displ foreign
```

Source	SS	df	MS		
				Number of obs	= 74
				F(4, 69)	= 39.37
Model	1699.02634	4	424.756584	Prob > F	= 0.0000
Residual	744.433124	69	10.7888859	R-squared	= 0.6953
				Adj R-squared	= 0.6777
Total	2443.45946	73	33.4720474	Root MSE	= 3.2846

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0173257	.0040488	-4.28	0.000	-.0254028	-.0092486
c.weight#c.weight	1.87e-06	6.89e-07	2.71	0.008	4.93e-07	3.24e-06
displacement	-.0101625	.0106236	-0.96	0.342	-.031356	.011031
foreign	-2.560016	1.123506	-2.28	0.026	-4.801349	-.3186832
_cons	58.23575	6.449882	9.03	0.000	45.36859	71.10291

Now we perform the link test on our new model:

```
. linktest
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =   81.08
       Model |  1699.39489     2  849.697445            Prob > F      =  0.0000
    Residual |   744.06457    71  10.4797827            R-squared     =  0.6955
-------------+------------------------------           Adj R-squared =  0.6869
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.2372

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        _hat |    1.141987   .7612218     1.50   0.138    -.3758456    2.659821
      _hatsq |   -.0031916   .0170194    -0.19   0.852    -.0371272    .0307441
       _cons |    -1.50305   8.196444    -0.18   0.855    -17.84629    14.84019
------------------------------------------------------------------------------
```

We now pass the link test.

◁

▷ Example 2

Above we followed a standard misinterpretation of the link test—when we discovered a problem, we focused on the explanatory variables of our model. We might consider varying exactly what the link test tests. The link test told us that our dependent variable was misspecified. For those with an engineering background, `mpg` is indeed a strange measure. It would make more sense to model energy consumption—gallons per mile—in terms of weight and displacement:

```
. gen gpm = 1/mpg
. regress gpm weight displ foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  3,    70) =   76.33
       Model |  .009157962     3  .003052654            Prob > F      =  0.0000
    Residual |  .002799666    70  .000039995            R-squared     =  0.7659
-------------+------------------------------           Adj R-squared =  0.7558
       Total |  .011957628    73  .000163803            Root MSE      =  .00632

------------------------------------------------------------------------------
         gpm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |   .0000144   2.15e-06     6.72   0.000     .0000102    .0000187
displacement |   .0000186   .0000186     1.00   0.319    -.0000184    .0000557
     foreign |   .0066981   .0020531     3.26   0.002     .0026034    .0107928
       _cons |   .0008917   .0043337     0.21   0.838    -.0077515     .009535
------------------------------------------------------------------------------
```

This model looks every bit as reasonable as our original model:

```
. linktest
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =  117.06
       Model |  .009175219     2  .004587609            Prob > F      =  0.0000
    Residual |  .002782409    71  .000039189            R-squared     =  0.7673
-------------+------------------------------           Adj R-squared =  0.7608
       Total |  .011957628    73  .000163803            Root MSE      =  .00626

------------------------------------------------------------------------------
         gpm |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        _hat |   .6608413    .515275     1.28   0.204    -.3665877     1.68827
      _hatsq |   3.275857   4.936655     0.66   0.509    -6.567553    13.11927
       _cons |    .008365   .0130468     0.64   0.523    -.0176496    .0343795
------------------------------------------------------------------------------
```

Specifying the model in terms of gallons per mile also solves the specification problem and results in a more parsimonious specification.

◁

▷ Example 3

The link test can be used with any single-equation estimation procedure, not solely regression. Let's turn our problem around and attempt to explain whether a car is manufactured outside the United States by its mileage rating and weight. To save paper, we will specify `logit`'s `nolog` option, which suppresses the iteration log:

```
. logit foreign mpg weight, nolog
Logistic regression                             Number of obs   =         74
                                                LR chi2(2)      =      35.72
                                                Prob > chi2     =     0.0000
Log likelihood = -27.175156                     Pseudo R2       =     0.3966

------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         mpg |  -.1685869   .0919175    -1.83   0.067    -.3487418     .011568
      weight |  -.0039067   .0010116    -3.86   0.000    -.0058894    -.001924
       _cons |   13.70837   4.518709     3.03   0.002     4.851859    22.56487
------------------------------------------------------------------------------
```

When we run `linktest` after `logit`, the result is another logit specification:

```
. linktest, nolog
Logistic regression                             Number of obs   =         74
                                                LR chi2(2)      =      36.83
                                                Prob > chi2     =     0.0000
Log likelihood = -26.615714                     Pseudo R2       =     0.4090

------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        _hat |   .8438531   .2738759     3.08   0.002     .3070661     1.38064
      _hatsq |  -.1559115   .1568642    -0.99   0.320    -.4633596     .1515366
       _cons |   .2630557   .4299598     0.61   0.541      -.57965     1.105761
------------------------------------------------------------------------------
```

The link test reveals no problems with our specification.

If there had been a problem, we would have been virtually forced to accept the misinterpretation of the link test—we would have reconsidered our specification of the independent variables. When using `logit`, we have no control over the specification of the dependent variable other than to change likelihood functions.

We admit to having seen a dataset once for which the link test rejected the logit specification. We did change the likelihood function, refitting the model using `probit`, and satisfied the link test. Probit has thinner tails than logit. In general, however, you will not be so lucky.

◁

❑ Technical note

You should specify the same options with `linktest` that you do with the estimation command, although you do not have to follow this advice as literally as we did in the preceding example. `logit`'s `nolog` option merely suppresses a part of the output, not what is estimated. We specified `nolog` both times to save paper.

If you are testing a tobit model, you must specify the censoring points just as you do with the `tobit` command.

If you are not sure which options are important, duplicate exactly what you specified on the estimation command.

If you do not specify `if` *exp* or `in` *range* with `linktest`, Stata will by default perform the link test on the same sample as the previous estimation. Suppose that you omitted some data when performing your estimation, but want to calculate the link test on all the data, which you might do if you believe the model is appropriate for all the data. You would type `linktest if e(sample) < .` to do this.

❑

Saved results

`linktest` saves the following in `r()`:

Scalars

`r(t)`	t statistic on `_hatsq`
`r(df)`	degrees of freedom

`linktest` is *not* an estimation command in the sense that it leaves previous estimation results unchanged. For instance, after running a regression and performing the link test, typing `regress` without arguments after the link test still replays the original regression.

For integrating an estimation command with `linktest`, `linktest` assumes that the name of the estimation command is stored in `e(cmd)` and that the name of the dependent variable is stored in `e(depvar)`. After estimation, it assumes that the number of degrees of freedom for the t test is given by `e(df_m)` if the macro is defined.

If the estimation command reports z statistics instead of t statistics, `linktest` will also report z statistics. The z statistic, however, is still returned in `r(t)`, and `r(df)` is set to a missing value.

Methods and formulas

`linktest` is implemented as an ado-file.

The link test is based on the idea that if a regression or regression-like equation is properly specified, you should be able to find no additional independent variables that are significant except by chance. One kind of specification error is called a link error. In regression, this means that the dependent variable needs a transformation or "link" function to properly relate to the independent variables. The idea of a link test is to add an independent variable to the equation that is especially likely to be significant if there is a link error.

Let

$$\mathbf{y} = f(\mathbf{X}\boldsymbol{\beta})$$

be the model and $\widehat{\boldsymbol{\beta}}$ be the parameter estimates. `linktest` calculates

$$\texttt{\_hat} = \mathbf{X}\widehat{\boldsymbol{\beta}}$$

and

$$\texttt{\_hatsq} = \texttt{\_hat}^2$$

The model is then refit with these two variables, and the test is based on the significance of `_hatsq`. This is the form suggested by Pregibon (1979) based on an idea of Tukey (1949). Pregibon (1980) suggests a slightly different method that has come to be known as "Pregibon's goodness-of-link test". We prefer the older version because it is universally applicable, straightforward, and a good second-order approximation. It can be applied to any single-equation estimation technique, whereas Pregibon's more recent tests are estimation-technique specific.

References

Pregibon, D. 1979. Data analytic methods for generalized linear models. PhD diss., University of Toronto.

——. 1980. Goodness of link tests for generalized linear models. *Applied Statistics* 29: 15–24.

Tukey, J. W. 1949. One degree of freedom for non-additivity. *Biometrics* 5: 232–242.

Also see

[R] **regress postestimation** — Postestimation tools for regress

Title

lnskew0 — Find zero-skewness log or Box–Cox transform

Syntax

Zero-skewness log transform

`lnskew0` *newvar* `=` *exp* [*if*] [*in*] [`,` *options*]

Zero-skewness Box–Cox transform

`bcskew0` *newvar* `=` *exp* [*if*] [*in*] [`,` *options*]

options	Description
Main	
`delta(#)`	increment for derivative of skewness function; default is `delta(0.02)` for `lnskew0` and `delta(0.01)` for `bcskew0`
`zero(#)`	value for determining convergence; default is `zero(0.001)`
`level(#)`	set confidence level; default is `level(95)`

Menu

lnskew0

Data > Create or change data > Other variable-creation commands > Zero-skewness log transform

bcskew0

Data > Create or change data > Other variable-creation commands > Box-Cox transform

Description

`lnskew0` creates $newvar = \ln(\pm exp - k)$, choosing k and the sign of *exp* so that the skewness of *newvar* is zero.

`bcskew0` creates $newvar = (exp^{\lambda} - 1)/\lambda$, the Box–Cox power transformation (Box and Cox 1964), choosing λ so that the skewness of *newvar* is zero. *exp* must be strictly positive. Also see [R] **boxcox** for maximum likelihood estimation of λ.

Options

Main

`delta(#)` specifies the increment used for calculating the derivative of the skewness function with respect to k (`lnskew0`) or λ (`bcskew0`). The default values are 0.02 for `lnskew0` and 0.01 for `bcskew0`.

`zero(#)` specifies a value for skewness to determine convergence that is small enough to be considered zero and is, by default, 0.001.

`level(#)` specifies the confidence level for the confidence interval for k (`lnskew0`) or λ (`bcskew0`). The confidence interval is calculated only if `level()` is specified. # is specified as an integer; 95 means 95% confidence intervals. The `level()` option is honored only if the number of observations exceeds 7.

Remarks

▷ Example 1: lnskew0

Using our automobile dataset (see [U] **1.2.2 Example datasets**), we want to generate a new variable equal to $\ln(\texttt{mpg} - k)$ to be approximately normally distributed. `mpg` records the miles per gallon for each of our cars. One feature of the normal distribution is that it has skewness 0.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. lnskew0 lnmpg = mpg
      Transform |          k     [95% Conf. Interval]       Skewness
----------------+---------------------------------------------------
      ln(mpg-k) |   5.383659      (not calculated)        -7.05e-06
```

This created the new variable $\texttt{lnmpg} = \ln(\texttt{mpg} - 5.384)$:

```
. describe lnmpg
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
lnmpg           float  %9.0g                  ln(mpg-5.383659)
```

Because we did not specify the `level()` option, no confidence interval was calculated. At the outset, we could have typed

```
. use http://www.stata-press.com/data/r12/auto, clear
(Automobile Data)
. lnskew0 lnmpg = mpg, level(95)
      Transform |          k     [95% Conf. Interval]       Skewness
----------------+---------------------------------------------------
      ln(mpg-k) |   5.383659    -17.12339   9.892416       -7.05e-06
```

The confidence interval is calculated under the assumption that $\ln(\texttt{mpg} - k)$ really does have a normal distribution. It would be perfectly reasonable to use `lnskew0`, even if we did not believe that the transformed variable would have a normal distribution—if we literally wanted the zero-skewness transform—although, then the confidence interval would be an approximation of unknown quality to the true confidence interval. If we now wanted to test the believability of the confidence interval, we could also test our new variable `lnmpg` by using `swilk` (see [R] **swilk**) with the `lnnormal` option.

◁

❑ Technical note

`lnskew0` and `bcskew0` report the resulting skewness of the variable merely to reassure you of the accuracy of its results. In our example above, `lnskew0` found k such that the resulting skewness was -7×10^{-6}, a number close enough to zero for all practical purposes. If we wanted to make it even smaller, we could specify the `zero()` option. Typing `lnskew0 new=mpg, zero(1e-8)` changes the estimated k to 5.383552 from 5.383659 and reduces the calculated skewness to -2×10^{-11}.

When you request a confidence interval, `lnskew0` may report the lower confidence interval as '`.`', which should be taken as indicating the lower confidence limit $k_L = -\infty$. (This cannot happen with `bcskew0`.)

As an example, consider a sample of size n on x and assume that the skewness of x is positive, but not significantly so, at the desired significance level—say, 5%. Then no matter how large and negative you make k_L, there is no value extreme enough to make the skewness of $\ln(x - k_L)$ equal the corresponding percentile (97.5 for a 95% confidence interval) of the distribution of skewness in a normal distribution of the same sample size. You cannot do this because the distribution of $\ln(x - k_L)$ tends to that of x—apart from location and scale shift—as $x \to \infty$. This "problem" never applies to the upper confidence limit, k_U, because the skewness of $\ln(x - k_U)$ tends to $-\infty$ as k tends upward to the minimum value of x.

❑

▷ Example 2: bcskew0

In example 1, using `lnskew0` with a variable such as `mpg` is probably undesirable. `mpg` has a natural zero, and we are shifting that zero arbitrarily. On the other hand, use of `lnskew0` with a variable such as temperature measured in Fahrenheit or Celsius would be more appropriate, as the zero is indeed arbitrary.

For a variable like `mpg`, it makes more sense to use the Box–Cox power transform (Box and Cox 1964):

$$y^{(\lambda)} = \frac{y^{\lambda} - 1}{\lambda}$$

λ is free to take on any value, but $y^{(1)} = y - 1$, $y^{(0)} = \ln(y)$, and $y^{(-1)} = 1 - 1/y$.

`bcskew0` works like `lnskew0`:

```
. bcskew0 bcmpg = mpg, level(95)
      Transform |          L     [95% Conf. Interval]       Skewness
----------------+---------------------------------------------------
    (mpg^L-1)/L |  -.3673283    -1.212752    .4339645       .0001898
```

The 95% confidence interval includes $\lambda = -1$ (λ is labeled `L` in the output), which has a rather more pleasing interpretation—gallons per mile—than $(\texttt{mpg}^{-0.3673} - 1)/(-0.3673)$. The confidence interval, however, is calculated assuming that the power transformed variable is normally distributed. It makes perfect sense to use `bcskew0`, even when you do not believe that the transformed variable will be normally distributed, but then the confidence interval is an approximation of unknown quality. If you believe that the transformed data are normally distributed, you can alternatively use `boxcox` to estimate λ; see [R] **boxcox**.

◁

Saved results

lnskew0 and bcskew0 save the following in r():

Scalars

r(gamma)	k (lnskew0)
r(lambda)	λ (bcskew0)
r(lb)	lower bound of confidence interval
r(ub)	upper bound of confidence interval
r(skewness)	resulting skewness of transformed variable

Methods and formulas

lnskew0 and bcskew0 are implemented as ado-files.

Skewness is as calculated by summarize; see [R] **summarize**. Newton's method with numeric, uncentered derivatives is used to estimate k (lnskew0) and λ (bcskew0). For lnskew0, the initial value is chosen so that the minimum of $x - k$ is 1, and thus $\ln(x - k)$ is 0. bcskew0 starts with $\lambda = 1$.

Acknowledgment

lnskew0 and bcskew0 were written by Patrick Royston of the MRC Clinical Trials Unit, London.

Reference

Box, G. E. P., and D. R. Cox. 1964. An analysis of transformations. *Journal of the Royal Statistical Society, Series B* 26: 211–252.

Also see

[R] **ladder** — Ladder of powers

[R] **boxcox** — Box–Cox regression models

[R] **swilk** — Shapiro–Wilk and Shapiro–Francia tests for normality

Title

log — Echo copy of session to file

Syntax

Report status of log file

```
log
log query [ logname | _all ]
```

Open log file

```
log using filename [ , append replace [ text | smcl ] name(logname) ]
```

Close log

```
log close [ logname | _all ]
```

Temporarily suspend logging or resume logging

```
log { off | on } [ logname ]
```

Report status of command log file

```
cmdlog
```

Open command log file

```
cmdlog using filename [ , append replace ]
```

Close command log, temporarily suspend logging, or resume logging

```
cmdlog { close | on | off }
```

Set default format for logs

```
set logtype { text | smcl } [ , permanently ]
```

Specify screen width

```
set linesize #
```

In addition to using the `log` command, you may access the capabilities of `log` by selecting **File > Log** from the menu and choosing one of the options in the list.

Menu

File > Log

Description

`log` allows you to make a full record of your Stata session. A log is a file containing what you type and Stata's output. You may start multiple log files at the same time, and you may refer to them with a *logname*. If you do not specify a *logname*, Stata will use the name `<unnamed>`.

`cmdlog` allows you to make a record of what you type during your Stata session. A command log contains only what you type, so it is a subset of a full log.

You can make full logs, command logs, or both simultaneously. Neither is produced until you tell Stata to start logging.

Command logs are always text files, making them easy to convert into do-files. (In this respect, it would make more sense if the default extension of a command log file was `.do` because command logs are do-files. The default is `.txt`, not `.do`, however, to keep you from accidentally overwriting your important do-files.)

Full logs are recorded in one of two formats: Stata Markup and Control Language (SMCL) or plain text. The default is SMCL, but you can use `set logtype` to change that, or you can specify an option to state the format you wish. We recommend SMCL because it preserves fonts and colors. SMCL logs can be converted to text or to other formats by using the `translate` command; see [R] **translate**. You can also use `translate` to produce printable versions of SMCL logs. SMCL logs can be viewed and printed from the Viewer, as can any text file; see [R] **view**.

When using multiple log files, you may have up to five SMCL logs and five text logs open at the same time.

`log` or `cmdlog`, typed without arguments, reports the status of logging. `log query`, when passed an optional *logname*, reports the status of that log.

`log using` and `cmdlog using` open a log file. `log close` and `cmdlog close` close the file. Between times, `log off` and `cmdlog off`, and `log on` and `cmdlog on`, can temporarily suspend and resume logging.

If *filename* is specified without an extension, one of the suffixes `.smcl`, `.log`, or `.txt` is added. The extension `.smcl` or `.log` is added by `log`, depending on whether the file format is SMCL or text. The extension `.txt` is added by `cmdlog`. If *filename* contains embedded spaces, remember to enclose it in double quotes.

`set logtype` specifies the default format in which full logs are to be recorded. Initially, full logs are recorded in SMCL format.

`set linesize` specifies the maximum width, in characters, of Stata output. Most commands in Stata do not respect `linesize`, because it is not important for most commands. Most users never need to `set linesize`, because it will automatically be reset if you resize your Results window. This is also why there is no `permanently` option allowed with `set linesize`. `set linesize` is for use with commands such as `list` and `display` and is typically used by programmers who wish the output of those commands to be wider or narrower than the current width of the Results window.

Options for use with both log and cmdlog

`append` specifies that results be appended to an existing file. If the file does not already exist, a new file is created.

`replace` specifies that *filename*, if it already exists, be overwritten. When you do not specify either `replace` or `append`, the file is assumed to be new. If the specified file already exists, an error message is issued and logging is not started.

Options for use with log

`text` and `smcl` specify the format in which the log is to be recorded. The default is complicated to describe but is what you would expect:

If you specify the file as *filename*`.smcl`, the default is to write the log in SMCL format (regardless of the value of `set logtype`).

If you specify the file as *filename*`.log`, the default is to write the log in text format (regardless of the value of `set logtype`).

If you type *filename* without an extension and specify neither the `smcl` option nor the `text` option, the default is to write the file according to the value of `set logtype`. If you have not `set logtype`, then that default is SMCL. Also, the *filename* you specified will be fixed to read *filename*`.smcl` if a SMCL log is being created or *filename*`.log` if a text log is being created.

If you specify either the `text` or `smcl` option, then what you specify determines how the log is written. If *filename* was specified without an extension, the appropriate extension is added for you.

If you open multiple log files, you may choose a different format for each file.

`name(`*logname*`)` specifies an optional name you may use to refer to the log while it is open. You can start multiple log files, give each a different *logname*, and then close, temporarily suspend, or resume them each individually.

Option for use with set logtype

`permanently` specifies that, in addition to making the change right now, the `logtype` setting be remembered and become the default setting when you invoke Stata.

Remarks

For a detailed explanation of logs, see [U] **15 Saving and printing output—log files**.

When you open a full log, the default is to show the name of the file and a time and date stamp:

```
. log using myfile
-------------------------------------------------------------------------------
      name:  <unnamed>
       log:  C:\data\proj1\myfile.smcl
  log type:  smcl
 opened on:  12 Jan 2011, 12:28:23
.
```

The above information will appear in the log. If you do not want this information to appear, precede the command by `quietly`:

```
. quietly log using myfile
```

quietly will not suppress any error messages or anything else you need to know.

Similarly, when you close a full log, the default is to show the full information,

```
. log close
      name:  <unnamed>
       log:  C:\data\proj1\myfile.smcl
  log type:  smcl
 closed on:  12 Jan 2011, 12:32:41
-------------------------------------------------------------------------------
```

and that information will also appear in the log. If you want to suppress that, type quietly log close.

Saved results

log and cmdlog save the following in r():

Macros

r(name)	*logname*
r(filename)	name of file
r(status)	on or off
r(type)	smcl or text

log query _all saves the following in r():

Scalars

r(numlogs)	number of open log files

For each open log file, log query _all also saves

r(name#)	*logname*
r(filename#)	name of file
r(status#)	on or off
r(type#)	smcl or text

where # varies between 1 and the value of r(numlogs). Be aware that # will not necessarily represent the order in which the log files were first opened, nor will it necessarily remain constant for a given log file upon multiple calls to log query.

Also see

[R] **translate** — Print and translate logs

[R] **query** — Display system parameters

[GSM] **16 Saving and printing results by using logs**

[GSW] **16 Saving and printing results by using logs**

[GSU] **16 Saving and printing results by using logs**

[U] **15 Saving and printing output—log files**

Title

logistic — Logistic regression, reporting odds ratios

Syntax

`logistic` *depvar indepvars* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`coef`	report estimated coefficients
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Binary outcomes > Logistic regression (reporting odds ratios)

Description

`logistic` fits a logistic regression model of *depvar* on *indepvars*, where *depvar* is a 0/1 variable (or, more precisely, a 0/non-0 variable). Without arguments, `logistic` redisplays the last `logistic` estimates. `logistic` displays estimates as odds ratios; to view coefficients, type `logit` after running `logistic`. To obtain odds ratios for any covariate pattern relative to another, see [R] **lincom**.

Options

Model

`noconstant`, `offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

`asis` forces retention of perfect predictor variables and their associated perfectly predicted observations and may produce instabilities in maximization; see [R] **probit**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`coef` causes `logistic` to report the estimated coefficients rather than the odds ratios (exponentiated coefficients). `coef` may be specified when the model is fit or may be used later to redisplay results. `coef` affects only how results are displayed and not how they are estimated.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

The following option is available with `logistic` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

logistic and logit
Robust estimate of variance

logistic and logit

`logistic` provides an alternative and preferred way to fit maximum-likelihood logit models, the other choice being `logit` ([R] **logit**).

First, let's dispose of some confusing terminology. We use the words logit and logistic to mean the same thing: maximum likelihood estimation. To some, one or the other of these words connotes transforming the dependent variable and using weighted least squares to fit the model, but that is not how we use either word here. Thus the `logit` and `logistic` commands produce the same results.

The `logistic` command is generally preferred to the `logit` command because `logistic` presents the estimates in terms of odds ratios rather than coefficients. To some people, this may seem disadvantageous, but you can type `logit` without arguments after `logistic` to see the underlying coefficients. You should be cautious when interpreting the odds ratio of the constant term. Usually, this odds ratio represents the baseline odds of the model when all predictor variables are set to zero. However, you must verify that a zero value for all predictor variables in the model actually makes sense before continuing with this interpretation.

Nevertheless, [R] **logit** is still worth reading because `logistic` shares the same features as `logit`, including omitting variables due to collinearity or one-way causation.

For an introduction to logistic regression, see Lemeshow and Hosmer (2005), Pagano and Gauvreau (2000, 470–487), or Pampel (2000); for a complete but nonmathematical treatment, see Kleinbaum and Klein (2010); and for a thorough discussion, see Hosmer and Lemeshow (2000). See Gould (2000) for a discussion of the interpretation of logistic regression. See Dupont (2009) or Hilbe (2009) for a discussion of logistic regression with examples using Stata. For a discussion using Stata with an emphasis on model specification, see Vittinghoff et al. (2005).

Stata has a variety of commands for performing estimation when the dependent variable is dichotomous or polytomous. See Long and Freese (2006) for a book devoted to fitting these models with Stata. Here is a list of some estimation commands that may be of interest. See [I] **estimation commands** for a complete list of all of Stata's estimation commands.

asclogit	[R] **asclogit**	Alternative-specific conditional logit (McFadden's choice) model
asmprobit	[R] **asmprobit**	Alternative-specific multinomial probit regression
asroprobit	[R] **asroprobit**	Alternative-specific rank-ordered probit regression
binreg	[R] **binreg**	Generalized linear models for the binomial family
biprobit	[R] **biprobit**	Bivariate probit regression
blogit	[R] **glogit**	Logit regression for grouped data
bprobit	[R] **glogit**	Probit regression for grouped data
clogit	[R] **clogit**	Conditional (fixed-effects) logistic regression
cloglog	[R] **cloglog**	Complementary log-log regression
exlogistic	[R] **exlogistic**	Exact logistic regression
glm	[R] **glm**	Generalized linear models
glogit	[R] **glogit**	Weighted least-squares logistic regression for grouped data
gprobit	[R] **glogit**	Weighted least-squares probit regression for grouped data
heckprob	[R] **heckprob**	Probit model with selection
hetprob	[R] **hetprob**	Heteroskedastic probit model
ivprobit	[R] **ivprobit**	Probit model with endogenous regressors
logit	[R] **logit**	Logistic regression, reporting coefficients
mlogit	[R] **mlogit**	Multinomial (polytomous) logistic regression
mprobit	[R] **mprobit**	Multinomial probit regression
nlogit	[R] **nlogit**	Nested logit regression (RUM-consistent and nonnormalized)
ologit	[R] **ologit**	Ordered logistic regression
oprobit	[R] **oprobit**	Ordered probit regression
probit	[R] **probit**	Probit regression
rologit	[R] **rologit**	Rank-ordered logistic regression
scobit	[R] **scobit**	Skewed logistic regression
slogit	[R] **slogit**	Stereotype logistic regression
svy: *cmd*	[SVY] **svy estimation**	Survey versions of many of these commands are available; see [SVY] **svy estimation**
xtcloglog	[XT] **xtcloglog**	Random-effects and population-averaged cloglog models
xtgee	[XT] **xtgee**	GEE population-averaged generalized linear models
xtlogit	[XT] **xtlogit**	Fixed-effects, random-effects, and population-averaged logit models
xtprobit	[XT] **xtprobit**	Random-effects and population-averaged probit models

▷ Example 1

Consider the following dataset from a study of risk factors associated with low birthweight described in Hosmer and Lemeshow (2000, 25).

```
. use http://www.stata-press.com/data/r12/lbw
(Hosmer & Lemeshow data)
. describe
Contains data from http://www.stata-press.com/data/r12/lbw.dta
  obs:           189                          Hosmer & Lemeshow data
 vars:            11                          15 Jan 2011 05:01
 size:         2,646
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
id              int    %8.0g                  identification code
low             byte   %8.0g                  birthweight<2500g
age             byte   %8.0g                  age of mother
lwt             int    %8.0g                  weight at last menstrual period
race            byte   %8.0g       race       race
smoke           byte   %8.0g                  smoked during pregnancy
ptl             byte   %8.0g                  premature labor history (count)
ht              byte   %8.0g                  has history of hypertension
ui              byte   %8.0g                  presence, uterine irritability
ftv             byte   %8.0g                  number of visits to physician
                                                during 1st trimester
bwt             int    %8.0g                  birthweight (grams)
-------------------------------------------------------------------------------
Sorted by:
```

We want to investigate the causes of low birthweight. Here `race` is a categorical variable indicating whether a person is white (`race` = 1), black (`race` = 2), or some other race (`race` = 3). We want indicator (dummy) variables for `race` included in the regression, so we will use factor variables.

```
. logistic low age lwt i.race smoke ptl ht ui
Logistic regression                               Number of obs   =        189
                                                  LR chi2(8)      =      33.22
                                                  Prob > chi2     =     0.0001
Log likelihood =   -100.724                       Pseudo R2       =     0.1416
------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .9732636   .0354759    -0.74   0.457     .9061578    1.045339
         lwt |   .9849634   .0068217    -2.19   0.029     .9716834    .9984249
             |
        race |
           2 |   3.534767   1.860737     2.40   0.016     1.259736    9.918406
           3 |   2.368079   1.039949     1.96   0.050     1.001356    5.600207
             |
       smoke |   2.517698    1.00916     2.30   0.021     1.147676    5.523162
         ptl |   1.719161   .5952579     1.56   0.118     .8721455    3.388787
          ht |   6.249602   4.322408     2.65   0.008     1.611152    24.24199
          ui |     2.1351   .9808153     1.65   0.099     .8677528      5.2534
       _cons |   1.586014   1.910496     0.38   0.702     .1496092     16.8134
------------------------------------------------------------------------------
```

The odds ratios are for a one-unit change in the variable. If we wanted the odds ratio for `age` to be in terms of 4-year intervals, we would type

```
. gen age4 = age/4
. logistic low age4 lwt i.race smoke ptl ht ui
(output omitted)
```

After `logistic`, we can type `logit` to see the model in terms of coefficients and standard errors:

```
. logit
Logistic regression                               Number of obs   =        189
                                                  LR chi2(8)      =      33.22
                                                  Prob > chi2     =     0.0001
Log likelihood =   -100.724                       Pseudo R2       =     0.1416
```

low	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age4	-.1084012	.1458017	-0.74	0.457	-.3941673	.1773649
lwt	-.0151508	.0069259	-2.19	0.029	-.0287253	-.0015763
race						
2	1.262647	.5264101	2.40	0.016	.2309024	2.294392
3	.8620792	.4391532	1.96	0.050	.0013548	1.722804
smoke	.9233448	.4008266	2.30	0.021	.137739	1.708951
ptl	.5418366	.346249	1.56	0.118	-.136799	1.220472
ht	1.832518	.6916292	2.65	0.008	.4769494	3.188086
ui	.7585135	.4593768	1.65	0.099	-.1418484	1.658875
_cons	.4612239	1.20459	0.38	0.702	-1.899729	2.822176

If we wanted to see the `logistic` output again, we would type `logistic` without arguments.

◁

▷ Example 2

We can specify the confidence interval for the odds ratios with the `level()` option, and we can do this either at estimation time or when replaying the model. For instance, to see our first model in example 1 with narrower, 90% confidence intervals, we might type

```
. logistic, level(90)
Logistic regression                               Number of obs   =        189
                                                  LR chi2(8)      =      33.22
                                                  Prob > chi2     =     0.0001
Log likelihood =   -100.724                       Pseudo R2       =     0.1416
```

low	Odds Ratio	Std. Err.	z	P>|z|	[90% Conf.	Interval]
age4	.8972675	.1308231	-0.74	0.457	.7059409	1.140448
lwt	.9849634	.0068217	-2.19	0.029	.9738063	.9962483
race						
2	3.534767	1.860737	2.40	0.016	1.487028	8.402379
3	2.368079	1.039949	1.96	0.050	1.149971	4.876471
smoke	2.517698	1.00916	2.30	0.021	1.302185	4.867819
ptl	1.719161	.5952579	1.56	0.118	.9726876	3.038505
ht	6.249602	4.322408	2.65	0.008	2.003487	19.49478
ui	2.1351	.9808153	1.65	0.099	1.00291	4.545424
_cons	1.586014	1.910496	0.38	0.702	.2186791	11.50288

◁

Robust estimate of variance

If you specify `vce(robust)`, Stata reports the robust estimate of variance described in [U] **20.20 Obtaining robust variance estimates**. Here is the model previously fit with the robust estimate of variance:

```
. logistic low age lwt i.race smoke ptl ht ui, vce(robust)
Logistic regression                             Number of obs   =        189
                                                Wald chi2(8)    =      29.02
                                                Prob > chi2     =     0.0003
Log pseudolikelihood =   -100.724               Pseudo R2       =     0.1416
```

low	Odds Ratio	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.9732636	.0329376	-0.80	0.423	.9108015	1.040009
lwt	.9849634	.0070209	-2.13	0.034	.9712984	.9988206
race						
2	3.534767	1.793616	2.49	0.013	1.307504	9.556051
3	2.368079	1.026563	1.99	0.047	1.012512	5.538501
smoke	2.517698	.9736417	2.39	0.017	1.179852	5.372537
ptl	1.719161	.7072902	1.32	0.188	.7675715	3.850476
ht	6.249602	4.102026	2.79	0.005	1.726445	22.6231
ui	2.1351	1.042775	1.55	0.120	.8197749	5.560858
_cons	1.586014	1.939482	0.38	0.706	.144345	17.42658

Also you can specify `vce(cluster` *clustvar*`)` and then, within cluster, relax the assumption of independence. To illustrate this, we have made some fictional additions to the low-birthweight data.

Say that these data are not a random sample of mothers but instead are a random sample of mothers from a random sample of hospitals. In fact, that may be true—we do not know the history of these data.

Hospitals specialize, and it would not be too incorrect to say that some hospitals specialize in more difficult cases. We are going to show two extremes. In one, all hospitals are alike, but we are going to estimate under the possibility that they might differ. In the other, hospitals are strikingly different. In both cases, we assume that patients are drawn from 20 hospitals.

In both examples, we will fit the same model, and we will type the same command to fit it. Below are the same data we have been using but with a new variable, `hospid`, that identifies from which of the 20 hospitals each patient was drawn (and which we have made up):

```
. use http://www.stata-press.com/data/r12/hospid1, clear
. logistic low age lwt i.race smoke ptl ht ui, vce(cluster hospid)
Logistic regression                               Number of obs   =        189
                                                  Wald chi2(8)    =      49.67
                                                  Prob > chi2     =     0.0000
Log pseudolikelihood =   -100.724                 Pseudo R2       =     0.1416
                                (Std. Err. adjusted for 20 clusters in hospid)
```

low	Odds Ratio	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.9732636	.0397476	-0.66	0.507	.898396	1.05437
lwt	.9849634	.0057101	-2.61	0.009	.9738352	.9962187
race						
2	3.534767	2.013285	2.22	0.027	1.157563	10.79386
3	2.368079	.8451325	2.42	0.016	1.176562	4.766257
smoke	2.517698	.8284259	2.81	0.005	1.321062	4.79826
ptl	1.719161	.6676221	1.40	0.163	.8030814	3.680219
ht	6.249602	4.066275	2.82	0.005	1.74591	22.37086
ui	2.1351	1.093144	1.48	0.138	.7827337	5.824014
_cons	1.586014	1.661913	0.44	0.660	.2034094	12.36639

The standard errors are similar to the standard errors we have previously obtained, whether we used the robust or conventional estimators. In this example, we invented the hospital IDs randomly.

Here are the results of the estimation with the same data but with a different set of hospital IDs:

```
. use http://www.stata-press.com/data/r12/hospid2
. logistic low age lwt i.race smoke ptl ht ui, vce(cluster hospid)
Logistic regression                               Number of obs   =        189
                                                  Wald chi2(8)    =       7.19
                                                  Prob > chi2     =     0.5167
Log pseudolikelihood =   -100.724                 Pseudo R2       =     0.1416
                                (Std. Err. adjusted for 20 clusters in hospid)
```

low	Odds Ratio	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.9732636	.0293064	-0.90	0.368	.9174862	1.032432
lwt	.9849634	.0106123	-1.41	0.160	.9643817	1.005984
race						
2	3.534767	3.120338	1.43	0.153	.6265521	19.9418
3	2.368079	1.297738	1.57	0.116	.8089594	6.932114
smoke	2.517698	1.570287	1.48	0.139	.7414969	8.548655
ptl	1.719161	.6799153	1.37	0.171	.7919045	3.732161
ht	6.249602	7.165454	1.60	0.110	.660558	59.12808
ui	2.1351	1.411977	1.15	0.251	.5841231	7.804266
_cons	1.586014	1.946253	0.38	0.707	.1431423	17.573

Note the strikingly larger standard errors. What happened? In these data, women most likely to have low-birthweight babies are sent to certain hospitals, and the decision on likeliness is based not just on age, smoking history, etc., but on other things that doctors can see but that are not recorded in our data. Thus merely because a woman is at one of the centers identifies her to be more likely to have a low-birthweight baby.

Saved results

logistic saves the following in e():

Scalars

e(N)	number of observations
e(N_cds)	number of completely determined successes
e(N_cdf)	number of completely determined failures
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance of model test
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	logistic
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(mns)	vector of means of the independent variables
e(rules)	information about perfect predictors
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`logistic` is implemented as an ado-file.

Define $\mathbf{x}_j$ as the (row) vector of independent variables, augmented by 1, and $\mathbf{b}$ as the corresponding estimated parameter (column) vector. The logistic regression model is fit by `logit`; see [R] **logit** for details of estimation.

The odds ratio corresponding to the ith coefficient is $\psi_i = \exp(b_i)$. The standard error of the odds ratio is $s_i^{\psi} = \psi_i s_i$, where s_i is the standard error of b_i estimated by `logit`.

Define $I_j = \mathbf{x}_j\mathbf{b}$ as the predicted index of the jth observation. The predicted probability of a positive outcome is

$$p_j = \frac{\exp(I_j)}{1+\exp(I_j)}$$

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`logistic` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **logistic postestimation** — Postestimation tools for logistic

[R] **brier** — Brier score decomposition

[R] **exlogistic** — Exact logistic regression

[R] **logit** — Logistic regression, reporting coefficients

[R] **roc** — Receiver operating characteristic (ROC) analysis

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtlogit** — Fixed-effects, random-effects, and population-averaged logit models

[U] **20 Estimation and postestimation commands**

Title

logistic postestimation — Postestimation tools for logistic

Description

The following postestimation commands are of special interest after `logistic`:

Command	Description
`estat classification`	report various summary statistics, including the classification table
`estat gof`	Pearson or Hosmer–Lemeshow goodness-of-fit test
`lroc`	compute area under ROC curve and graph the curve
`lsens`	graph sensitivity and specificity versus probability cutoff

These commands are not appropriate after the `svy` prefix.

For information about these commands, see below.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Special-interest postestimation commands

`estat classification` reports various summary statistics, including the classification table.

`estat gof` reports the Pearson goodness-of-fit test or the Hosmer–Lemeshow goodness-of-fit test.

`lroc` graphs the ROC curve and calculates the area under the curve.

`lsens` graphs sensitivity and specificity versus probability cutoff and optionally creates new variables containing these data.

`estat classification`, `estat gof`, `lroc`, and `lsens` produce statistics and graphs either for the estimation sample or for any set of observations. However, they always use the estimation sample by default. When weights, `if`, or `in` is used with `logistic`, it is not necessary to repeat the qualifier with these commands when you want statistics computed for the estimation sample. Specify `if`, `in`, or the `all` option only when you want statistics computed for a set of observations other than the estimation sample. Specify weights (only `fweights` are allowed with these commands) only when you want to use a different set of weights.

By default, `estat classification`, `estat gof`, `lroc`, and `lsens` use the last model fit by `logistic`. You may also directly specify the model to the `lroc` and `lsens` commands by inputting a vector of coefficients with the `beta()` option and passing the name of the dependent variable *depvar*.

`estat classification` and `estat gof` require that the current estimation results be from `logistic`, `logit`, or `probit`. `lroc` and `lsens` commands may also be used after `logit` or `probit`. `estat classification`, `lroc`, and `lsens` may also be used after `ivprobit`.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [, *statistic* `nooffset` `rules` `asif`]

statistic	Description
Main	
`pr`	probability of a positive outcome; the default
`xb`	linear prediction
`stdp`	standard error of the prediction
* `dbeta`	Pregibon (1981) $\Delta\widehat{\beta}$ influence statistic
* `deviance`	deviance residual
* `dx2`	Hosmer and Lemeshow (2000) $\Delta\,\chi^2$ influence statistic
* `ddeviance`	Hosmer and Lemeshow (2000) $\Delta\,D$ influence statistic
* `hat`	Pregibon (1981) leverage
* `number`	sequential number of the covariate pattern
* `residuals`	Pearson residuals; adjusted for number sharing covariate pattern
* `rstandard`	standardized Pearson residuals; adjusted for number sharing covariate pattern
`score`	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

`pr`, `xb`, `stdp`, and `score` are the only options allowed with `svy` estimation results.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of a positive outcome.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`dbeta` calculates the Pregibon (1981) $\Delta\widehat{\beta}$ influence statistic, a standardized measure of the difference in the coefficient vector that is due to deletion of the observation along with all others that share the same covariate pattern. In Hosmer and Lemeshow (2000, 144–145) jargon, this statistic is M-asymptotic; that is, it is adjusted for the number of observations that share the same covariate pattern.

`deviance` calculates the deviance residual.

`dx2` calculates the Hosmer and Lemeshow (2000, 174) $\Delta\chi^2$ influence statistic, reflecting the decrease in the Pearson χ^2 that is due to the deletion of the observation and all others that share the same covariate pattern.

`ddeviance` calculates the Hosmer and Lemeshow (2000, 174) ΔD influence statistic, which is the change in the deviance residual that is due to deletion of the observation and all others that share the same covariate pattern.

`hat` calculates the Pregibon (1981) leverage or the diagonal elements of the hat matrix adjusted for the number of observations that share the same covariate pattern.

`number` numbers the covariate patterns—observations with the same covariate pattern have the same `number`. Observations not used in estimation have `number` set to missing. The first covariate pattern is numbered 1, the second 2, and so on.

`residuals` calculates the Pearson residual as given by Hosmer and Lemeshow (2000, 145) and adjusted for the number of observations that share the same covariate pattern.

`rstandard` calculates the standardized Pearson residual as given by Hosmer and Lemeshow (2000, 173) and adjusted for the number of observations that share the same covariate pattern.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

Options

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `logistic`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`rules` requests that Stata use any rules that were used to identify the model when making the prediction. By default, Stata calculates missing for excluded observations. See example 1 in [R] **logit postestimation**.

`asif` requests that Stata ignore the rules and the exclusion criteria and calculate predictions for all observations possible by using the estimated parameter from the model. See example 1 in [R] **logit postestimation**.

Syntax for estat classification

```
estat classification [ if ] [ in ] [ weight ] [ , class_options ]
```

class_options	Description
Main	
all	display summary statistics for all observations in the data
cutoff(#)	positive outcome threshold; default is cutoff(0.5)

fweights are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Postestimation > Reports and statistics

Options for estat classification

Main

all requests that the statistic be computed for all observations in the data, ignoring any if or in restrictions specified by logistic.

cutoff(#) specifies the value for determining whether an observation has a predicted positive outcome. An observation is classified as positive if its predicted probability is $\geq$ #. The default is 0.5.

Syntax for estat gof

```
estat gof [ if ] [ in ] [ weight ] [ , gof_options ]
```

gof_options	Description
Main	
group(#)	perform Hosmer–Lemeshow goodness-of-fit test using # quantiles
all	execute test for all observations in the data
outsample	adjust degrees of freedom for samples outside estimation sample
table	display table of groups used for test

fweights are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Postestimation > Reports and statistics

Options for estat gof

Main

`group(#)` specifies the number of quantiles to be used to group the data for the Hosmer–Lemeshow goodness-of-fit test. `group(10)` is typically specified. If this option is not given, the Pearson goodness-of-fit test is computed using the covariate patterns in the data as groups.

`all` requests that the statistic be computed for all observations in the data, ignoring any `if` or `in` restrictions specified with `logistic`.

`outsample` adjusts the degrees of freedom for the Pearson and Hosmer–Lemeshow goodness-of-fit tests for samples outside the estimation sample. See *Samples other than the estimation sample* later in this entry.

`table` displays a table of the groups used for the Hosmer–Lemeshow or Pearson goodness-of-fit test with predicted probabilities, observed and expected counts for both outcomes, and totals for each group.

Syntax for lroc

`lroc` [*depvar*] [*if*] [*in*] [*weight*] [`,` *lroc_options*]

lroc_options	Description
Main	
`all`	compute area under ROC curve and graph curve for all observations
`nograph`	suppress graph
Advanced	
`beta(`*matname*`)`	row vector containing coefficients for a logistic model
Plot	
cline_options	change the look of the line
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

`fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Binary outcomes > Postestimation > ROC curve after logistic/logit/probit/ivprobit

Options for lroc

Main

`all` requests that the statistic be computed for all observations in the data, ignoring any `if` or `in` restrictions specified by `logistic`.

`nograph` suppresses graphical output.

Advanced

`beta(`*matname*`)` specifies a row vector containing coefficients for a logistic model. The columns of the row vector must be labeled with the corresponding names of the independent variables in the data. The dependent variable *depvar* must be specified immediately after the command name. See *Models other than the last fitted model* later in this entry.

Plot

cline_options, *marker_options*, and *marker_label_options* affect the rendition of the ROC curve—the plotted points connected by lines. These options affect the size and color of markers, whether and how the markers are labeled, and whether and how the points are connected; see [G-3] ***cline_options***, [G-3] ***marker_options***, and [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for lsens

`lsens` [*depvar*] [*if*] [*in*] [*weight*] [`,` *lsens_options*]

lsens_options	Description
Main	
`all`	graph all observations in the data
`genprob(`*varname*`)`	create variable containing probability cutoffs
`gensens(`*varname*`)`	create variable containing sensitivity
`genspec(`*varname*`)`	create variable containing specificity
`replace`	overwrite existing variables
`nograph`	suppress the graph
Advanced	
`beta(`*matname*`)`	row vector containing coefficients for the model
Plot	
connect_options	affect rendition of the plotted points connected by lines
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

`fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Binary outcomes > Postestimation > Sensitivity/specificity plot

Options for lsens

Main

`all` requests that the statistic be computed for all observations in the data, ignoring any `if` or `in` restrictions specified with `logistic`.

`genprob(`*varname*`)`, `gensens(`*varname*`)`, and `genspec(`*varname*`)` specify the names of new variables created to contain, respectively, the probability cutoffs and the corresponding sensitivity and specificity.

`replace` requests that existing variables specified for `genprob()`, `gensens()`, or `genspec()` be overwritten.

`nograph` suppresses graphical output.

Advanced

`beta(`*matname*`)` specifies a row vector containing coefficients for a logistic model. The columns of the row vector must be labeled with the corresponding names of the independent variables in the data. The dependent variable *depvar* must be specified immediately after the command name. See *Models other than the last fitted model* later in this entry.

Plot

connect_options affect the rendition of the plotted points connected by lines; see *connect_options* in [G-2] **graph twoway scatter**.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Remarks are presented under the following headings:

predict after logistic
predict without options
predict with the xb and stdp options
predict with the residuals option
predict with the number option
predict with the deviance option
predict with the rstandard option
predict with the hat option
predict with the dx2 option
predict with the ddeviance option
predict with the dbeta option
estat classification
estat gof
lroc
lsens
Samples other than the estimation sample
Models other than the last fitted model

predict after logistic

`predict` is used after `logistic` to obtain predicted probabilities, residuals, and influence statistics for the estimation sample. The suggested diagnostic graphs below are from Hosmer and Lemeshow (2000), where they are more elaborately explained. Also see Collett (2003, 129–168) for a thorough discussion of model checking.

predict without options

Typing `predict` *newvar* after estimation calculates the predicted probability of a positive outcome.

In example 1 of [R] **logistic**, we ran the model `logistic low age lwt i.race smoke ptl ht ui`. We obtain the predicted probabilities of a positive outcome by typing

```
. use http://www.stata-press.com/data/r12/lbw
(Hosmer & Lemeshow data)
. logistic low age lwt i.race smoke ptl ht ui
  (output omitted)
. predict p
(option pr assumed; Pr(low))
. summarize p low
```

Variable	Obs	Mean	Std. Dev.	Min	Max
p	189	.3121693	.1913915	.0272559	.8391283
low	189	.3121693	.4646093	0	1

predict with the xb and stdp options

`predict` with the `xb` option calculates the linear combination $x_j\mathbf{b}$, where x_j are the independent variables in the jth observation and $\mathbf{b}$ is the estimated parameter vector. This is sometimes known as the index function because the cumulative distribution function indexed at this value is the probability of a positive outcome.

With the `stdp` option, `predict` calculates the standard error of the prediction, which is *not* adjusted for replicated covariate patterns in the data. The influence statistics described below are adjusted for replicated covariate patterns in the data.

predict with the residuals option

`predict` can calculate more than predicted probabilities. The Pearson residual is defined as the square root of the contribution of the covariate pattern to the Pearson χ^2 goodness-of-fit statistic, signed according to whether the observed number of positive responses within the covariate pattern is less than or greater than expected. For instance,

```
. predict r, residuals
. summarize r, detail
```

Pearson residual

Percentiles	Smallest		
1% -1.750923	-2.283885		
5% -1.129907	-1.750923		
10% -.9581174	-1.636279	Obs	189
25% -.6545911	-1.636279	Sum of Wgt.	189
50% -.3806923		Mean	-.0242299
	Largest	Std. Dev.	.9970949
75% .8162894	2.23879		
90% 1.510355	2.317558	Variance	.9941981
95% 1.747948	3.002206	Skewness	.8618271
99% 3.002206	3.126763	Kurtosis	3.038448

We notice the prevalence of a few large positive residuals:

```
. sort r
. list id r low p age race in -5/l
```

	id	r	low	p	age	race
185.	33	2.224501	1	.1681123	19	white
186.	57	2.23879	1	.166329	15	white
187.	16	2.317558	1	.1569594	27	other
188.	77	3.002206	1	.0998678	26	white
189.	36	3.126763	1	.0927932	24	white

predict with the number option

Covariate patterns play an important role in logistic regression. Two observations are said to share the same covariate pattern if the independent variables for the two observations are identical. Although we might think of having individual observations, the statistical information in the sample can be summarized by the covariate patterns, the number of observations with that covariate pattern, and the number of positive outcomes within the pattern. Depending on the model, the number of covariate patterns can approach or be equal to the number of observations, or it can be considerably less.

Stata calculates all the residual and diagnostic statistics in terms of covariate patterns, not observations. That is, all observations with the same covariate pattern are given the same residual and diagnostic statistics. Hosmer and Lemeshow (2000, 145–145) argue that such "M-asymptotic" statistics are more useful than "N-asymptotic" statistics.

To understand the difference, think of an observed positive outcome with predicted probability of 0.8. Taking the observation in isolation, the residual must be positive—we expected 0.8 positive responses and observed 1. This may indeed be the correct residual, but not necessarily. Under the M-asymptotic definition, we ask how many successes we observed across all observations with this covariate pattern. If that number were, say, six, and there were a total of 10 observations with this covariate pattern, then the residual is negative for the covariate pattern—we expected eight positive outcomes but observed six. `predict` makes this kind of calculation and then attaches the same residual to all observations in the covariate pattern.

Occasionally, you might want to find all observations sharing a covariate pattern. `number` allows you to do this:

```
. predict pattern, number
. summarize pattern
```

Variable	Obs	Mean	Std. Dev.	Min	Max
pattern	189	89.2328	53.16573	1	182

We previously fit the model `logistic low age lwt i.race smoke ptl ht ui` over 189 observations. There are 182 covariate patterns in our data.

predict with the deviance option

The deviance residual is defined as the square root of the contribution to the likelihood-ratio test statistic of a saturated model versus the fitted model. It has slightly different properties from the Pearson residual (see Hosmer and Lemeshow [2000, 145–147]):

```
. predict d, deviance
. summarize d, detail
                    deviance residual
-------------------------------------------------------------
      Percentiles      Smallest
 1%    -1.843472      -1.911621
 5%     -1.33477      -1.843472
10%    -1.148316      -1.843472       Obs                 189
25%    -.8445325      -1.674869       Sum of Wgt.         189
50%    -.5202702                      Mean           -.1228811
                       Largest        Std. Dev.       1.049237
75%     .9129041       1.894089
90%     1.541558       1.924457       Variance        1.100898
95%     1.673338       2.146583       Skewness        .6598857
99%     2.146583       2.180542       Kurtosis        2.036938
```

predict with the rstandard option

Pearson residuals do not have a standard deviation equal to 1. `rstandard` generates Pearson residuals normalized to have an *expected* standard deviation equal to 1.

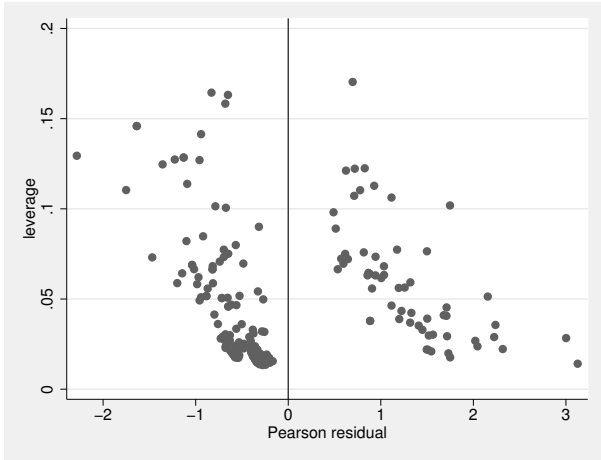
```
. predict rs, rstandard
. summarize r rs
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
           r |       189   -.0242299    .9970949  -2.283885   3.126763
          rs |       189   -.0279135    1.026406    -2.4478   3.149081

. correlate r rs
(obs=189)
             |        r       rs
-------------+------------------
           r |   1.0000
          rs |   0.9998   1.0000
```

Remember that we previously created `r` containing the (unstandardized) Pearson residuals. In these data, whether we use standardized or unstandardized residuals does not matter much.

predict with the hat option

`hat` calculates the leverage of a covariate pattern—a scaled measure of distance in terms of the independent variables. Large values indicate covariate patterns far from the average covariate pattern that can have a large effect on the fitted model even if the corresponding residual is small. Consider the following graph:

```
. predict h, hat
. scatter h r, xline(0)
```



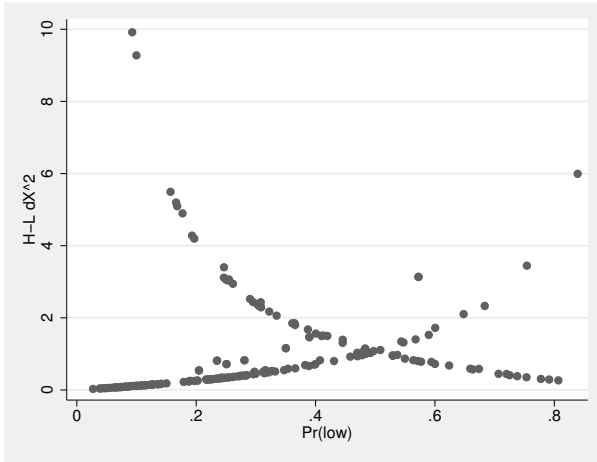
The points to the left of the vertical line are observed negative outcomes; here our data contain almost as many covariate patterns as observations, so most covariate patterns are unique. In such unique patterns, we observe either 0 or 1 success and expect p, thus forcing the sign of the residual. If we had fewer covariate patterns—if we did not have continuous variables in our model—there would be no such interpretation, and we would not have drawn the vertical line at 0.

Points on the left and right edges of the graph represent large residuals—covariate patterns that are not fit well by our model. Points at the top of our graph represent high leverage patterns. When analyzing the influence of observations on the model, we are most interested in patterns with high leverage and small residuals—patterns that might otherwise escape our attention.

predict with the dx2 option

There are many ways to measure influence, and `hat` is one example. `dx2` measures the decrease in the Pearson χ^2 goodness-of-fit statistic that would be caused by deleting an observation (and all others sharing the covariate pattern):

```
. predict dx2, dx2
. scatter dx2 p
```



Paraphrasing Hosmer and Lemeshow (2000, 178–179), the points going from the top left to the bottom right correspond to covariate patterns with the number of positive outcomes equal to the number in the group; the points on the other curve correspond to 0 positive outcomes. In our data, most of the covariate patterns are unique, so the points tend to lie along one or the other curves; the points that are off the curves correspond to the few repeated covariate patterns in our data in which all the outcomes are not the same.

We examine this graph for large values of `dx2`—there are two at the top left.

predict with the ddeviance option

Another measure of influence is the change in the deviance residuals due to deletion of a covariate pattern:

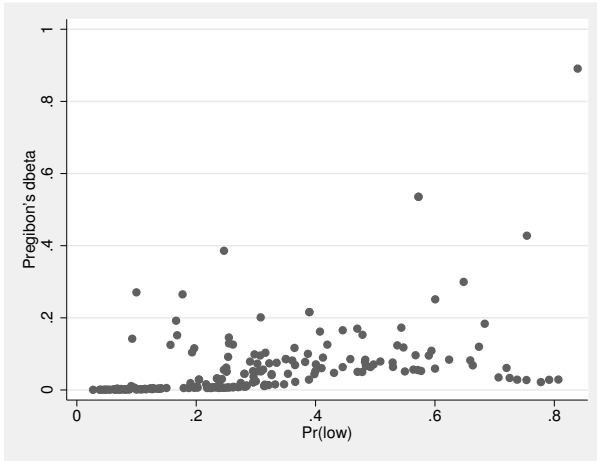
```
. predict dd, ddeviance
```

As with `dx2`, we typically graph `ddeviance` against the probability of a positive outcome. We direct you to Hosmer and Lemeshow (2000, 178) for an example and for the interpretation of this graph.

predict with the dbeta option

One of the more direct measures of influence of interest to model fitters is the Pregibon (1981) `dbeta` measure, a measure of the change in the coefficient vector that would be caused by deleting an observation (and all others sharing the covariate pattern):

```
. predict db, dbeta
. scatter db p
```



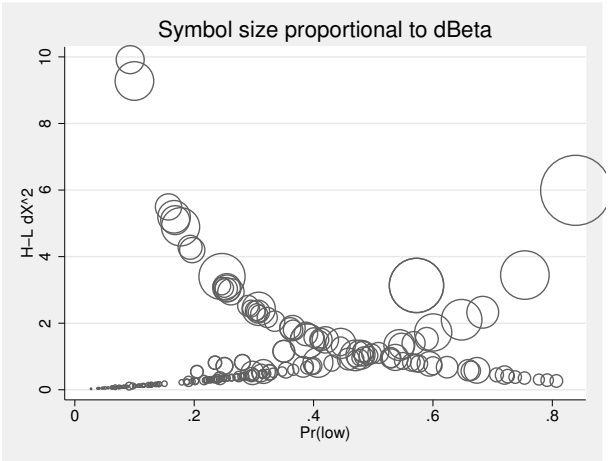
One observation has a large effect on the estimated coefficients. We can easily find this point:

```
. sort db
. list in 1
```

```
189.
+-------------------------------------------------------------------------------------------------------------+
|  id   low   age   lwt   race   smoke   ptl   ht   ui   ftv   bwt                                            |
| 188     0    25    95  white       1     3    0    1     0  3637                                            |
|-------------------------------------------------------------------------------------------------------------|
|       p          r   pattern          d          rs          h                                             |
| .8391283 -2.283885       117 -1.911621    -2.4478  .1294439                                                 |
|-------------------------------------------------------------------------------------------------------------|
|          dx2              dd              db                                                                |
|     5.991726        4.197658        .8909163                                                                |
+-------------------------------------------------------------------------------------------------------------+
```

Hosmer and Lemeshow (2000, 180) suggest a graph that combines two of the influence measures:

```
. scatter dx2 p [w=db], title("Symbol size proportional to dBeta") mfcolor(none)
(analytic weights assumed)
```



We can easily spot the most influential points by the `dbeta` and `dx2` measures.

estat classification

▷ Example 1

`estat classification` presents the classification statistics and classification table after `logistic`.

```
. use http://www.stata-press.com/data/r12/lbw, clear
(Hosmer & Lemeshow data)
. logistic low age lwt i.race smoke ptl ht ui
  (output omitted)
. estat classification
Logistic model for low
                 -------- True --------
Classified |         D             ~D  |        Total
-----------+--------------------------+-----------------
     +     |        21             12  |           33
     -     |        38            118  |          156
-----------+--------------------------+-----------------
   Total   |        59            130  |          189
Classified + if predicted Pr(D) >= .5
True D defined as low != 0
--------------------------------------------------------
Sensitivity                     Pr( +| D)   35.59%
Specificity                     Pr( -|~D)   90.77%
Positive predictive value       Pr( D| +)   63.64%
Negative predictive value       Pr(~D| -)   75.64%
--------------------------------------------------------
False + rate for true ~D        Pr( +|~D)    9.23%
False - rate for true D         Pr( -| D)   64.41%
False + rate for classified +   Pr(~D| +)   36.36%
False - rate for classified -   Pr( D| -)   24.36%
--------------------------------------------------------
Correctly classified                        73.54%
--------------------------------------------------------
```

By default, estat classification uses a cutoff of 0.5, although you can vary this with the cutoff() option. You can use the lsens command to review the potential cutoffs; see *lsens* below.

◁

estat gof

estat gof computes goodness-of-fit tests: either the Pearson χ^2 test or the Hosmer–Lemeshow test.

By default, estat classification, estat gof, lroc, and lsens compute statistics for the estimation sample by using the last model fit by logistic. However, samples other than the estimation sample can be specified; see *Samples other than the estimation sample* later in this entry.

▷ Example 2

estat gof, typed without options, presents the Pearson χ^2 goodness-of-fit test for the fitted model. The Pearson χ^2 goodness-of-fit test is a test of the observed against expected number of responses using cells defined by the covariate patterns; see *predict with the number option* earlier in this entry for the definition of covariate patterns.

```
. estat gof
Logistic model for low, goodness-of-fit test
       number of observations =       189
 number of covariate patterns =       182
            Pearson chi2(173) =       179.24
                  Prob > chi2 =         0.3567
```

Our model fits reasonably well. However, the number of covariate patterns is close to the number of observations, making the applicability of the Pearson χ^2 test questionable but not necessarily inappropriate. Hosmer and Lemeshow (2000, 147–150) suggest regrouping the data by ordering on the predicted probabilities and then forming, say, 10 nearly equal-sized groups. estat gof with the group() option does this:

```
. estat gof, group(10)
Logistic model for low, goodness-of-fit test
  (Table collapsed on quantiles of estimated probabilities)
     number of observations =       189
           number of groups =        10
    Hosmer-Lemeshow chi2(8) =         9.65
                  Prob > chi2 =         0.2904
```

Again we cannot reject our model. If we specify the table option, estat gof displays the groups along with the expected and observed number of positive responses (low-birthweight babies):

```
. estat gof, group(10) table
```

Logistic model for low, goodness-of-fit test

(Table collapsed on quantiles of estimated probabilities)

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.0827	0	1.2	19	17.8	19
2	0.1276	2	2.0	17	17.0	19
3	0.2015	6	3.2	13	15.8	19
4	0.2432	1	4.3	18	14.7	19
5	0.2792	7	4.9	12	14.1	19
6	0.3138	7	5.6	12	13.4	19
7	0.3872	6	6.5	13	12.5	19
8	0.4828	7	8.2	12	10.8	19
9	0.5941	10	10.3	9	8.7	19
10	0.8391	13	12.8	5	5.2	18

```
      number of observations =       189
            number of groups =        10
    Hosmer-Lemeshow chi2(8) =      9.65
                Prob > chi2 =      0.2904
```

◁

❑ Technical note

`estat gof` with the `group()` option puts all observations with the same predicted probabilities into the same group. If, as in the previous example, we request 10 groups, the groups that `estat gof` makes are $[p_0, p_{10}]$, $(p_{10}, p_{20}]$, $(p_{20}, p_{30}]$, …, $(p_{90}, p_{100}]$, where p_k is the kth percentile of the predicted probabilities, with p_0 the minimum and p_{100} the maximum.

If there are many ties at the quantile boundaries, as will often happen if all independent variables are categorical and there are only a few of them, the sizes of the groups will be uneven. If the totals in some of the groups are small, the χ^2 statistic for the Hosmer–Lemeshow test may be unreliable. In this case, fewer groups should be specified, or the Pearson goodness-of-fit test may be a better choice.

❑

▷ Example 3

The `table` option can be used without the `group()` option. We would not want to specify this for our current model because there were 182 covariate patterns in the data, caused by including the two continuous variables, `age` and `lwt`, in the model. As an aside, we fit a simpler model and specify `table` with `estat gof`:

```
. logistic low i.race smoke ui
Logistic regression                               Number of obs   =        189
                                                  LR chi2(4)      =      18.80
                                                  Prob > chi2     =     0.0009
Log likelihood = -107.93404                       Pseudo R2       =     0.0801
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
race						
2	3.052746	1.498087	2.27	0.023	1.166747	7.987382
3	2.922593	1.189229	2.64	0.008	1.316457	6.488285
smoke	2.945742	1.101838	2.89	0.004	1.415167	6.131715
ui	2.419131	1.047359	2.04	0.041	1.035459	5.651788
_cons	.1402209	.0512295	-5.38	0.000	.0685216	.2869447

```
. estat gof, table
```

Logistic model for low, goodness-of-fit test

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.1230	3	4.9	37	35.1	40
2	0.2533	1	1.0	3	3.0	4
3	0.2907	16	13.7	31	33.3	47
4	0.2923	15	12.6	28	30.4	43
5	0.2997	3	3.9	10	9.1	13
6	0.4978	4	4.0	4	4.0	8
7	0.4998	4	4.5	5	4.5	9
8	0.5087	2	1.5	1	1.5	3
9	0.5469	2	4.4	6	3.6	8
10	0.5577	6	5.6	4	4.4	10
11	0.7449	3	3.0	1	1.0	4

Group	Prob	race	smoke	ui
1	0.1230	white	0	0
2	0.2533	white	0	1
3	0.2907	other	0	0
4	0.2923	white	1	0
5	0.2997	black	0	0
6	0.4978	other	0	1
7	0.4998	white	1	1
8	0.5087	black	0	1
9	0.5469	other	1	0
10	0.5577	black	1	0
11	0.7449	other	1	1

```
      number of observations =       189
 number of covariate patterns =        11
             Pearson chi2(6) =         5.71
                 Prob > chi2 =         0.4569
```

◁

❑ Technical note

`logistic` and `estat gof` keep track of the estimation sample. If you type `logistic ... if x==1`, then when you type `estat gof`, the statistics will be calculated on the `x==1` subsample of the data automatically.

You should specify `if` or `in` with `estat gof` only when you wish to calculate statistics for a set of observations other than the estimation sample. See *Samples other than the estimation sample* later in this entry.

If the `logistic` model was fit with `fweights`, `estat gof` properly accounts for the weights in its calculations. (`estat gof` does not allow `pweights`.) You do not have to specify the weights when you run `estat gof`. Weights should be specified with `estat gof` only when you wish to use a different set of weights.

❑

lroc

Stata also has a suite of commands for performing both parametric and nonparametric receiver operating characteristic (ROC) analysis. See [R] **roc** for an overview of these commands.

`lroc` graphs the ROC curve—a graph of sensitivity versus one minus specificity as the cutoff c is varied—and calculates the area under it. Sensitivity is the fraction of observed positive-outcome cases that are correctly classified; specificity is the fraction of observed negative-outcome cases that are correctly classified. When the purpose of the analysis is classification, you must choose a cutoff.

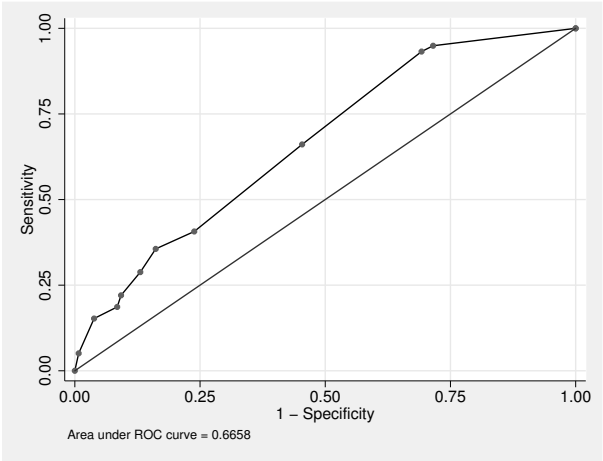
The curve starts at $(0, 0)$, corresponding to $c = 1$, and continues to $(1, 1)$, corresponding to $c = 0$. A model with no predictive power would be a 45° line. The greater the predictive power, the more bowed the curve, and hence the area beneath the curve is often used as a measure of the predictive power. A model with no predictive power has area 0.5; a perfect model has area 1.

The ROC curve was first discussed in signal detection theory (Peterson, Birdsall, and Fox 1954) and then was quickly introduced into psychology (Tanner and Swets 1954). It has since been applied in other fields, particularly medicine (for instance, Metz [1978]). For a classic text on ROC techniques, see Green and Swets (1966).

▷ Example 4

ROC curves are typically used when the point of the analysis is classification—which it is not in our low-birthweight model. Nevertheless, the ROC curve is

```
. lroc
Logistic model for low
number of observations =       189
area under ROC curve   =    0.6658
```

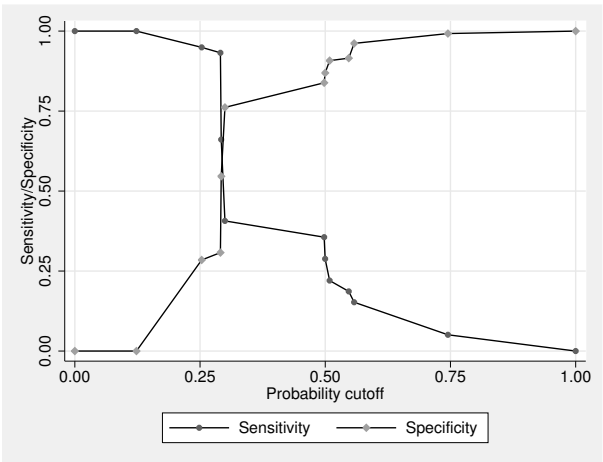


We see that the area under the curve is 0.6658.

lsens

`lsens` also plots sensitivity and specificity; it plots both sensitivity and specificity versus probability cutoff c. The graph is equivalent to what you would get from `estat classification` if you varied the cutoff probability from 0 to 1.

```
. lsens
```



`lsens` optionally creates new variables containing the probability cutoff, sensitivity, and specificity.

```
. lsens, genprob(p) gensens(sens) genspec(spec) nograph
```

The variables created will have $M + 2$ distinct nonmissing values: one for each of the M covariate patterns, one for $c = 0$, and another for $c = 1$. Values are recorded for $p = 0$, for each of the observed predicted probabilities, and for $p = 1$. The total number of observations required to do this can be fewer than _N, the same as _N, or _N + 1, or _N + 2. If more observations are added, they are added at the end of the dataset and the values of the original variables are set to missing in the added observations. How the values added align with existing observations is irrelevant.

Samples other than the estimation sample

`estat gof`, `estat classification`, `lroc`, and `lsens` can be used with samples other than the estimation sample. By default, these commands remember the estimation sample used with the last `logistic` command. To override this, simply use an `if` or `in` restriction to select another set of observations, or specify the `all` option to force the command to use all the observations in the dataset.

If you use `estat gof` with a sample that is completely different from the estimation sample (that is, no overlap), you should also specify the `outsample` option so that the χ^2 statistic properly adjusts the degrees of freedom upward. For an overlapping sample, the conservative thing to do is to leave the degrees of freedom the same as they are for the estimation sample.

▷ Example 5

We want to develop a model for predicting low-birthweight babies. One approach would be to divide our data into two groups, a developmental sample and a validation sample. See Lemeshow and Gall (1994) and Tilford, Roberson, and Fiser (1995) for more information on developing prediction models and severity-scoring systems.

We will do this with the low-birthweight data that we considered previously. First, we randomly divide the data into two samples.

```
. use http://www.stata-press.com/data/r12/lbw, clear
(Hosmer & Lemeshow data)
. set seed 1
. gen r = runiform()
. sort r
. gen group = 1 if _n <= _N/2
(95 missing values generated)
. replace group = 2 if group >=.
(95 real changes made)
```

Then we fit a model using the first sample (`group` = 1), which is our developmental sample.

```
. logistic low age lwt i.race smoke ptl ht ui if group==1
Logistic regression                             Number of obs   =         94
                                                LR chi2(8)      =      29.14
                                                Prob > chi2     =     0.0003
Log likelihood = -44.293342                     Pseudo R2       =     0.2475

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |     .91542   .0553937    -1.46   0.144     .8130414    1.03069
         lwt |   .9744276   .0112295    -2.25   0.025     .9526649    .9966874
             |
        race |
           2 |   5.063678    3.78442     2.17   0.030     1.170327    21.90913
           3 |   2.606209   1.657608     1.51   0.132     .7492483    9.065522
             |
       smoke |    .909912   .5252898    -0.16   0.870     .2934966    2.820953
         ptl |   3.033543   1.507048     2.23   0.025     1.145718     8.03198
          ht |   21.07656   22.64788     2.84   0.005     2.565304    173.1652
          ui |    .988479   .6699458    -0.02   0.986     .2618557    3.731409
       _cons |   30.73641   56.82168     1.85   0.064     .8204589    1151.462
------------------------------------------------------------------------------
```

To test calibration in the developmental sample, we calculate the Hosmer–Lemeshow goodness-of-fit test by using `estat gof`.

```
. estat gof, group(10)
Logistic model for low, goodness-of-fit test
  (Table collapsed on quantiles of estimated probabilities)
      number of observations =        94
            number of groups =        10
     Hosmer-Lemeshow chi2(8) =      6.67
                 Prob > chi2 =      0.5721
```

We did not specify an `if` statement with `estat gof` because we wanted to use the estimation sample. Because the test is not significant, we are satisfied with the fit of our model.

Running `lroc` gives a measure of the discrimination:

```
. lroc, nograph
Logistic model for low
number of observations =       94
area under ROC curve   =   0.8156
```

Now we test the calibration of our model by performing a goodness-of-fit test on the validation sample. We specify the `outsample` option so that the number of degrees of freedom is 10 rather than 8.

```
. estat gof if group==2, group(10) table outsample
Logistic model for low, goodness-of-fit test
  (Table collapsed on quantiles of estimated probabilities)
```

Group	Prob	Obs_1	Exp_1	Obs_0	Exp_0	Total
1	0.0725	1	0.4	9	9.6	10
2	0.1202	4	0.8	5	8.2	9
3	0.1549	3	1.3	7	8.7	10
4	0.1888	1	1.5	8	7.5	9
5	0.2609	3	2.2	7	7.8	10
6	0.3258	4	2.7	5	6.3	9
7	0.4217	2	3.7	8	6.3	10
8	0.4915	3	4.1	6	4.9	9
9	0.6265	4	5.5	6	4.5	10
10	0.9737	4	7.1	5	1.9	9

```
      number of observations =        95
            number of groups =        10
    Hosmer-Lemeshow chi2(10) =        28.03
                Prob > chi2 =         0.0018
```

We must acknowledge that our model does not fit well on the validation sample. The model's discrimination in the validation sample is appreciably lower, as well.

```
. lroc if group==2, nograph
Logistic model for low
number of observations =       95
area under ROC curve   =   0.5839
```

◁

Models other than the last fitted model

By default, `estat classification`, `estat gof`, `lroc`, and `lsens` use the last model fit by `logistic`. You may also directly specify the model to `lroc` and `lsens` by inputting a vector of coefficients with the `beta()` option and passing the name of the dependent variable *depvar* to these commands.

▷ Example 6

Suppose that someone publishes the following logistic model of low birthweight:

$$\Pr(\texttt{low}=1) = F(-0.02\,\texttt{age} - 0.01\,\texttt{lwt} + 1.3\,\texttt{black} + 1.1\,\texttt{smoke} + 0.5\,\texttt{ptl} + 1.8\,\texttt{ht} + 0.8\,\texttt{ui} + 0.5)$$

where F is the cumulative logistic distribution. These coefficients are not odds ratios; they are the equivalent of what `logit` produces.

We can see whether this model fits our data. First we enter the coefficients as a row vector and label its columns with the names of the independent variables plus `_cons` for the constant (see [P] **matrix define** and [P] **matrix rownames**).

```
. use http://www.stata-press.com/data/r12/lbw3, clear
(Hosmer & Lemeshow data)
. matrix input b = (-.02, -.01, 1.3, 1.1, .5, 1.8, .8, .5)
. matrix colnames b = age lwt black smoke ptl ht ui _cons
```

Here we use `lroc` to examine the predictive ability of the model:

```
. lroc low, beta(b) nograph
Logistic model for low
number of observations =      189
area under ROC curve   =   0.7275
```

The area under the curve indicates that this model does have some predictive power. We could also obtain a graph of sensitivity and specificity as a function of the cutoff probability by typing

```
. lsens low, beta(b)
```

◁

Saved results

`estat classification` saves the following in `r()`:

Scalars

`r(P_corr)`	percent correctly classified
`r(P_p1)`	sensitivity
`r(P_n0)`	specificity
`r(P_p0)`	false-positive rate given true negative
`r(P_n1)`	false-negative rate given true positive
`r(P_1p)`	positive predictive value
`r(P_0n)`	negative predictive value
`r(P_0p)`	false-positive rate given classified positive
`r(P_1n)`	false-negative rate given classified negative

`estat gof` saves the following in `r()`:

Scalars

`r(N)`	number of observations
`r(m)`	number of covariate patterns or groups
`r(df)`	degrees of freedom
`r(chi2)`	χ^2

`lroc` saves the following in `r()`:

Scalars

`r(N)`	number of observations
`r(area)`	area under the ROC curve

`lsens` saves the following in `r()`:

Scalars

`r(N)`	number of observations

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Methods and formulas are presented under the following headings:

estat gof
predict after logistic
estat classification and lsens
lroc

estat gof

Let M be the total number of covariate patterns among the N observations. View the data as collapsed on covariate patterns $j = 1, 2, \ldots, M$, and define m_j as the total number of observations having covariate pattern j and y_j as the total number of positive responses among observations with covariate pattern j. Define p_j as the predicted probability of a positive outcome in covariate pattern j.

The Pearson χ^2 goodness-of-fit statistic is

$$\chi^2 = \sum_{j=1}^{M} \frac{(y_j - m_j p_j)^2}{m_j p_j (1 - p_j)}$$

This χ^2 statistic has approximately $M - k$ degrees of freedom for the estimation sample, where k is the number of independent variables, including the constant. For a sample outside the estimation sample, the statistic has M degrees of freedom.

The Hosmer–Lemeshow goodness-of-fit χ^2 (Hosmer and Lemeshow 1980; Lemeshow and Hosmer 1982; Hosmer, Lemeshow, and Klar 1988) is calculated similarly, except that rather than using the M covariate patterns as the group definition, the quantiles of the predicted probabilities are used to form groups. Let $G = \#$ be the number of quantiles requested with `group(#)`. The smallest index $1 \leq q(i) \leq M$, such that

$$W_{q(i)} = \sum_{j=1}^{q(i)} m_j \geq \frac{N}{G}$$

gives $p_{q(i)}$ as the upper boundary of the ith quantile for $i = 1, 2, \ldots, G$. Let $q(0) = 1$ denote the first index.

The groups are then

$$[p_{q(0)}, p_{q(1)}], (p_{q(1)}, p_{q(2)}], \ldots, (p_{q(G-1)}, p_{q(G)}]$$

If the `table` option is given, the upper boundaries $p_{q(1)}, \ldots, p_{q(G)}$ of the groups appear next to the group number on the output.

The resulting χ^2 statistic has approximately $G - 2$ degrees of freedom for the estimation sample. For a sample outside the estimation sample, the statistic has G degrees of freedom.

predict after logistic

Index j will now be used to index observations, not covariate patterns. Define M_j for each observation as the total number of observations sharing j's covariate pattern. Define Y_j as the total number of positive responses among observations sharing j's covariate pattern.

The Pearson residual for the jth observation is defined as

$$r_j = \frac{Y_j - M_j p_j}{\sqrt{M_j p_j (1 - p_j)}}$$

For $M_j > 1$, the deviance residual d_j is defined as

$$d_j = \pm \left(2 \left[Y_j \ln\left(\frac{Y_j}{M_j p_j} \right) + (M_j - Y_j) \ln\left\{ \frac{M_j - Y_j}{M_j (1 - p_j)} \right\} \right] \right)^{1/2}$$

where the sign is the same as the sign of $(Y_j - M_j p_j)$. In the limiting cases, the deviance residual is given by

$$d_j = \begin{cases} -\sqrt{2M_j|\ln(1-p_j)|} & \text{if } Y_j = 0 \\ \sqrt{2M_j|\ln p_j|} & \text{if } Y_j = M_j \end{cases}$$

The *unadjusted* diagonal elements of the hat matrix $h_{\mathrm{U}j}$ are given by $h_{\mathrm{U}j} = (\mathbf{X}\mathbf{V}\mathbf{X}')_{jj}$, where V is the estimated covariance matrix of parameters. The adjusted diagonal elements h_j created by `hat` are then $h_j = M_j p_j(1-p_j)h_{\mathrm{U}j}$.

The standardized Pearson residual $r_{\mathrm{S}j}$ is $r_j/\sqrt{1-h_j}$.

The Pregibon (1981) $\Delta\widehat{\beta}_j$ influence statistic is

$$\Delta\widehat{\beta}_j = \frac{r_j^2 h_j}{(1-h_j)^2}$$

The corresponding change in the Pearson χ^2 is $r_{\mathrm{S}j}^2$. The corresponding change in the deviance residual is $\Delta D_j = d_j^2/(1-h_j)$.

estat classification and lsens

Again let j index observations. Define c as the `cutoff()` specified by the user or, if not specified, as 0.5. Let p_j be the predicted probability of a positive outcome and y_j be the actual outcome, which we will treat as 0 or 1, although Stata treats it as 0 and non-0, excluding missing observations.

A prediction is classified as *positive* if $p_j \geq c$ and otherwise is classified as *negative*. The classification is *correct* if it is *positive* and $y_j = 1$ or if it is *negative* and $y_j = 0$.

Sensitivity is the fraction of $y_j = 1$ observations that are correctly classified. *Specificity* is the percentage of $y_j = 0$ observations that are correctly classified.

lroc

The ROC curve is a graph of *specificity* against $(1 - \textit{sensitivity})$. This is guaranteed to be a monotone nondecreasing function because the number of correctly predicted successes increases and the number of correctly predicted failures decreases as the classification cutoff c decreases.

The area under the ROC curve is the area on the bottom of this graph and is determined by integrating the curve. The vertices of the curve are determined by sorting the data according to the predicted index, and the integral is computed using the trapezoidal rule.

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Also see

[R] **logistic** — Logistic regression, reporting odds ratios

[U] **20 Estimation and postestimation commands**

Title

logit — Logistic regression, reporting coefficients

Syntax

`logit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`or`	report odds ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`nocoef`	do not display coefficient table; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()`, `nocoef`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`nocoef` and `coeflegend` do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Binary outcomes > Logistic regression

Description

`logit` fits a logit model for a binary response by maximum likelihood; it models the probability of a positive outcome given a set of regressors. *depvar* equal to nonzero and nonmissing (typically *depvar* equal to one) indicates a positive outcome, whereas *depvar* equal to zero indicates a negative outcome.

Also see [R] **logistic**; `logistic` displays estimates as odds ratios. Many users prefer the `logistic` command to `logit`. Results are the same regardless of which you use—both are the maximum-likelihood estimator. Several auxiliary commands that can be run after `logit`, `probit`, or `logistic` estimation are described in [R] **logistic postestimation**. A list of related estimation commands is given in [R] **logistic**.

If estimating on grouped data, see [R] **glogit**.

Options

Model

`noconstant`, `offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

`asis` forces retention of perfect predictor variables and their associated perfectly predicted observations and may produce instabilities in maximization; see [R] **probit**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`or` reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. `or` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

The following options are available with `logit` but are not shown in the dialog box:

`nocoef` specifies that the coefficient table not be displayed. This option is sometimes used by program writers but is of no use interactively.

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Basic usage
Model identification

Basic usage

`logit` fits maximum likelihood models with dichotomous dependent (left-hand-side) variables coded as 0/1 (or, more precisely, coded as 0 and not-0).

▷ Example 1

We have data on the make, weight, and mileage rating of 22 foreign and 52 domestic automobiles. We wish to fit a logit model explaining whether a car is foreign on the basis of its weight and mileage. Here is an overview of our data:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. keep make mpg weight foreign
. describe
Contains data from http://www.stata-press.com/data/r12/auto.dta
  obs:            74                          1978 Automobile Data
 vars:             4                          13 Apr 2011 17:45
 size:         1,702                          (_dta has notes)
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
make            str18  %-18s                  Make and Model
mpg             int    %8.0g                  Mileage (mpg)
weight          int    %8.0gc                 Weight (lbs.)
foreign         byte   %8.0g       origin     Car type
-------------------------------------------------------------------------------
Sorted by:  foreign
     Note:  dataset has changed since last saved
. inspect foreign
foreign:  Car type                              Number of Observations
-----------------------                    ------------------------------
                                                Total   Integers   Nonintegers
|   #                          Negative           -          -          -
|   #                          Zero              52         52          -
|   #                          Positive          22         22          -
|   #                                           ----       ----       ----
|   #   #                      Total              74         74          -
|   #   #                      Missing            -
+-----------------------                        ----
0                       1                      74
   (2 unique values)
      foreign is labeled and all values are documented in the label.
```

The variable `foreign` takes on two unique values, 0 and 1. The value 0 denotes a domestic car, and 1 denotes a foreign car.

The model that we wish to fit is

$$\Pr(\texttt{foreign} = 1) = F(\beta_0 + \beta_1\texttt{weight} + \beta_2\texttt{mpg})$$

where $F(z) = e^z/(1 + e^z)$ is the cumulative logistic distribution.

To fit this model, we type

```
. logit foreign weight mpg
Iteration 0:   log likelihood =  -45.03321
Iteration 1:   log likelihood = -29.238536
Iteration 2:   log likelihood = -27.244139
Iteration 3:   log likelihood = -27.175277
Iteration 4:   log likelihood = -27.175156
Iteration 5:   log likelihood = -27.175156
Logistic regression                               Number of obs   =         74
                                                  LR chi2(2)      =      35.72
                                                  Prob > chi2     =     0.0000
Log likelihood = -27.175156                       Pseudo R2       =     0.3966
------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0039067   .0010116    -3.86   0.000    -.0058894    -.001924
         mpg |  -.1685869   .0919175    -1.83   0.067    -.3487418     .011568
       _cons |   13.70837   4.518709     3.03   0.002     4.851859    22.56487
------------------------------------------------------------------------------
```

We find that heavier cars are less likely to be foreign and that cars yielding better gas mileage are also less likely to be foreign, at least holding the weight of the car constant.

◁

❑ Technical note

Stata interprets a value of 0 as a negative outcome (failure) and treats all other values (except missing) as positive outcomes (successes). Thus if your dependent variable takes on the values 0 and 1, then 0 is interpreted as failure and 1 as success. If your dependent variable takes on the values 0, 1, and 2, then 0 is still interpreted as failure, but both 1 and 2 are treated as successes.

If you prefer a more formal mathematical statement, when you type `logit` y x, Stata fits the model

$$\Pr(y_j \neq 0 \mid \mathbf{x}_j) = \frac{\exp(\mathbf{x}_j\boldsymbol{\beta})}{1+\exp(\mathbf{x}_j\boldsymbol{\beta})}$$

❑

Model identification

The `logit` command has one more feature, and it is probably the most useful. `logit` automatically checks the model for identification and, if it is underidentified, drops whatever variables and observations are necessary for estimation to proceed. (`logistic`, `probit`, and `ivprobit` do this as well.)

▷ Example 2

Have you ever fit a logit model where one or more of your independent variables perfectly predicted one or the other outcome?

For instance, consider the following data:

Outcome y	Independent variable x
0	1
0	1
0	0
1	0

Say that we wish to predict the outcome on the basis of the independent variable. The outcome is always zero whenever the independent variable is one. In our data, $\Pr(y = 0 \mid x = 1) = 1$, which means that the logit coefficient on x must be minus infinity with a corresponding infinite standard error. At this point, you may suspect that we have a problem.

Unfortunately, not all such problems are so easily detected, especially if you have a lot of independent variables in your model. If you have ever had such difficulties, you have experienced one of the more unpleasant aspects of computer optimization. The computer has no idea that it is trying to solve for an infinite coefficient as it begins its iterative process. All it knows is that at each step, making the coefficient a little bigger, or a little smaller, works wonders. It continues on its merry way until either 1) the whole thing comes crashing to the ground when a numerical overflow error occurs or 2) it reaches some predetermined cutoff that stops the process. In the meantime, you have been waiting. The estimates that you finally receive, if you receive any at all, may be nothing more than numerical roundoff.

Stata watches for these sorts of problems, alerts us, fixes them, and properly fits the model.

Let's return to our automobile data. Among the variables we have in the data is one called `repair`, which takes on three values. A value of 1 indicates that the car has a poor repair record, 2 indicates an average record, and 3 indicates a better-than-average record. Here is a tabulation of our data:

```
. use http://www.stata-press.com/data/r12/repair, clear
(1978 Automobile Data)
. tabulate foreign repair
```

	repair			
Car type	1	2	3	Total
Domestic	10	27	9	46
Foreign	0	3	9	12
Total	10	30	18	58

All the cars with poor repair records (`repair` = 1) are domestic. If we were to attempt to predict `foreign` on the basis of the repair records, the predicted probability for the `repair` = 1 category would have to be zero. This in turn means that the logit coefficient must be minus infinity, and that would set most computer programs buzzing.

Let's try Stata on this problem.

```
. logit foreign b3.repair
note: 1.repair != 0 predicts failure perfectly
      1.repair dropped and 10 obs not used
Iteration 0:   log likelihood = -26.992087
Iteration 1:   log likelihood = -22.483187
Iteration 2:   log likelihood = -22.230498
Iteration 3:   log likelihood = -22.229139
Iteration 4:   log likelihood = -22.229138
Logistic regression                               Number of obs   =         48
                                                  LR chi2(1)      =       9.53
                                                  Prob > chi2     =     0.0020
Log likelihood = -22.229138                       Pseudo R2       =     0.1765
------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      repair |
          1  |          0  (empty)
          2  |  -2.197225   .7698003    -2.85   0.004    -3.706005   -.6884436
             |
       _cons |  -1.98e-16   .4714045    -0.00   1.000    -.9239359    .9239359
------------------------------------------------------------------------------
```

Remember that all the cars with poor repair records (`repair` = 1) are domestic, so the model cannot be fit, or at least it cannot be fit if we restrict ourselves to finite coefficients. Stata noted that fact "note: 1.repair !=0 predicts failure perfectly". This is Stata's mathematically precise way of saying what we said in English. When `repair` is 1, the car is domestic.

Stata then went on to say "1.repair dropped and 10 obs not used". This is Stata eliminating the problem. First `1.repair` had to be removed from the model because it would have an infinite coefficient. Then the 10 observations that led to the problem had to be eliminated, as well, so as not to bias the remaining coefficients in the model. The 10 observations that are not used are the 10 domestic cars that have poor repair records.

Stata then fit what was left of the model, using the remaining observations. Because no observations remained for cars with poor repair records, Stata reports "(empty)" in the row for `repair` = 1.

◁

❑ Technical note

Stata is pretty smart about catching problems like this. It will catch "one-way causation by a dummy variable", as we demonstrated above.

Stata also watches for "two-way causation", that is, a variable that perfectly determines the outcome, both successes and failures. Here Stata says, "so-and-so predicts outcome perfectly" and stops. Statistics dictates that no model can be fit.

Stata also checks your data for collinear variables; it will say, "so-and-so omitted because of collinearity". No observations need to be eliminated in this case, and model fitting will proceed without the offending variable.

It will also catch a subtle problem that can arise with continuous data. For instance, if we were estimating the chances of surviving the first year after an operation, and if we included in our model `age`, and if all the persons over 65 died within the year, Stata would say, "age $>$ 65 predicts failure perfectly". It would then inform us about the fix-up it takes and fit what can be fit of our model.

logit (and logistic, probit, and ivprobit) will also occasionally display messages such as

```
Note: 4 failures and 0 successes completely determined.
```

There are two causes for a message like this. The first—and most unlikely—case occurs when a continuous variable (or a combination of a continuous variable with other continuous or dummy variables) is simply a great predictor of the dependent variable. Consider Stata's auto.dta dataset with 6 observations removed.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. drop if foreign==0 & gear_ratio > 3.1
(6 observations deleted)
. logit foreign mpg weight gear_ratio, nolog
Logistic regression                             Number of obs   =         68
                                                LR chi2(3)      =      72.64
                                                Prob > chi2     =     0.0000
Log likelihood = -6.4874814                     Pseudo R2       =     0.8484

------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         mpg |  -.4944907   .2655508    -1.86   0.063    -1.014961    .0259792
      weight |  -.0060919    .003101    -1.96   0.049    -.0121698   -.000014
  gear_ratio |   15.70509   8.166234     1.92   0.054     -.300436    31.71061
       _cons |  -21.39527   25.41486    -0.84   0.400    -71.20747    28.41694
------------------------------------------------------------------------------
Note: 4 failures and 0 successes completely determined.
```

There are no missing standard errors in the output. If you receive the "completely determined" message and have one or more missing standard errors in your output, see the second case discussed below.

Note gear_ratio's large coefficient. logit thought that the 4 observations with the smallest predicted probabilities were essentially predicted perfectly.

```
. predict p
(option pr assumed; Pr(foreign))
. sort p
. list p in 1/4

     +-----------+
     |         p |
     |-----------|
  1. | 1.34e-10  |
  2. | 6.26e-09  |
  3. | 7.84e-09  |
  4. | 1.49e-08  |
     +-----------+
```

If this happens to you, you do not have to do anything. Computationally, the model is sound. The second case discussed below requires careful examination.

The second case occurs when the independent terms are all dummy variables or continuous ones with repeated values (for example, age). Here one or more of the estimated coefficients will have missing standard errors. For example, consider this dataset consisting of 5 observations.

```
. use http://www.stata-press.com/data/r12/logitxmpl, clear
. list, separator(0)
```

	y	x1	x2
1.	0	0	0
2.	0	0	0
3.	0	1	0
4.	1	1	0
5.	0	0	1
6.	1	0	1

```
. logit y x1 x2
Iteration 0:   log likelihood =  -3.819085
Iteration 1:   log likelihood = -2.9527336
Iteration 2:   log likelihood = -2.8110282
Iteration 3:   log likelihood = -2.7811973
Iteration 4:   log likelihood = -2.7746107
Iteration 5:   log likelihood = -2.7730128
  (output omitted)
Iteration 15996: log likelihood = -2.7725887  (not concave)
Iteration 15997: log likelihood = -2.7725887  (not concave)
Iteration 15998: log likelihood = -2.7725887  (not concave)
Iteration 15999: log likelihood = -2.7725887  (not concave)
Iteration 16000: log likelihood = -2.7725887  (not concave)
convergence not achieved
Logistic regression                               Number of obs   =          6
                                                  LR chi2(1)      =       2.09
                                                  Prob > chi2     =     0.1480
Log likelihood = -2.7725887                       Pseudo R2       =     0.2740

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          x1 |     18.3704          2     9.19   0.000     14.45047    22.29033
          x2 |     18.3704          .        .       .            .           .
       _cons |    -18.3704   1.414214   -12.99   0.000    -21.14221    -15.5986
------------------------------------------------------------------------------
Note: 2 failures and 0 successes completely determined.
convergence not achieved
r(430);
```

Three things are happening here. First, `logit` iterates almost forever and then declares nonconvergence. Second, `logit` can fit the outcome (`y` = 0) for the covariate pattern `x1` = 0 and `x2` = 0 (that is, the first two observations) perfectly. This observation is the "2 failures and 0 successes completely determined". Third, if this observation is dropped, then `x1`, `x2`, and the constant are collinear.

This is the cause of the nonconvergence, the message "completely determined", and the missing standard errors. It happens when you have a covariate pattern (or patterns) with only one outcome and there is collinearity when the observations corresponding to this covariate pattern are dropped.

If this happens to you, confirm the causes. First, identify the covariate pattern with only one outcome. (For your data, replace `x1` and `x2` with the independent variables of your model.)

```
. egen pattern = group(x1 x2)
. quietly logit y x1 x2, iterate(100)
. predict p
(option pr assumed; Pr(y))
```

```
. summarize p
```

Variable	Obs	Mean	Std. Dev.	Min	Max
p	6	.3333333	.2581989	1.05e-08	.5

If successes were completely determined, that means that there are predicted probabilities that are almost 1. If failures were completely determined, that means that there are predicted probabilities that are almost 0. The latter is the case here, so we locate the corresponding value of `pattern`:

```
. tabulate pattern if p < 1e-7
```

group(x1 x2)	Freq.	Percent	Cum.
1	2	100.00	100.00
Total	2	100.00	

Once we omit this covariate pattern from the estimation sample, `logit` can deal with the collinearity:

```
. logit y x1 x2 if pattern !=1, nolog
note: x2 omitted because of collinearity
Logistic regression                             Number of obs   =          4
                                                LR chi2(1)      =       0.00
                                                Prob > chi2     =     1.0000
Log likelihood = -2.7725887                     Pseudo R2       =     0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
x1	0	2	0.00	1.000	-3.919928	3.919928
x2	0	(omitted)				
_cons	0	1.414214	0.00	1.000	-2.771808	2.771808

We omit the collinear variable. Then we must decide whether to include or omit the observations with `pattern` $= 1$. We could include them,

```
. logit y x1, nolog
Logistic regression                             Number of obs   =          6
                                                LR chi2(1)      =       0.37
                                                Prob > chi2     =     0.5447
Log likelihood = -3.6356349                     Pseudo R2       =     0.0480
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
x1	1.098612	1.825742	0.60	0.547	-2.479776	4.677001
_cons	-1.098612	1.154701	-0.95	0.341	-3.361784	1.164559

or exclude them,

```
. logit y x1 if pattern != 1, nolog
Logistic regression                             Number of obs   =          4
                                                LR chi2(1)      =       0.00
                                                Prob > chi2     =     1.0000
Log likelihood = -2.7725887                     Pseudo R2       =     0.0000

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          x1 |          0           2     0.00   1.000    -3.919928    3.919928
       _cons |          0    1.414214     0.00   1.000    -2.771808    2.771808
------------------------------------------------------------------------------
```

If the covariate pattern that predicts outcome perfectly is meaningful, you may want to exclude these observations from the model. Here you would report that covariate pattern such and such predicted outcome perfectly and that the best model for the rest of the data is .... But, more likely, the perfect prediction was simply the result of having too many predictors in the model. Then you would omit the extraneous variables from further consideration and report the best model for all the data.

❑

Saved results

`logit` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_cds)`	number of completely determined successes
`e(N_cdf)`	number of completely determined failures
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(r2_p)`	pseudo-R-squared
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance of model test
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	logit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(mns)	vector of means of the independent variables
e(rules)	information about perfect predictors
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

logit is implemented as an ado-file.

Cramer (2003, chap. 9) surveys the prehistory and history of the logit model. The word "logit" was coined by Berkson (1944) and is analogous to the word "probit". For an introduction to probit and logit, see, for example, Aldrich and Nelson (1984), Cameron and Trivedi (2010), Greene (2012), Jones (2007), Long (1997), Long and Freese (2006), Pampel (2000), or Powers and Xie (2008).

The likelihood function for logit is

$$\ln L = \sum_{j \in S} w_j \ln F(\mathbf{x}_j\mathbf{b}) + \sum_{j \notin S} w_j \ln\{1 - F(\mathbf{x}_j\mathbf{b})\}$$

where S is the set of all observations j, such that $y_j \neq 0$, $F(z) = e^z/(1+e^z)$, and w_j denotes the optional weights. $\ln L$ is maximized as described in [R] **maximize**.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. The scores are calculated as $\mathbf{u}_j = \{1 - F(\mathbf{x}_j\mathbf{b})\}\mathbf{x}_j$ for the positive outcomes and $-F(\mathbf{x}_j\mathbf{b})\mathbf{x}_j$ for the negative outcomes.

`logit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

Joseph Berkson (1899–1982) was born in New York City and studied at the College of the City of New York, Columbia, and Johns Hopkins, earning both an MD and a doctorate in statistics. He then worked at Johns Hopkins before moving to the Mayo Clinic in 1931 as a biostatistician. Among many other contributions, his most influential one drew upon a long-sustained interest in the logistic function, especially his 1944 paper on bioassay, in which he introduced the term "logit". Berkson was a frequent participant in controversy—sometimes humorous, sometimes bitter—on subjects such as the evidence for links between smoking and various diseases and the relative merits of probit and logit methods and of different calculation methods.

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Also see

[R] **logit postestimation** — Postestimation tools for logit

[R] **brier** — Brier score decomposition

[R] **exlogistic** — Exact logistic regression

[R] **glogit** — Logit and probit regression for grouped data

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **probit** — Probit regression

[R] **roc** — Receiver operating characteristic (ROC) analysis

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtlogit** — Fixed-effects, random-effects, and population-averaged logit models

[U] **20 Estimation and postestimation commands**

Title

logit postestimation — Postestimation tools for logit

Description

The following postestimation commands are of special interest after `logit`:

Command	Description
`estat classification`	report various summary statistics, including the classification table
`estat gof`	Pearson or Hosmer–Lemeshow goodness-of-fit test
`lroc`	compute area under ROC curve and graph the curve
`lsens`	graph sensitivity and specificity versus probability cutoff

These commands are not appropriate after the `svy` prefix.

For information about these commands, see [R] **logistic postestimation**.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset rules asif]
```

statistic	Description
Main	
pr	probability of a positive outcome; the default
xb	linear prediction
stdp	standard error of the prediction
* dbeta	Pregibon (1981) $\Delta\widehat{\beta}$ influence statistic
* deviance	deviance residual
* dx2	Hosmer and Lemeshow (2000) $\Delta\,\chi^2$ influence statistic
* ddeviance	Hosmer and Lemeshow (2000) $\Delta\,D$ influence statistic
* hat	Pregibon (1981) leverage
* number	sequential number of the covariate pattern
* residuals	Pearson residuals; adjusted for number sharing covariate pattern
* rstandard	standardized Pearson residuals; adjusted for number sharing covariate pattern
score	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

`pr`, `xb`, `stdp`, and `score` are the only options allowed with `svy` estimation results.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of a positive outcome.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`dbeta` calculates the Pregibon (1981) $\Delta\widehat{\beta}$ influence statistic, a standardized measure of the difference in the coefficient vector that is due to deletion of the observation along with all others that share the same covariate pattern. In Hosmer and Lemeshow (2000, 144–145) jargon, this statistic is M-asymptotic; that is, it is adjusted for the number of observations that share the same covariate pattern.

`deviance` calculates the deviance residual.

`dx2` calculates the Hosmer and Lemeshow (2000, 174) $\Delta\chi^2$ influence statistic, reflecting the decrease in the Pearson χ^2 that is due to deletion of the observation and all others that share the same covariate pattern.

`ddeviance` calculates the Hosmer and Lemeshow (2000, 174) ΔD influence statistic, which is the change in the deviance residual that is due to deletion of the observation and all others that share the same covariate pattern.

`hat` calculates the Pregibon (1981) leverage or the diagonal elements of the hat matrix adjusted for the number of observations that share the same covariate pattern.

`number` numbers the covariate patterns—observations with the same covariate pattern have the same `number`. Observations not used in estimation have `number` set to missing. The first covariate pattern is numbered 1, the second 2, and so on.

`residuals` calculates the Pearson residual as given by Hosmer and Lemeshow (2000, 145) and adjusted for the number of observations that share the same covariate pattern.

`rstandard` calculates the standardized Pearson residual as given by Hosmer and Lemeshow (2000, 173) and adjusted for the number of observations that share the same covariate pattern.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

Options

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `logit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`rules` requests that Stata use any rules that were used to identify the model when making the prediction. By default, Stata calculates missing for excluded observations.

`asif` requests that Stata ignore the rules and exclusion criteria and calculate predictions for all observations possible by using the estimated parameter from the model.

Remarks

Once you have fit a logit model, you can obtain the predicted probabilities by using the `predict` command for both the estimation sample and other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**. Here we will make only a few more comments.

`predict` without arguments calculates the predicted probability of a positive outcome, that is, $\Pr(y_j = 1) = F(\mathbf{x}_j\mathbf{b})$. With the `xb` option, `predict` calculates the linear combination $\mathbf{x}_j\mathbf{b}$, where $\mathbf{x}_j$ are the independent variables in the jth observation and $\mathbf{b}$ is the estimated parameter vector. This is sometimes known as the index function because the cumulative distribution function indexed at this value is the probability of a positive outcome.

In both cases, Stata remembers any rules used to identify the model and calculates missing for excluded observations, unless `rules` or `asif` is specified. For information about the other statistics available after `predict`, see [R] **logistic postestimation**.

▷ Example 1

In example 2 of [R] **logit**, we fit the logit model `logit foreign b3.repair`. To obtain predicted probabilities, type

```
. use http://www.stata-press.com/data/r12/repair
(1978 Automobile Data)
. logit foreign b3.repair
note: 1.repair != 0 predicts failure perfectly
      1.repair dropped and 10 obs not used
  (output omitted)
. predict p
(option pr assumed; Pr(foreign))
(10 missing values generated)
```

```
. summarize foreign p
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
     foreign |         58    .2068966    .4086186          0          1
           p |         48         .25    .1956984         .1         .5
```

Stata remembers any rules used to identify the model and sets predictions to missing for any excluded observations. `logit` dropped the variable `1.repair` from our model and excluded 10 observations. Thus when we typed `predict p`, those same 10 observations were again excluded, and their predictions were set to missing.

`predict`'s `rules` option uses the rules in the prediction. During estimation, we were told "1.repair != 0 predicts failure perfectly", so the rule is that when `1.repair` is not zero, we should predict 0 probability of success or a positive outcome:

```
. predict p2, rules
(option pr assumed; Pr(foreign))
. summarize foreign p p2
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
     foreign |         58    .2068966    .4086186          0          1
           p |         48         .25    .1956984         .1         .5
          p2 |         58    .2068966    .2016268          0         .5
```

`predict`'s `asif` option ignores the rules and exclusion criteria and calculates predictions for all observations possible by using the estimated parameters from the model:

```
. predict p3, asif
(option pr assumed; Pr(foreign))
. summarize foreign p p2 p3
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
     foreign |         58    .2068966    .4086186          0          1
           p |         48         .25    .1956984         .1         .5
          p2 |         58    .2068966    .2016268          0         .5
          p3 |         58    .2931035    .2016268         .1         .5
```

Which is right? What `predict` does by default is the most conservative approach. If many observations had been excluded because of a simple rule, we could be reasonably certain that the `rules` prediction is correct. The `asif` prediction is correct only if the exclusion is a fluke, and we would be willing to exclude the variable from the analysis anyway. Then, however, we would refit the model to include the excluded observations.

◁

▷ Example 2

We can use the command `margins, contrast` after `logit` to make comparisons on the probability scale. Let's fit a model predicting low birthweight from characteristics of the mother:

```
. use http://www.stata-press.com/data/r12/lbw, clear
(Hosmer & Lemeshow data)
```

```
. logit low age i.race i.smoke ptl i.ht i.ui
Iteration 0:   log likelihood =   -117.336
Iteration 1:   log likelihood = -103.81846
Iteration 2:   log likelihood = -103.40486
Iteration 3:   log likelihood = -103.40384
Iteration 4:   log likelihood = -103.40384
Logistic regression                             Number of obs   =        189
                                                LR chi2(7)      =      27.86
                                                Prob > chi2     =     0.0002
Log likelihood = -103.40384                     Pseudo R2       =     0.1187
```

low	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.0403293	.0357127	-1.13	0.259	-.1103249	.0296663
race						
2	1.009436	.5025122	2.01	0.045	.0245302	1.994342
3	1.001908	.4248342	2.36	0.018	.1692485	1.834568
1.smoke	.9631876	.3904357	2.47	0.014	.1979477	1.728427
ptl	.6288678	.3399067	1.85	0.064	-.0373371	1.295073
1.ht	1.358142	.6289555	2.16	0.031	.125412	2.590872
1.ui	.8001832	.4572306	1.75	0.080	-.0959724	1.696339
_cons	-1.184127	.9187461	-1.29	0.197	-2.984837	.6165818

The coefficients are log odds-ratios: conditional on the other predictors, smoking during pregnancy is associated with an increase of 0.96 in the log odds-ratios of low birthweight. The model is linear in the log odds-scale, so the estimate of 0.96 has the same interpretation, whatever the values of the other predictors might be. We could convert 0.96 to an odds ratio by replaying the results with `logit, or`.

But what if we want to talk about the probability of low birthweight, and not the odds? Then we will need the command `margins, contrast`. We will use the `r.` contrast operator to compare each level of `smoke` with a reference level. (`smoke` has only two levels, so there will be only one comparison: a comparison of smokers with nonsmokers.)

```
. margins r.smoke, contrast
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(low), predict()
```

	df	chi2	P>chi2
smoke	1	6.32	0.0119

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
smoke (1 vs 0)	.1832779	.0728814	.0404329	.3261229

We see that maternal smoking is associated with an 18.3% increase in the probability of low birthweight. (We received a contrast in the probability scale because predicted probabilities are the default when `margins` is used after `logit`.)

The contrast of 18.3% is a difference of margins that are computed by averaging over the predictions for observations in the estimation sample. If the values of the other predictors were different, the contrast for `smoke` would be different, too. Let's estimate the contrast for 25-year-old mothers:

```
. margins r.smoke, contrast at(age=25)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(low), predict()
at           : age             =          25
```

	df	chi2	P>chi2
smoke	1	6.19	0.0129

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
smoke (1 vs 0)	.1808089	.0726777	.0383632	.3232547

Specifying a maternal `age` of 25 changed the contrast to 18.1%. Our contrast of probabilities changed because the `logit` model is nonlinear in the probability scale. A contrast of log odds-ratios would not have changed.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

See *Methods and formulas* of [R] **logistic postestimation** for details.

References

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Also see

[R] **logit** — Logistic regression, reporting coefficients

[R] **logistic postestimation** — Postestimation tools for logistic

[U] **20 Estimation and postestimation commands**

Title

loneway — Large one-way ANOVA, random effects, and reliability

Syntax

`loneway` *response_var group_var* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`mean`	expected value of F distribution; default is 1
`median`	median of F distribution; default is 1
`exact`	exact confidence intervals (groups must be equal with no weights)
`level(#)`	set confidence level; default is `level(95)`

`by` is allowed; see [D] **by**.
`aweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Linear models and related > ANOVA/MANOVA > Large one-way ANOVA

Description

`loneway` fits one-way analysis-of-variance (ANOVA) models on datasets with many levels of *group_var* and presents different ancillary statistics from `oneway` (see [R] **oneway**):

Feature	`oneway`	`loneway`
Fit one-way model	x	x
on fewer than 376 levels	x	x
on more than 376 levels		x
Bartlett's test for equal variance	x	
Multiple-comparison tests	x	
Intragroup correlation and SE		x
Intragroup correlation confidence interval		x
Est. reliability of group-averaged score		x
Est. SD of group effect		x
Est. SD within group		x

Options

Main

`mean` specifies that the expected value of the $F_{k-1,N-k}$ distribution be used as the reference point F_m in the estimation of ρ instead of the default value of 1.

`median` specifies that the median of the $F_{k-1,N-k}$ distribution be used as the reference point F_m in the estimation of ρ instead of the default value of 1.

`exact` requests that exact confidence intervals be computed, as opposed to the default asymptotic confidence intervals. This option is allowed only if the groups are equal in size and weights are not used.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals of the coefficients. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

Remarks

Remarks are presented under the following headings:

The one-way ANOVA model
R-squared
The random-effects ANOVA model
Intraclass correlation
Estimated reliability of the group-averaged score

The one-way ANOVA model

▷ Example 1

`loneway`'s output looks like that of `oneway`, except that `loneway` presents more information at the end. Using our automobile dataset, we have created a (numeric) variable called `manufacturer_grp` identifying the manufacturer of each car, and within each manufacturer we have retained a maximum of four models, selecting those with the lowest mpg. We can compute the intraclass correlation of mpg for all manufacturers with at least four models as follows:

```
. use http://www.stata-press.com/data/r12/auto7
(1978 Automobile Data)
. loneway mpg manufacturer_grp if nummake == 4
              One-way Analysis of Variance for mpg: Mileage (mpg)

                                              Number of obs =        36
                                                  R-squared =    0.5228

    Source                SS         df       MS            F     Prob > F
------------------------------------------------------------------------
Between manufactur~p   621.88889       8    77.736111      3.70     0.0049
Within manufactur~p       567.75      27    21.027778
------------------------------------------------------------------------
Total                  1189.6389      35    33.989683

         Intraclass       Asy.
         correlation      S.E.       [95% Conf. Interval]
         ------------------------------------------------
            0.40270     0.18770        0.03481     0.77060

         Estimated SD of manufactur~p effect     3.765247
         Estimated SD within manufactur~p        4.585605
         Est. reliability of a manufactur~p mean   .72950
              (evaluated at n=4.00)
```

◁

In addition to the standard one-way ANOVA output, `loneway` produces the R-squared, the estimated standard deviation of the group effect, the estimated standard deviation within group, the intragroup correlation, the estimated reliability of the group-averaged mean, and, for unweighted data, the asymptotic standard error and confidence interval for the intragroup correlation.

R-squared

The R-squared is, of course, simply the underlying R^2 for a regression of *response_var* on the levels of *group_var*, or `mpg` on the various manufacturers here.

The random-effects ANOVA model

`loneway` assumes that we observe a variable, y_{ij}, measured for n_i elements within k groups or classes such that

$$y_{ij} = \mu + \alpha_i + \epsilon_{ij}, \quad i = 1, 2, \ldots, k, \quad j = 1, 2, \ldots, n_i$$

and α_i and ϵ_{ij} are independent zero-mean random variables with variance σ_α^2 and σ_ϵ^2, respectively. This is the random-effects ANOVA model, also known as the components-of-variance model, in which it is typically assumed that the y_{ij} are normally distributed.

The interpretation with respect to our example is that the observed value of our response variable, `mpg`, is created in two steps. First, the ith manufacturer is chosen, and a value, α_i, is determined—the typical `mpg` for that manufacturer less the overall `mpg` μ. Then a deviation, ϵ_{ij}, is chosen for the jth model within this manufacturer. This is how much that particular automobile differs from the typical `mpg` value for models from this manufacturer.

For our sample of 36 car models, the estimated standard deviations are $\sigma_\alpha = 3.8$ and $\sigma_\epsilon = 4.6$. Thus a little more than half of the variation in `mpg` between cars is attributable to the car model, with the rest attributable to differences between manufacturers. These standard deviations differ from those that would be produced by a (standard) fixed-effects regression in that the regression would require the sum within each manufacturer of the ϵ_{ij}, $\epsilon_{i.}$ for the ith manufacturer, to be zero, whereas these estimates merely impose the constraint that the sum is *expected* to be zero.

Intraclass correlation

There are various estimators of the intraclass correlation, such as the pairwise estimator, which is defined as the Pearson product-moment correlation computed over all possible pairs of observations that can be constructed within groups. For a discussion of various estimators, see Donner (1986). `loneway` computes what is termed the analysis of variance, or ANOVA, estimator. This intraclass correlation is the theoretical upper bound on the variation in *response_var* that is explainable by *group_var*, of which R-squared is an overestimate because of the serendipity of fitting. This correlation is comparable to an R-squared—you do not have to square it.

In our example, the intra-`manu` correlation, the correlation of `mpg` within manufacturer, is 0.40. Because `aweights` were not used and the default correlation was computed (that is, the `mean` and `median` options were not specified), `loneway` also provided the asymptotic confidence interval and standard error of the intraclass correlation estimate.

Estimated reliability of the group-averaged score

The estimated reliability of the group-averaged score or mean has an interpretation similar to that of the intragroup correlation; it is a comparable number if we average *response_var* by *group_var*, or `mpg` by `manu` in our example. It is the theoretical upper bound of a regression of manufacturer-averaged `mpg` on characteristics of manufacturers. Why would we want to collapse our 36-observation dataset into a 9-observation dataset of manufacturer averages? Because the 36 observations might be a mirage. When General Motors builds cars, do they sometimes put a Pontiac label and sometimes a Chevrolet label on them, so that it appears in our data as if we have two cars when we really have

only one, replicated? If that were the case, and if it were the case for many other manufacturers, then we would be forced to admit that we do not have data on 36 cars; we instead have data on nine manufacturer-averaged characteristics.

Saved results

`loneway` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(rho_t)`	estimated reliability
`r(rho)`	intraclass correlation	`r(se)`	asymp. SE of intraclass correlation
`r(lb)`	lower bound of 95% CI for rho	`r(sd_w)`	estimated SD within group
`r(ub)`	upper bound of 95% CI for rho	`r(sd_b)`	estimated SD of group effect

Methods and formulas

`loneway` is implemented as an ado-file.

The mean squares in the `loneway`'s ANOVA table are computed as

$$\text{MS}_\alpha = \sum_i w_{i\cdot}(\overline{y}_{i\cdot} - \overline{y}_{\cdot\cdot})^2/(k-1)$$

and

$$\text{MS}_\epsilon = \sum_i \sum_j w_{ij}(y_{ij} - \overline{y}_{i\cdot})^2/(N-k)$$

in which

$$w_{i\cdot} = \sum_j w_{ij} \quad w_{\cdot\cdot} = \sum_i w_{i\cdot} \quad \overline{y}_{i\cdot} = \sum_j w_{ij}y_{ij}/w_{i\cdot} \quad \text{and} \quad \overline{y}_{\cdot\cdot} = \sum_i w_{i\cdot}\overline{y}_{i\cdot}/w_{\cdot\cdot}$$

The corresponding expected values of these mean squares are

$$E(\text{MS}_\alpha) = \sigma^2_\epsilon + g\sigma^2_\alpha \qquad \text{and} \qquad E(\text{MS}_\epsilon) = \sigma^2_\epsilon$$

in which

$$g = \frac{w_{\cdot\cdot} - \sum_i w^2_{i\cdot}/w_{\cdot\cdot}}{k-1}$$

In the unweighted case, we get

$$g = \frac{N - \sum_i n^2_i/N}{k-1}$$

As expected, $g = m$ for the case of no weights and equal group sizes in the data, that is, $n_i = m$ for all i. Replacing the expected values with the observed values and solving yields the ANOVA estimates of σ^2_α and σ^2_ϵ. Substituting these into the definition of the intraclass correlation

$$\rho = \frac{\sigma^2_\alpha}{\sigma^2_\alpha + \sigma^2_\epsilon}$$

yields the ANOVA estimator of the intraclass correlation:

$$\rho_A = \frac{F_{\text{obs}} - 1}{F_{\text{obs}} - 1 + g}$$

F_{obs} is the observed value of the F statistic from the ANOVA table. For no weights and equal n_i, ρ_A = roh, which is the intragroup correlation defined by Kish (1965). Two slightly different estimators are available through the `mean` and `median` options (Gleason 1997). If either of these options is specified, the estimate of ρ becomes

$$\rho = \frac{F_{\text{obs}} - F_m}{F_{\text{obs}} + (g-1)F_m}$$

For the `mean` option, $F_m = E(F_{k-1,N-K}) = (N-k)/(N-k-2)$, that is, the expected value of the ANOVA table's F statistic. For the `median` option, F_m is simply the median of the F statistic. Setting F_m to 1 gives ρ_A, so for large samples, these different point estimators are essentially the same. Also, because the intraclass correlation of the random-effects model is by definition nonnegative, for any of the three possible point estimators, ρ is truncated to zero if F_{obs} is less than F_m.

For no weighting, interval estimators for ρ_A are computed. If the groups are equal sized (all n_i equal) and the `exact` option is specified, the following exact (assuming that the y_{ij} are normally distributed) $100(1-\alpha)\%$ confidence interval is computed:

$$\left\{ \frac{F_{\text{obs}} - F_m F_u}{F_{\text{obs}} + (g-1)F_m F_u}, \frac{F_{\text{obs}} - F_m F_l}{F_{\text{obs}} + (g-1)F_m F_l} \right\}$$

with $F_m = 1$, $F_l = F_{\alpha/2,k-1,N-k}$, and $F_u = F_{1-\alpha/2,k-1,N-k}$, $F_{\cdot,k-1,N-k}$ being the cumulative distribution function for the F distribution with $k-1$ and $N-k$ degrees of freedom. If `mean` or `median` is specified, F_m is defined as above. If the groups are equal sized and `exact` is not specified, the following asymptotic $100(1-\alpha)\%$ confidence interval for ρ_A is computed,

$$\left[\rho_A - z_{\alpha/2}\sqrt{V(\rho_A)}, \rho_A + z_{\alpha/2}\sqrt{V(\rho_A)} \right]$$

where $z_{\alpha/2}$ is the $100(1-\alpha/2)$ percentile of the standard normal distribution and $\sqrt{V(\rho_A)}$ is the asymptotic standard error of ρ defined below. This confidence interval is also available for unequal groups. It is not applicable and, therefore, not computed for the estimates of ρ provided by the `mean` and `median` options. Again, because the intraclass coefficient is nonnegative, if the lower bound is negative for either confidence interval, it is truncated to zero. As might be expected, the coverage probability of a truncated interval is higher than its nominal value.

The asymptotic standard error of ρ_A, assuming that the y_{ij} are normally distributed, is also computed when appropriate, namely, for unweighted data and when ρ_A is computed (neither the `mean` option nor the `median` option is specified):

$$V(\rho_A) = \frac{2(1-\rho)^2}{g^2}(A + B + C)$$

with

$$A = \frac{\{1+\rho(g-1)\}^2}{N-k}$$

$$B = \frac{(1-\rho)\{1+\rho(2g-1)\}}{k-1}$$

$$C = \frac{\rho^2\{\sum n_i^2 - 2N^{-1}\sum n_i^3 + N^{-2}(\sum n_i^2)^2\}}{(k-1)^2}$$

and ρ_A is substituted for ρ (Donner 1986).

The estimated reliability of the group-averaged score, known as the Spearman–Brown prediction formula in the psychometric literature (Winer, Brown, and Michels 1991, 1014), is

$$\rho_t = \frac{t\rho}{1 + (t-1)\rho}$$

for group size t. `loneway` computes ρ_t for $t = g$.

The estimated standard deviation of the group effect is $\sigma_\alpha = \sqrt{(\text{MS}_\alpha - \text{MS}_\epsilon)/g}$. This deviation comes from the assumption that an observation is derived by adding a group effect to a within-group effect.

The estimated standard deviation within group is the square root of the mean square due to error, or $\sqrt{\text{MS}_\epsilon}$.

Acknowledgment

We thank John Gleason of Syracuse University (retired) for his contributions to improving `loneway`.

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Winer, B. J., D. R. Brown, and K. M. Michels. 1991. *Statistical Principles in Experimental Design*. 3rd ed. New York: McGraw–Hill.

Also see

[R] **anova** — Analysis of variance and covariance

[R] **oneway** — One-way analysis of variance

Title

lowess — Lowess smoothing

Syntax

`lowess` *yvar xvar* [*if*] [*in*] [, *options*]

options	Description
Main	
`mean`	running-mean smooth; default is running-line least squares
`noweight`	suppress weighted regressions; default is tricube weighting function
`bwidth(#)`	use # for the bandwidth; default is `bwidth(0.8)`
`logit`	transform dependent variable to logits
`adjust`	adjust smoothed mean to equal mean of dependent variable
`nograph`	suppress graph
`generate(`*newvar*`)`	create *newvar* containing smoothed values of *yvar*
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Smoothed line	
`lineopts(`*cline_options*`)`	affect rendition of the smoothed line
Add plots	
`addplot(`*plot*`)`	add other plots to generated graph
Y axis, X axis, Titles, Legend, Overall, By	
twoway_options	any of the options documented in [G-3] ***twoway_options***

yvar and *xvar* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

Menu

Statistics > Nonparametric analysis > Lowess smoothing

Description

`lowess` carries out a locally weighted regression of *yvar* on *xvar*, displays the graph, and optionally saves the smoothed variable.

Warning: `lowess` is computationally intensive and may therefore take a long time to run on a slow computer. Lowess calculations on 1,000 observations, for instance, require performing 1,000 regressions.

Options

Main

`mean` specifies running-mean smoothing; the default is running-line least-squares smoothing.

`noweight` prevents the use of Cleveland's (1979) tricube weighting function; the default is to use the weighting function.

`bwidth(#)` specifies the bandwidth. Centered subsets of `bwidth()` $\times N$ observations are used for calculating smoothed values for each point in the data except for the end points, where smaller, uncentered subsets are used. The greater the `bwidth()`, the greater the smoothing. The default is 0.8.

`logit` transforms the smoothed *yvar* into logits. Predicted values less than 0.0001 or greater than 0.9999 are set to $1/N$ and $1 - 1/N$, respectively, before taking logits.

`adjust` adjusts the mean of the smoothed *yvar* to equal the mean of *yvar* by multiplying by an appropriate factor. This option is useful when smoothing binary (0/1) data.

`nograph` suppresses displaying the graph.

`generate(`*newvar*`)` creates *newvar* containing the smoothed values of *yvar*.

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Smoothed line

`lineopts(`*cline_options*`)` affects the rendition of the lowess-smoothed line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall, By

twoway_options are any of the options documented in [G-3] ***twoway_options***. These include options for titling the graph (see [G-3] ***title_options***), options for saving the graph to disk (see [G-3] ***saving_option***), and the `by()` option (see [G-3] ***by_option***).

Remarks

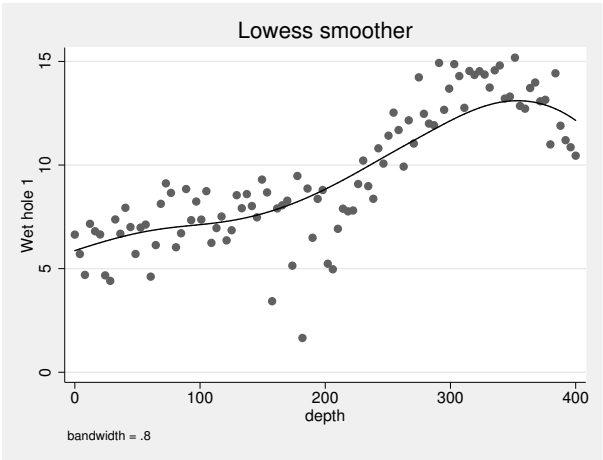
By default, `lowess` provides locally weighted scatterplot smoothing. The basic idea is to create a new variable (*newvar*) that, for each *yvar* y_i, contains the corresponding smoothed value. The smoothed values are obtained by running a regression of *yvar* on *xvar* by using only the data (x_i, y_i) and a few of the data near this point. In `lowess`, the regression is weighted so that the central point (x_i, y_i) gets the highest weight and points that are farther away (based on the distance $|x_j - x_i|$) receive less weight. The estimated regression line is then used to predict the smoothed value $\widehat{y}_i$ for y_i only. The procedure is repeated to obtain the remaining smoothed values, which means that a separate weighted regression is performed for every point in the data.

Lowess is a desirable smoother because of its locality—it tends to follow the data. Polynomial smoothing methods, for instance, are global in that what happens on the extreme left of a scatterplot can affect the fitted values on the extreme right.

Example 1

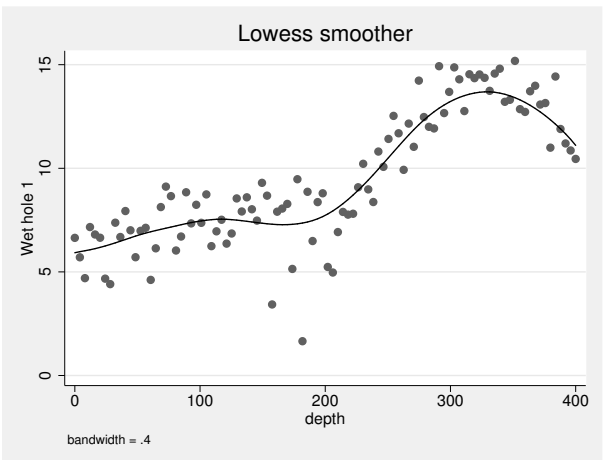
The amount of smoothing is affected by `bwidth(#)`. You are warned to experiment with different values. For instance,

```
. use http://www.stata-press.com/data/r12/lowess1
(example data for lowess)
. lowess h1 depth
```



Now compare that with

```
. lowess h1 depth, bwidth(.4)
```

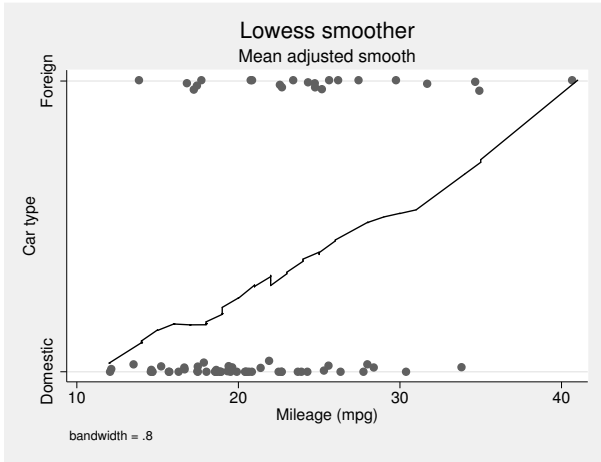


In the first case, the default bandwidth of 0.8 is used, meaning that 80% of the data are used in smoothing each point. In the second case, we explicitly specified a bandwidth of 0.4. Smaller bandwidths follow the original data more closely.

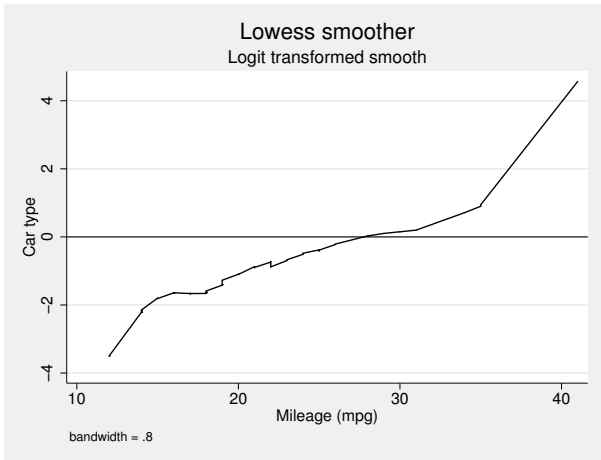
Example 2

Two `lowess` options are especially useful with binary (0/1) data: `adjust` and `logit`. `adjust` adjusts the resulting curve (by multiplication) so that the mean of the smoothed values is equal to the mean of the unsmoothed values. `logit` specifies that the smoothed curve be in terms of the log of the odds ratio:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. lowess foreign mpg, ylabel(0 "Domestic" 1 "Foreign") jitter(5) adjust
```




```
. lowess foreign mpg, logit yline(0)
```



With binary data, if you do not use the `logit` option, it is a good idea to specify `graph`'s `jitter()` option; see [G-2] **graph twoway scatter**. Because the underlying data (whether the car was manufactured outside the United States here) take on only two values, raw data points are more likely to be on top of each other, thus making it impossible to tell how many points there are. `graph`'s `jitter()` option adds some noise to the data to shift the points around. This noise affects only the location of points on the graph, not the lowess curve.

When you specify the `logit` option, the display of the raw data is suppressed.

◁

❑ Technical note

`lowess` can be used for more than just lowess smoothing. Lowess can be usefully thought of as a combination of two smoothing concepts: the use of predicted values from regression (rather than means) for imputing a smoothed value and the use of the tricube weighting function (rather than a constant weighting function). `lowess` allows you to combine these concepts freely. You can use line smoothing without weighting (specify `noweight`), mean smoothing with tricube weighting (specify `mean`), or mean smoothing without weighting (specify `mean` and `noweight`).

❑

Methods and formulas

`lowess` is implemented as an ado-file.

Let y_i and x_i be the two variables, and assume that the data are ordered so that $x_i \leq x_{i+1}$ for $i = 1, \ldots, N-1$. For each y_i, a smoothed value y_i^s is calculated.

The subset used in calculating y_i^s is indices $i_- = \max(1, i-k)$ through $i_+ = \min(i+k, N)$, where $k = \lfloor (N \times \texttt{bwidth} - 0.5)/2 \rfloor$. The weights for each of the observations between $j = i_-, \ldots, i_+$ are either 1 (`noweight`) or the tricube (default),

$$w_j = \left\{ 1 - \left(\frac{|x_j - x_i|}{\Delta} \right)^3 \right\}^3$$

where $\Delta = 1.0001 \max(x_{i_+} - x_i, x_i - x_{i_-})$. The smoothed value y_i^s is then the (weighted) mean or the (weighted) regression prediction at x_i.

William Swain Cleveland (1943–) studied mathematics and statistics at Princeton and Yale. He worked for several years at Bell Labs in New Jersey and now teaches statistics and computer science at Purdue. He has made key contributions in many areas of statistics, including graphics and data visualization, time series, environmental applications, and analysis of Internet traffic data.

Acknowledgment

`lowess` is a modified version of a command originally written by Patrick Royston of the MRC Clinical Trials Unit, London.

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Also see

[D] **ipolate** — Linearly interpolate (extrapolate) values

[R] **smooth** — Robust nonlinear smoother

[R] **lpoly** — Kernel-weighted local polynomial smoothing

Title

lpoly — Kernel-weighted local polynomial smoothing

Syntax

`lpoly` *yvar xvar* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Main	
`kernel(`*kernel*`)`	specify kernel function; default is `kernel(epanechnikov)`
`bwidth(`*#* | *varname*`)`	specify kernel bandwidth
`degree(`*#*`)`	specify degree of the polynomial smooth; default is `degree(0)`
`generate(`[*newvar*$_x$] *newvar*$_s$`)`	store smoothing grid in *newvar*$_x$ and smoothed points in *newvar*$_s$
`n(`*#*`)`	obtain the smooth at *#* points; default is min(N, 50)
`at(`*varname*`)`	obtain the smooth at the values specified by *varname*
`nograph`	suppress graph
`noscatter`	suppress scatterplot only
SE/CI	
`ci`	plot confidence bands
`level(`*#*`)`	set confidence level; default is `level(95)`
`se(`*newvar*`)`	store standard errors in *newvar*
`pwidth(`*#*`)`	specify pilot bandwidth for standard error calculation
`var(`*#* | *varname*`)`	specify estimates of residual variance
Scatterplot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Smoothed line	
`lineopts(`*cline_options*`)`	affect rendition of the smoothed line
CI plot	
`ciopts(`*cline_options*`)`	affect rendition of the confidence bands
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

kernel	Description
epanechnikov	Epanechnikov kernel function; the default
epan2	alternative Epanechnikov kernel function
biweight	biweight kernel function
cosine	cosine trace kernel function
gaussian	Gaussian kernel function
parzen	Parzen kernel function
rectangle	rectangle kernel function
triangle	triangle kernel function

fweights and aweights are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Nonparametric analysis > Local polynomial smoothing

Description

lpoly performs a kernel-weighted local polynomial regression of *yvar* on *xvar* and displays a graph of the smoothed values with (optional) confidence bands.

Options

Main

kernel(*kernel*) specifies the kernel function for use in calculating the weighted local polynomial estimate. The default is kernel(epanechnikov).

bwidth(*#* | *varname*) specifies the half-width of the kernel—the width of the smoothing window around each point. If bwidth() is not specified, a rule-of-thumb (ROT) bandwidth estimator is calculated and used. A local variable bandwidth may be specified in *varname*, in conjunction with an explicit smoothing grid using the at() option.

degree(*#*) specifies the degree of the polynomial to be used in the smoothing. The default is degree(0), meaning local-mean smoothing.

generate([*newvar*$_x$] *newvar*$_s$) stores the smoothing grid in *newvar*$_x$ and the smoothed values in *newvar*$_s$. If at() is not specified, then both *newvar*$_x$ and *newvar*$_s$ must be specified. Otherwise, only *newvar*$_s$ is to be specified.

n(*#*) specifies the number of points at which the smooth is to be calculated. The default is $\min(N, 50)$, where N is the number of observations.

at(*varname*) specifies a variable that contains the values at which the smooth should be calculated. By default, the smoothing is done on an equally spaced grid, but you can use at() to instead perform the smoothing at the observed x's, for example. This option also allows you to more easily obtain smooths for different variables or different subsamples of a variable and then overlay the estimates for comparison.

nograph suppresses drawing the graph of the estimated smooth. This option is often used with the generate() option.

noscatter suppresses superimposing a scatterplot of the observed data over the smooth. This option is useful when the number of resulting points would be so large as to clutter the graph.

SE/CI

`ci` plots confidence bands, using the confidence level specified in `level()`.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`se(`*newvar*`)` stores the estimates of the standard errors in *newvar*. This option requires specifying `generate()` or `at()`.

`pwidth(#)` specifies the pilot bandwidth to be used for standard-error computations. The default is chosen to be 1.5 times the value of the ROT bandwidth selector. If you specify `pwidth()` without specifying `se()` or `ci`, then the `ci` option is assumed.

`var(#` | *varname*`)` specifies an estimate of a constant residual variance or a variable containing estimates of the residual variances at each grid point required for standard-error computation. By default, the residual variance at each smoothing point is estimated by the normalized weighted residual sum of squares obtained from locally fitting a polynomial of order $p + 2$, where p is the degree specified in `degree()`. `var(`*varname*`)` is allowed only if `at()` is specified. If you specify `var()` without specifying `se()` or `ci`, then the `ci` option is assumed.

Scatterplot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Smoothed line

`lineopts(`*cline_options*`)` affects the rendition of the smoothed line; see [G-3] ***cline_options***.

CI plot

`ciopts(`*cline_options*`)` affects the rendition of the confidence bands; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Remarks are presented under the following headings:

Introduction
Local polynomial smoothing
Choice of a bandwidth
Confidence bands

Introduction

The last 25 years or so has seen a significant outgrowth in the literature on scatterplot smoothing, otherwise known as univariate nonparametric regression. Of most appeal is the idea of making no assumptions about the functional form for the expected value of a response given a regressor, but instead allowing the data to "speak for themselves". Various methods and estimators fall into the category of nonparametric regression, including local mean smoothing as described independently by Nadaraya (1964) and Watson (1964), the Gasser and Müller (1979) estimator, locally weighted scatterplot smoothing (LOWESS) as described by Cleveland (1979), wavelets (for example, Donoho [1995]), and splines (Eubank 1999), to name a few. Much of the vast literature focuses on automating the amount of smoothing to be performed and dealing with the bias/variance tradeoff inherent to this type of estimation. For example, for Nadaraya–Watson the amount of smoothing is controlled by choosing a *bandwidth*.

Smoothing via local polynomials is by no means a new idea but instead one that has been rediscovered in recent years in articles such as Fan (1992). A natural extension of the local mean smoothing of Nadaraya–Watson, local polynomial regression involves fitting the response to a polynomial form of the regressor via locally weighted least squares. Higher-order polynomials have better bias properties than the zero-degree local polynomials of the Nadaraya–Watson estimator; in general, higher-order polynomials do not require bias adjustment at the boundary of the regression space. For a definitive reference on local polynomial smoothing, see Fan and Gijbels (1996).

Local polynomial smoothing

Consider a set of scatterplot data $\{(x_1, y_1), \ldots, (x_n, y_n)\}$ from the model

$$y_i = m(x_i) + \sigma(x_i)\epsilon_i \tag{1}$$

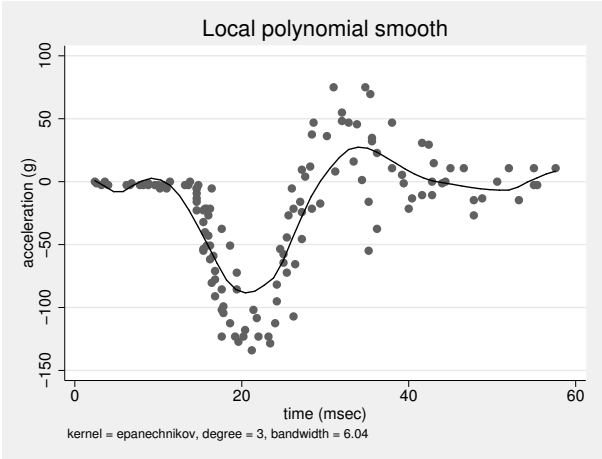
for some unknown mean and variance functions $m(\cdot)$ and $\sigma^2(\cdot)$, and symmetric errors ϵ_i with $E(\epsilon_i) = 0$ and $\mathrm{Var}(\epsilon_i) = 1$. The goal is to estimate $m(x_0) = E[Y|X = x_0]$, making no assumption about the functional form of $m(\cdot)$.

`lpoly` estimates $m(x_0)$ as the constant term (intercept) of a regression, weighted by the kernel function specified in `kernel()`, of *yvar* on the polynomial terms $(xvar - x_0), (xvar - x_0)^2, \ldots, (xvar - x_0)^p$ for each smoothing point x_0. The degree of the polynomial, p, is specified in `degree()`, the amount of smoothing is controlled by the bandwidth specified in `bwidth()`, and the chosen kernel function is specified in `kernel()`.

▷ Example 1

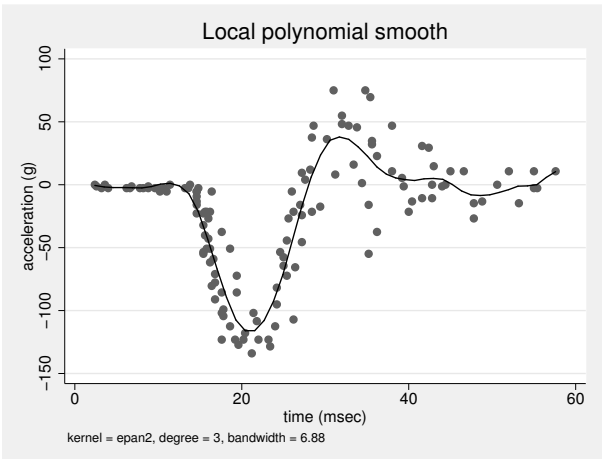
Consider the motorcycle data as examined (among other places) in Fan and Gijbels (1996). The data consist of 133 observations and measure the acceleration (`accel` measured in grams [g]) of a dummy's head during impact over time (`time` measured in milliseconds). For these data, we use `lpoly` to fit a local cubic polynomial with the default bandwidth (obtained using the ROT method) and the default Epanechnikov kernel.

```
. use http://www.stata-press.com/data/r12/motorcycle
(Motorcycle data from Fan & Gijbels (1996))
. lpoly accel time, degree(3)
```



The default bandwidth and kernel settings do not provide a satisfactory fit in this example. To improve the fit, we can either supply a different bandwidth by using the `bwidth()` option or specify a different kernel by using the `kernel()` option. For example, using the alternative Epanechnikov kernel, `kernel(epan2)`, below provides a better fit for these data.

```
. lpoly accel time, degree(3) kernel(epan2)
```



◁

❑ Technical note

`lpoly` allows specifying in `degree()` both odd and even orders of the polynomial to be used for the smoothing. However, the odd-order, $2k+1$, polynomial approximations are preferable. They have

an extra parameter compared with the even-order, $2k$, approximations, which leads to a significant bias reduction and there is no increase of variability associated with adding this extra parameter. Using an odd order when estimating the regression function is therefore usually sufficient. For a more thorough discussion, see Fan and Gijbels (1996).

❑

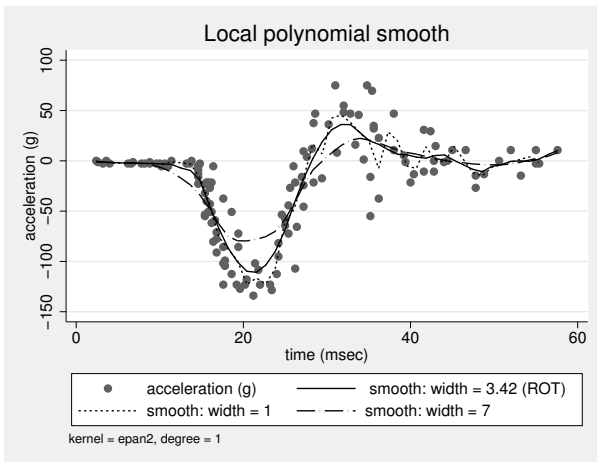
Choice of a bandwidth

The choice of a bandwidth is crucial for many smoothing techniques, including local polynomial smoothing. In general, using a large bandwidth gives smooths with a large bias, whereas a small bandwidth may result in highly variable smoothed values. Various techniques exist for optimal bandwidth selection. By default, `lpoly` uses the ROT method to estimate the bandwidth used for the smoothing; see *Methods and formulas* for details.

▷ Example 2

Using the `motorcycle` data, we demonstrate how a local linear polynomial fit changes using different bandwidths.

```
. lpoly accel time, degree(1) kernel(epan2) bwidth(1) generate(at smooth1)
> nograph
. lpoly accel time, degree(1) kernel(epan2) bwidth(7) at(at) generate(smooth2)
> nograph
. label variable smooth1 "smooth: width = 1"
. label variable smooth2 "smooth: width = 7"
. lpoly accel time, degree(1) kernel(epan2) at(at) addplot(line smooth* at)
> legend(label(2 "smooth: width = 3.42 (ROT)")) note("kernel = epan2, degree = 1")
```

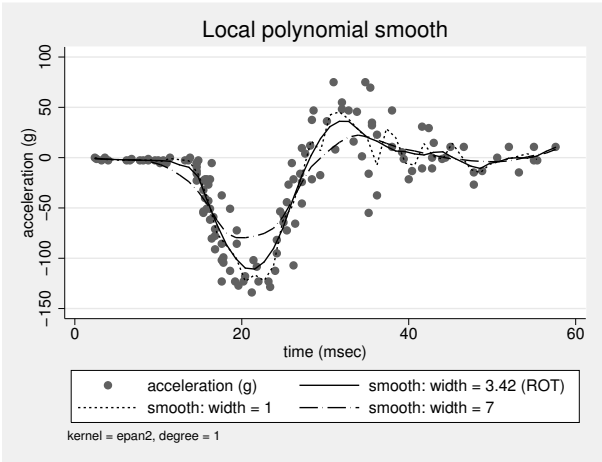


From this graph, we can see that the local linear polynomial fit with larger bandwidth (`width = 7`) corresponds to a smoother line but fails to fit the curvature of the scatterplot data. The smooth obtained using the width equal to one seems to fit most data points, but the corresponding line has several spikes indicating larger variability. The smooth obtained using the ROT bandwidth estimator seems to have a good tradeoff between the fit and variability in this example.

In the above, we also demonstrated how the `generate()` and `addplot()` options may be used to produce overlaid plots obtained from `lpoly` with different options. The `nograph` option saves time when you need to save only results with `generate()`.

However, to avoid generating variables manually, one can use `twoway lpoly` instead; see [G-2] **graph twoway lpoly** for more details.

```
. twoway scatter accel time ||
>         lpoly accel time, degree(1) kernel(epan2) lpattern(solid) ||
>         lpoly accel time, degree(1) kernel(epan2) bwidth(1)       ||
>         lpoly accel time, degree(1) kernel(epan2) bwidth(7)       ||
>     , legend(label(2 "smooth: width = 3.42 (ROT)") label(3 "smooth: width = 1")
>              label(4 "smooth: width = 7"))
>       title("Local polynomial smooth") note("kernel = epan2, degree = 1")
>       xtitle("time (msec)") ytitle("acceleration (g)")
```



The ROT estimate is commonly used as an initial guess for the amount of smoothing; this approach may be sufficient when the choice of a bandwidth is less important. In other cases, you can pick your own bandwidth.

When the shape of the regression function has a combination of peaked and flat regions, a variable bandwidth may be preferable over the constant bandwidth to allow for different degrees of smoothness in different regions. The `bwidth()` option allows you to specify the values of the local variable bandwidths as those stored in a variable in your data.

Similar issues with bias and variability arise when choosing a pilot bandwidth (the `pwidth()` option) used to compute standard errors of the local polynomial smoother. The default value is chosen to be $1.5 \times$ ROT. For a review of methods for pilot bandwidth selection, see Fan and Gijbels (1996).

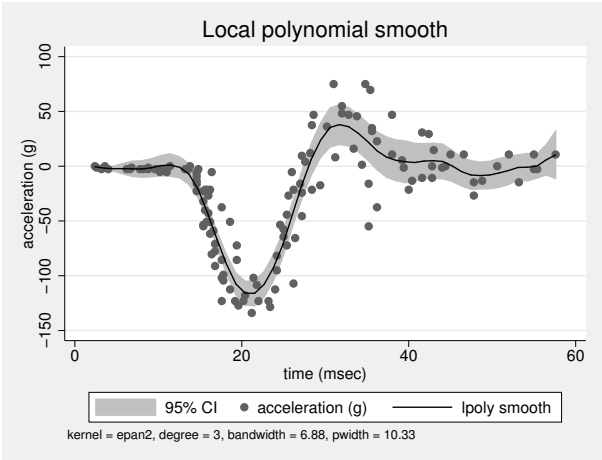
Confidence bands

The established asymptotic normality of the local polynomial estimators under certain conditions allows the construction of approximate confidence bands. `lpoly` offers the `ci` option to plot these bands.

▷ Example 3

Let us plot the confidence bands for the local polynomial fit from example 1.

```
. lpoly accel time, degree(3) kernel(epan2) ci
```



You can obtain graphs with overlaid confidence bands by using `twoway lpolyci`; see [G-2] **graph twoway lpolyci** for examples.

◁

Constructing the confidence intervals involves computing standard errors obtained by taking a square root of the estimate of the conditional variance of the local polynomial estimator at each grid point x_0. Estimating the conditional variance requires fitting a polynomial of a higher order locally by using a different bandwidth, the pilot bandwidth. The value of the pilot bandwidth may be supplied by using `pwidth()`. By default, the value of $1.5 \times$ ROT is used. Also, estimates of the residual variance $\sigma^2(x_0)$ at each grid point, x_0, are required to obtain the estimates of the conditional variances. These estimates may be supplied by using the `var()` option. By default, they are computed using the normalized weighted residual sum of squares from a local polynomial fit of a higher order. See *Methods and formulas* for details. The standard errors may be saved by using `se()`.

Saved results

`lpoly` saves the following in `r()`:

Scalars

`r(degree)`	smoothing polynomial degree	`r(bwidth)`	bandwidth of the smooth
`r(ngrid)`	number of successful regressions	`r(pwidth)`	pilot bandwidth
`r(N)`	sample size		

Macros

`r(kernel)`	name of kernel

Methods and formulas

`lpoly` is implemented as an ado-file.

Consider model (1), written in matrix notation,

$$\mathbf{y} = m(\mathbf{x}) + \epsilon$$

where $\mathbf{y}$ and $\mathbf{x}$ are the $n \times 1$ vectors of scatterplot values, ϵ is the $n \times 1$ vector of errors with zero mean and covariance matrix $\mathbf{\Sigma} = \text{diag}\{\sigma(x_i)\}\mathbf{I}_n$, and $m()$ and $\sigma()$ are some unknown functions. Define $m(x_0) = E[Y|X = x_0]$ and $\sigma^2(x_0) = \text{Var}[Y|X = x_0]$ to be the conditional mean and conditional variance of random variable Y (residual variance), respectively, for some realization x_0 of random variable X.

The method of local polynomial smoothing is based on the approximation of $m(x)$ locally by a pth order polynomial in $(x - x_0)$ for some x in the neighborhood of x_0. For the scatterplot data $\{(x_1, y_1), \ldots, (x_n, y_n)\}$, the pth-order local polynomial smooth $\widehat{m}(x_0)$ is equal to $\widehat{\beta}_0$, an estimate of the intercept of the weighted linear regression,

$$\widehat{\beta} = (\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}\mathbf{X}^T\mathbf{W}\mathbf{y} \tag{2}$$

where $\widehat{\beta} = (\widehat{\beta}_0, \widehat{\beta}_1, \ldots, \widehat{\beta}_p)^T$ is the vector of estimated regression coefficients (with $\{\widehat{\beta}_j = (j!)^{-1}\widehat{m}^{(j)}(x)|_{x=x_0},\ j = 0, \ldots, p\}$ also representing estimated coefficients from a corresponding Taylor expansion); $\mathbf{X} = \{(x_i - x_0)^j\}_{i,j=1,0}^{n,p}$ is a design matrix; and $\mathbf{W} = \text{diag}\{K_h(x_i - x_0)\}_{n\times n}$ is a weighting matrix with weights $K_h(\cdot)$ defined as $K_h(x) = h^{-1}K(x/h)$, with $K(\cdot)$ being a kernel function and h defining a bandwidth. The kernels are defined in *Methods and formulas* of [R] **kdensity**.

The default bandwidth is obtained using the ROT method of bandwidth selection. The ROT bandwidth is the plugin estimator of the asymptotically optimal constant bandwidth. This is the bandwidth that minimizes the conditional weighted mean integrated squared error. The ROT plugin bandwidth selector for the smoothing bandwidth h is defined as follows; assuming constant residual variance $\sigma^2(x_0) = \sigma^2$ and odd degree p:

$$\widehat{h} = C_{0,p}(K)\left[\frac{\widehat{\sigma}^2 \int w_0(x)dx}{n\int\{\widehat{m}^{(p+1)}(x)\}^2 w_0(x)f(x)dx}\right]^{1/(2p+3)} \tag{3}$$

where $C_{0,p}(K)$ is a constant, as defined in Fan and Gijbels (1996), that depends on the kernel function $K(\cdot)$, and the degree of a polynomial p and w_0 is chosen to be an indicator function on the interval $[\min_{\mathbf{x}} + 0.05 \times \text{range}_{\mathbf{x}}, \max_{\mathbf{x}} - 0.05 \times \text{range}_{\mathbf{x}}]$ with $\min_{\mathbf{x}}$, $\max_{\mathbf{x}}$, and $\text{range}_{\mathbf{x}}$ being, respectively, the minimum, maximum, and the range of $\mathbf{x}$. To obtain the estimates of a constant residual variance, $\widehat{\sigma}^2$, and $(p+1)$th order derivative of $m(x)$, denoted as $\widehat{m}^{(p+1)}(x)$, a polynomial in $\mathbf{x}$ of order $(p+3)$ is fit globally to $\mathbf{y}$. $\widehat{\sigma}^2$ is estimated as a standardized residual sum of squares from this fit.

The expression for the asymptotically optimal constant bandwidth used in constructing the ROT bandwidth estimator is derived for the odd-order polynomial approximations. For even-order polynomial fits the expression would depend not only on $m^{(p+1)}(x)$ but also on $m^{(p+2)}(x)$ and the design density and its derivative, $f(x)$ and $f'(x)$. Therefore, the ROT bandwidth selector would require estimation of these additional quantities. Instead, for an even-degree p of the local polynomial, `lpoly` uses the value of the ROT estimator (3) computed using degree $p + 1$. As such, for even degrees this is not a plugin estimator of the asymptotically optimal constant bandwidth.

The estimates of the conditional variance of local polynomial estimators are obtained using

$$\widehat{\mathrm{Var}}\{\widehat{m}(x_0)|X=x_0\} = \widehat{\sigma}^2_m(x_0) = (\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}(\mathbf{X}^T\mathbf{W}^2\mathbf{X})(\mathbf{X}^T\mathbf{W}\mathbf{X})^{-1}\widehat{\sigma}^2(x_0) \qquad (4)$$

where $\widehat{\sigma}^2(x_0)$ is estimated by the normalized weighted residual sum of squares from the $(p+2)$th order polynomial fit using pilot bandwidth $h^\star$.

When the bias is negligible the normal-approximation method yields a $(1-\alpha)\times 100\%$ confidence interval for $m(x_0)$,

$$\left\{\widehat{m}(x_0) - z_{(1-\alpha/2)}\widehat{\sigma}_m(x_0),\ \widehat{m}(x_0) + z_{(1-\alpha/2)}\widehat{\sigma}_m(x_0)\right\}$$

where $z_{(1-\alpha/2)}$ is the $(1-\alpha/2)$th quantile of the standard Gaussian distribution, and $\widehat{m}(x_0)$ and $\widehat{\sigma}_m(x_0)$ are as defined in (2) and (4), respectively.

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Also see

[R] **kdensity** — Univariate kernel density estimation

[R] **lowess** — Lowess smoothing

[R] **smooth** — Robust nonlinear smoother

[G-2] **graph twoway lpoly** — Local polynomial smooth plots

[G-2] **graph twoway lpolyci** — Local polynomial smooth plots with CIs

Title

lrtest — Likelihood-ratio test after estimation

Syntax

`lrtest` *modelspec*$_1$ [*modelspec*$_2$] [`,` *options*]

where *modelspec* is

name | `.` | `(`*namelist*`)`

where *name* is the name under which estimation results were saved using `estimates store` (see [R] **estimates store**), and "`.`" refers to the last estimation results, whether or not these were already stored.

options	Description
`stats`	display statistical information about the two models
`dir`	display descriptive information about the two models
`df(#)`	override the automatic degrees-of-freedom calculation; seldom used
`force`	force testing even when apparently invalid

Menu

Statistics > Postestimation > Tests > Likelihood-ratio test

Description

`lrtest` performs a likelihood-ratio test of the null hypothesis that the parameter vector of a statistical model satisfies some smooth constraint. To conduct the test, both the unrestricted and the restricted models must be fit using the maximum likelihood method (or some equivalent method), and the results of at least one must be stored using `estimates store`; see [R] **estimates store**.

modelspec$_1$ and *modelspec*$_2$ specify the restricted and unrestricted model in any order. *modelspec*$_1$ and *modelspec*$_2$ cannot have names in common; for example, `lrtest (A B C) (C D E)` is not allowed because both model specifications include `C`. If *modelspec*$_2$ is not specified, the last estimation result is used; this is equivalent to specifying *modelspec*$_2$ as a period (`.`).

`lrtest` supports composite models specified by a parenthesized list of model names. In a composite model, we assume that the log likelihood and dimension (number of free parameters) of the full model are obtained as the sum of the log-likelihood values and dimensions of the constituting models.

`lrtest` provides an important alternative to `test` (see [R] **test**) for models fit via maximum likelihood or equivalent methods.

Options

`stats` displays statistical information about the unrestricted and restricted models, including the information indices of Akaike and Schwarz.

`dir` displays descriptive information about the unrestricted and restricted models; see `estimates dir` in [R] **estimates store**.

`df(#)` is seldom specified; it overrides the automatic degrees-of-freedom calculation.

`force` forces the likelihood-ratio test calculations to take place in situations where `lrtest` would normally refuse to do so and issue an error. Such situations arise when one or more assumptions of the test are violated, for example, if the models were fit with `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweights`; when the dependent variables in the two models differ; when the null log likelihoods differ; when the samples differ; or when the estimation commands differ. If you use the `force` option, there is no guarantee as to the validity or interpretability of the resulting test.

Remarks

The standard way to use `lrtest` is to do the following:

1. Fit either the restricted model or the unrestricted model by using one of Stata's estimation commands and then store the results using `estimates store` *name*.
2. Fit the alternative model (the unrestricted or restricted model) and then type '`lrtest` *name* `.`'. `lrtest` determines for itself which of the two models is the restricted model by comparing the degrees of freedom.

Often you may want to store the alternative model with `estimates store` $name_2$, for instance, if you plan additional tests against models yet to be fit. The likelihood-ratio test is then obtained as `lrtest` *name* $name_2$.

Remarks are presented under the following headings:

Nested models
Composite models

Nested models

`lrtest` may be used with any estimation command that reports a log likelihood, including `heckman`, `logit`, `poisson`, `stcox`, and `streg`. You must check that one of the model specifications implies a statistical model that is *nested within* the model implied by the other specification. Usually, this means that both models are fit with the same estimation command (for example, both are fit by `logit`, with the same dependent variables) and that the set of covariates of one model is a subset of the covariates of the other model. Second, `lrtest` is valid only for models that are fit by maximum likelihood or by some equivalent method, so it does not apply to models that were fit with probability weights or clusters. Specifying the `vce(robust)` option similarly would indicate that you are worried about the valid specification of the model, so you would not use `lrtest`. Third, `lrtest` assumes that under the null hypothesis, the test statistic is (approximately) distributed as chi-squared. This assumption is not true for likelihood-ratio tests of "boundary conditions", such as tests for the presence of overdispersion or random effects (Gutierrez, Carter, and Drukker 2001).

▷ Example 1

We have data on infants born with low birthweights along with the characteristics of the mother (Hosmer and Lemeshow 2000; see also [R] **logistic**). We fit the following model:

```
. use http://www.stata-press.com/data/r12/lbw
(Hosmer & Lemeshow data)
. logistic low age lwt i.race smoke ptl ht ui
Logistic regression                               Number of obs   =        189
                                                  LR chi2(8)      =      33.22
                                                  Prob > chi2     =     0.0001
Log likelihood =   -100.724                       Pseudo R2       =     0.1416

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .9732636   .0354759    -0.74   0.457     .9061578    1.045339
         lwt |   .9849634   .0068217    -2.19   0.029     .9716834    .9984249
             |
        race |
          2  |   3.534767   1.860737     2.40   0.016     1.259736    9.918406
          3  |   2.368079   1.039949     1.96   0.050     1.001356    5.600207
             |
       smoke |   2.517698    1.00916     2.30   0.021     1.147676    5.523162
         ptl |   1.719161   .5952579     1.56   0.118     .8721455    3.388787
          ht |   6.249602   4.322408     2.65   0.008     1.611152    24.24199
          ui |     2.1351   .9808153     1.65   0.099     .8677528      5.2534
       _cons |   1.586014   1.910496     0.38   0.702     .1496092    16.8134
------------------------------------------------------------------------------
```

We now wish to test the constraint that the coefficients on `age`, `lwt`, `ptl`, and `ht` are all zero or, equivalently here, that the odds ratios are all 1. One solution is to type

```
. test age lwt ptl ht
 ( 1)  [low]age = 0
 ( 2)  [low]lwt = 0
 ( 3)  [low]ptl = 0
 ( 4)  [low]ht = 0
           chi2(  4) =   12.38
         Prob > chi2 =    0.0147
```

This test is based on the inverse of the information matrix and is therefore based on a quadratic approximation to the likelihood function; see [R] **test**. A more precise test would be to refit the model, applying the proposed constraints, and then calculate the likelihood-ratio test.

We first save the current model:

```
. estimates store full
```

We then fit the constrained model, which here is the model omitting `age`, `lwt`, `ptl`, and `ht`:

```
. logistic low i.race smoke ui
Logistic regression                               Number of obs   =        189
                                                  LR chi2(4)      =      18.80
                                                  Prob > chi2     =     0.0009
Log likelihood = -107.93404                       Pseudo R2       =     0.0801

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        race |
          2  |   3.052746   1.498087     2.27   0.023     1.166747    7.987382
          3  |   2.922593   1.189229     2.64   0.008     1.316457    6.488285
             |
       smoke |   2.945742   1.101838     2.89   0.004     1.415167    6.131715
          ui |   2.419131   1.047359     2.04   0.041     1.035459    5.651788
       _cons |   .1402209   .0512295    -5.38   0.000     .0685216    .2869447
------------------------------------------------------------------------------
```

That done, `lrtest` compares this model with the model we previously saved:

```
. lrtest full .
Likelihood-ratio test                                 LR chi2(4)  =     14.42
(Assumption: . nested in full)                        Prob > chi2 =    0.0061
```

Let's compare results. `test` reported that `age`, `lwt`, `ptl`, and `ht` were jointly significant at the 1.5% level; `lrtest` reports that they are significant at the 0.6% level. Given the quadratic approximation made by `test`, we could argue that `lrtest`'s results are more accurate.

`lrtest` explicates the assumption that, from a comparison of the degrees of freedom, it has assessed that the last fit model (`.`) is nested within the model stored as `full`. In other words, `full` is the unconstrained model and `.` is the constrained model.

The names in "`(Assumption: . nested in full)`" are actually links. Click on a name, and the results for that model are replayed.

◁

Aside: The `nestreg` command provides a simple syntax for performing likelihood-ratio tests for nested model specifications; see [R] **nestreg**. In the previous example, we fit a full `logistic` model, used `estimates store` to store the `full` model, fit a constrained `logistic` model, and used `lrtest` to report a likelihood-ratio test between two models. To do this with one call to `nestreg`, use the `lrtable` option.

❑ Technical note

`lrtest` determines the degrees of freedom of a model as the rank of the (co)variance matrix `e(V)`. There are two issues here. First, the *numerical* determination of the rank of a matrix is a subtle problem that can, for instance, be affected by the scaling of the variables in the model. The rank of a matrix depends on the number of (independent) linear combinations of coefficients that sum exactly to zero. In the world of numerical mathematics, it is hard to tell whether a very small number is really nonzero or is a real zero that happens to be slightly off because of roundoff error from the finite precision with which computers make floating-point calculations. Whether a small number is being classified as one or the other, typically on the basis of a threshold, affects the determined degrees of freedom. Although Stata generally makes sensible choices, it is bound to make mistakes occasionally. The moral of this story is to make sure that the calculated degrees of freedom are as you expect before interpreting the results.

❑

❑ Technical note

A second issue involves `regress` and related commands such as `anova`. Mainly for historical reasons, `regress` does not treat the residual variance, σ^2, the same way that it treats the regression coefficients. Type `estat vce` after `regress`, and you will see the regression coefficients, not $\widehat{\sigma}^2$. Most estimation commands for models with ancillary parameters (for example, `streg` and `heckman`) treat all parameters as equals. There is nothing technically wrong with `regress` here; we are usually focused on the regression coefficients, and their estimators are uncorrelated with $\widehat{\sigma}^2$. But, formally, σ^2 adds a degree of freedom to the model, which does not matter if you are comparing two regression models by a likelihood-ratio test. This test depends on the difference in the degrees of freedom, and hence being "off by 1" in each does not matter. But, if you are comparing a regression model with a larger model—for example, a heteroskedastic regression model fit by `arch`—the automatic determination of the degrees of freedom is incorrect, and you must specify the `df(#)` option.

❑

Example 2

Returning to the low-birthweight data in the example 1, we now wish to test that the coefficient on `2.race` is equal to that on `3.race`. The base model is still stored under the name `full`, so we need only fit the constrained model and perform the test. With z as the index of the logit model, the base model is

$$z = \beta_0 + \beta_1\texttt{age} + \beta_2\texttt{lwt} + \beta_3\texttt{2.race} + \beta_4\texttt{3.race} + \cdots$$

If $\beta_3 = \beta_4$, this can be written as

$$z = \beta_0 + \beta_1\texttt{age} + \beta_2\texttt{lwt} + \beta_3(\texttt{2.race} + \texttt{3.race}) + \cdots$$

We can fit the constrained model as follows:

```
. constraint 1 2.race = 3.race
. logistic low age lwt i.race smoke ptl ht ui, constraints(1)
Logistic regression                                     Number of obs   =        189
                                                        Wald chi2(7)    =      25.17
Log likelihood =  -100.9997                             Prob > chi2     =     0.0007
 ( 1)  [low]2.race - [low]3.race = 0
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.9716799	.0352638	-0.79	0.429	.9049649	1.043313
lwt	.9864971	.0064627	-2.08	0.038	.9739114	.9992453
race						
2	2.728186	1.080207	2.53	0.011	1.255586	5.927907
3	2.728186	1.080207	2.53	0.011	1.255586	5.927907
smoke	2.664498	1.052379	2.48	0.013	1.228633	5.778414
ptl	1.709129	.5924776	1.55	0.122	.8663666	3.371691
ht	6.116391	4.215585	2.63	0.009	1.58425	23.61385
ui	2.09936	.9699702	1.61	0.108	.8487997	5.192407
_cons	1.309371	1.527398	0.23	0.817	.1330839	12.8825

Comparing this model with our original model, we obtain

```
. lrtest full .
Likelihood-ratio test                                   LR chi2(1)  =      0.55
(Assumption: . nested in full)                          Prob > chi2 =    0.4577
```

By comparison, typing `test 2.race=3.race` after fitting our base model results in a significance level of 0.4572. Alternatively, we can first store the restricted model, here using the name `equal`. Next `lrtest` is invoked specifying the names of the restricted and unrestricted models (we do not care about the order). This time, we also add the option `stats` requesting a table of model statistics, including the model selection indices AIC and BIC.

```
. estimates store equal
. lrtest equal full, stats
Likelihood-ratio test                                   LR chi2(1)  =      0.55
(Assumption: equal nested in full)                      Prob > chi2 =    0.4577
```

Model	Obs	ll(null)	ll(model)	df	AIC	BIC
equal	189	.	-100.9997	8	217.9994	243.9334
full	189	-117.336	-100.724	9	219.448	248.6237

Note: N=Obs used in calculating BIC; see **[R] BIC note**

Composite models

`lrtest` supports composite models; that is, models that can be fit by fitting a series of simpler models or by fitting models on subsets of the data. Theoretically, a composite model is one in which the likelihood function, $L(\theta)$, of the parameter vector, θ, can be written as the product

$$L(\theta) = L_1(\theta_1) \times L_2(\theta_2) \times \cdots \times L_k(\theta_k)$$

of likelihood terms with $\theta = (\theta_1, \ldots, \theta_k)$ a partitioning of the full parameter vector. In such a case, the full-model likelihood $L(\theta)$ is maximized by maximizing the likelihood terms $L_j(\theta_j)$ in turn. Obviously, $\log L(\widehat{\theta}) = \sum_{j=1}^{k} \log L_j(\widehat{\theta}_j)$. The degrees of freedom for the composite model is obtained as the sum of the degrees of freedom of the constituting models.

▷ Example 3

As an example of the application of composite models, we consider a test of the hypothesis that the coefficients of a statistical model do not differ between different portions ("regimes") of the covariate space. Economists call a test for such a hypothesis a *Chow test*.

We continue the analysis of the data on children of low birthweight by using logistic regression modeling and study whether the regression coefficients are the same among the three races: white, black, and other. A likelihood-ratio Chow test can be obtained by fitting the logistic regression model for each of the races and then comparing the combined results with those of the model previously stored as `full`. Because the full model included dummies for the three races, this version of the Chow test allows the intercept of the logistic regression model to vary between the regimes (races).

```
. logistic low age lwt smoke ptl ht ui if 1.race, nolog
Logistic regression                             Number of obs   =         96
                                                LR chi2(6)      =      13.86
                                                Prob > chi2     =     0.0312
Log likelihood = -45.927061                     Pseudo R2       =     0.1311

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .9869674   .0527757    -0.25   0.806     .8887649    1.096021
         lwt |   .9900874   .0106101    -0.93   0.353     .9695089    1.011103
       smoke |   4.208697   2.680133     2.26   0.024      1.20808    14.66222
         ptl |   1.592145   .7474264     0.99   0.322     .6344379    3.995544
          ht |   2.900166   3.193537     0.97   0.334     .3350554     25.1032
          ui |   1.229523   .9474768     0.27   0.789     .2715165    5.567715
       _cons |   .4891008    .993785    -0.35   0.725     .0091175    26.23746
------------------------------------------------------------------------------

. estimates store white
```

```
. logistic low age lwt smoke ptl ht ui if 2.race, nolog
Logistic regression                               Number of obs   =         26
                                                  LR chi2(6)      =      10.12
                                                  Prob > chi2     =     0.1198
Log likelihood = -12.654157                       Pseudo R2       =     0.2856

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .8735313   .1377846    -0.86   0.391     .6412332    1.189983
         lwt |   .9747736    .016689    -1.49   0.136     .9426065    1.008038
       smoke |   16.50373   24.37044     1.90   0.058     .9133647    298.2083
         ptl |   4.866916    9.33151     0.83   0.409     .1135573    208.5895
          ht |   85.05605   214.6382     1.76   0.078     .6049308    11959.27
          ui |   67.61338   133.3313     2.14   0.033     1.417399    3225.322
       _cons |    48.7249   169.9216     1.11   0.265     .0523961    45310.94
------------------------------------------------------------------------------

. estimates store black
. logistic low age lwt smoke ptl ht ui if 3.race, nolog
Logistic regression                               Number of obs   =         67
                                                  LR chi2(6)      =      14.06
                                                  Prob > chi2     =     0.0289
Log likelihood = -37.228444                       Pseudo R2       =     0.1589

------------------------------------------------------------------------------
         low | Odds Ratio   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .9263905   .0665386    -1.06   0.287     .8047407     1.06643
         lwt |   .9724499    .015762    -1.72   0.085     .9420424    1.003839
       smoke |   .7979034   .6340585    -0.28   0.776     .1680885    3.787586
         ptl |   2.845675   1.777944     1.67   0.094     .8363053    9.682908
          ht |   7.767503   10.00537     1.59   0.112     .6220764    96.98826
          ui |   2.925006   2.046473     1.53   0.125     .7423107    11.52571
       _cons |   49.09444   113.9165     1.68   0.093     .5199275    4635.769
------------------------------------------------------------------------------

. estimates store other
```

We are now ready to perform the likelihood-ratio Chow test:

```
. lrtest (full) (white black other), stats
Likelihood-ratio test                             LR chi2(12) =       9.83
                                                  Prob > chi2 =     0.6310

Assumption: (full) nested in (white, black, other)

-----------------------------------------------------------------------------
       Model |  Obs       ll(null)   ll(model)     df          AIC         BIC
-------------+---------------------------------------------------------------
        full |  189       -117.336    -100.724      9      219.448    248.6237
       white |   96       -52.85752   -45.92706      7    105.8541    123.8046
       black |   26       -17.71291   -12.65416      7    39.30831    48.11499
       other |   67       -44.26039   -37.22844      7    88.45689    103.8897
-----------------------------------------------------------------------------
                Note:  N=Obs used in calculating BIC; see [R] BIC note
```

We cannot reject the hypothesis that the logistic regression model applies to each of the races at any reasonable significance level. By specifying the `stats` option, we can verify the degrees of freedom of the test: $12 = 7 + 7 + 7 - 9$. We can obtain the same test by fitting an expanded model with interactions between all covariates and `race`.

```
. logistic low race##c.(age lwt smoke ptl ht ui)
Logistic regression                               Number of obs   =        189
                                                  LR chi2(20)     =      43.05
                                                  Prob > chi2     =     0.0020
Log likelihood = -95.809661                       Pseudo R2       =     0.1835
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
race						
2	99.62137	402.0829	1.14	0.254	.0365434	271578.9
3	100.3769	309.586	1.49	0.135	.2378638	42358.38
age	.9869674	.0527757	-0.25	0.806	.8887649	1.096021
lwt	.9900874	.0106101	-0.93	0.353	.9695089	1.011103
smoke	4.208697	2.680133	2.26	0.024	1.20808	14.66222
ptl	1.592145	.7474264	0.99	0.322	.6344379	3.995544
ht	2.900166	3.193537	0.97	0.334	.3350554	25.1032
ui	1.229523	.9474768	0.27	0.789	.2715165	5.567715
race#c.age						
2	.885066	.1474079	-0.73	0.464	.638569	1.226714
3	.9386232	.0840486	-0.71	0.479	.7875366	1.118695
race#c.lwt						
2	.9845329	.0198857	-0.77	0.440	.9463191	1.02429
3	.9821859	.0190847	-0.93	0.355	.9454839	1.020313
race#c.smoke						
2	3.921338	6.305992	0.85	0.395	.167725	91.67917
3	.1895844	.1930601	-1.63	0.102	.025763	1.395113
race#c.ptl						
2	3.05683	6.034089	0.57	0.571	.0638301	146.3918
3	1.787322	1.396789	0.74	0.457	.3863582	8.268285
race#c.ht						
2	29.328	80.7482	1.23	0.220	.1329492	6469.623
3	2.678295	4.538712	0.58	0.561	.0966916	74.18702
race#c.ui						
2	54.99155	116.4274	1.89	0.058	.8672471	3486.977
3	2.378976	2.476124	0.83	0.405	.309335	18.29579
_cons	.4891008	.993785	-0.35	0.725	.0091175	26.23746

```
. lrtest full .
Likelihood-ratio test                             LR chi2(12) =       9.83
(Assumption: full nested in .)                    Prob > chi2 =     0.6310
```

Applying `lrtest` for the full model against the model with all interactions yields the same test statistic and p-value as for the full model against the composite model for the three regimes. Here the specification of the model with interactions was convenient, and `logistic` had no problem computing the estimates for the expanded model. In models with more complicated likelihoods, such as Heckman's selection model (see [R] **heckman**) or complicated survival-time models (see [ST] **streg**), fitting the models with all interactions may be numerically demanding and may be much more time consuming than fitting a series of models separately for each regime.

Given the model with all interactions, we could also test the hypothesis of no differences among the regions (races) by a Wald version of the Chow test by using the `testparm` command; see [R] **test**.

```
. testparm race#c.(age lwt smoke ptl ht ui)
 ( 1)  [low]2.race#c.age = 0
 ( 2)  [low]3.race#c.age = 0
 ( 3)  [low]2.race#c.lwt = 0
 ( 4)  [low]3.race#c.lwt = 0
 ( 5)  [low]2.race#c.smoke = 0
 ( 6)  [low]3.race#c.smoke = 0
 ( 7)  [low]2.race#c.ptl = 0
 ( 8)  [low]3.race#c.ptl = 0
 ( 9)  [low]2.race#c.ht = 0
 (10)  [low]3.race#c.ht = 0
 (11)  [low]2.race#c.ui = 0
 (12)  [low]3.race#c.ui = 0
           chi2( 12) =    8.24
         Prob > chi2 =    0.7663
```

We conclude that, here, the Wald version of the Chow test is similar to the likelihood-ratio version of the Chow test.

◁

Saved results

`lrtest` saves the following in `r()`:

Scalars

`r(p)`	level of significance
`r(df)`	degrees of freedom
`r(chi2)`	LR test statistic

Programmers wishing their estimation commands to be compatible with `lrtest` should note that `lrtest` requires that the following results be returned:

`e(cmd)`	name of estimation command
`e(ll)`	log likelihood
`e(V)`	variance–covariance matrix of the estimators
`e(N)`	number of observations

`lrtest` also verifies that `e(N)`, `e(ll_0)`, and `e(depvar)` are consistent between two noncomposite models.

Methods and formulas

`lrtest` is implemented as an ado-file.

Let L_0 and L_1 be the log-likelihood values associated with the full and constrained models, respectively. The test statistic of the likelihood-ratio test is $\text{LR} = -2(L_1 - L_0)$. If the constrained model is true, LR is approximately χ^2 distributed with $d_0 - d_1$ degrees of freedom, where d_0 and d_1 are the model degrees of freedom associated with the full and constrained models, respectively (Greene 2012, 526–527).

`lrtest` determines the degrees of freedom of a model as the rank of `e(V)`, computed as the number of nonzero diagonal elements of `invsym(e(V))`.

References

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Also see

[R] **test** — Test linear hypotheses after estimation

[R] **testnl** — Test nonlinear hypotheses after estimation

[R] **nestreg** — Nested model statistics

Title

lv — Letter-value displays

Syntax

```
lv [varlist] [if] [in] [, generate tail(#)]
```

by is allowed; see [D] **by**.

Menu

Statistics > Summaries, tables, and tests > Distributional plots and tests > Letter-value display

Description

lv shows a letter-value display (Tukey 1977, 44–49; Hoaglin 1983) for each variable in *varlist*. If no variables are specified, letter-value displays are shown for each numeric variable in the data.

Options

Main

generate adds four new variables to the data: _mid, containing the midsummaries; _spread, containing the spreads; _psigma, containing the pseudosigmas; and _z2, containing the squared values from a standard normal distribution corresponding to the particular letter value. If the variables _mid, _spread, _psigma, and _z2 already exist, their contents are replaced. At most, only the first 11 observations of each variable are used; the remaining observations contain missing. If *varlist* specifies more than one variable, the newly created variables contain results for the last variable specified. The generate option may not be used with the by prefix.

tail(#) indicates the inverse of the tail density through which letter values are to be displayed: 2 corresponds to the median (meaning half in each tail), 4 to the fourths (roughly the 25th and 75th percentiles), 8 to the eighths, and so on. # may be specified as 4, 8, 16, 32, 64, 128, 256, 512, or 1,024 and defaults to a value of # that has corresponding depth just greater than 1. The default is taken as 1,024 if the calculation results in a number larger than 1,024. Given the intelligent default, this option is rarely specified.

Remarks

Letter-value displays are a collection of observations drawn systematically from the data, focusing especially on the tails rather than the middle of the distribution. The displays are called letter-value displays because letters have been (almost arbitrarily) assigned to tail densities:

Letter	Tail area	Letter	Tail area
M	1/2	B	1/64
F	1/4	A	1/128
E	1/8	Z	1/256
D	1/16	Y	1/512
C	1/32	X	1/1024

Example 1

We have data on the mileage ratings of 74 automobiles. To obtain a letter-value display, we type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. lv mpg
 #      74              Mileage (mpg)
                  ------------------------------

 M      37.5 |                  20              |    spread  pseudosigma
 F        19 |          18     21.5          25 |         7    5.216359
 E        10 |          15     21.5          28 |        13    5.771728
 D       5.5 |          14    22.25        30.5 |      16.5    5.576303
 C         3 |          14     24.5          35 |        21    5.831039
 B         2 |          12     23.5          35 |        23    5.732448
 A       1.5 |          12       25          38 |        26    6.040635
         1   |          12     26.5          41 |        29     6.16562

                                                |  # below     # above
inner fence  |         7.5                 35.5 |         0           1
outer fence  |          -3                   46 |         0           0
```

The decimal points can be made to line up and thus the output made more readable by specifying a display format for the variable; see [U] **12.5 Formats: Controlling how data are displayed**.

```
. format mpg %9.2f
. lv mpg
 #      74              Mileage (mpg)
                  ------------------------------

 M      37.5 |                20.00              |    spread  pseudosigma
 F        19 |       18.00    21.50       25.00 |      7.00        5.22
 E        10 |       15.00    21.50       28.00 |     13.00        5.77
 D       5.5 |       14.00    22.25       30.50 |     16.50        5.58
 C         3 |       14.00    24.50       35.00 |     21.00        5.83
 B         2 |       12.00    23.50       35.00 |     23.00        5.73
 A       1.5 |       12.00    25.00       38.00 |     26.00        6.04
         1   |       12.00    26.50       41.00 |     29.00        6.17

                                                |  # below     # above
inner fence  |       7.50                 35.50 |         0           1
outer fence  |      -3.00                 46.00 |         0           0
```

At the top, the number of observations is indicated as 74. The first line shows the statistics associated with M, the letter value that puts half the density in each tail, or the median. The median has *depth* 37.5 (that is, in the ordered data, M is 37.5 observations in from the extremes) and has value 20. The next line shows the statistics associated with F or the fourths. The fourths have depth 19 (that is, in the ordered data, the lower fourth is observation 19, and the upper fourth is observation $74 - 19 + 1$), and the values of the lower and upper fourths are 18 and 25. The number in the middle is the point halfway between the fourths—called a midsummary. If the distribution were perfectly symmetric, the midsummary would equal the median. The spread is the difference between the lower and upper summaries ($25 - 18 = 7$). For fourths, half the data lie within a 7-mpg band. The pseudosigma is a calculation of the standard deviation using only the lower and upper summaries and assuming that the variable is normally distributed. If the data really were normally distributed, all the pseudosigmas would be roughly equal.

After the letter values, the line labeled with depth 1 reports the minimum and maximum values. Here the halfway point between the extremes is 26.5, which is greater than the median, indicating that 41 is more extreme than 12, at least relative to the median. And with each letter value, the

midsummaries are increasing—our data are skewed. The pseudosigmas are also increasing, indicating that the data are spreading out relative to a normal distribution, although, given the evident skewness, this elongation may be an artifact of the skewness.

At the end is an attempt to identify outliers, although the points so identified are merely outside some predetermined cutoff. Points outside the inner fence are called *outside values* or *mild outliers*. Points outside the outer fence are called *severe outliers*. The inner fence is defined as $(3/2)$IQR and the outer fence as 3IQR above and below the F summaries, where the interquartile range (IQR) is the spread of the fourths.

◁

❑ Technical note

The form of the letter-value display has varied slightly with different authors. `lv` displays appear as described by Hoaglin (1983) but as modified by Emerson and Stoto (1983), where they included the midpoint of each of the spreads. This format was later adopted by Hoaglin (1985). If the distribution is symmetric, the midpoints will all be roughly equal. On the other hand, if the midpoints vary systematically, the distribution is skewed.

The pseudosigmas are obtained from the lower and upper summaries for each letter value. For each letter value, they are the standard deviation a normal distribution would have if its spread for the given letter value were to equal the observed spread. If the pseudosigmas are all roughly equal, the data are said to have *neutral elongation*. If the pseudosigmas increase systematically, the data are said to be more elongated than a normal, that is, have thicker tails. If the pseudosigmas decrease systematically, the data are said to be less elongated than a normal, that is, have thinner tails.

Interpretation of the number of mild and severe outliers is more problematic. The following discussion is drawn from Hamilton (1991):

Obviously, the presence of any such outliers does not rule out that the data have been drawn from a normal distribution; in large datasets, there will most certainly be observations outside $(3/2)$IQR and 3IQR. Severe outliers, however, make up about two per million (0.0002%) of a normal population. In samples, they lie far enough out to have substantial effects on means, standard deviations, and other classical statistics. The 0.0002%, however, should be interpreted carefully; outliers appear more often in small samples than one might expect from population proportions because of sampling variation in estimated quartiles. Monte Carlo simulation by Hoaglin, Iglewicz, and Tukey (1986) obtained these results on the percentages and numbers of outliers in random samples from a normal population:

	percentage		number	
n	any outliers	severe	any outliers	severe
10	2.83	.362	.283	.0362
20	1.66	.074	.332	.0148
50	1.15	.011	.575	.0055
100	.95	.002	.95	.002
200	.79	.001	1.58	.002
300	.75	.001	2.25	.003
∞	.70	.0002	∞	∞

Thus the presence of any severe outliers in samples of less than 300 is sufficient to reject normality. Hoaglin, Iglewicz, and Tukey (1981) suggested the approximation $0.00698 + 0.4/n$ for the fraction of mild outliers in a sample of size n or, equivalently, $0.00698n + 0.4$ for the number of outliers.

❑

Example 2

The `generate` option adds the `_mid`, `_spread`, `_psigma`, and `_z2` variables to our data, making possible many of the diagnostic graphs suggested by Hoaglin (1985).

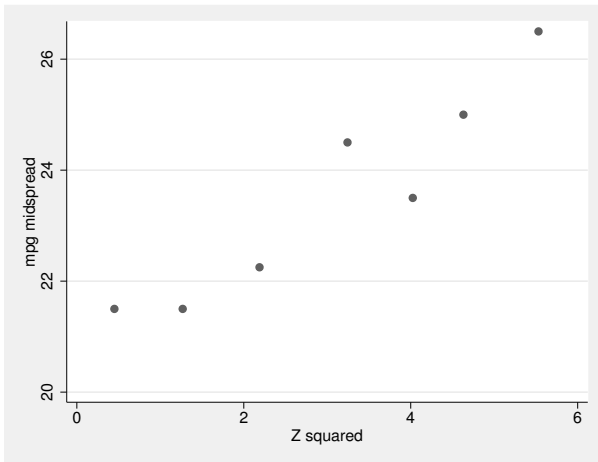
```
. lv mpg, generate
  (output omitted)
. list _mid _spread _psigma _z2 in 1/12
```

	_mid	_spread	_psigma	_z2
1.	20	.	.	.
2.	21.5	7	5.216359	.4501955
3.	21.5	13	5.771728	1.26828
4.	22.25	16.5	5.576303	2.188846
5.	24.5	21	5.831039	3.24255
6.	23.5	23	5.732448	4.024532
7.	25	26	6.040635	4.631499
8.	.	.	.	.
9.	.	.	.	.
10.	.	.	.	.
11.	26.5	29	6.16562	5.53073
12.	.	.	.	.

Observations 12 through the end are missing for these new variables. The definition of the observations is always the same. The first observation contains the M summary; the second, the F; the third, the E; and so on. Observation 11 always contains the summary for depth 1. Observations 8–10—corresponding to letter values Z, Y, and X—contain missing because these statistics were not calculated. We have only 74 observations, and their depth would be 1.

Hoaglin (1985) suggests graphing the midsummary against z^2. If the distribution is not skewed, the points in the resulting graph will be along a horizontal line:

```
. scatter _mid _z2
```



The graph clearly indicates the skewness of the distribution. We might also graph `_psigma` against `_z2` to examine elongation.

Saved results

lv saves the following in r():

Scalars

r(N)	number of observations	r(u_C)	upper 32nd
r(min)	minimum	r(l_B)	lower 64th
r(max)	maximum	r(u_B)	upper 64th
r(median)	median	r(l_A)	lower 128th
r(l_F)	lower 4th	r(u_A)	upper 128th
r(u_F)	upper 4th	r(l_Z)	lower 256th
r(l_E)	lower 8th	r(u_Z)	upper 256th
r(u_E)	upper 8th	r(l_Y)	lower 512th
r(l_D)	lower 16th	r(u_Y)	upper 512th
r(u_D)	upper 16th	r(l_X)	lower 1024th
r(l_C)	lower 32nd	r(u_X)	upper 1024th

The lower/upper 8ths, 16ths, ..., 1024ths will be defined only if there are sufficient data.

Methods and formulas

lv is implemented as an ado-file.

Let N be the number of (nonmissing) observations on x, and let $x_{(i)}$ refer to the ordered data when i is an integer. Define $x_{(i+0.5)} = (x_{(i)} + x_{(i+1)})/2$; the median is defined as $x_{\{(N+1)/2\}}$.

Define $x_{[d]}$ as the pair of numbers $x_{(d)}$ and $x_{(N+1-d)}$, where d is called the *depth*. Thus $x_{[1]}$ refers to the minimum and maximum of the data. Define $m = (N+1)/2$ as the depth of the median, $f = (\lfloor m \rfloor + 1)/2$ as the depth of the fourths, $e = (\lfloor f \rfloor + 1)/2$ as the depth of the eighths, and so on. Depths are reported on the far left of the letter-value display. The corresponding fourths of the data are $x_{[f]}$, the eighths are $x_{[e]}$, and so on. These values are reported inside the display. The middle value is defined as the corresponding midpoint of $x_{[\cdot]}$. The spreads are defined as the difference in $x_{[\cdot]}$.

The corresponding point z_i on a standard normal distribution is obtained as (Hoaglin 1985, 456–457)

$$z_i = \begin{cases} F^{-1}\{(d_i - 1/3)/(N + 1/3)\} & \text{if } d_i > 1 \\ F^{-1}\{0.695/(N + 0.390)\} & \text{otherwise} \end{cases}$$

where d_i is the depth of the letter value. The corresponding pseudosigma is obtained as the ratio of the spread to $-2z_i$ (Hoaglin 1985, 431).

Define $(F_l, F_u) = x_{[f]}$. The inner fence has cutoffs $F_l - \frac{3}{2}(F_u - F_l)$ and $F_u + \frac{3}{2}(F_u - F_l)$. The outer fence has cutoffs $F_l - 3(F_u - F_l)$ and $F_u + 3(F_u - F_l)$.

The inner-fence values reported by lv are almost equal to those used by graph, box to identify outside points. The only difference is that graph uses a slightly different definition of fourths, namely, the 25th and 75th percentiles as defined by summarize; see [R] **summarize**.

References

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Fox, J. 1990. Describing univariate distributions. In *Modern Methods of Data Analysis*, ed. J. Fox and J. S. Long, 58–125. Newbury Park, CA: Sage.

Hamilton, L. C. 1991. sed4: Resistant normality check and outlier identification. *Stata Technical Bulletin* 3: 15–18. Reprinted in *Stata Technical Bulletin Reprints*, vol. 1, pp. 86–90. College Station, TX: Stata Press.

Hoaglin, D. C. 1983. Letter values: A set of selected order statistics. In *Understanding Robust and Exploratory Data Analysis*, ed. D. C. Hoaglin, F. Mosteller, and J. W. Tukey, 33–57. New York: Wiley.

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Hoaglin, D. C., B. Iglewicz, and J. W. Tukey. 1981. Small-sample performance of a resistant rule for outlier detection. In *1980 Proceedings of the Statistical Computing Section*. Washington, DC: American Statistical Association.

——. 1986. Performance of some resistant rules for outlier labeling. *Journal of the American Statistical Association* 81: 991–999.

Tukey, J. W. 1977. *Exploratory Data Analysis*. Reading, MA: Addison–Wesley.

Also see

[R] **diagnostic plots** — Distributional diagnostic plots

[R] **stem** — Stem-and-leaf displays

[R] **summarize** — Summary statistics

Title

margins — Marginal means, predictive margins, and marginal effects

Syntax

`margins` [*marginlist*] [*if*] [*in*] [*weight*] [`,` *response_options* *options*]

where *marginlist* is a list of factor variables or interactions that appear in the current estimation results. The variables may be typed with or without the `i.` prefix, and you may use any factor-variable syntax:

```
. margins i.sex i.group i.sex#i.group
. margins sex group sex#i.group
. margins sex##group
```

response_options	Description
Main	
`predict(`*pred_opt*`)`	estimate margins for `predict,` *pred_opt*
`expression(`*pnl_exp*`)`	estimate margins for *pnl_exp*
`dydx(`*varlist*`)`	estimate marginal effect of variables in *varlist*
`eyex(`*varlist*`)`	estimate elasticities of variables in *varlist*
`dyex(`*varlist*`)`	estimate semielasticity—$d(y)/d(\ln x)$
`eydx(`*varlist*`)`	estimate semielasticity—$d(\ln y)/d(x)$
`continuous`	treat factor-level indicators as continuous

options	Description
Main	
`grand`	add the overall margin; default if no *marginlist*
At	
`at(`*atspec*`)`	estimate margins at specified values of covariates
`atmeans`	estimate margins at the means of covariates
`asbalanced`	treat all factor variables as balanced
if/in/over	
`over(`*varlist*`)`	estimate margins at unique values of *varlist*
`subpop(`*subspec*`)`	estimate margins for subpopulation
Within	
`within(`*varlist*`)`	estimate margins at unique values of the nesting factors in *varlist*
SE	
`vce(delta)`	estimate SEs using delta method; the default
`vce(unconditional)`	estimate SEs allowing for sampling of covariates
`nose`	do not estimate SEs

Advanced

noweights	ignore weights specified in estimation
noesample	do not restrict margins to the estimation sample
emptycells(*empspec*)	treatment of empty cells for balanced factors
estimtolerance(*tol*)	specify numerical tolerance used to determine estimable functions; default is estimtolerance(1e-5)
noestimcheck	suppress estimability checks
force	estimate margins despite potential problems
chainrule	use the chain rule when computing derivatives
nochainrule	do not use the chain rule

Reporting

level(#)	set confidence level; default is level(95)
mcompare(*method*)	adjust for multiple comparisons; default is mcompare(noadjust)
noatlegend	suppress legend of fixed covariate values
post	post margins and their VCE as estimation results
display_options	control column formats, row spacing, and line width

method	Description
noadjust	do not adjust for multiple comparisons; the default
bonferroni [adjustall]	Bonferroni's method; adjust across all terms
sidak [adjustall]	Šidák's method; adjust across all terms
scheffe	Scheffé's method

Time-series operators are allowed if they were used in the estimation.

See at() under *Options* for a description of *atspec*.

fweights, aweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Postestimation > Marginal means and predictive margins

Statistics > Postestimation > Marginal effects

Description

Margins are statistics calculated from predictions of a previously fit model at fixed values of some covariates and averaging or otherwise integrating over the remaining covariates.

The margins command estimates margins of responses for specified values of covariates and presents the results as a table.

Capabilities include estimated marginal means, least-squares means, average and conditional marginal and partial effects (which may be reported as derivatives or as elasticities), average and conditional adjusted predictions, and predictive margins.

Options

Warning: The option descriptions are brief and use jargon. Skip to Remarks if you are reading about `margins` *for the first time.*

Main

`predict(`*pred_opt*`)` and `expression(`*pnl_exp*`)` are mutually exclusive; they specify the response. If neither is specified, the response will be the default prediction that would be produced by `predict` after the underlying estimation command.

`predict(`*pred_opt*`)` specifies the option(s) to be specified with the `predict` command to produce the variable that will be used as the response. After estimation by `logistic`, you could specify `predict(xb)` to obtain linear predictions rather than the `predict` command's default, the probabilities.

`expression(`*pnl_exp*`)` specifies the response as an expression. See [R] **predictnl** for a full description of *pnl_exp*. After estimation by `logistic`, you might specify `expression(exp(predict(xb)))` to use relative odds rather than probabilities as the response. For examples, see *Example 12: Margins of a specified expression*.

`dydx(`*varlist*`)`, `eyex(`*varlist*`)`, `dyex(`*varlist*`)`, and `eydx(`*varlist*`)` request that `margins` report derivatives of the response with respect to *varlist* rather than on the response itself. `eyex()`, `dyex()`, and `eydx()` report derivatives as elasticities; see *Expressing derivatives as elasticities*.

`continuous` is relevant only when one of `dydx()` or `eydx()` is also specified. It specifies that the levels of factor variables be treated as continuous; see *Derivatives versus discrete differences*. This option is implied if there is a single-level factor variable specified in `dydx()` or `eydx()`.

`grand` specifies that the overall margin be reported. `grand` is assumed when *marginlist* is empty.

At

`at(`*atspec*`)` specifies values for covariates to be treated as fixed.

`at(age=20)` fixes covariate `age` to the value specified. `at()` may be used to fix continuous or factor covariates.

`at(age=20 sex=1)` simultaneously fixes covariates `age` and `sex` at the values specified.

`at(age=(20 30 40 50))` fixes age first at 20, then at 30, ... `margins` produces separate results for each specified value.

`at(age=(20(10)50))` does the same as `at(age=(20 30 40 50))`; that is, you may specify a numlist.

`at((mean) age (median) distance)` fixes the covariates at the summary statistics specified. `at((p25) _all)` fixes all covariates at their 25th percentile values. See *Syntax of at()* for the full list of summary-statistic modifiers.

`at((mean) _all (median) x x2=1.2 z=(1 2 3))` is read from left to right, with latter specifiers overriding former ones. Thus all covariates are fixed at their means except for `x` (fixed at its median), `x2` (fixed at 1.2), and `z` (fixed first at 1, then at 2, and finally at 3).

`at((means) _all (asobserved) x2)` is a convenient way to set all covariates except `x2` to the mean.

Multiple `at()` options can be specified, and each will produce a different set of margins.

See *Syntax of at()* for more information.

`atmeans` specifies that covariates be fixed at their means and is shorthand for `at((mean) _all)`. `atmeans` differs from `at((mean) _all)` in that `atmeans` will affect subsequent `at()` options. For instance,

```
. margins ..., atmeans  at((p25) x)  at((p75) x)
```

produces two sets of margins with both sets evaluated at the means of all covariates except `x`.

`asbalanced` is shorthand for `at((asbalanced) _factor)` and specifies that factor covariates be evaluated as though there were an equal number of observations in each level; see *Obtaining margins as though the data were balanced*. `asbalanced` differs from `at((asbalanced) _factor)` in that `asbalanced` will affect subsequent `at()` options in the same way as `atmeans` does.

if/in/over

`over(`*varlist*`)` specifies that separate sets of margins be estimated for the groups defined by *varlist*. The variables in *varlist* must contain nonnegative integer values. The variables need not be covariates in your model. When `over()` is combined with the `vce(unconditional)` option, each group is treated as a subpopulation; see [SVY] **subpopulation estimation**.

`subpop(`[*varname*] [*if*]`)` is intended for use with the `vce(unconditional)` option. It specifies that margins be estimated for the single subpopulation identified by the indicator variable or by the `if` expression or by both. Zero indicates that the observation be excluded; nonzero, that it be included; and missing value, that it be treated as outside of the population (and so ignored). See [SVY] **subpopulation estimation** for why `subpop()` is preferred to `if` expressions and `in` ranges when also using `vce(unconditional)`. If `subpop()` is used without `vce(unconditional)`, it is treated merely as an additional `if` qualifier.

Within

`within(`*varlist*`)` allows for nested designs. *varlist* contains the nesting variable(s) over which margins are to be estimated. See *Obtaining margins with nested designs*. As with `over(`*varlist*`)`, when `within(`*varlist*`)` is combined with `vce(unconditional)`, each level of the variables in *varlist* is treated as a subpopulation.

SE

`vce(delta)` and `vce(unconditional)` specify how the VCE and, correspondingly, standard errors are calculated.

`vce(delta)` is the default. The delta method is applied to the formula for the response and the VCE of the estimation command. This method assumes that values of the covariates used to calculate the response are given or, if all covariates are not fixed using `at()`, that the data are given.

`vce(unconditional)` specifies that the covariates that are not fixed be treated in a way that accounts for their having been sampled. The VCE is estimated using the linearization method. This method allows for heteroskedasticity or other violations of distributional assumptions and allows for correlation among the observations in the same manner as `vce(robust)` and `vce(cluster ...)`, which may have been specified with the estimation command. This method also accounts for complex survey designs if the data are `svyset`. See *Obtaining margins with survey data and representative samples*.

`nose` suppresses calculation of the VCE and standard errors. See *Requirements for model specification* for an example of the use of this option.

Advanced

noweights specifies that any weights specified on the previous estimation command be ignored by margins. By default, margins uses the weights specified on the estimator to average responses and to compute summary statistics. If weights are specified on the margins command, they override previously specified weights, making it unnecessary to specify noweights. The noweights option is not allowed after svy: estimation when the vce(unconditional) option is specified.

noesample specifies that margins not restrict its computations to the estimation sample used by the previous estimation command. See *Example 15: Margins evaluated out of sample*.

With the default delta-method VCE, noesample margins may be estimated on samples other than the estimation sample; such results are valid under the assumption that the data used are treated as being given.

You can specify noesample and vce(unconditional) together, but if you do, you should be sure that the data in memory correspond to the original e(sample). To show that you understand that, you must also specify the force option. Be aware that making the vce(unconditional) calculation on a sample different from the estimation sample would be equivalent to estimating the coefficients on one set of data and computing the scores used by the linearization on another set; see [P] **_robust**.

emptycells(strict) and emptycells(reweight) are relevant only when the asbalanced option is also specified. emptycells() specifies how empty cells are handled in interactions involving factor variables that are being treated as balanced; see *Obtaining margins as though the data were balanced*.

emptycells(strict) is the default; it specifies that margins involving empty cells be treated as not estimable.

emptycells(reweight) specifies that the effects of the observed cells be increased to accommodate any missing cells. This makes the margin estimable but changes its interpretation. emptycells(reweight) is implied when the within() option is specified.

estimtolerance(*tol*) specifies the numerical tolerance used to determine estimable functions. The default is estimtolerance(1e-5).

A linear combination of the model coefficients z is found to be not estimable if

$$\texttt{mreldif}(z,\ z \times H) > tol$$

where H is defined in *Methods and formulas*.

noestimcheck specifies that margins not check for estimability. By default, the requested margins are checked and those found not estimable are reported as such. Nonestimability is usually caused by empty cells. If noestimcheck is specified, estimates are computed in the usual way and reported even though the resulting estimates are manipulable, which is to say they can differ across equivalent models having different parameterizations. See *Estimability of margins*.

force instructs margins to proceed in some situations where it would otherwise issue an error message because of apparent violations of assumptions. Do not be casual about specifying force. You need to understand and fully evaluate the statistical issues. For an example of the use of force, see *Using margins after the estimates use command*.

chainrule and nochainrule specify whether margins uses the chain rule when numerically computing derivatives. You need not specify these options when using margins after any official Stata estimator; margins will choose the appropriate method automatically.

Specify nochainrule after estimation by a user-written command. We recommend using nochainrule, even though chainrule is usually safe and is always faster. nochainrule is safer because it makes no assumptions about how the parameters and covariates join to form the response.

nochainrule is implied when the expression() option is specified.

Reporting

level(#) specifies the confidence level, as a percentage, for confidence intervals. The default is level(95) or as set by set level; see [U] 20.7 Specifying the width of confidence intervals.

mcompare(*method*) specifies the method for computing p-values and confidence intervals that account for multiple comparisons within a factor-variable term.

Most methods adjust the comparisonwise error rate, α_c, to achieve a prespecified experimentwise error rate, α_e.

mcompare(noadjust) is the default; it specifies no adjustment.

$$\alpha_c = \alpha_e$$

mcompare(bonferroni) adjusts the comparisonwise error rate based on the upper limit of the Bonferroni inequality

$$\alpha_e \leq m\alpha_c$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = \alpha_e/m$$

mcompare(sidak) adjusts the comparisonwise error rate based on the upper limit of the probability inequality

$$\alpha_e \leq 1 - (1 - \alpha_c)^m$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = 1 - (1 - \alpha_e)^{1/m}$$

This adjustment is exact when the m comparisons are independent.

mcompare(scheffe) controls the experimentwise error rate using the F or χ^2 distribution with degrees of freedom equal to the rank of the term.

mcompare(*method* adjustall) specifies that the multiple-comparison adjustments count all comparisons across all terms rather than performing multiple comparisons term by term. This leads to more conservative adjustments when multiple variables or terms are specified in *marginslist*. This option is compatible only with the bonferroni and sidak methods.

noatlegend specifies that the legend showing the fixed values of covariates be suppressed.

post causes margins to behave like a Stata estimation (e-class) command. margins posts the vector of estimated margins along with the estimated variance–covariance matrix to e(), so you can treat the estimated margins just as you would results from any other estimation command. For example, you could use test to perform simultaneous tests of hypotheses on the margins, or you could use lincom to create linear combinations. See *Example 10: Testing margins—contrasts of margins*.

display_options: vsquish, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch.

vsquish specifies that the blank space separating factor-variable terms or time-series–operated variables from other variables in the model be suppressed.

cformat(%*fmt*) specifies how to format margins, standard errors, and confidence limits in the table of estimated margins.

`pformat(%`*fmt*`)` specifies how to format p-values in the table of estimated margins.

`sformat(%`*fmt*`)` specifies how to format test statistics in the table of estimated margins.

`nolstretch` specifies that the width of the table of estimated margins not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the table of estimated margins up to the width of the Results window. To change the default, use `set lstretch off`. `nolstretch` is not shown in the dialog box.

Remarks

Remarks are presented under the following headings:

Introduction
Obtaining margins of responses
- *Example 1: A simple case after regress*
- *Example 2: A simple case after logistic*
- *Example 3: Average response versus response at average*
- *Example 4: Multiple margins from one command*
- *Example 5: Margins with interaction terms*
- *Example 6: Margins with continuous variables*
- *Example 7: Margins of continuous variables*
- *Example 8: Margins of interactions*
- *Example 9: Decomposing margins*
- *Example 10: Testing margins—contrasts of margins*
- *Example 11: Margins of a specified prediction*
- *Example 12: Margins of a specified expression*
- *Example 13: Margins with multiple outcomes (responses)*
- *Example 14: Margins with multiple equations*
- *Example 15: Margins evaluated out of sample*

Obtaining margins of derivatives of responses (a.k.a. marginal effects)
- *Do not specify marginlist when you mean over()*
- *Use at() freely, especially with continuous variables*
- *Expressing derivatives as elasticities*
- *Derivatives versus discrete differences*
- *Example 16: Average marginal effect (partial effects)*
- *Example 17: Average marginal effect of all covariates*
- *Example 18: Evaluating marginal effects over the response surface*

Obtaining margins with survey data and representative samples
- *Example 19: Inferences for populations, margins of response*
- *Example 20: Inferences for populations, marginal effects*
- *Example 21: Inferences for populations with svyset data*

Standardizing margins
Obtaining margins as though the data were balanced
- *Balancing using asbalanced*
- *Balancing by standardization*
- *Balancing nonlinear responses*
- *Treating a subset of covariates as balanced*
- *Using fvset design*
- *Balancing in the presence of empty cells*

Obtaining margins with nested designs
- *Introduction*
- *Margins with nested designs as though the data were balanced*
- *Coding of nested designs*

Special topics
- *Requirements for model specification*
- *Estimability of margins*
- *Manipulability of tests*
- *Using margins after the estimates use command*
- *Syntax of at()*
- *Estimation commands that may be used with margins*

Glossary

Introduction

margins is a postestimation command, a command for use after you have fit a model using an estimation command such as regress or logistic, or using almost any other estimation command.

margins estimates and reports margins of responses and margins of derivatives of responses, also known as marginal effects. A margin is a statistic based on a fitted model in which some of or all the covariates are fixed. Marginal effects are changes in the response for change in a covariate, which can be reported as a derivative, elasticity, or semielasticity.

Obtaining margins of responses

What we call margins of responses are also known as predictive margins, adjusted predictions, and recycled predictions. When applied to balanced data, margins of responses are also called estimated marginal means and least-squares means.

A margin is a statistic based on a fitted model calculated over a dataset in which some of or all the covariates are fixed at values different from what they really are. For instance, after a linear regression fit on males and females, the marginal mean (margin of mean) for males is the predicted mean of the dependent variable, where every observation is treated as if it represents a male; thus those observations that in fact do represent males are included, as well as those observations that represent females. The marginal mean for female would be similarly obtained by treating all observations as if they represented females.

In making the calculation, sex is treated as male or female everywhere it appears in the model. The model might be

```
. regress y age bp i.sex sex#c.age sex#c.bp
```

and then, in making the marginal calculation of the mean for males and females, margins not only accounts for the direct effect of i.sex but also for the indirect effects of sex#c.age and sex#c.bp.

The response being margined can be any statistic produced by [R] **predict**, or any expression of those statistics.

Standard errors are obtained by the delta method, at least by default. The delta method assumes that the values at which the covariates are evaluated to obtain the marginal responses are fixed. When your sample represents a population, whether you are using svy or not (see [SVY] **svy**), you can specify margins' vce(unconditional) option and margins will produce standard errors that account for the sampling variability of the covariates. Some researchers reserve the term predictive margins to describe this.

The best way to understand margins is to see some examples. You can run the following examples yourself if you type

```
. use http://www.stata-press.com/data/r12/margex
(Artificial data for margins)
```

Example 1: A simple case after regress

```
. regress y i.sex i.group
  (output omitted)
. margins sex
Predictive margins                              Number of obs   =       3000
Model VCE    : OLS
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	60.56034	.5781782	104.74	0.000	59.42713	61.69355
1	78.88236	.5772578	136.65	0.000	77.75096	80.01377

The numbers reported in the "Margin" column are average values of `y`. Based on a linear regression of `y` on `sex` and `group`, 60.6 would be the average value of `y` if everyone in the data were treated as if they were male, and 78.9 would be the average value if everyone were treated as if they were female.

Example 2: A simple case after logistic

`margins` may be used after almost any estimation command.

```
. logistic outcome i.sex i.group
  (output omitted)
. margins sex
Predictive margins                              Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1286796	.0111424	11.55	0.000	.106841	.1505182
1	.1905087	.0089719	21.23	0.000	.1729241	.2080933

The numbers reported in the "Margin" column are average predicted probabilities. Based on a logistic regression of `outcome` on `sex` and `group`, 0.13 would be the average probability of `outcome` if everyone in the data were treated as if they were male, and 0.19 would be the average probability if everyone were treated as if they were female.

`margins` reports average values after `regress` and average probabilities after `logistic`. By default, `margins` makes tables of whatever it is that `predict` (see [R] **predict**) predicts by default. Alternatively, `margins` can make tables of anything that `predict` can produce if you use `margins`' `predict()` option; see *Example 11: Margins of a specified prediction*.

Example 3: Average response versus response at average

In example 2, margins reported average probabilities of outcome for sex = 0 and sex = 1. If we instead wanted the predicted probabilities evaluated at the mean of the covariates, we would specify margins' atmeans option. We previously typed

```
. logistic outcome i.sex i.group
  (output omitted)
. margins sex
  (output omitted)
```

and now we type

```
. margins sex, atmeans
Adjusted predictions                              Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
at           : 0.sex           =    .4993333 (mean)
               1.sex           =    .5006667 (mean)
               1.group         =    .3996667 (mean)
               2.group         =    .3726667 (mean)
               3.group         =    .2276667 (mean)
```

	Delta-method Margin	Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.0966105	.0089561	10.79	0.000	.0790569	.1141641
1	.1508362	.0118064	12.78	0.000	.127696	.1739764

The prediction at the average of the covariates is different from the average of the predictions. The first is the expected probability of a person with average characteristics, a person who, in another problem, might be 3/4 married and have 1.2 children. The second is the average of the probability among actual persons in the data.

When you specify atmeans or any other at option, margins reports the values used for the covariates in the legend above the table. margins lists the values for all the covariates, including values it may not use, in the results that follow. In this example, margins reported means for sex even though those means were not used. They were not used because we asked for the margins of sex, so sex was fixed first at 0 and then at 1.

If you wish to suppress this legend, specify the nolegend option.

Example 4: Multiple margins from one command

More than one margin can be reported by just one margins command. You can type

```
. margins sex group
```

and doing that is equivalent in terms of the output to typing

```
. margins sex
. margins group
```

When multiple margins are requested on the same command, each is estimated separately. There is, however, a difference when you also specify margins' post option. Then the variance–covariance matrix for all margins requested is posted, and that is what allows you to test equality of margins, etc. Testing equality of margins is covered in *Example 10: Testing margins—contrasts of margins*.

In any case, below we request margins for sex and for group.

```
. margins sex group
Predictive margins                              Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1286796	.0111424	11.55	0.000	.106841	.1505182
1	.1905087	.0089719	21.23	0.000	.1729241	.2080933
group						
1	.2826207	.0146234	19.33	0.000	.2539593	.311282
2	.1074814	.0094901	11.33	0.000	.0888812	.1260817
3	.0291065	.0073417	3.96	0.000	.0147169	.043496

Example 5: Margins with interaction terms

The estimation command on which margins bases its calculations may contain interaction terms, such as an interaction of sex and group:

```
. logistic outcome i.sex i.group sex#group
  (output omitted)
. margins sex group
Predictive margins                              Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1561738	.0132774	11.76	0.000	.1301506	.182197
1	.1983749	.0101546	19.54	0.000	.1784723	.2182776
group						
1	.3211001	.0176403	18.20	0.000	.2865257	.3556744
2	.1152127	.0099854	11.54	0.000	.0956417	.1347838
3	.0265018	.0109802	2.41	0.016	.0049811	.0480226

We fit the model by typing logistic outcome i.sex i.group sex#group, but the meaning would have been the same had we typed logistic outcome sex##group.

As mentioned in example 4, the results for sex and the results for group are calculated independently, and we would have obtained the same results had we typed margins sex followed by margins group.

The margin for male (sex = 0) is 0.16. The probability 0.16 is the average probability if everyone in the data were treated as if sex = 0, including sex = 0 in the main effect and sex = 0 in the interaction of sex with group.

Had we specified margins sex, atmeans, we would have obtained not average probabilities but the probabilities evaluated at the average. Rather than obtaining 0.16, we would have obtained 0.10

for sex = 0. The 0.10 is calculated by taking the fitted model, plugging in sex = 0 everywhere, and plugging in the average value of the group indicator variables everywhere they are used. That is, rather than treating the group indicators as being (1, 0, 0), (0, 1, 0), or (0, 0, 1) depending on observation, the group indicators are treated as being (0.40, 0.37, 0.23), which are the average values of group = 1, group = 2, and group = 3.

Example 6: Margins with continuous variables

To the above example, we will add the continuous covariate age to the model and then rerun margins sex group.

```
. logistic outcome i.sex i.group sex#group age
  (output omitted)
. margins sex group
Predictive margins                              Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1600644	.0125653	12.74	0.000	.1354368	.184692
1	.1966902	.0100043	19.66	0.000	.1770821	.2162983
group						
1	.2251302	.0123233	18.27	0.000	.200977	.2492834
2	.150603	.0116505	12.93	0.000	.1277685	.1734376
3	.0736157	.0337256	2.18	0.029	.0075147	.1397167

Compared with the results presented in example 5, results for sex change little, but results for groups 1 and 3 change markedly. The tables differ because now we are adjusting for the continuous covariate age, as well as for sex and group.

We will continue examining interactions in example 8. Because we have added a continuous variable, let's take a detour to explain how to obtain margins for continuous variables and to explain their interpretation.

Example 7: Margins of continuous variables

Continuing with our example of

```
. logistic outcome i.sex i.group sex#group age
```

let's examine the continuous covariate age.

You are not allowed to type margins age; doing that will produce an error:

```
. margins age
'age' not found in list of covariates
r(322);
```

The message "'age' not found in list of covariates" is margins' way of saying, "Yes, age might be in the model, but if it is, it is not included as a factor variable; it is in as a continuous variable." Sometimes, Stata is overly terse. margins might also say that because age is continuous there are an infinite number of values at which it could evaluate the margins. At what value(s) should age be fixed? margins requires more guidance with continuous covariates. We can provide that guidance by using the at() option and typing

```
. margins, at(age=40)
```

To understand why that yields the desired result, let us tell you that if you were to type

```
. margins
```

`margins` would report the overall margin—the margin that holds nothing constant. Because our model is logistic, the average value of the predicted probabilities would be reported. The `at()` option fixes one or more covariates to the value(s) specified and can be used with both factor and continuous variables. Thus, if you typed `margins, at(age=40)`, then `margins` would average over the data the responses for everybody, setting `age=40`. Here is what happens when you type that:

```
. margins, at(age=40)
Predictive margins                                Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
at           : age             =          40
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	.1133603	.0070731	16.03	0.000	.0994972	.1272234

Reported is the margin for `age` $= 40$, adjusted for the other covariates in our model.

If we wanted to obtain the margins for age 30, 35, 40, 45, and 50, we could type

```
. margins, at(age=(30 35 40 45 50))
```

or, equivalently,

```
. margins, at(age=(30(5)50))
```

Example 8: Margins of interactions

Our model is

```
. logistic outcome i.sex i.group sex#group age
```

We can obtain the margins of all possible combinations of the levels of `sex` and the levels of `group` by typing

```
. margins sex#group
Predictive margins                                Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex#group						
0 1	.2379605	.0237178	10.03	0.000	.1914745	.2844465
0 2	.0658294	.0105278	6.25	0.000	.0451953	.0864636
0 3	.0538001	.0136561	3.94	0.000	.0270347	.0805656
1 1	.2158632	.0112968	19.11	0.000	.1937218	.2380045
1 2	.2054406	.0183486	11.20	0.000	.1694781	.2414032
1 3	.085448	.0533914	1.60	0.110	-.0191973	.1900932

The first line in the table reports the marginal probability for sex = 0 and group = 1. That is, it reports the estimated probability if everyone in the data were treated as if they were sex = 0 and group = 1.

Also reported are all the other combinations of sex and group.

By the way, we could have typed margins sex#group even if our fitted model did not include sex#group. Estimation is one thing, and asking questions about the nature of the estimates is another. margins does, however, require that i.sex and i.group appear somewhere in the model, because fixing a value outside the model would just produce the grand margin, and you can separately ask for that if you want it by typing margins without arguments.

Example 9: Decomposing margins

We have the model

```
. logistic outcome i.sex i.group sex#group age
```

In example 6, we typed margins sex and obtained 0.160 for males and 0.197 for females. We are going to decompose each of those numbers. Let us explain:

1. The margin for males, 0.160, treats everyone as if they were male, and that amounts to simultaneously
    1a. treating males as males and
    1b. treating females as males.
2. The margin for females, 0.197, treats everyone as if they were female, and that amounts to simultaneously
    2a. treating males as females and
    2b. treating females as females.

The margins 1a and 1b are the decomposition of 1, and the margins 2a and 2b are the decomposition of 2.

We could obtain 1a and 2a by typing

```
. margins if sex==0, at(sex=(0 1))
```

because the qualifier if sex==0 would restrict margins to running on only the males. Similarly, we could obtain 1b and 2b by typing

```
. margins if sex==1, at(sex=(0 1))
```

We run these examples below:

```
. margins if sex==0, at(sex=(0 1))
Predictive margins                                Number of obs   =       1498
Model VCE    : OIM
Expression   : Pr(outcome), predict()
1._at        : sex             =           0
2._at        : sex             =           1
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_at						
1	.0794393	.0062147	12.78	0.000	.0672586	.0916199
2	.1335584	.0127351	10.49	0.000	.1085981	.1585187

```
. margins if sex==1, at(sex=(0 1))
Predictive margins                                Number of obs   =       1502
Model VCE    : OIM
Expression   : Pr(outcome), predict()
1._at        : sex             =           0
2._at        : sex             =           1
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_at						
1	.2404749	.0199709	12.04	0.000	.2013326	.2796171
2	.2596538	.0104756	24.79	0.000	.2391219	.2801857

Putting together the results from example 6 and the results above, we have

Margin treating everybody as themself	0.170
Margin treating everybody as male	0.160
Margin treating male as male	0.079
Margin treating female as male	0.240
Margin treating everybody as female	0.197
Margin treating male as female	0.134
Margin treating female as female	0.260

Example 10: Testing margins—contrasts of margins

Continuing with the previous example, it would be interesting to test the equality of 2b and 1b, to test whether the average probability of a positive outcome for females treated as females is equal to that for females treated as males. That test would be different from testing the overall significance of `sex` in our model. The test performed on our model would be a test of whether the probability of a positive outcome differs between males and females when they have equal values of the other covariates. The test of equality of margins is a test of whether the *average* probabilities differ given the different pattern of values of the other covariates that the two sexes have in our data.

We can also perform such tests by treating the results from `margins` as estimation results. There are three steps required to perform tests on margins. First, you must arrange it so that all the margins of interest are reported by just one `margins` command. Second, you must specify `margins`' `post` option. Third, you perform the test with the `test` command.

Such tests and comparisons can be readily performed by contrasting margins; see [R] **margins, contrast**. Also see *Contrasts of margins—effects (discrete marginal effects)* in [R] **marginsplot**.

In the previous example, we used two commands to obtain our results, namely,

```
. margins if sex==0, at(sex=(0 1))
. margins if sex==1, at(sex=(0 1))
```

We could, however, have obtained the same results by typing just one command:

```
. margins, over(sex) at(sex=(0 1))
```

Performing `margins, over(sex)` first restricts the sample to `sex==0` and then restricts it to `sex==1`, and that is equivalent to the two different `if` conditions that we specified before.

To test whether females treated as females is equal to females treated as males, we will need to type

```
. margins, over(sex) at(sex=(0 1)) post
. test _b[2._at#1.sex] = _b[1._at#1.sex]
```

We admit that the second command may seem to have come out of nowhere. When we specify `post` on the `margins` command, `margins` behaves as if it were an estimation command, which means that 1) it posts its estimates and full VCE to `e()`, 2) it gains the ability to replay results just as any estimation command can, and 3) it gains access to the standard postestimation commands. Item 3 explains why we could use `test`. We learned that we wanted to test `_b[2._at#1.sex]` and `_b[1._at#1.sex]` by replaying the estimation results, but this time with the standard estimation command `coeflegend` option. So what we typed was

```
. margins, over(sex) at(sex=(0 1)) post
. margins, coeflegend
. test _b[2._at#1.sex] = _b[1._at#1.sex]
```

We will let you try `margins, coeflegend` for yourself. The results of running the other two commands are

```
. margins, over(sex) at(sex=(0 1)) post
Predictive margins                                 Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : sex
1._at        : 0.sex
                    sex              =           0
               1.sex
                    sex              =           0
2._at        : 0.sex
                    sex              =           1
               1.sex
                    sex              =           1
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_at#sex						
1 0	.0794393	.0062147	12.78	0.000	.0672586	.0916199
1 1	.2404749	.0199709	12.04	0.000	.2013326	.2796171
2 0	.1335584	.0127351	10.49	0.000	.1085981	.1585187
2 1	.2596538	.0104756	24.79	0.000	.2391219	.2801857

```
. test _b[2._at#1.sex] = _b[1._at#1.sex]
 ( 1)  - 1bn._at#1.sex + 2._at#1.sex = 0
           chi2(  1) =    0.72
         Prob > chi2 =    0.3951
```

We can perform the same test in one command using contrasts of margins:

```
. logistic outcome i.sex i.group sex#group age
  (output omitted)
. margins, over(sex) at(sex=(0 1)) contrast(atcontrast(r._at) wald)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : sex
1._at        : 0.sex
                    sex             =           0
               1.sex
                    sex             =           0
2._at        : 0.sex
                    sex             =           1
               1.sex
                    sex             =           1
```

	df	chi2	P>chi2
_at@sex			
(2 vs 1) 0	1	14.59	0.0001
(2 vs 1) 1	1	0.72	0.3951
Joint	2	16.13	0.0003

	Delta-method			
	Contrast	Std. Err.	[95% Conf.	Interval]
_at@sex				
(2 vs 1) 0	.0541192	.0141706	.0263453	.081893
(2 vs 1) 1	.0191789	.0225516	-.0250215	.0633793

We refitted our logistic model because its estimation results were replaced when we posted our margins. The syntax to perform the contrast we want is admittedly not obvious. Contrasting (testing) across `at()` groups is more difficult than contrasting across the margins themselves or across `over()` groups, because we have no natural place for the contrast operators (`r.`, in our case). We also explicitly requested Wald tests of the contrasts, which are not provided by default. Nevertheless, the chi-squared statistic and its p-value for `(2 vs 1)` for `sex` $= 1$ matches the results of our `test` command. We also obtain the test of whether the response of males treated as males is equal to the response of males treated as females.

For a gentler introduction to contrasts of margins, see [R] **margins, contrast**.

Example 11: Margins of a specified prediction

We will fit the model

```
. use http://www.stata-press.com/data/r12/margex
. tobit ycn i.sex i.group sex#group age, ul(90)
```

and we will tell the following story about the variables: We run a peach orchard where we allow people to pick their own peaches. A person receives one empty basket in exchange for $20, along with the right to enter the orchard. There is no official limit on how many peaches a person can pick, but only 90 peaches will fit into a basket. The dependent variable in the above tobit model, `ycn`, is the number of peaches picked. We use tobit, a special case of censored-normal regression, because `ycn` is censored at 90.

After fitting this model, if we typed

```
. margins sex
```

we would obtain the margins for males and for females of the uncensored number of peaches picked. We would obtain that because `predict` after `tobit` produces the uncensored number by default. To obtain the censored prediction, we would have to specify `predict`'s `ystar(.,90)` option. If we want the margins based on that response, we type

```
. margins sex, predict(ystar(.,90))
```

The results of typing that are

```
. tobit ycn i.sex i.group sex#group age, ul(90)
  (output omitted)
. margins sex, predict(ystar(.,90))
Predictive margins                              Number of obs   =       3000
Model VCE    : OIM
Expression   : E(ycn*|ycn<90), predict(ystar(.,90))
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	62.21804	.5996928	103.75	0.000	61.04266	63.39342
1	78.34272	.455526	171.98	0.000	77.4499	79.23553

In our previous examples, `sex` = 1 has designated females, so evidently the females visiting our orchard are better at filling baskets than the men.

Example 12: Margins of a specified expression

Continuing with our peach orchard example and the previously fit model

```
. use http://www.stata-press.com/data/r12/margex
. tobit ycn i.sex i.group sex#group age, ul(90)
```

let's examine how well our baskets are working for us. What is the proportion of the number of peaches actually picked to the number that would have been picked were the baskets larger? As mentioned in example 11, `predict, ystar(.,90)` produces the expected number picked given the limit of basket size. `predict, xb` would predict the expected number without a limit. We want the ratio of those two predictions. That ratio will measure as a proportion how well the baskets work. Thus we could type

```
. margins sex, expression(predict(ystar(.,90))/predict(xb))
```

That would give us the proportion for everyone treated as male and everyone treated as female, but what we want to know is how well baskets work for true males and true females, so we will type

```
. margins, over(sex) expression(predict(ystar(.,90))/predict(xb))
```

```
. margins, over(sex) expression(predict(ystar(0,90))/predict(xb))
Predictive margins                                Number of obs   =       3000
Model VCE    : OIM
Expression   : predict(ystar(0,90))/predict(xb)
over         : sex
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.9811785	.0013037	752.60	0.000	.9786233	.9837337
1	.9419962	.0026175	359.88	0.000	.936866	.9471265

By the way, we could count the number of peaches saved by the limited basket size during the period of data collection by typing

```
. count
  3000
. margins, expression(3000*(predict(xb)-predict(ystar(.,90))))
  (output omitted)
```

The number of peaches saved turns outs to be 9,183.

Example 13: Margins with multiple outcomes (responses)

Estimation commands such as `mlogit` and `mprobit` (see [R] **mlogit** and [R] **mprobit**) calculate multiple responses, and those multiple responses are reflected in the options available with `predict` after estimation. Obtaining margins for such estimators is thus the same as obtaining margins of a specified prediction, which was demonstrated in example 11. The solution is to include the *predict_opt* that selects the desired response in `margins`' `predict(`*predict_opt*`)` option.

If we fit the multinomial logistic model

```
. mlogit group i.sex age
```

then to obtain the margins for the probability that `group` = 1, we would type

```
. margins sex, predict(outcome(1))
```

and to obtain the margins for the probability that `group` = 3, we would type

```
. margins sex, predict(outcome(3))
```

We learned about the `outcome(1)` and `outcome(3)` options by looking in [R] **mlogit postestimation**. For an example using `margins` with a multiple-outcome estimator, see example 4 in [R] **mlogit postestimation**.

Example 14: Margins with multiple equations

Estimation commands such as `mvreg`, `manova`, `sureg`, and `reg3` (see [R] **mvreg**, [MV] **manova**, [R] **sureg**, and [R] **reg3**) fit multiple equations. Obtaining margins for such estimators is the same as obtaining margins with multiple outcomes (see example 13), which in turn is the same as obtaining margins of a specified prediction (see example 11). You place the relevant option from the estimator's `predict` command into `margins`' `predict(`*predict_opt*`)` option.

If we fit the seemingly unrelated regression model

```
. sureg (y = i.sex age) (distance = i.sex i.group)
```

we can obtain the marginal means of y for males and females by typing

```
. margins sex, predict(equation(y))
```

and we can obtain the marginal means of distance by typing

```
. margins sex, predict(equation(distance))
```

We could obtain the difference between the margins of y and distance by typing

```
. margins sex, expression(predict(equation(y)) -
> predict(equation(distance)))
```

More examples can be found in [MV] **manova** and [MV] **manova postestimation**.

Example 15: Margins evaluated out of sample

You can fit your model on one dataset and use margins on another if you specify margins' noesample option. Remember that margins reports estimated average responses, and, unless you lock all the covariates at fixed values by using the at() option, the remaining variables are allowed to vary as they are observed to vary in the data. That is indeed the point of using margins. The fitted model provides the basis for adjusting for the remaining variables, and the data provide their values. The predictions produced by margins are of interest assuming the data used by margins are in some sense interesting or representative. In some cases, you might need to fit your model on one set of data and perform margins on another.

In example 11, we fit the model

```
. tobit ycn i.sex i.group sex#group age, ul(90)
```

and we told a story about our peach orchard in which we charged people $20 to collect a basket of peaches, where baskets could hold at most 90 peaches. Let us now tell you that we believe the data on which we estimated those margins were unrepresentative, or at least, we have a more representative sample stored in another .dta file. That dataset includes the demographics of our customers but does not include counts of peaches picked. It is a lot of work counting those peaches.

Thus we will fit our model just as we did previously using the detailed data, but we will bring the other, more representative dataset into memory before issuing the margins sex, predict(ystar(.,90)) command, and we will add noesample to it.

```
. use http://www.stata-press.com/data/r12/margex
(Artificial data for margins)
. tobit ycn i.sex i.group sex#group age, ul(90)
  (output omitted)
. use http://www.stata-press.com/data/r12/peach
. margins sex, predict(ystar(.,90)) noesample
Predictive margins                              Number of obs   =       2727
Model VCE    : OIM
Expression   : E(ycn*|ycn<90), predict(ystar(.,90))
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	56.79774	1.003727	56.59	0.000	54.83047	58.76501
1	75.02146	.643742	116.54	0.000	73.75975	76.28317

In example 12, we produced an estimate of the number of peaches saved by the limited-size baskets. We can update that estimate using the new demographic data by typing

```
. count
  2727
. margins, exp(2727*(predict(xb)-predict(ystar(.,90)))) noesample
  (output omitted)
```

By running the above, we find that the updated number of peaches saved is 6,408.

Obtaining margins of derivatives of responses (a.k.a. marginal effects)

Derivatives of responses are themselves responses, so everything said above in *Obtaining margins of responses* is equally true of derivatives of responses, and every example above could be repeated here substituting the derivative of the response for the response.

Derivatives are of interest because they are an informative way of summarizing fitted results. The change in a response for a change in the covariate is easy to understand and to explain. In simple models, one hardly needs `margins` to assist in obtaining such margins. Consider the simple linear regression

$$y = \beta_0 + \beta_1 \times \text{sex} + \beta_2 \times \text{age} + \epsilon$$

The derivatives of the responses are

$$dy/d(\text{sex}) = \beta_1$$
$$dy/d(\text{age}) = \beta_2$$

The derivatives are the fitted coefficients. How does y change between males and females? It changes by β_1. How does y change with age? It changes by β_2 per year.

If you make the model a little more complicated, however, the need for margins arises. Consider the model

$$y = \beta_0 + \beta_1 \times \text{sex} + \beta_2 \times \text{age} + \beta_3 \times \text{age}^2 + \epsilon$$

Now the derivative with respect to age is

$$dy/d(\text{age}) = \beta_2 + 2 \times \beta_3 \times \text{age}$$

The change in y for a change in age itself changes with age, and so to better understand the fitted results, you might want to make a table of the change in y for a change in age for age $= 30$, age $= 40$, and age $= 50$. `margins` can do that.

Consider an even more complicated model, such as

$$\begin{aligned} y = {} & \beta_0 + \beta_1 \times \text{sex} + \beta_2 \times \text{age} + \beta_3 \times \text{age}^2 + \beta_4 \times \text{bp} + \beta_5 \times \text{sex} \times \text{bp} + \beta_6 \times \text{tmt} \\ & + \beta_7 \times \text{tmt} \times \text{age} + \beta_8 \times \text{tmt} \times \text{age}^2 + \epsilon \end{aligned} \tag{1}$$

The derivatives are

$$dy/d(\text{sex}) = \beta_1 + \beta_5 \times \text{bp}$$

$$dy/d(\text{age}) = \beta_2 + 2 \times \beta_3 \times \text{age} + \beta_7 \times \text{tmt} + 2 \times \beta_8 \times \text{tmt} \times \text{age}$$
$$dy/d(\text{bp}) = \beta_4 + \beta_5 \times \text{sex}$$

$$dy/d(\text{tmt}) = \beta_6 + \beta_7 \times \text{age} + \beta_8 \times \text{age}^2$$

At this point, `margins` becomes indispensable.

Do not specify marginlist when you mean over()

`margins` has the same syntax when used with derivatives of responses as when used with responses. To obtain derivatives, one specifies the `dydx()` option. If we wanted to examine the response variable $dy/d(\text{tmt})$, we would specify `margins`' `dydx(tmt)` option. The rest of the `margins` command has the same syntax as ordinarily, although one tends to specify different syntactical elements. For instance, one usually does not specify a *marginlist*. If we typed

```
. margins sex, dydx(tmt)
```

we would obtain $dy/d(\text{tmt})$ calculated first as if everyone were male and then as if everyone were female. At the least, we would probably want to specify

```
. margins sex, dydx(tmt) grand
```

so as also to obtain $dy/d(\text{tmt})$, the overall margin, the margin with everyone having their own value of sex. Usually, however, all we want is the overall margin, and because `grand` is the default when the *marginlist* is not specified, we would just type

```
. margins, dydx(tmt)
```

Alternatively, if we were interested in the decomposition by sex, then rather than type `margins sex, dydx(tmt)`, we probably want to type

```
. margins, over(sex) dydx(tmt)
```

This command gives us the average effect of tmt for males and again for females rather than the average effect with everyone treated as male and then again with everyone treated as female.

Use at() freely, especially with continuous variables

Another option one tends to use more often with derivatives of responses than one does with responses is `at()`. Such use is often to better understand or to communicate how the response varies, or, in technical jargon, to explore the nature of the response surface.

For instance, the effect $dy/d(\text{tmt})$ in (1) is equal to $\beta_6 + \beta_7 \times \text{age} + \beta_8 \times \text{age}^2$, and so simply to understand how treatment varies with age, we may want to fix age at various values. We might type

```
. margins, dydx(tmt) over(sex) at(age=(30 40 50))
```

Expressing derivatives as elasticities

You specify the `dydx(`*varname*`)` option on the `margins` command to use $dy/d(\textit{varname})$ as the response variable. If you want that derivative expressed as an elasticity, you can specify `eyex(`*varname*`)`, `eydx(`*varname*`)`, or `dyex(`*varname*`)`. You substitute `e` for `d` where you want an elasticity. The formulas are

$$\begin{aligned}
\texttt{dydx()} &= dy/dx \\
\texttt{eyex()} &= dy/dx \times (x/y) \\
\texttt{eydx()} &= dy/dx \times (1/y) \\
\texttt{dyex()} &= dy/dx \times (x)
\end{aligned}$$

and the interpretations are

`dydx()`:		change in y for a		change in x
`eyex()`:	proportional	change in y for a	proportional	change in x
`eydx()`:	proportional	change in y for a		change in x
`dyex()`:		change in y for a	proportional	change in x

As `margins` always does with response functions, calculations are made at the observational level and are then averaged. Let's assume that in observation 5, $dy/dx = 0.5$, $y = 15$, and $x = 30$; then

$$\texttt{dydx()} = 0.5$$
$$\texttt{eyex()} = 1.0$$
$$\texttt{eydx()} = 0.03$$
$$\texttt{dyex()} = 15.0$$

Many social scientists would informally explain the meaning of `eyex()` $= 1$ as "y increases 100% when x increases 100%" or as "y doubles when x doubles", although neither statement is literally true. `eyex()`, `eydx()`, and `dyex()` are rates evaluated at a point, just as `dydx()` is a rate, and all such interpretations are valid only for small (infinitesimal) changes in x. It is true that `eyex()` $= 1$ means y increases with x at a rate such that, if the rate were constant, y would double if x doubled. This issue of casual interpretation is no different from casually interpreting `dydx()` as if it represents the response to a unit change. It is not necessarily true that `dydx()` $= 0.5$ means that "y increases by 0.5 if x increases by 1". It is true that "y increases with x at a rate such that, if the rate were constant, y would increase by 0.5 if x increased by 1".

`dydx()`, `eyex()`, `eydx()`, and `dyex()` may be used with continuous x variables. `dydx()` and `eydx()` may also be used with factor variables.

Derivatives versus discrete differences

In (1),

$$y = \beta_0 + \beta_1 \times \text{sex} + \beta_2 \times \text{age} + \beta_3 \times \text{age}^2 + \beta_4 \times \text{bp} + \beta_5 \times \text{sex} \times \text{bp} + \beta_6 \times \text{tmt} + \beta_7 \times \text{tmt} \times \text{age} + \beta_8 \times \text{tmt} \times \text{age}^2 + \epsilon$$

Let us call your attention to the derivatives of y with respect to age and sex:

$$dy/d(\text{age}) = \beta_2 + 2 \times \beta_3 \times \text{age} + \beta_7 \times \text{tmt} + 2 \times \beta_8 \times \text{tmt} \times \text{age} \tag{2}$$

$$dy/d(\text{sex}) = \beta_1 + \beta_5 \times \text{bp} \tag{3}$$

`age` is presumably a continuous variable and (2) is precisely how `margins` calculates its derivatives when you type `margins, dydx(age)`. `sex`, however, is presumably a factor variable, and `margins` does not necessarily make the calculation using (3) were you to type `margins, dydx(sex)`. We will explain, but let us first clarify what we mean by a continuous and a factor variable. Say that you fit (1) by typing

```
. regress y i.sex age c.age#c.age i.bp bp#sex
> i.tmt tmt#c.age tmt#c.age#c.age
```

It is important that sex entered the model as a factor variable. It would not do to type regress y sex ... because then sex would be a continuous variable, or at least it would be a continuous variable from Stata's point of view. The model estimates would be the same, but margins' understanding of those estimates would be a little different. With the model estimated using i.sex, margins understands that either sex is 0 or sex is 1. With the model estimated using sex, margins thinks sex is continuous and, for instance, sex = 1.5 is a possibility.

margins calculates dydx() differently for continuous and for factor variables. For continuous variables, margins calculates dy/dx. For factor variables, margins calculates the discrete first-difference from the base category. To obtain that for sex, write down the model and then subtract from it the model evaluated at the base category for sex, which is sex = 0. If you do that, you will get the same formula as we obtained for the derivative, namely,

$$\text{discrete difference}\{(\text{sex}=1)-(\text{sex}=0)\} = \beta_1 + \beta_5 \times \text{bp}$$

We obtain the same formula because our model is linear regression. Outside of linear regression, and outside of linear response functions generally, the discrete difference is not equal to the derivative. The discrete difference is not equal to the derivative for logistic regression, probit, etc. The discrete difference calculation is generally viewed as better for factor variables than the derivative calculation because the discrete difference is what would actually be observed.

If you want the derivative calculation for your factor variables, specify the continuous option on the margins command.

Example 16: Average marginal effect (partial effects)

Concerning the title of this example, the way we use the term marginal effect, the effects of factor variables are calculated using discrete first-differences. If you wanted the continuous calculation, you would specify margins' continuous option in what follows.

```
. use http://www.stata-press.com/data/r12/margex
(Artificial data for margins)
. logistic outcome treatment##group age c.age#c.age treatment#c.age
  (output omitted)
. margins, dydx(treatment)
Average marginal effects                        Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
dy/dx w.r.t. : 1.treatment
```

	dy/dx	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
1.treatment	.0385625	.0162848	2.37	0.018	.0066449	.0704801

```
Note: dy/dx for factor levels is the discrete change from the base level.
```

The average marginal effect of treatment on the probability of a positive outcome is 0.039.

Example 17: Average marginal effect of all covariates

We will continue with the model

```
. logistic outcome treatment##group age c.age#c.age treatment#c.age
```

if we wanted the average marginal effects for all covariates, we would type `margins, dydx(*)` or `margins, dydx(_all)`; they mean the same thing. This is probably the most common way `margins, dydx()` is used.

```
. margins, dydx(*)
Average marginal effects                        Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
dy/dx w.r.t. : 1.treatment 2.group 3.group age
```

	dy/dx	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
1.treatment	.0385625	.0162848	2.37	0.018	.0066449	.0704801
group						
2	-.0776906	.0181584	-4.28	0.000	-.1132805	-.0421007
3	-.1505652	.0400882	-3.76	0.000	-.2291366	-.0719937
age	.0095868	.0007796	12.30	0.000	.0080589	.0111148

```
Note: dy/dx for factor levels is the discrete change from the base level.
```

Example 18: Evaluating marginal effects over the response surface

Continuing with the model

```
. logistic outcome treatment##group age c.age#c.age treatment#c.age
```

What follows maps out the entire response surface of our fitted model. We report the marginal effect of treatment evaluated at `age` $= 20, 30, \ldots, 60$, by each level of group.

```
. margins group, dydx(treatment) at(age=(20(10)60))
Conditional marginal effects                      Number of obs   =       3000
Model VCE    : OIM

Expression   : Pr(outcome), predict()
dy/dx w.r.t. : 1.treatment

1._at        : age             =          20

2._at        : age             =          30

3._at        : age             =          40

4._at        : age             =          50

5._at        : age             =          60
```

	dy/dx	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
1.treatment						
_at#group						
1 1	-.0208409	.0152862	-1.36	0.173	-.0508013	.0091196
1 2	.009324	.0059896	1.56	0.120	-.0024155	.0210635
1 3	.0006558	.0048682	0.13	0.893	-.0088856	.0101972
2 1	-.0436964	.0279271	-1.56	0.118	-.0984325	.0110397
2 2	.0382959	.0120405	3.18	0.001	.014697	.0618949
2 3	.0064564	.0166581	0.39	0.698	-.0261929	.0391057
3 1	-.055676	.0363191	-1.53	0.125	-.1268601	.015508
3 2	.1152235	.0209858	5.49	0.000	.074092	.156355
3 3	.0284808	.0471293	0.60	0.546	-.0638908	.1208524
4 1	-.027101	.0395501	-0.69	0.493	-.1046177	.0504158
4 2	.2447682	.0362623	6.75	0.000	.1736954	.315841
4 3	.0824401	.1025028	0.80	0.421	-.1184616	.2833418
5 1	.0292732	.0587751	0.50	0.618	-.0859239	.1444703
5 2	.3757777	.0578106	6.50	0.000	.2624709	.4890844
5 3	.1688268	.1642191	1.03	0.304	-.1530368	.4906904

Note: dy/dx for factor levels is the discrete change from the base level.

Obtaining margins with survey data and representative samples

The standard errors and confidence intervals produced by `margins` are based by default on the delta method applied to the VCE of the current estimates. Delta-method standard errors treat the covariates at which the response is evaluated as given or fixed. Such standard errors are appropriate if you specify `at()` to fix the covariates, and they are appropriate when you are making inferences about groups exactly like your sample whether you specify `at()` or not.

On the other hand, if you have a representative sample of the population or if you have complex survey data and if you want to make inferences about the underlying population, you need to account for the variation in the covariates that would arise in repeated sampling. You do that using `vce(unconditional)`, which invokes a different standard-error calculation based on Korn and Graubard (1999). Syntactically, there are three cases. They all involve specifying the `vce(unconditional)` option on the `margins` command:

1. *You have a representative random sample, and you have not* `svyset` *your data.*
   When you fit the model, you need to specify the `vce(robust)` or `vce(cluster` *clustvar*`)` option. When you issue the `margins` command, you need to specify the `vce(unconditional)` option.

2. *You have a weighted sample, and you have not* `svyset` *your data.*
   You need to specify `[pw=weight]` when you fit the model and, of course, specify the `vce(unconditional)` option on the `margins` command. You do not need to specify the weights on the `margins` command because `margins` will obtain them from the estimation results.

3. *You have* `svyset` *your data, whether it be a simple random sample or something more complex including weights, strata, sampling units, or poststratification.*
   You need to use the `svy` prefix when you fit the model. You need to specify `vce(unconditional)` when you issue the `margins` command. You do not need to respecify the weights.

   Even though the data are `svyset`, and even though the estimation was `svy` estimation, `margins` does not default to `vce(unconditional)`. It does not default to `vce(unconditional)` because there are valid reasons to want the data-specific, `vce(delta)` standard-error estimates. Whether you specify `vce(unconditional)` or not, `margins` uses the weights, so you do not need to respecify them even if you are using `vce(unconditional)`.

`vce(unconditional)` is allowed only after estimation with `vce(robust)`, `vce(cluster ...)`, or the `svy` prefix. If the VCE of the current estimates was specified as clustered, so will be the VCE estimates of `margins`. If the estimates were from a survey estimation, the survey settings in the dataset will be used by `margins`.

When you use `vce(unconditional)`, never specify `if` *exp* or `in` *range* on the `margins` command; instead, specify the `subpop(if` *exp*`)` option. You do that for the usual reasons; see [SVY] **subpopulation estimation**. If you specify `over(`*varlist*`)` to examine subgroups, the subgroups will automatically be treated as subpopulations.

Example 19: Inferences for populations, margins of response

In example 6, we fit the model

```
. logistic outcome i.sex i.group sex#group age
```

and we obtained margins by sex and margins by group,

```
. margins sex group
```

If our data were randomly drawn from the population of interest and we wanted to account for this, we would have typed

```
. logistic outcome i.sex i.group sex#group age, vce(robust)
. margins sex group, vce(unconditional)
```

We do that below:

```
. logistic outcome i.sex i.group sex#group age, vce(robust)
  (output omitted)
. margins sex group, vce(unconditional)
Predictive margins                                Number of obs   =       3000
Expression   : Pr(outcome), predict()
```

	Unconditional Margin	Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1600644	.0131685	12.16	0.000	.1342546	.1858743
1	.1966902	.0104563	18.81	0.000	.1761963	.2171841
group						
1	.2251302	.0127069	17.72	0.000	.200225	.2500354
2	.150603	.0118399	12.72	0.000	.1273972	.1738088
3	.0736157	.0343188	2.15	0.032	.0063522	.1408793

The estimated margins are the same as they were in example 6, but the standard errors and confidence intervals differ, although not by much. Given that we have 3,000 observations in our randomly drawn sample, we should expect this.

Example 20: Inferences for populations, marginal effects

In example 17, we fit a logistic model and then obtained the average marginal effects for all covariates by typing

```
. logistic outcome treatment##group age c.age#c.age treatment#c.age
. margins, dydx(*)
```

To repeat that and also obtain standard errors for our population, we would type

```
. logistic outcome treatment##group age c.age#c.age treatment#c.age,
> vce(robust)
. margins, dydx(*) vce(unconditional)
```

The results are

```
. logistic outcome treatment##group age c.age#c.age treatment#c.age, vce(robust)
  (output omitted)
. margins, dydx(*) vce(unconditional)
Average marginal effects                          Number of obs   =       3000
Expression   : Pr(outcome), predict()
dy/dx w.r.t. : 1.treatment 2.group 3.group age
```

	Unconditional dy/dx	Std. Err.	z	P>|z|	[95% Conf.	Interval]
1.treatment	.0385625	.0163872	2.35	0.019	.0064442	.0706808
group						
2	-.0776906	.0179573	-4.33	0.000	-.1128863	-.0424949
3	-.1505652	.0411842	-3.66	0.000	-.2312848	-.0698456
age	.0095868	.0007814	12.27	0.000	.0080553	.0111183

```
Note: dy/dx for factor levels is the discrete change from the base level.
```

Example 21: Inferences for populations with svyset data

See example 3 in [SVY] **svy postestimation**.

Standardizing margins

A standardized margin is the margin calculated on data different from the data used to fit the model. Typically, the word standardized is reserved for situations in which the alternate population is a reference population, which may be real or artificial, and which is treated as fixed.

Say that you work for a hospital and have fit a model of mortality on the demographic characteristics of the hospital's patients. At this stage, were you to type

```
. margins
```

you would obtain the mortality rate for your hospital. You have another dataset, `hstandard.dta`, that contains demographic characteristics of patients across all hospitals along with the population of each hospital recorded in the `pop` variable. You could obtain the expected mortality rate at your hospital if your patients matched the characteristics of the standard population by typing

```
. use http://www.stata-press.com/data/r12/hstandard, clear
. margins [fw=pop], noesample
```

You specified `noesample` because the margin is being calculated on data other than the data used to estimate the model. You specified `[fw=pop]` because the reference dataset you are using included population counts, as many reference datasets do.

Obtaining margins as though the data were balanced

Here we discuss what are commonly called estimated marginal means or least-squares means. These are margins assuming that all levels of factor variables are equally likely or, equivalently, that the design is balanced. The seminal reference on these margins is Searle, Speed, and Milliken (1980).

In designed experiments, observations are often allocated in a balanced way so that the variances can be easily compared and decomposed. At the Acme Portable Widget Company, they are experimenting with a new machine. The machine has three temperature settings and two pressure settings; a combination of settings will be optimal on any particular day, determined by the weather. At start-up, one runs a quick test and chooses the optimal setting for the day. Across different days, each setting will be used about equally, says the manufacturer.

In experiments with the machine, 10 widgets were collected for stress testing at each of the settings over a six-week period. We wish to know the average stress-test value that can be expected from these machines over a long period.

Balancing using asbalanced

The data were intended to be balanced, but unfortunately, the stress test sometimes destroys samples before the stress can be measured. Thus even though the experiment was designed to be balanced, the data are not balanced. You specify the `asbalanced` option to estimate the margins as if the data were balanced. We will type

```
. use http://www.stata-press.com/data/r12/acmemanuf
. regress y pressure##temp
. margins, asbalanced
```

So that you can compare the asbalanced results with the observed results, we will also include margins without the asbalanced option in what follows:

```
. use http://www.stata-press.com/data/r12/acmemanuf
. regress y pressure##temp
  (output omitted)
. margins
Predictive margins                              Number of obs   =         49
Model VCE    : OLS
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	109.9214	1.422629	77.27	0.000	107.1331	112.7097

```
. margins, asbalanced
Adjusted predictions                            Number of obs   =         49
Model VCE    : OLS
Expression   : Linear prediction, predict()
at           : pressure         (asbalanced)
               temp             (asbalanced)
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	115.3758	1.530199	75.40	0.000	112.3767	118.375

❑ Technical note

Concerning how asbalanced calculations are performed, if a factor variable has l levels, then each level's coefficient contributes to the response weighted by $1/l$. If two factors, a and b, interact, then each coefficient associated with their interaction is weighted by $1/(l_a \times l_b)$.

If a balanced factor interacts with a continuous variable, then each coefficient in the interaction is applied to the value of the continuous variable, and the results are weighted equally. So, if the factor being interacted has l_a levels, the effect of each coefficient on the value of the continuous covariate is weighted by $1/l_a$.

❑

Balancing by standardization

To better understand the balanced results, we can perform the balancing ourselves by using the standardizing method shown in *Standardizing margins*. To do that, we will input a balanced dataset and then type margins, noesample.

```
. use http://www.stata-press.com/data/r12/acmemanuf
. regress y pressure##temp
  (output omitted)
. drop _all
. input pressure temp
     pressure       temp
  1. 1 1
  2. 1 2
  3. 1 3
  4. 2 1
  5. 2 2
  6. 2 3
  7. end
. margins, noesample
Predictive margins                                Number of obs   =          6
Model VCE    : OLS
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	115.3758	1.530199	75.40	0.000	112.3767	118.375

We obtain the same results as previously.

Balancing nonlinear responses

If our testing had produced a binary outcome, say, acceptable/unacceptable, rather than a continuous variable, we would type

```
. use http://www.stata-press.com/data/r12/acmemanuf, clear
. logistic acceptable pressure##temp
. margins, asbalanced
```

The result of doing that would be 0.680. If we omitted the `asbalanced` option, the result would have been 0.667. The two results are so similar because `acmemanuf.dta` is nearly balanced.

Even though the `asbalanced` option can be used on both linear and nonlinear responses, such as probabilities, there is an issue of which you should be aware. The most widely used formulas for balancing responses apply the balancing to the linear prediction, average that as if it were balanced, and then apply the nonlinear transform. That is the calculation that produced 0.680.

An alternative would be to apply the standardization method. That amounts to making the linear predictions observation by observation, applying the nonlinear transform to each, and then averaging the nonlinear result as if it were balanced. You could do that by typing

```
. use http://www.stata-press.com/data/r12/acmemanuf, clear
. logistic acceptable pressure##temp
. clear
. input pressure temp
  (see above for entered data)
. margins, noesample
```

The result from the standardization procedure would be 0.672. These two ways of averaging nonlinear responses are discussed in detail in Lane and Nelder (1982) within the context of general linear models.

Concerning the method used by the `asbalanced` option, if your data start balanced and you have a nonlinear response, you will get different results with and without the `asbalanced` option!

Treating a subset of covariates as balanced

So far, we have treated all the covariates as if they were balanced. `margins` will allow you to treat a subset of the covariates as balanced, too. For instance, you might be performing an experiment in which you are randomly allocating patients to a treatment arm and so want to balance on arm, but you do not want to balance the other characteristics because you want mean effects for the experiment's population.

In this example, we will imagine that the outcome of the experiment is continuous. We type

```
. use http://www.stata-press.com/data/r12/margex, clear
. regress y arm##sex sex##agegroup
. margins, at((asbalanced) arm)
```

If we wanted results balanced on `agegroup` as well, we could type

```
. margins, at((asbalanced) arm agegroup)
```

If we wanted results balanced on all three covariates, we could type

```
. margins, at((asbalanced) arm agegroup sex)
```

or we could type

```
. margins, at((asbalanced) _factor)
```

or we could type

```
. margins, asbalanced
```

Using fvset design

As a convenience feature, equivalent to

```
. regress y arm##sex sex##agegroup
. margins, at((asbalanced) arm sex)
```

is

```
. fvset design asbalanced arm sex
. regress y arm##sex sex##agegroup
. margins
```

The advantage of the latter is that you have to set the variables as balanced only once. This is useful when balancing is a design characteristic of certain variables and you wish to avoid accidentally treating them as unbalanced.

If you `save` your data after `fvset`ting, the settings will be remembered in future sessions. If you want to clear the setting(s), type

```
. fvset clear varlist
```

See [R] **fvset**.

Balancing in the presence of empty cells

The issue of empty cells is not exclusively an issue of balancing, but there are special considerations when balancing. Empty cells are discussed generally in *Estimability of margins*.

An empty cell is an interaction of levels of two or more factor variables for which you have no data. Usually, margins involving empty cells cannot be estimated. When balancing, there is an alternate definition of the margin that allows the margin to be estimated. `margins` makes the alternate calculation when you specify the `emptycells(reweight)` option. By default, `margins` uses the `emptycells(strict)` option.

If you have empty cells in your data and you request margins involving the empty cells, those margins will be marked as not estimable even if you specify the `asbalanced` option.

```
. use http://www.stata-press.com/data/r12/estimability, clear
(margins estimability)
. regress y sex##group
  (output omitted)
. margins sex, asbalanced
Adjusted predictions                              Number of obs   =         69
Model VCE    : OLS
Expression   : Linear prediction, predict()
Empty cells  : reweight
at           : sex             (asbalanced)
               group           (asbalanced)
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	21.91389	1.119295	19.58	0.000	19.72011	24.10767
1	.	(not estimable)				

This example is discussed in *Estimability of margins*, although without the `asbalanced` option. What is said there is equally relevant to the `asbalanced` case. For reasons explained there, the margin for `sex` = 1 cannot be estimated.

The margin for `sex` = 1 can be estimated in the `asbalanced` case if you are willing to make an assumption. Remember that `margins` makes the balanced calculation by summing the responses associated with the levels and then dividing by the number of levels. If you specify `emptycells(reweight)`, `margins` sums what is available and divides by the number available. Thus you are assuming that, whatever the responses in the empty cells, those responses are such that they would not change the overall mean of what is observed.

The results of specifying `emptycells(reweight)` are

```
. margins sex, asbalanced emptycells(reweight)
Adjusted predictions                              Number of obs   =         69
Model VCE    : OLS
Expression   : Linear prediction, predict()
Empty cells  : reweight
at           : sex             (asbalanced)
               group           (asbalanced)
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	21.91389	1.119295	19.58	0.000	19.72011	24.10767
1	24.85185	1.232304	20.17	0.000	22.43658	27.26712

Obtaining margins with nested designs

Introduction

Factors whose meaning depends on other factors are called nested factors, and the factors on which their meaning depends are called the nesting factors. For instance, assume that we have a sample of patients and each patient is assigned to one doctor. Then patient is nested within doctor. Let the identifiers of the first 5 observations of our data be

Doctor	Patient	Name
1	1	Fred
1	2	Mary
1	3	Bob
2	1	Karen
2	2	Hank

The first patient on one doctor's list has nothing whatsoever to do with the first patient on another doctor's list. The meaning of `patient` = 1 is defined only when the value of `doctor` is supplied.

Nested factors enter into models as interactions of nesting and nested; the nested factor does not appear by itself. We might estimate a model such as

```
. regress y ... i.doctor doctor#patient ...
```

You do not include `i.patient` because the coding for patient has no meaning except within doctor. Patient 1 is Fred for doctor 1 and Karen for doctor 2, etc.

`margins` provides an option to help account for the structure of nested models. The `within(`*varlist*`)` option specifies that `margins` estimate and report a set of margins for the value combinations of *varlist*. We might type

```
. margins, within(doctor)
```

Margin calculations are performed first for `doctor` = 1, then for `doctor` = 2, and so on.

Sometimes you need to specify `within()`, and other times you do not. Let's consider the particular model

```
. regress y i.doctor doctor#patient i.sex sex#doctor#patient
```

The guidelines are the following:

1. You may compute overall margins by typing
   `margins`.
2. You may compute overall margins within levels of a nesting factor by typing
   `margins, within(doctor)`.
3. You may compute margins of a nested factor within levels of its nesting factor by typing
   `margins patient, within(doctor)`.
4. You may compute margins of factors in your model, as long as the factor does not nest other factors and is not nested within other factors, by typing
   `margins sex`.
5. You may not compute margins of a nesting factor, such as `margins doctor`, because they are not estimable.

For examples using `within()`, see [R] **anova**.

Margins with nested designs as though the data were balanced

To obtain margins with nested designs as though the data were balanced, the guidelines are the same as above except that 1) you add the `asbalanced` option and 2) whenever you do not specify `within()`, you specify `emptycells(reweight)`. The updated guidelines are

1. You may compute overall margins by typing
   `margins, asbalanced emptycells(reweight)`.
2. You may compute overall margins within levels of a nesting factor by typing
   `margins, asbalanced within(doctor)`.
3. You may compute margins of a nested factor within levels of its nesting factor by typing
   `margins patient, asbalanced within(doctor)`.
4. You may compute margins of factors in your model, as long as the factor does not nest other factors and is not nested within other factors, by typing
   `margins sex, asbalanced emptycells(reweight)`.
5. You may not compute margins of a nesting factor, such as `margins doctor`, because they are not estimable.

Just as explained in *Using fvset design*, rather than specifying the `asbalanced` option, you may set the balancing characteristic on the factor variables once and for all by using the command `fvset design asbalanced` *varlist*.

❑ Technical note

Specifying either `emptycells(reweight)` or `within(`*varlist*`)` causes `margins` to rebalance over all empty cells in your model. If you have interactions in your model that are not involved in the nesting, `margins` will lose its ability to detect estimability.

❑

❑ Technical note

Careful readers will note that the description of `within(`*varlist*`)` matches closely the description of `over(`*varlist*`)`. The concept of nesting is similar to the concept of subpopulations. `within()` differs from `over()` in that it gracefully handles the missing cells when margins are computed as balanced.

❑

Coding of nested designs

In the *Introduction* to this section, we showed a coding of the nested variable `patient`, where the coding started over with each `doctor`:

Doctor	Patient	Name
1	1	Fred
1	2	Mary
1	3	Bob
2	1	Karen
2	2	Hank

That coding style is not required. The data could just as well have been coded

Doctor	Patient	Name
1	1	Fred
1	2	Mary
1	3	Bob
2	4	Karen
2	5	Hank

or even

Doctor	Patient	Name
1	1037239	Fred
1	2223942	Mary
1	0611393	Bob
2	4433329	Karen
2	6110271	Hank

Actually, either of the above two alternatives are better than the first one because `margins` will be better able to give you feedback about estimability should you make a mistake following the guidelines. On the other hand, both of these two alternatives require more memory at the estimation step. If you run short of memory, you will need to recode your patient ID to the first coding style, which you could do by typing

```
. sort doctor patient
. by doctor: gen newpatient = _n
```

Alternatively, you can `set emptycells drop` and continue to use your patient ID variable just as it is coded. If you do this, we recommend that you remember to type `set emptycells keep` when you are finished; `margins` is better able to determine estimability that way. If you regularly work with large nested models, you can `set emptycells keep, permanently` so that the setting persists across sessions. See [R] **set emptycells**.

Special topics

Requirements for model specification

The results that `margins` reports are based on the most recently fit model or, in Stata jargon, the most recently issued estimation command. Here we discuss 1) mechanical requirements for how you specify that estimation command, 2) work-arounds to use when those restrictions prove impossible, and 3) requirements for `margins`' `predict(`*pred_opt*`)` option to work.

Concerning 1, when you specify the estimation command, covariates that are logically factor variables must be Stata factor variables, and that includes indicator variables, binary variables, and dummies. It will not do to type

```
. regress y ... female ...
```

even if `female` is a 0/1 variable. You must type

```
. regress y ... i.female ...
```

If you violate this rule, you will not get incorrect results, but you will discover that you will be unable to obtain margins on `female`:

```
. margins female
factor female not found in e(b)
r(111);
```

It is also important that if the same continuous variable appears in your model more than once, differently transformed, those transforms be performed via Stata's factor-variable notation. It will not do to type

```
. generate age2 = age^2
. regress y ... age age2 ...
```

You must type

```
. regress y ... age c.age#c.age ...
```

You must do that because `margins` needs to know everywhere that variable appears in the model if it is to be able to set covariates to fixed values.

Concerning 2, sometimes the transformations you desire may not be achievable using the factor-variable notation; in those situations, there is a work-around. Let's assume you wish to estimate

```
. generate age1_5 = age^1.5
. regress y ... age age1_5 ...
```

There is no factor-variable notation for including `age` and $\texttt{age}^{1.5}$ in a model, so obviously you are going to obtain the estimates by typing just what we have shown. In what follows, it would be okay if there are interactions of `age` and `age1_5` with other variables specified by the factor-variable notation, so the model could just as well be

```
. regress y ... age age1_5 sex#c.age sex#c.age1_5 ...
```

Let's assume you have fit one of these two models. On any subsequent `margins` command where you leave age free to vary, there will be no issue. You can type

```
. margins female
```

and results will be correct. Issues arise when you attempt to fix age at predetermined values. The following would produce incorrect results:

```
. margins female, at(age=20)
```

The results would be incorrect because they leave age1_5 free to vary, and, logically, fixing age implies that age1_5 should also be fixed. Because we were unable to state the relationship between age and age1_5 using the factor-variable notation, margins does not know to fix age1_5 at $20^{1.5}$ when it fixes age at 20. To get the correct results, you must fix the value of age1_5 yourself:

```
. margins female, at(age=20 age1_5=89.442719)
```

That command produces correct results. In the command, 89.442719 is $20^{1.5}$.

In summary, when there is a functional relationship between covariates of your model and that functional relationship is not communicated to margins via the factor-variable notation, then it becomes your responsibility to ensure that all variables that are functionally related are set to the appropriate fixed values when any one of them is set to a fixed value.

Concerning 3, we wish to amend our claim that you can calculate margins for anything that predict will produce. We need to add a qualifier. Let us show you an example where the statement is not true. After regress, predict will predict something it calls pr(*a*,*b*), which is the probability $a \leq y \leq b$. Yet if we attempted to use pr() with margins after estimation by regress, we would obtain

```
. margins sex, predict(pr(10,20))
prediction is a function of possibly stochastic quantities other than e(b)
r(498);
```

What we should have stated was that you can calculate margins for anything that predict will produce for which all the estimated quantities used in its calculation appear in e(V), the estimated VCE. pr() is a function of $\boldsymbol{\beta}$, the estimated coefficients, and of s^2, the estimated variance of the residual. regress does not post the variance of the residual variance (sic) in e(V), or even estimate it, and therefore, predict(pr(10,20)) cannot be specified with margins after estimation by regress.

It is unlikely that you will ever encounter these kinds of problems because there are so few predictions where the components are not posted to e(V). If you do encounter the problem, the solution may be to specify nose to suppress the standard-error calculation. If the problem is not with computing the margin, but with computing its standard error, margins will report the result:

```
. margins sex, predict(pr(10,20)) nose
  (output appears with SEs, tests, and CIs left blank)
```

❑ Technical note

Programmers: If you run into this after running an estimation command that you have written, be aware that as of Stata 11, you are supposed to set in e(marginsok) the list of options allowed with predict that are okay to use with margins. When that list is not set, margins looks for violations of its assumptions and, if it finds any, refuses to proceed.

❑

Estimability of margins

Sometimes `margins` will report that a margin cannot be estimated:

```
. use http://www.stata-press.com/data/r12/estimability, clear
(margins estimability)
. regress y sex##group
  (output omitted)
. margins sex
Predictive margins                                Number of obs   =         69
Model VCE    : OLS
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	21	.8500245	24.71	0.000	19.33398	22.66602
1	.	(not estimable)				

In the above output, the margin for `sex` $= 0$ is estimated, but the margin for `sex` $= 1$ is not estimable. This occurs because of empty cells. An empty cell is an interaction of levels of two or more factor variables for which you have no data. In the example, the lack of estimability arises because we have two empty cells:

```
. table sex group
```

	group				
sex	1	2	3	4	5
0	2	9	27	8	2
1	9	9	3		

To calculate the marginal mean response for `sex` $= 1$, we have no responses to average over for `group` $= 4$ and `group` $= 5$. We obviously could calculate that mean for the observations that really are `sex` $= 1$, but remember, the marginal calculation for `sex` $= 1$ treats everyone as if female, and we will thus have 8 and 2 observations for which we have no basis for estimating the response.

There is no solution for this problem unless you are willing to treat the data as if it were balanced and adjust your definition of a margin; see *Balancing in the presence of empty cells*.

Manipulability of tests

Manipulability is a problem that arises with some tests, and in particular, arises with Wald tests. Tests of margins are based on Wald tests, hence our interest. This is a generic issue and not specific to the `margins` command.

Let's understand the problem. Consider performing a test of whether some statistic ϕ is 0. Whatever the outcome of that test, it would be desirable if the outcome were the same were we to test whether the sqrt(ϕ) were 0, or whether ϕ^2 were 0, or whether any other monotonic transform of ϕ were 0 (for ϕ^2, we were considering only the positive half of the number line). If a test does not have that property, it is manipulable.

Wald tests are manipulable, and that means the tests produced by `margins` are manipulable. You can see this for yourself by typing

```
. use http://www.stata-press.com/data/r12/margex, clear
. replace y = y - 65
. regress y sex##group
. margins
. margins, expression(predict(xb)^2)
```

We would prefer if the test against zero produced by `margins` was equal to the test produced by `margins, expression(predict(xb)^2)`. But alas, they produce different results. The first produces $z = 12.93$, and the second produces $z = 12.57$.

The difference is not much in our example, but behind the scenes, we worked to make it small. We subtracted 65 from `y` so that the experiment would be for a case where it might be reasonable that you would be testing against 0. One does not typically test whether the mean income in the United States is zero or whether the mean blood pressure of live patients is zero. Had we left `y` as it was originally, we would have obtained $z = 377$ and $z = 128$. We did not want to show that comparison to you first because the mean of `y` is so far from 0 that you probably would never be testing it. The corresponding difference in ϕ is tiny.

Regardless of the example, it is important that you base your tests in the metric where the likelihood surface is most quadratic. For further discussion on manipulability, see *Manipulability* in [R] **predictnl**.

This manipulability is not limited to Wald tests after estimation; you can also see the manipulability of results produced by linear regression just by applying nonlinear transforms to a covariate (Phillips and Park 1988; Gould 1996).

Using margins after the estimates use command

Assume you fit and used `estimates save` (see [R] **estimates save**) to save the estimation results:

```
. regress y sex##group age c.age*c.age if site==1
. ...
. estimates save mymodel
(file mymodel.ster saved)
```

Later, perhaps in a different Stata session, you reload the estimation results by typing

```
. estimates use mymodel
```

You plan to use `margins` with the reloaded results. You must remember that `margins` bases its results not only on the current estimation results but also on the current data in memory. Before you can use `margins`, you must reload the dataset on which you fit the model or, if you wish to produce standardized margins, some other dataset.

```
. use mydata, clear
(data for fitting models)
```

If the dataset you loaded contained the data for standardization, you can stop reading; you know that to produce standardized margins, you need to specify the `noesample` option.

We reloaded the original data and want to produce margins for the estimation sample. In addition to the data, `margins` requires that `e(sample)` be set, as `margins` will remind us:

```
. margins sex
e(sample) does not identify the estimation sample
r(322);
```

The best solution is to use estimates esample to rebuild e(sample):

```
. estimates esample: y sex group age if site==1
```

If we knew we had no missing values in y and the covariates, we could type

```
. estimates esample: if site==1
```

Either way, margins would now work:

```
. margins sex
(usual output appears)
```

There is an alternative. We do not recommend it, but we admit that we have used it. Rather than rebuilding e(sample), you can use margins' noesample option to tell margins to skip using e(sample). You could then specify the appropriate if statement (if necessary) to identify the estimation sample:

```
. estimates use mymodel
. use mydata, clear
(data for fitting models)
. margins sex if !missing(y, sex, group age) & site==1, noesample
(usual output appears)
```

In the above, we are not really running on a sample different from the estimation sample; we are merely using noesample to fool margins, and then we are specifying on the margins command the conditions equivalent to re-create e(sample).

If we wish to obtain vce(unconditional) results, however, noesample will be insufficient. We must also specify the force option,

```
. margins sex if !missing(y, sex, group age) & site==1,
> vce(unconditional) noesample force
(usual output appears)
```

Regardless of the approach you choose—resetting e(sample) or specifying noesample and possibly force—make sure you are right. In the vce(delta) case, you want to be right to ensure that you obtain the results you want. In the vce(unconditional) case, you need to be right because otherwise results will be statistically invalid.

Syntax of at()

In at(*atspec*), *atspec* may contain one or more of the following specifications:

varlist

(*stat*) *varlist*

varname = #

varname = (*numlist*)

where

1. *varname*s must be covariates in the previously fit model (estimation command).
2. Variable names (whether in *varname* or *varlist*) may be continuous variables, factor variables, or specific level variables, such as age, group, or 3.group.

3. *varlist* may also be one of three standard lists:
    a. _all (all covariates),
    b. _factor (all factor-variable covariates), or
    c. _continuous (all continuous covariates).
4. Specifications are processed from left to right with latter specifications overriding previous ones.
5. *stat* can be any of the following:

stat	Description	Variables allowed
asobserved	at observed values in the sample (default)	all
mean	means (default for *varlist*)	all
median	medians	continuous
p1	1st percentile	continuous
p2	2nd percentile	continuous
...	3rd–49th percentiles	continuous
p50	50th percentile (same as median)	continuous
...	51st–97th percentiles	continuous
p98	98th percentile	continuous
p99	99th percentile	continuous
min	minimums	continuous
max	maximums	continuous
zero	fixed at zero	continuous
base	base level	factors
asbalanced	all levels equally probable and sum to 1	factors

Any *stat* except zero, base, and asbalanced may be prefixed with an o to get the overall statistic—the sample over all over() groups. For example, omean, omedian, and op25. Overall statistics differ from their correspondingly named statistics only when the over() or within() option is specified. When no *stat* is specified, mean is assumed.

Estimation commands that may be used with margins

margins may be used after most estimation commands.

margins cannot be used after estimation commands that do not produce full variance matrices, such as exlogistic and expoisson (see [R] **exlogistic** and [R] **expoisson**).

margins is all about covariates and cannot be used after estimation commands that do not post the covariates, which eliminates gmm (see [R] **gmm**).

margins cannot be used after estimation commands that have an odd data organization, and that excludes asclogit, asmprobit, asroprobit, and nlogit (see [R] **asclogit**, [R] **asmprobit**, [R] **asroprobit**, and [R] **nlogit**).

Glossary

adjusted mean. A *margin* when the response is the linear predictor from linear regression, ANOVA, etc. For some authors, adjusting also implies adjusting for unbalanced data. See *Obtaining margins of responses* and see *Obtaining margins as though the data were balanced*.

average marginal effect. See *marginal effect and average marginal effect*.

average partial effect. See *partial effect and average partial effect*.

conditional margin. A *margin* when the response is evaluated at fixed values of all the covariates. If any covariates are left to vary, the margin is called a predictive margin.

effect. The effect of x is the derivative of the *response* with respect to covariate x, or it is the difference in responses caused by a discrete change in x. Also see *marginal effect*.

The effect of x measures the change in the response for a change in x. Derivatives or differences might be reported as elasticities. If x is continuous, the effect is measured continuously. If x is a factor, the effect is measured with respect to each level of the factor and may be calculated as a discrete difference or as a continuous change, as measured by the derivative. `margins` calculates the discrete difference by default and calculates the derivative if the `continuous` option is specified.

elasticity and **semielasticity**. The elasticity of y with respect to x is $d(\ln y)/d(\ln x) = (x/y)\times(dy/dx)$, which is approximately equal to the proportional change in y for a proportional change in x.

The semielasticity of y with respect to x is either 1) $dy/d(\ln x) = x \times (dy/dx)$ or 2) $d(\ln y)/dx = (1/y) \times (dy/dx)$, which is approximately 1) the change in y for a proportional change in x or 2) the proportional change in y for a change in x.

empty cell. An interaction of levels of two or more factor variables for which you have no data. For instance, you have sex interacted with group in your model, and in your data there are no females in group 1. Empty cells affect which margins can be estimated; see *Estimability of margins*.

estimability. Estimability concerns whether a margin can be uniquely estimated (identified); see *Estimability of margins*.

estimated marginal mean. This is one of the few terms that has the same meaning across authors. An estimated marginal mean is a margin assuming the levels of each factor covariate are equally likely (balanced), including interaction terms. This is obtained using `margins'` `asbalanced` option. In addition, there is an alternate definition of estimated marginal mean in which margins involving empty cells are redefined so that they become estimable. This is invoked by `margins'` `emptycells(reweight)` option. See *Balancing in the presence of empty cells*.

least-squares mean. Synonym for *estimated marginal mean*.

margin. A statistic calculated from predictions or other statistics of a previously fit model at fixed values of some covariates and averaging or otherwise integrating over the remaining covariates. The prediction or other statistic on which the margin is based is called the response.

If all the covariates are fixed, then the margin is called a conditional margin. If any covariates are left to vary, the margin is called a predictive margin.

In this documentation, we divide margins on the basis of whether the statistic is a response or a derivative of a response; see *Obtaining margins of responses* and *Obtaining margins of derivatives of responses*.

marginal effect and **average marginal effect**. The marginal effect of x is the *margin* of the *effect* of x. The term is popular with social scientists, and because of that, you might think the word marginal in marginal effect means derivative because of terms like marginal cost and marginal revenue. Marginal used in that way, however, refers to the derivative of revenue and the derivative

of cost; it refers to the numerator, whereas marginal effect refers to the denominator. Moreover, *effect* is already a derivative or difference.

Some researchers interpret marginal in marginal effect to mean instantaneous, and thus a marginal effect is the instantaneous derivative rather than the discrete first-difference, corresponding to `margins`' `continuous` option. Researchers who use marginal in this way refer to the discrete difference calculation of an effect as a partial effect.

Other researchers define marginal effect to be the margin when all covariates are held fixed and the average marginal effect when some covariates are not fixed.

out-of-sample prediction. Predictions made in one dataset using the results from a model fit on another. Sample here refers to the sample on which the model was fit, and out-of-sample refers to the dataset on which the predictions are made.

partial effect and **average partial effect**. Some authors restrict the term *marginal effect* to mean derivatives and use the term partial effect to denote discrete differences; see *marginal effect and average marginal effect*.

population marginal mean. The theoretical (true) value that is estimated by *estimated marginal mean*. We avoid this term because it can be confused with the concept of a population in survey statistics, with which the population marginal mean has no connection.

posting results, **posting margins**. A Stata concept having to do with saving the results from the `margins` command in `e()` so that those results can be used as if they were estimation results, thus allowing the subsequent use of postestimation commands, such as `test`, `testnl`, `lincom`, and `nlcom` (see [R] **test**, [R] **testnl**, [R] **lincom**, and [R] **nlcom**). This is achieved by specifying `margins`' `post` option. See *Example 10: Testing margins—contrasts of margins*.

predictive margin. A *margin* in which all the covariates are not fixed. When all covariates are fixed, it is called a *conditional margin*.

recycled prediction. A synonym for *predictive margin*.

response. A prediction or other statistic derived from combining the parameter estimates of a fitted model with data or specified values on covariates. Derivatives of responses are themselves responses. Responses are what we take *margins* of.

standardized margin. The margin calculated on data different from the data used to fit the model. The term standardized is usually reserved for situations in which the alternate population is a reference population, which may be real or artificial, and which is treated as fixed.

subpopulation. A subset of your sample that represents a subset of the population, such as the males in a sample of people. In survey contexts when it is desired to account for sampling of the covariates, standard errors for marginal statistics and effects need to account for both the population and the subpopulation. This is accomplished by specifying the `vce(unconditional)` option and one of the `subpop()` or `over()` options. In fact, the above is allowed even when your data are not `svyset` because `vce(unconditional)` implies that the sample represents a population.

Saved results

`margins` saves the following in `r()`:

Scalars

`r(N)`	number of observations
`r(N_sub)`	subpopulation observations
`r(N_clust)`	number of clusters
`r(N_psu)`	number of sampled PSUs, survey data only
`r(N_strata)`	number of strata, survey data only
`r(df_r)`	variance degrees of freedom, survey data only
`r(N_poststrata)`	number of post strata, survey data only
`r(k_margins)`	number of terms in *marginlist*
`r(k_by)`	number of subpopulations
`r(k_at)`	number of `at()` options
`r(level)`	confidence level of confidence intervals

Macros

`r(cmd)`	`margins`
`r(cmdline)`	command as typed
`r(est_cmd)`	`e(cmd)` from original estimation results
`r(est_cmdline)`	`e(cmdline)` from original estimation results
`r(title)`	title in output
`r(subpop)`	*subspec* from `subpop()`
`r(model_vce)`	*vcetype* from estimation command
`r(model_vcetype)`	Std. Err. title from estimation command
`r(vce)`	*vcetype* specified in `vce()`
`r(vcetype)`	title used to label Std. Err.
`r(clustvar)`	name of cluster variable
`r(margins)`	*marginlist*
`r(predict_label)`	label from `predict()`
`r(expression)`	response expression
`r(xvars)`	*varlist* from `dydx()`, `dyex()`, `eydx()`, or `eyex()`
`r(derivatives)`	"", "dy/dx", "dy/ex", "ey/dx", "ey/ex"
`r(over)`	*varlist* from `over()`
`r(within)`	*varlist* from `within()`
`r(by)`	union of `r(over)` and `r(within)` lists
`r(by#)`	interaction notation identifying the #th subpopulation
`r(atstats#)`	the #th `at()` specification
`r(emptycells)`	*empspec* from `emptycells()`
`r(mcmethod)`	*method* from `mcompare()`
`r(mcadjustall)`	`adjustall` or empty

Matrices

`r(b)`	estimates
`r(V)`	variance–covariance matrix of the estimates
`r(Jacobian)`	Jacobian matrix
`r(_N)`	sample size corresponding to each margin estimate
`r(at)`	matrix of values from the `at()` options
`r(chainrule)`	chainrule information from the fitted model
`r(error)`	margin estimability codes; `0` means estimable, `8` means not estimable
`r(table)`	matrix containing the margins with their standard errors, test statistics, p-values, and confidence intervals

margins with the post option also saves the following in e():

Scalars

e(N)	number of observations
e(N_sub)	subpopulation observations
e(N_clust)	number of clusters
e(N_psu)	number of sampled PSUs, survey data only
e(N_strata)	number of strata, survey data only
e(df_r)	variance degrees of freedom, survey data only
e(N_poststrata)	number of post strata, survey data only
e(k_margins)	number of terms in *marginlist*
e(k_by)	number of subpopulations
e(k_at)	number of at() options

Macros

e(cmd)	margins
e(cmdline)	command as typed
e(est_cmd)	e(cmd) from original estimation results
e(est_cmdline)	e(cmdline) from original estimation results
e(title)	title in estimation output
e(subpop)	*subspec* from subpop()
e(model_vce)	*vcetype* from estimation command
e(model_vcetype)	Std. Err. title from estimation command
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(clustvar)	name of cluster variable
e(margins)	*marginlist*
e(predict_label)	label from predict()
e(expression)	prediction expression
e(xvars)	*varlist* from dydx(), dyex(), eydx(), or eyex()
e(derivatives)	"", "dy/dx", "dy/ex", "ey/dx", "ey/ex"
e(over)	*varlist* from over()
e(within)	*varlist* from within()
e(by)	union of r(over) and r(within) lists
e(by#)	interaction notation identifying the #th subpopulation
e(atstats#)	the #th at() specification
e(emptycells)	*empspec* from emptycells()
e(mcmethod)	*method* from mcompare()
e(mcadjustall)	adjustall or empty

Matrices

e(b)	estimates
e(V)	variance–covariance matrix of the estimates
e(Jacobian)	Jacobian matrix
e(_N)	sample size corresponding to each margin estimate
e(at)	matrix of values from the at() options
e(chainrule)	chainrule information from the fitted model

Functions

e(sample)	marks estimation sample

Methods and formulas

margins is implemented as an ado-file.

Margins are statistics calculated from predictions of a previously fit model at fixed values of some covariates and averaging or otherwise integrating over the remaining covariates. There are many names for the different statistics that margins can compute: estimates marginal means (see Searle, Speed, and Milliken [1980]), predictive margins (see Graubard and Korn [2004]), marginal effects (see Greene [2012]), and average marginal/partial effects (see Wooldridge [2010] and Bartus [2005]).

Methods and formulas are presented under the following headings:

Notation
Marginal effects
Fixing covariates and balancing factors
Estimable functions
Standard errors conditional on the covariates
Unconditional standard errors

Notation

Let $\boldsymbol{\theta}$ be the vector of parameters in the current model fit, let $\mathbf{z}$ be a vector of covariate values, and let $f(\mathbf{z}, \boldsymbol{\theta})$ be a scalar-valued function returning the value of the predictions of interest. The following table illustrates the parameters and default prediction for several of Stata's estimation commands.

Command	$\boldsymbol{\theta}$	$\mathbf{z}$	$f(\mathbf{z}, \boldsymbol{\theta})$
`regress`	$\boldsymbol{\beta}$	$\mathbf{x}$	$\mathbf{x}\boldsymbol{\beta}$
`cloglog`	$\boldsymbol{\beta}$	$\mathbf{x}$	$1 - e^{-e^{x\beta}}$
`logit`	$\boldsymbol{\beta}$	$\mathbf{x}$	$1/(1 + e^{-x\beta})$
`poisson`	$\boldsymbol{\beta}$	$\mathbf{x}$	$e^{x\beta}$
`probit`	$\boldsymbol{\beta}$	$\mathbf{x}$	$\Phi(\mathbf{x}\boldsymbol{\beta})$
`biprobit`	$\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \rho$	$\mathbf{x}_1, \mathbf{x}_2$	$\Phi_2(\mathbf{x}_1\boldsymbol{\beta}_1, \mathbf{x}_2\boldsymbol{\beta}_2, \rho)$
`mlogit`	$\boldsymbol{\beta}_1, \boldsymbol{\beta}_2, \ldots, \boldsymbol{\beta}_k$	$\mathbf{x}$	$e^{-x\beta_1}/(\sum_i e^{-x\beta_i})$
`nbreg`	$\boldsymbol{\beta}$, $\ln\alpha$	$\mathbf{x}$	$e^{x\beta}$

$\Phi()$ and $\Phi_2()$ are cumulative distribution functions: $\Phi()$ for the standard normal distribution and $\Phi_2()$ for the standard bivariate normal distribution.

`margins` computes estimates of

$$p(\boldsymbol{\theta}) = \frac{1}{M_{S_\mathrm{p}}} \sum_{j=1}^{M} \delta_j(S_\mathrm{p}) f(\mathbf{z}_j, \boldsymbol{\theta})$$

where $\delta_j(S_\mathrm{p})$ identifies elements within the subpopulation S_p (for the prediction of interest),

$$\delta_j(S_\mathrm{p}) = \begin{cases} 1, & j \in S_\mathrm{p} \\ 0, & j \notin S_\mathrm{p} \end{cases}$$

M_{S_p} is the subpopulation size,

$$M_{S_\mathrm{p}} = \sum_{j=1}^{M} \delta_j(S_\mathrm{p})$$

and M is the population size.

Let $\widehat{\boldsymbol{\theta}}$ be the vector of parameter estimates. Then `margins` estimates $p(\boldsymbol{\theta})$ via

$$\widehat{p} = \frac{1}{w_\cdot} \sum_{j=1}^{N} \delta_j(S_\mathrm{p}) w_j f(\mathbf{z}_j, \widehat{\boldsymbol{\theta}})$$

where

$$w_{\cdot} = \sum_{j=1}^{N} \delta_j(S_{\mathrm{p}}) w_j$$

$\delta_j(S_{\mathrm{p}})$ indicates whether observation j is in subpopulation S_{p}, w_j is the weight for the jth observation, and N is the sample size.

Marginal effects

`margins` also computes marginal/partial effects. For the marginal effect of continuous covariate x, `margins` computes

$$\widehat{p} = \frac{1}{w_{\cdot}} \sum_{j=1}^{N} \delta_j(S_{\mathrm{p}}) w_j h(\mathbf{z}_j, \widehat{\boldsymbol{\theta}})$$

where

$$h(\mathbf{z}, \boldsymbol{\theta}) = \frac{\partial f(\mathbf{z}, \boldsymbol{\theta})}{\partial x}$$

The marginal effect for level k of factor variable A is the simple contrast (a.k.a. difference) comparing its margin with the margin at the base level.

$$h(\mathbf{z}, \boldsymbol{\theta}) = f(\mathbf{z}, \boldsymbol{\theta} | A = k) - f(\mathbf{z}, \boldsymbol{\theta} | A = \mathrm{base})$$

Fixing covariates and balancing factors

`margins` controls the values in each $\mathbf{z}$ vector through the *marginlist*, the `at()` option, the `atmeans` option, and the `asbalanced` and `emptycells()` options. Suppose $\mathbf{z}$ is composed of the elements from the equation specification

```
A##B x
```

where `A` is a factor variable with a levels, `B` is a factor variable with b levels, and `x` is a continuous covariate. To simplify the notation for this discussion, assume the levels of `A` and `B` start with 1 and are contiguous. Then

$$\mathbf{z} = (A_1, \ldots, A_a, B_1, \ldots, B_b, A_1B_1, A_1B_2, \ldots, A_aB_b, x, 1)$$

where A_i, B_j, and A_iB_j represent the indicator values for the factor variables `A` and `B` and the interaction `A#B`.

When factor `A` is in the *marginlist*, `margins` replaces `A` with i and then computes the mean of the subsequent prediction, for $i = 1, \ldots, a$. When the interaction term `A#B` is in the *marginlist*, `margins` replaces `A` with i and `B` with j, and then computes the mean of the subsequent prediction, for all combinations of $i = 1, \ldots, a$ and $j = 1, \ldots, b$.

The `at()` option sets model covariates to fixed values. For example, `at(x=15)` causes `margins` to temporarily set x to 15 for each observation in the dataset before computing any predictions. Similarly, `at((median) x)` causes `margins` to temporarily set x to the median of `x` using the current dataset.

When factor variable `A` is specified as `asbalanced`, `margins` sets each A_i to $1/a$. Thus each $\mathbf{z}$ vector will look like

$$\mathbf{z} = (1/a, \ldots, 1/a, B_1, \ldots, B_b, B_1/a, B_2/a, \ldots, B_b/a, x, 1)$$

If `B` is also specified as `asbalanced`, then each B_j is set to $1/b$, and each $\mathbf{z}$ vector will look like

$$\mathbf{z} = (1/a, \ldots, 1/a, 1/b, \ldots, 1/b, 1/ab, 1/ab, \ldots, 1/ab, x, 1)$$

If `emptycells(reweight)` is also specified, then `margins` uses a different balancing weight for each element of $\mathbf{z}$, depending on how many empty cells the element is associated with. Let δ_{ij} indicate that the ijth cell of `A#B` was observed in the estimation sample.

$$\delta_{ij} = \begin{cases} 0, & \texttt{A}=i \text{ and } \texttt{B}=j \text{ was an empty cell} \\ 1, & \text{otherwise} \end{cases}$$

For the grand margin, the affected elements of $\mathbf{z}$ and their corresponding balancing weights are

$$A_i = \frac{\sum_j \delta_{ij}}{\sum_k \sum_j \delta_{kj}}$$

$$B_j = \frac{\sum_i \delta_{ij}}{\sum_i \sum_k \delta_{ik}}$$

$$A_i B_j = \frac{\delta_{ij}}{\sum_k \sum_l \delta_{kl}}$$

For the jth margin of `B`, the affected elements of $\mathbf{z}$ and their corresponding balancing weights are

$$A_i = \frac{\delta_{ij}}{\sum_k \delta_{kj}}$$

$$B_l = \begin{cases} 1, & \text{if } l = j \text{ and not all } \delta_{ij} \text{ are zero} \\ 0, & \text{otherwise} \end{cases}$$

$$A_i B_l = \frac{\delta_{il}}{\sum_k \delta_{kl}} B_l$$

Estimable functions

The fundamental idea behind estimable functions is clearly defined in the statistical literature for linear models; see Searle (1971). Assume that we are working with the following linear model:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{e}$$

where $\mathbf{y}$ is an $N \times 1$ vector of responses, $\mathbf{X}$ is an $N \times p$ matrix of covariate values, $\mathbf{b}$ is a $p \times 1$ vector of coefficients, and $\mathbf{e}$ is a vector of random errors. Assuming a constant variance for the random errors, the normal equations for the least-squares estimator, $\widehat{\mathbf{b}}$, are

$$\mathbf{X}'\mathbf{X}\widehat{\mathbf{b}} = \mathbf{X}'\mathbf{y}$$

When $\mathbf{X}$ is not of full column rank, we will need a generalized inverse (g-inverse) of $\mathbf{X}'\mathbf{X}$ to solve for $\widehat{\mathbf{b}}$. Let $\mathbf{G}$ be a g-inverse of $\mathbf{X}'\mathbf{X}$.

Searle (1971) defines a linear function of the parameters as *estimable* if it is identically equal to some linear function of the expected values of the $\mathbf{y}$ vector. Let $\mathbf{H} = \mathbf{G}\mathbf{X}'\mathbf{X}$. Then this definition simplifies to the following rule:

$$\mathbf{z}\mathbf{b} \text{ is estimable if } \mathbf{z} = \mathbf{z}\mathbf{H}$$

`margins` generalizes this to nonlinear functions by assuming the prediction function $f(\mathbf{z}, \boldsymbol{\theta})$ is a function of one or more of the linear predictions from the equations in the model that $\boldsymbol{\theta}$ represents.

$$f(\mathbf{z}, \boldsymbol{\theta}) = h(\mathbf{z}_1\boldsymbol{\beta}_1, \mathbf{z}_2\boldsymbol{\beta}_2, \ldots, \mathbf{z}_k\boldsymbol{\beta}_k)$$

$\mathbf{z}_i\boldsymbol{\beta}_i$ is considered estimable if $\mathbf{z}_i = \mathbf{z}_i\mathbf{H}_i$, where $\mathbf{H}_i = \mathbf{G}_i\mathbf{X}_i'\mathbf{X}_i$, $\mathbf{G}_i$ is a g-inverse for $\mathbf{X}_i'\mathbf{X}_i$, and $\mathbf{X}_i$ is the matrix of covariates from the ith equation of the fitted model. `margins` considers $p(\boldsymbol{\theta})$ to be estimable if every $\mathbf{z}_i\boldsymbol{\beta}_i$ is estimable.

Standard errors conditional on the covariates

By default, `margins` uses the delta method to estimate the variance of $\widehat{p}$.

$$\widehat{\text{Var}}(\widehat{p} \,|\, \mathbf{z}) = \mathbf{v}'\mathbf{V}\mathbf{v}$$

where $\mathbf{V}$ is a variance estimate for $\widehat{\boldsymbol{\theta}}$ and

$$\mathbf{v} = \left.\frac{\partial \widehat{p}}{\partial \boldsymbol{\theta}}\right|_{\theta=\widehat{\theta}}$$

This variance estimate is conditional on the $\mathbf{z}$ vectors used to compute the marginalized predictions.

Unconditional standard errors

`margins` with the `vce(unconditional)` option uses linearization to estimate the unconditional variance of $\widehat{\boldsymbol{\theta}}$. Linearization uses the variance estimator for the total of a score variable for $\widehat{p}$ as an approximate estimator for $\text{Var}(\widehat{p})$; see [SVY] **variance estimation**. `margins` requires that the model was fit using some form of linearized variance estimator and that `predict, scores` computes the appropriate score values for the linearized variance estimator.

The score for $\widehat{p}$ from the jth observation is given by

$$s_j = \frac{\partial \widehat{p}}{\partial w_j} = -\frac{\delta_j(S_{\rm p})}{w.}\widehat{p} + \frac{\delta_j(S_{\rm p})}{w.} f(\mathbf{z}_j, \widehat{\boldsymbol{\theta}}) + \frac{1}{w.}\sum_{i=1}^{N} \delta_i(S_{\rm p}) w_i \frac{\partial f(\mathbf{z}_i, \widehat{\boldsymbol{\theta}})}{\partial w_j}$$

The remaining partial derivative can be decomposed using the chain rule.

$$\frac{\partial f(\mathbf{z}_i, \widehat{\boldsymbol{\theta}})}{\partial w_j} = \left(\left. \frac{\partial f(\mathbf{z}_i, \boldsymbol{\theta})}{\partial \boldsymbol{\theta}} \right|_{\theta=\widehat{\theta}} \right) \left(\frac{\partial \widehat{\boldsymbol{\theta}}}{\partial w_j} \right)'$$

This is the inner product of two vectors, the second of which is not a function of the i index. Thus the score is

$$s_j = -\frac{\delta_j(S_{\rm p})}{w.}\widehat{p} + \frac{\delta_j(S_{\rm p})}{w.} f(\mathbf{z}_j, \widehat{\boldsymbol{\theta}}) + \left(\left. \frac{\partial \widehat{p}}{\partial \boldsymbol{\theta}} \right|_{\theta=\widehat{\theta}} \right) \left(\frac{\partial \widehat{\boldsymbol{\theta}}}{\partial w_j} \right)'$$

If $\widehat{\boldsymbol{\theta}}$ was derived from a system of equations (such as in linear regression or maximum likelihood estimation), then $\widehat{\boldsymbol{\theta}}$ is the solution to

$$\mathbf{G}(\boldsymbol{\theta}) = \sum_{j=1}^{N} \delta_j(S_{\rm m}) w_j \mathbf{g}(\boldsymbol{\theta}, \mathbf{y}_j, \mathbf{x}_j) = \mathbf{0}$$

where $S_{\rm m}$ identifies the subpopulation used to fit the model, $\mathbf{g}()$ is the model's gradient function, and $\mathbf{y}_j$ and $\mathbf{x}_j$ are the values of the dependent and independent variables for the jth observation. We can use linearization to derive a first-order approximation for $\partial\widehat{\boldsymbol{\theta}}/\partial w_j$.

$$\mathbf{G}(\widehat{\boldsymbol{\theta}}) \approx \mathbf{G}(\boldsymbol{\theta}_0) + \left. \frac{\partial \mathbf{G}(\boldsymbol{\theta})}{\partial \boldsymbol{\theta}} \right|_{\theta=\theta_0} (\widehat{\boldsymbol{\theta}} - \boldsymbol{\theta}_0)$$

Let $\mathbf{H}$ be the Hessian matrix

$$\mathbf{H} = \left. \frac{\partial \mathbf{G}(\boldsymbol{\theta})}{\partial \boldsymbol{\theta}} \right|_{\theta=\theta_0}$$

Then

$$\widehat{\boldsymbol{\theta}} \approx \boldsymbol{\theta}_0 + (-\mathbf{H})^{-1}\mathbf{G}(\boldsymbol{\theta}_0)$$

and

$$\frac{\partial\widehat{\boldsymbol{\theta}}}{\partial w_j} \approx (-\mathbf{H})^{-1}\left.\frac{\partial\mathbf{G}(\boldsymbol{\theta})}{\partial w_j}\right|_{\theta=\widehat{\theta}} = (-\mathbf{H})^{-1}\delta_j(S_{\rm m})\mathbf{g}(\widehat{\boldsymbol{\theta}},\mathbf{y}_j,\mathbf{x}_j)$$

The computed value of the score for $\widehat{p}$ for the jth observation is

$$s_j = \mathbf{v}'\mathbf{u}_j$$

where

$$\mathbf{v} = \begin{bmatrix} -\dfrac{\widehat{p}}{w.} \\ \dfrac{1}{w.} \\ \dfrac{\partial\widehat{p}}{\partial\widehat{\boldsymbol{\theta}}}(-\mathbf{H})^{-1} \end{bmatrix}$$

and

$$\mathbf{u}_j = \begin{bmatrix} \delta_j(S_{\rm p}) \\ \delta_j(S_{\rm p})f(\mathbf{z}_j,\widehat{\boldsymbol{\theta}}) \\ \delta_j(S_{\rm m})\mathbf{g}(\widehat{\boldsymbol{\theta}},\mathbf{y}_j,\mathbf{x}_j) \end{bmatrix}$$

Thus the variance estimate for $\widehat{p}$ is

$$\widehat{\rm Var}(\widehat{p}) = \mathbf{v}'\widehat{\rm Var}(\widehat{\mathbf{U}})\mathbf{v}$$

where

$$\widehat{\mathbf{U}} = \sum_{j=1}^{N} w_j\mathbf{u}_j$$

`margins` uses the model-based variance estimates for $(-\mathbf{H})^{-1}$ and the scores from `predict` for $\mathbf{g}(\widehat{\boldsymbol{\theta}},\mathbf{y}_j,\mathbf{x}_j)$.

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Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **margins, contrast** — Contrasts of margins

[R] **margins, pwcompare** — Pairwise comparisons of margins

[R] **margins postestimation** — Postestimation tools for margins

[R] **marginsplot** — Graph results from margins (profile plots, etc.)

[R] **lincom** — Linear combinations of estimators

[R] **nlcom** — Nonlinear combinations of estimators

[R] **predict** — Obtain predictions, residuals, etc., after estimation

[R] **predictnl** — Obtain nonlinear predictions, standard errors, etc., after estimation

[U] **20 Estimation and postestimation commands**

Title

margins postestimation — Postestimation tools for margins

Description

The following standard postestimation command is available after `margins`:

Command	Description
`marginsplot`	graph the results from margins—profile plots, interaction plots, etc.

For information on `marginsplot`, see [R] **marginsplot**.

The following standard postestimation commands are available after `margins, post`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	estimation sample summary; `estat summarize` only
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

Remarks

Continuing with the example from *Example 8: Margins of interactions* in [R] **margins**, we use the dataset and reestimate the logistic model of `outcome`:

```
. use http://www.stata-press.com/data/r12/margex
(Artificial data for margins)
. logistic outcome sex##group age
```

(*output omitted*)

We then estimate the margins for males and females and post the margins as estimation results with a full VCE.

```
. margins sex, post
Predictive margins                                Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Delta-method					
	Margin	Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1600644	.0125653	12.74	0.000	.1354368	.184692
1	.1966902	.0100043	19.66	0.000	.1770821	.2162983

We can now use `nlcom` (see [R] **nlcom**) to estimate a risk ratio of females to males using the average probabilities for females and males posted by `margins`:

```
. nlcom (risk_ratio: _b[1.sex] / _b[0.sex])
  risk_ratio:  _b[1.sex] / _b[0.sex]
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
risk_ratio	1.228819	.1149538	10.69	0.000	1.003514	1.454124

We could similarly estimate the average risk difference between females and males:

```
. nlcom (risk_diff: _b[1.sex] - _b[0.sex])
   risk_diff:  _b[1.sex] - _b[0.sex]
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
risk_diff	.0366258	.0160632	2.28	0.023	.0051425	.068109

Also see

[R] **margins** — Marginal means, predictive margins, and marginal effects

[U] **20 Estimation and postestimation commands**

Title

margins, contrast — Contrasts of margins

Syntax

```
margins [marginlist] [if] [in] [weight] [, contrast margins_options]

margins [marginlist] [if] [in] [weight] [, contrast(suboptions) margins_options]
```

where *marginlist* is a list of factor variables or interactions that appear in the current estimation results. The variables may be typed with or without contrast operators, and you may use any factor-variable syntax:

```
. margins sex##group, contrast
. margins sex##g.group, contrast
. margins sex@group, contrast
```

See the operators (*op.*) table in [R] **contrast** for the list of contrast operators. Contrast operators may also be specified on the variables in `margins`' `over()` and `within()` options to perform contrasts across the levels of those variables.

See [R] **margins** for the available *margins_options*.

suboptions	Description
Contrast	
`overall`	add a joint hypothesis test for all specified contrasts
`lincom`	treat user-defined contrasts as linear combinations
`atcontrast(`*op*`[ ._at ])`	apply the *op*`.` contrast operator to the groups defined by `at()`
`atjoint`	test jointly across all groups defined by `at()`
`overjoint`	test jointly across all levels of the unoperated `over()` variables
`withinjoint`	test jointly across all levels of the unoperated `within()` variables
`marginswithin`	perform contrasts within the levels of the unoperated terms in *marginlist*
`cieffects`	show effects table with confidence intervals
`pveffects`	show effects table with p-values
`effects`	show effects table with confidence intervals and p-values
`nowald`	suppress table of Wald tests
`noatlevels`	report only the overall Wald test for terms that use the within `@` or nested `|` operator
`nosvyadjust`	compute unadjusted Wald tests for survey results

`fweights`, `aweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Postestimation > Contrasts of margins

Description

`margins` with the `contrast` option or with contrast operators performs contrasts of margins. This extends the capabilities of `contrast` to any of the nonlinear responses, predictive margins, or other margins that can be estimated by `margins`.

Suboptions

Contrast

`overall` specifies that a joint hypothesis test over all terms be performed.

`lincom` specifies that user-defined contrasts be treated as linear combinations. The default is to require that all user-defined contrasts sum to zero. (Summing to zero is part of the definition of a contrast.)

`atcontrast(`*op*`[ ._at ])` specifies that the *op*`.` contrast operator be applied to the groups defined by the `at()` option(s). The default behavior, by comparison, is to perform tests and contrasts within the groups defined by the `at()` option(s).

See example 6 in *Remarks*.

`atjoint` specifies that joint tests be performed across all groups defined by the `at()` option. The default behavior, by comparison, is to perform contrasts and tests within each group.

See example 5 in *Remarks*.

`overjoint` specifies how unoperated variables in the `over()` option are treated.

Each variable in the `over()` option may be specified either with or without a contrast operator. For contrast-operated variables, the specified contrast comparisons are always performed.

`overjoint` specifies that joint tests be performed across all levels of the unoperated variables. The default behavior, by comparison, is to perform contrasts and tests within each combination of levels of the unoperated variables.

See example 3 in *Remarks*.

`withinjoint` specifies how unoperated variables in the `within()` option are treated.

Each variable in the `within()` option may be specified either with or without a contrast operator. For contrast-operated variables, the specified contrast comparisons are always performed.

`withinjoint` specifies that joint tests be performed across all levels of the unoperated variables. The default behavior, by comparison, is to perform contrasts and tests within each combination of levels of the unoperated variables.

`marginswithin` specifies how unoperated variables in *marginlist* are treated.

Each variable in *marginlist* may be specified either with or without a contrast operator. For contrast-operated variables, the specified contrast comparisons are always performed.

`marginswithin` specifies that contrasts and tests be performed within each combination of levels of the unoperated variables. The default behavior, by comparison, is to perform joint tests across all levels of the unoperated variables.

See example 4 in *Remarks*.

`cieffects` specifies that a table containing a confidence interval for each individual contrast be reported.

`pveffects` specifies that a table containing a p-value for each individual contrast be reported.

`effects` specifies that a single table containing a confidence interval and p-value for each individual contrast be reported.

`nowald` suppresses the table of Wald tests.

`noatlevels` indicates that only the overall Wald test be reported for each term containing within or nested (`@` or `|`) operators.

`nosvyadjust` is for use with `svy` estimation commands. It specifies that the Wald test be carried out without the default adjustment for the design degrees of freedom. That is to say the test is carried out as $W/k \sim F(k,d)$ rather than as $(d-k+1)W/(kd) \sim F(k,d-k+1)$, where k is the dimension of the test and d is the total number of sampled PSUs minus the total number of strata.

Remarks

Remarks are presented under the following headings:

Contrasts of margins
Contrasts and the over() option
The overjoint suboption
The marginswithin suboption
Contrasts and the at() option
Conclusion

Contrasts of margins

▷ Example 1

Estimating contrasts of margins is as easy as adding a contrast operator to the variable name. Let's review *Example 2: A simple case after logistic* of [R] **margins**. Variable `sex` is coded `0` for males and `1` for females.

```
. use http://www.stata-press.com/data/r12/margex
. logistic outcome i.sex i.group
  (output omitted)
. margins sex
Predictive margins                              Number of obs   =       3000
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	Delta-method Margin	Std. Err.	z	P>|z|	[95% Conf.	Interval]
sex						
0	.1286796	.0111424	11.55	0.000	.106841	.1505182
1	.1905087	.0089719	21.23	0.000	.1729241	.2080933

The first margin, 0.13, is the average probability of a positive outcome, treating everyone as if they were male. The second margin, 0.19, is the average probability of a positive outcome, treating everyone as if they were female. We can compare females with males by rerunning `margins` and adding a contrast operator:

```
. margins r.sex
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	df	chi2	P>chi2
sex	1	16.61	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
sex				
(1 vs 0)	.0618291	.0151719	.0320927	.0915656

The `r.` prefix for `sex` is the reference-category contrast operator—see [R] **contrast**. (The default reference category is zero, the lowest value of `sex`.) Contrast operators in a *marginlist* work just as they do in the *termlist* of a `contrast` command.

The contrast estimate of 0.06 says that unconditional on group, females on average are about 6% more likely than males to have a positive outcome. The chi-squared statistic of 16.61 shows that the contrast is significantly different from zero.

You may be surprised that we did not need to include the `contrast` option to estimate our contrast. If we had included the option, our output would not have changed:

```
. margins r.sex, contrast
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	df	chi2	P>chi2
sex	1	16.61	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
sex				
(1 vs 0)	.0618291	.0151719	.0320927	.0915656

The `contrast` option is useful mostly for its suboptions, which control the output and how contrasts are estimated in more complicated situations. But `contrast` may be specified on its own (without contrast operators or suboptions) if we do not need estimates or confidence intervals:

```
. margins sex group, contrast
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	df	chi2	P>chi2
sex	1	16.61	0.0000
group	2	225.76	0.0000

Each chi-squared statistic is a joint test of constituent contrasts. The test for group has two degrees of freedom because group has three levels.

◁

Contrasts and the over() option

▷ Example 2

It is common to estimate margins at combinations of factor levels, and margins, contrast includes several suboptions for contrasting such margins. Let's fit a model with two categorical predictors and their interaction:

```
. logistic outcome group##agegroup
Logistic regression                             Number of obs   =       3000
                                                LR chi2(8)      =     520.64
                                                Prob > chi2     =     0.0000
Log likelihood = -1105.7504                     Pseudo R2       =     0.1906
```

outcome	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
group						
2	.834507	.5663738	-0.27	0.790	.2206611	3.15598
3	.2146729	.1772897	-1.86	0.062	.0425407	1.083303
agegroup						
2	3.54191	2.226951	2.01	0.044	1.032882	12.14576
3	16.23351	9.61188	4.71	0.000	5.086452	51.80955
group# agegroup						
2 2	.4426927	.3358505	-1.07	0.283	.1000772	1.958257
2 3	.440672	.3049393	-1.18	0.236	.1135259	1.71055
3 2	1.160885	1.103527	0.16	0.875	.1801543	7.480553
3 3	.4407912	.4034688	-0.89	0.371	.0733	2.650709
_cons	.0379747	.0223371	-5.56	0.000	.0119897	.1202762

Each of group and agegroup has three levels. To compare each age group with the reference category on the probability scale, we can again use margins with the r. contrast operator.

```
. margins r.agegroup
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
```

	df	chi2	P>chi2
agegroup			
(2 vs 1)	1	10.04	0.0015
(3 vs 1)	1	224.44	0.0000
Joint	2	238.21	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
agegroup				
(2 vs 1)	.044498	.0140448	.0169706	.0720253
(3 vs 1)	.2059281	.0137455	.1789874	.2328688

Our model includes an interaction, though, so it would be nice to estimate the contrasts separately for each value of `group`. We need the `over()` option:

```
. margins r.agegroup, over(group)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : group
```

	df	chi2	P>chi2
agegroup@group			
(2 vs 1) 1	1	6.94	0.0084
(2 vs 1) 2	1	1.18	0.2783
(2 vs 1) 3	1	3.10	0.0783
(3 vs 1) 1	1	173.42	0.0000
(3 vs 1) 2	1	57.77	0.0000
(3 vs 1) 3	1	5.12	0.0236
Joint	6	266.84	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
agegroup@group				
(2 vs 1) 1	.0819713	.0311208	.0209757	.142967
(2 vs 1) 2	.0166206	.0153309	-.0134275	.0466686
(2 vs 1) 3	.0243462	.0138291	-.0027583	.0514508
(3 vs 1) 1	.3447797	.0261811	.2934658	.3960937
(3 vs 1) 2	.1540882	.0202722	.1143554	.193821
(3 vs 1) 3	.0470319	.0207774	.006309	.0877548

The effect of `agegroup` appears to be greatest for the first level of `group`.

Including a variable in the `over()` option is not equivalent to including the variable in the main *marginlist*. The variables in the *marginlist* are manipulated in the analysis, so that we can measure, for example, the effect of being in age group 3 and not age group 1. (The manipulation could be mimicked by running `replace` and then `predict`, but the manipulations actually performed by `margins` do not change the data in memory.) The variables in the `over()` option are not so manipulated—the values of the `over()` variables are left as they were observed, and the *marginlist* variables are manipulated separately for each observed `over()` group. For more information, see *Do not specify marginlist when you mean over()* in [R] **margins**.

◁

The overjoint suboption

▷ Example 3

Each variable in an `over()` option may be specified with or without contrast operators. Our option `over(group)` did not include a contrast operator, so `margins` estimated the contrasts separately for each level of `group`. If we had instead specified `over(r.group)`, we would have received differences of the contrasts:

```
. margins r.agegroup, over(r.group)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : group
```

	df	chi2	P>chi2
group#agegroup			
(2 vs 1) (2 vs 1)	1	3.55	0.0596
(2 vs 1) (3 vs 1)	1	33.17	0.0000
(3 vs 1) (2 vs 1)	1	2.86	0.0906
(3 vs 1) (3 vs 1)	1	79.36	0.0000
Joint	4	83.88	0.0000

	Delta-method			
	Contrast	Std. Err.	[95% Conf.	Interval]
group#agegroup				
(2 vs 1) (2 vs 1)	-.0653508	.0346921	-.133346	.0026445
(2 vs 1) (3 vs 1)	-.1906915	.0331121	-.25559	-.1257931
(3 vs 1) (2 vs 1)	-.0576251	.0340551	-.1243719	.0091216
(3 vs 1) (3 vs 1)	-.2977479	.0334237	-.3632572	-.2322385

The contrasts are double differences: the estimate of -0.19, for example, says that the difference in the probability of success between age group 3 and age group 1 is smaller in group 2 than in group 1. We can jointly test pairs of the double differences with the `overjoint` suboption:

```
. margins r.agegroup, over(group) contrast(overjoint)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : group
```

	df	chi2	P>chi2
group#agegroup			
(joint) (2 vs 1)	2	3.62	0.1641
(joint) (3 vs 1)	2	79.45	0.0000
Joint	4	83.88	0.0000

The `contrast(overjoint)` option overrides the default behavior of `over()` and requests joint tests over the levels of the unoperated variable `group`. The chi-squared statistic of 3.62 tests that the first and third contrasts from the previous table are jointly zero. The chi-squared statistic of 79.45 jointly tests the other pair of contrasts.

◁

The marginswithin suboption

▷ Example 4

Another suboption that may usefully be combined with `over()` is `marginswithin`. `marginswithin` requests that contrasts be performed within the levels of unoperated variables in the main *marginlist*, instead of performing them jointly across the levels. `marginswithin` affects only unoperated variables because contrast operators take precedence over suboptions.

Let's first look at the default behavior, which occurs when `marginswithin` is not specified:

```
. margins agegroup, over(r.group) contrast(effects)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : group
```

	df	chi2	P>chi2
group#agegroup			
(2 vs 1) (joint)	2	33.94	0.0000
(3 vs 1) (joint)	2	83.38	0.0000
Joint	4	83.88	0.0000

	Contrast	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
group# agegroup						
(2 vs 1) (2 vs base)	-.0653508	.0346921	-1.88	0.060	-.133346	.0026445
(3 vs 1) (3 vs base)	-.1906915	.0331121	-5.76	0.000	-.25559	-.1257931
(2 vs 1) (3 vs 1)	-.0576251	.0340551	-1.69	0.091	-.1243719	.0091216
(3 vs 1) (3 vs base)	-.2977479	.0334237	-8.91	0.000	-.3632572	-.2322385

Here `agegroup` in the main *marginlist* is an unoperated variable, so `margins` by default performs joint tests across the levels of `agegroup`: the chi-squared statistic of 33.94, for example, jointly tests whether the first two contrast estimates in the lower table differ significantly from zero.

When we specify marginswithin, the contrasts will instead be performed within the levels of agegroup:

```
. margins agegroup, over(r.group) contrast(marginswithin effects)
Contrasts of predictive margins
Model VCE    : OIM
Expression   : Pr(outcome), predict()
over         : group
```

	df	chi2	P>chi2
group@agegroup			
(2 vs 1) 1	1	0.06	0.7991
(2 vs 1) 2	1	7.55	0.0060
(2 vs 1) 3	1	68.39	0.0000
(3 vs 1) 1	1	1.80	0.1798
(3 vs 1) 2	1	10.47	0.0012
(3 vs 1) 3	1	159.89	0.0000
Joint	6	186.87	0.0000

	Contrast	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
group@ agegroup						
(2 vs 1) 1	-.0058686	.0230533	-0.25	0.799	-.0510523	.039315
(2 vs 1) 2	-.0712194	.0259246	-2.75	0.006	-.1220308	-.0204081
(2 vs 1) 3	-.1965602	.0237688	-8.27	0.000	-.2431461	-.1499742
(3 vs 1) 1	-.0284991	.0212476	-1.34	0.180	-.0701436	.0131453
(3 vs 1) 2	-.0861243	.0266137	-3.24	0.001	-.1382862	-.0339624
(3 vs 1) 3	-.326247	.0258009	-12.64	0.000	-.3768159	-.2756781

The joint tests in the top table have been replaced by one-degree-of-freedom tests, one for each combination of the two reference comparisons and three levels of agegroup. The reference-category contrasts for group have been performed within levels of agegroup.

◁

Contrasts and the at() option

▷ Example 5

The at() option of margins is used to set predictors to particular values. When at() is used, contrasts are by default performed within each at() level:

```
. margins r.agegroup, at(group=(1/3))
Contrasts of adjusted predictions
Model VCE    : OIM
Expression   : Pr(outcome), predict()
1._at        : group           =           1
2._at        : group           =           2
3._at        : group           =           3
```

	df	chi2	P>chi2
agegroup@_at			
(2 vs 1) 1	1	6.94	0.0084
(2 vs 1) 2	1	1.18	0.2783
(2 vs 1) 3	1	3.10	0.0783
(3 vs 1) 1	1	173.42	0.0000
(3 vs 1) 2	1	57.77	0.0000
(3 vs 1) 3	1	5.12	0.0236
Joint	6	266.84	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
agegroup@_at				
(2 vs 1) 1	.0819713	.0311208	.0209757	.142967
(2 vs 1) 2	.0166206	.0153309	-.0134275	.0466686
(2 vs 1) 3	.0243462	.0138291	-.0027583	.0514508
(3 vs 1) 1	.3447797	.0261811	.2934658	.3960937
(3 vs 1) 2	.1540882	.0202722	.1143554	.193821
(3 vs 1) 3	.0470319	.0207774	.006309	.0877548

Our option `at(group=(1/3))` manipulates the values of `group` and is therefore not equivalent to `over(group)`. We see that the reference-category contrasts for `agegroup` have been performed within each `at()` level. For a similar example that uses the `._at` operator instead of the `at()` option, see *Contrasts of at() groups—discrete effects* in [R] **marginsplot**.

The default within behavior of `at()` may be changed to joint behavior with the `atjoint` suboption:

```
. margins r.agegroup, at(group=(1/3)) contrast(atjoint)
Contrasts of adjusted predictions
Model VCE    : OIM
Expression   : Pr(outcome), predict()
1._at        : group           =           1
2._at        : group           =           2
3._at        : group           =           3
```

	df	chi2	P>chi2
_at#agegroup			
(joint) (2 vs 1)	2	3.62	0.1641
(joint) (3 vs 1)	2	79.45	0.0000
Joint	4	83.88	0.0000

Now the tests are performed jointly over the levels of `group`, the `at()` variable. The `atjoint` suboption is the analogue for `at()` of the `overjoint` suboption from example 3.

◁

▷ Example 6

What if we would like to apply a contrast operator, like `r.`, to the `at()` levels? It is not possible to specify the operator inside the `at()` option. Instead, we need a new suboption, `atcontrast()`:

```
. margins r.agegroup, at(group=(1/3)) contrast(atcontrast(r))
Contrasts of adjusted predictions
Model VCE    : OIM
Expression   : Pr(outcome), predict()
1._at        : group           =           1
2._at        : group           =           2
3._at        : group           =           3
```

	df	chi2	P>chi2
_at#agegroup			
(2 vs 1) (2 vs 1)	1	3.55	0.0596
(2 vs 1) (3 vs 1)	1	33.17	0.0000
(3 vs 1) (2 vs 1)	1	2.86	0.0906
(3 vs 1) (3 vs 1)	1	79.36	0.0000
Joint	4	83.88	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
_at#agegroup				
(2 vs 1) (2 vs 1)	-.0653508	.0346921	-.133346	.0026445
(2 vs 1) (3 vs 1)	-.1906915	.0331121	-.25559	-.1257931
(3 vs 1) (2 vs 1)	-.0576251	.0340551	-.1243719	.0091216
(3 vs 1) (3 vs 1)	-.2977479	.0334237	-.3632572	-.2322385

When we specify `contrast(atcontrast(r))`, `margins` will apply the `r.` reference-category operator to the levels of `group`, the variable specified inside `at()`. The default reference category is `1`, the lowest level of `group`.

Conclusion

`margins, contrast` is a powerful command, and its abundance of suboptions may seem daunting. The suboptions are in the service of only three goals, however. There are three things that `margins, contrast` can do with a factor variable or a set of `at()` definitions:

1. Perform contrasts across the levels of the factor or set (as in example 1).
2. Perform a joint test across the levels of the factor or set (as in example 5).
3. Perform other tests and contrasts within each level of the factor or set (as in example 4).

The default behavior for variables specified inside `at()`, `over()`, and `within()` is to perform contrasts within groups; the default behavior for variables in the *marginlist* is to perform joint tests across groups.

◁

Saved results

`margins, contrast` saves the following additional items in `r()`:

Scalars
- `r(k_terms)` — number of terms participating in contrasts

Macros
- `r(cmd)` — `contrast`
- `r(cmd2)` — `margins`
- `r(overall)` — `overall` or empty

Matrices
- `r(L)` — matrix of contrasts applied to the margins
- `r(chi2)` — vector of χ^2 statistics
- `r(p)` — vector of p-values corresponding to `r(chi2)`
- `r(df)` — vector of degrees of freedom corresponding to `r(p)`

`margins, contrast` with the `post` option also saves the following additional items in `e()`:

Scalars
- `e(k_terms)` — number of terms participating in contrasts

Macros
- `e(cmd)` — `contrast`
- `e(cmd2)` — `margins`
- `e(overall)` — `overall` or empty

Matrices
- `e(L)` — matrix of contrasts applied to the margins
- `e(chi2)` — vector of χ^2 statistics
- `e(p)` — vector of p-values corresponding to `e(chi2)`
- `e(df)` — vector of degrees of freedom corresponding to `e(p)`

Methods and formulas

See *Methods and formulas* in [R] **margins** and *Methods and formulas* in [R] **contrast**.

Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **margins** — Marginal means, predictive margins, and marginal effects

[R] **margins postestimation** — Postestimation tools for margins

[R] **margins, pwcompare** — Pairwise comparisons of margins

[R] **nlcom** — Nonlinear combinations of estimators

[R] **predict** — Obtain predictions, residuals, etc., after estimation

[R] **predictnl** — Obtain nonlinear predictions, standard errors, etc., after estimation

[R] **pwcompare** — Pairwise comparisons

Title

margins, pwcompare — Pairwise comparisons of margins

Syntax

```
margins [marginlist] [if] [in] [weight] [, pwcompare margins_options]

margins [marginlist] [if] [in] [weight] [, pwcompare(suboptions) margins_options]
```

where *marginlist* is a list of factor variables or interactions that appear in the current estimation results. The variables may be typed with or without the `i.` prefix, and you may use any factor-variable syntax:

```
. margins i.sex i.group i.sex#i.group, pwcompare
. margins sex group sex#i.group, pwcompare
. margins sex##group, pwcompare
```

See [R] **margins** for the available *margins_options*.

suboptions	Description
Pairwise comparisons	
`cieffects`	show effects table with confidence intervals; the default
`pveffects`	show effects table with p-values
`effects`	show effects table with confidence intervals and p-values
`cimargins`	show table of margins and confidence intervals
`groups`	show table of margins and group codes
`sort`	sort the margins or contrasts in each term

`fweights`, `aweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Postestimation > Pairwise comparisons of margins

Description

`margins` with the `pwcompare` option performs pairwise comparisons of margins. `margins, pwcompare` extends the capabilities of `pwcompare` to any of the nonlinear responses, predictive margins, or other margins that can be estimated by `margins`.

Suboptions

Pairwise comparisons

`cieffects` specifies that a table of the pairwise comparisons with their standard errors and confidence intervals be reported. This is the default.

`pveffects` specifies that a table of the pairwise comparisons with their standard errors, test statistics, and p-values be reported.

`effects` specifies that a table of the pairwise comparisons with their standard errors, test statistics, p-values, and confidence intervals be reported.

`cimargins` specifies that a table of the margins with their standard errors and confidence intervals be reported.

`groups` specifies that a table of the margins with their standard errors and group codes be reported. Margins with the same letter in the group code are not significantly different at the specified significance level.

`sort` specifies that the reported tables be sorted on the margins or contrasts in each term.

Remarks

You should be familiar with the concepts and syntax of both `margins` and `pwcompare` before using the `pwcompare` option of `margins`. These remarks build on those in [R] **margins** and [R] **pwcompare**.

`margins` can perform pairwise comparisons of any of the margins that it estimates.

In the *Continuous covariates* example in [R] **marginsplot**, we fit a logistic regression model using the NHANES II dataset, ignoring the complex survey nature of the data. Our dependent variable is `highbp`, an indicator for whether a person has high blood pressure. We fit a fully interacted model including two factor variables representing gender and age group as well as the continuous covariate, `bmi`.

```
. use http://www.stata-press.com/data/r12/nhanes2
. logistic highbp sex##agegrp##c.bmi
  (output omitted)
```

By default, `margins` will compute the predictive margins of the probability of a positive outcome for each of the terms in *marginlist* after logistic regression. We will margin on `agegrp` so that `margins` will estimate the average predicted probabilities of having high blood pressure conditional on being in each of the six age groups and unconditional on sex and BMI. We can specify the `pwcompare` option to obtain all possible pairwise comparisons of these predictive margins:

```
. margins agegrp, pwcompare
Pairwise comparisons of predictive margins
Model VCE    : OIM
Expression   : Pr(highbp), predict()
```

	Contrast	Delta-method Std. Err.	Unadjusted [95% Conf.	Interval]
agegrp				
2 vs 1	.0182344	.0069751	.0045635	.0319054
3 vs 1	.08395	.0097271	.0648852	.1030148
4 vs 1	.1443977	.0111944	.122457	.1663383
5 vs 1	.1517272	.0082323	.1355922	.1678622
6 vs 1	.1443064	.0126661	.1194813	.1691314
3 vs 2	.0657156	.010205	.0457141	.0857171
4 vs 2	.1261632	.0116121	.1034039	.1489225
5 vs 2	.1334928	.0087919	.116261	.1507245
6 vs 2	.1260719	.0130367	.1005205	.1516234
4 vs 3	.0604477	.0134464	.0340932	.0868021
5 vs 3	.0677772	.0111023	.046017	.0895374
6 vs 3	.0603564	.0146942	.0315562	.0891565
5 vs 4	.0073296	.012408	-.0169898	.0316489
6 vs 4	-.0000913	.0157041	-.0308707	.0306882
6 vs 5	-.0074208	.0137504	-.0343712	.0195295

This table gives each of the pairwise differences with confidence intervals. We can see that the confidence interval in the row labeled `(2 vs 1)` does not include zero. At the 5% level, the predictive margins for the first and second age groups are significantly different. The same is true of many of the other comparisons. With many pairwise comparisons, output in this format can be difficult to sort through. We can put some structure on this by adding the `group` suboption:

```
. margins agegrp, pwcompare(group)
Pairwise comparisons of predictive margins
Model VCE    : OIM
Expression   : Pr(highbp), predict()
```

	Margin	Delta-method Std. Err.	Unadjusted Groups
agegrp			
1	.0375314	.004423	
2	.0557658	.0053934	
3	.1214814	.0086634	
4	.181929	.0102836	A
5	.1892586	.0069432	A
6	.1818377	.0118687	A

```
Note: Margins sharing a letter in the group label
      are not significantly different at the 5%
      level.
```

The group output includes the predictive margins for each age group and letters denoting margins that are not significantly different from each other. In this case, there is not a letter associated with the first age group in the "Unadjusted Groups" column. This missingness indicates that the average predicted probability for this age group is significantly different from the average predicted probability for each of the other age groups at the 5% significance level. The absence of a letter next to the second and third age groups is interpreted in a similar manner. The fourth, fifth, and sixth age groups each

have an A in the "Unadjusted Groups" column, which indicates that the average predicted probabilities for these groups are not significantly different at our 5% level.

We can also include the mcompare(bonferroni) option to perform tests using Bonferroni's method to account for making multiple comparisons.

```
. margins agegrp, pwcompare(group) mcompare(bonferroni)
Pairwise comparisons of predictive margins
Model VCE    : OIM
Expression   : Pr(highbp), predict()
```

	Number of Comparisons
agegrp	15

	Margin	Delta-method Std. Err.	Bonferroni Groups
agegrp			
1	.0375314	.004423	B
2	.0557658	.0053934	B
3	.1214814	.0086634	
4	.181929	.0102836	A
5	.1892586	.0069432	A
6	.1818377	.0118687	A

```
Note: Margins sharing a letter in the group label
      are not significantly different at the 5%
      level.
```

We now see the letter B on the rows corresponding to the first and second age groups. At the 5% level and using Bonferroni's adjustment, the predictive margins for the probability in the first and second age groups are not significantly different.

Saved results

margins, pwcompare saves the following additional items in r():

Scalars

r(k_terms)	number of terms participating in pairwise comparisons

Macros

r(cmd)	pwcompare
r(cmd2)	margins
r(group#)	group code for the #th margin in r(b)
r(mcmethod_vs)	*method* from mcompare()
r(mctitle_vs)	title for *method* from mcompare()
r(mcadjustall_vs)	adjustall or empty

Matrices

r(b)	margin estimates
r(V)	variance–covariance matrix of the margin estimates
r(b_vs)	margin difference estimates
r(V_vs)	variance–covariance margin difference of the margin estimates
r(error_vs)	margin difference estimability codes; 0 means estimable, 8 means not estimable
r(table_vs)	matrix containing the margin differences with their standard errors, test statistics, p-values, and confidence intervals
r(L)	matrix that produces the margin differences

`margins, pwcompare` with the `post` option also saves the following additional items in `e()`:

Scalars	
`e(k_terms)`	number of terms participating in pairwise comparisons
Macros	
`e(cmd)`	`pwcompare`
`e(cmd2)`	`margins`
Matrices	
`e(b)`	margin estimates
`e(V)`	variance–covariance matrix of the margin estimates
`e(b_vs)`	margin difference estimates
`e(V_vs)`	variance–covariance margin difference of the margin estimates
`e(error_vs)`	margin difference estimability codes; `0` means estimable, `8` means not estimable
`e(L)`	matrix that produces the margin differences

Methods and formulas

See *Methods and formulas* in [R] **margins** and *Methods and formulas* in [R] **pwcompare**.

Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **margins** — Marginal means, predictive margins, and marginal effects

[R] **margins postestimation** — Postestimation tools for margins

[R] **nlcom** — Nonlinear combinations of estimators

[R] **predict** — Obtain predictions, residuals, etc., after estimation

[R] **predictnl** — Obtain nonlinear predictions, standard errors, etc., after estimation

[R] **pwcompare** — Pairwise comparisons

Title

marginsplot — Graph results from margins (profile plots, etc.)

Syntax

```
marginsplot [ , options ]
```

options	Description
Main	
`xdimension(`*dimlist* `[ , `*dimopts*`])`	use *dimlist* to define x axis
`plotdimension(`*dimlist* `[ , `*dimopts*`])`	create plots for groups in *dimlist*
`bydimension(`*dimlist* `[ , `*dimopts*`])`	create subgraphs for groups in *dimlist*
`graphdimension(`*dimlist* `[ , `*dimopts*`])`	create graphs for groups in *dimlist*
`horizontal`	swap x and y axes
`noci`	do not plot confidence intervals
`name(`*name* | *stub* `[ , replace ])`	name of graph, or stub if multiple graphs
Labels	
`allxlabels`	place ticks and labels on the x axis for each value
`nolabels`	label groups with their values, not their labels
`allsimplelabels`	forgo variable name and equal signs in all labels
`nosimplelabels`	include variable name and equal signs in all labels
`separator(`*string*`)`	separator for labels when multiple variables are specified in a dimension
`noseparator`	do not use a separator
Plot	
`plotopts(`*plot_options*`)`	affect rendition of all margin plots
`plot#opts(`*plot_options*`)`	affect rendition of #th margin plot
`recast(`*plottype*`)`	plot margins using *plottype*
CI plot	
`ciopts(`*rcap_options*`)`	affect rendition of all confidence-interval plots
`ci#opts(`*rcap_options*`)`	affect rendition of #th confidence-interval plot
`recastci(`*plottype*`)`	plot confidence intervals using *plottype*
Pairwise	
`unique`	plot only unique pairwise comparisons
`csort`	sort comparison categories first
Add plots	
`addplot(`*plot*`)`	add other plots to the graph
Y axis, X axis, Titles, Legend, Overall, By	
twoway_options	any options documented in [G-3] ***twoway_options***
`byopts(`*byopts*`)`	how subgraphs are combined, labeled, etc.

where *dimlist* may be any of the dimensions across which margins were computed in the immediately preceding `margins` command; see [R] **margins**. That is to say, *dimlist* may be any variable used in the `margins` command, including variables specified in the `at()`, `over()`, and `within()` options. More advanced specifications of *dimlist* are covered in *Addendum: Advanced uses of dimlist*.

dimopts	Description
`labels(`*lablist*`)`	list of quoted strings to label each level of the dimension
`elabels(`*elablist*`)`	list of enumerated labels
`nolabels`	label groups with their values, not their labels
`allsimplelabels`	forgo variable name and equal signs in all labels
`nosimplelabels`	include variable name and equal signs in all labels
`separator(`*string*`)`	separator for labels when multiple variables are specified in the dimension
`noseparator`	do not use a separator

where *lablist* is defined as

"label" [*"label"* [...]]

elablist is defined as

 # "label" [*# "label"* [...]]

and the #s are the indices of the levels of the dimension—1 is the first level, 2 is the second level, and so on.

plot_options	Description
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
cline_options	change look of the line

Menu

Statistics > Postestimation > Margins plots and profile plots

Description

`marginsplot` graphs the results of the immediately preceding `margins` command; see [R] **margins**. Common names for some of the graphs that `marginsplot` can produce are profile plots and interaction plots.

Options

Main

`xdimension()`, `plotdimension()`, `bydimension()`, and `graphdimension()` specify the variables from the preceding `margins` command whose group levels will be used for the graph's x axis, plots, `by()` subgraphs, and graphs.

marginsplot chooses default dimensions based on the margins command. In most cases, the first variable appearing in an at() option and evaluated over more than one value is used for the x axis. If no at() variable meets this condition, the first variable in the *marginlist* is usually used for the x axis and the remaining variables determine the plotted lines or markers. Pairwise comparisons and graphs of marginal effects (derivatives) have different defaults. In all cases, you may override the defaults and explicitly control which variables are used on each dimension of the graph by using these dimension options.

Each of these options supports suboptions that control the labeling of the dimension—axis labels for xdimension(), plot labels for plotdimension(), subgraph titles for bydimension(), and graph titles for graphdimension() titles.

For examples using the dimension options, see *Controlling the graph's dimensions*.

xdimension(*dimlist* [, *dimopts*]) specifies the variables for the x axis in *dimlist* and controls the content of those labels with *dimopts*.

plotdimension(*dimlist* [, *dimopts*]) specifies in *dimlist* the variables whose group levels determine the plots and optionally specifies in *dimopts* the content of the plots' labels.

bydimension(*dimlist* [, *dimopts*]) specifies in *dimlist* the variables whose group levels determine the by() subgraphs and optionally specifies in *dimopts* the content of the subgraphs' titles. For an example using by(), see *Three-way interactions*.

graphdimension(*dimlist* [, *dimopts*]) specifies in *dimlist* the variables whose group levels determine the graphs and optionally specifies in *dimopts* the content of the graphs' titles.

horizontal reverses the default x and y axes. By default, the y axis represents the estimates of the margins and the x axis represents one or more factors or continuous covariates. Specifying horizontal swaps the axes so that the x axis represents the estimates of the margins. This option can be useful if the labels on the factor or continuous covariates are long.

The horizontal option is discussed in *Horizontal is sometimes better*.

noci removes plots of the pointwise confidence intervals. The default is to plot the confidence intervals.

name(*name* | *stub* [, replace]) specifies the name of the graph or graphs. If the graphdimension() option is specified, or if the default action is to produce multiple graphs, then the argument of name() is taken to be *stub* and graphs named *stub*1, *stub*2, ... are created.

The replace suboption causes existing graphs with the specified name or names to be replaced.

If name() is not specified, default names are used and the graphs may be replaced by subsequent marginsplot or other graphing commands.

Labels

With the exception of allxlabels, all these options may be specified either directly as options or as *dimopts* within options xdimension(), plotdimension(), bydimension(), and graphdimension(). When specified in one of the dimension options, only the labels for that dimension are affected. When specified outside the dimension options, all labels on all dimensions are affected. Specifications within the dimension options take precedence.

allxlabels specifies that tick marks and labels be placed on the x axis for each value of the x-dimension variables. By default, if there are more than 25 ticks, default graph axis labeling rules are applied. Labeling may also be specified using the standard graph twoway x-axis label rules and options—xlabel(); see [G-3] ***axis_label_options***.

`nolabels` specifies that value labels not be used to construct graph labels and titles for the group levels in the dimension. By default, if a variable in a dimension has value labels, those labels are used to construct labels and titles for axis ticks, plots, subgraphs, and graphs.

Graphs of contrasts and pairwise comparisons are an exception to this rule and are always labeled with values rather than value labels.

`allsimplelabels` and `nosimplelabels` control whether graphs' labels and titles include just the values of the variables or include variable names and equal signs. The default is to use just the value label for variables that have value labels and to use variable names and equal signs for variables that do not have value labels. An example of the former is "Female" and the latter is "country=2".

Sometimes value labels are universally descriptive, and sometimes they have meaning only when considered in relation to their variable. For example, "Male" and "Female" are typically universal, regardless of the variable from which they are taken. "High" and "Low" may not have meaning unless you know they are in relation to a specific measure, say, blood-pressure level. The `allsimplelabels` and `nosimplelabels` options let you override the default labeling.

`allsimplelabels` specifies that all titles and labels use just the value or value label of the variable.

`nosimplelabels` specifies that all titles and labels include *varname*`=` before the value or value label of the variable.

`separator(`*string*`)` and `noseparator` control the separator between label sections when more than one variable is used to specify a dimension. The default separator is a comma followed by a space, but no separator may be requested with `noseparator` or the default may be changed to any string with `separator()`.

For example, if `plotdimension(a b)` is specified, the plot labels in our graph legend might be "a=1, b=1", "a=1, b=2", ... Specifying `separator(:)` would create labels "a=1:b=1", "a=1:b=2", ...

Plot

`plotopts(`*plot_options*`)` affects the rendition of all margin plots. The *plot_options* can affect the size and color of markers, whether and how the markers are labeled, and whether and how the points are connected; see [G-3] ***marker_options***, [G-3] ***marker_label_options***, and [G-3] ***cline_options***.

These settings may be overridden for specific plots by using the `plot#opts()` option.

`plot#opts(`*plot_options*`)` affects the rendition of the #th margin plot. The *plot_options* can affect the size and color of markers, whether and how the markers are labeled, and whether and how the points are connected; see [G-3] ***marker_options***, [G-3] ***marker_label_options***, and [G-3] ***cline_options***.

`recast(`*plottype*`)` specifies that margins be plotted using *plottype*. *plottype* may be `scatter`, `line`, `connected`, `bar`, `area`, `spike`, `dropline`, or `dot`; see [G-2] **graph twoway**. When `recast()` is specified, the plot-rendition options appropriate to the specified *plottype* may be used in lieu of *plot_options*. For details on those options, follow the appropriate link from [G-2] **graph twoway**.

For an example using `recast()`, see *Continuous covariates*.

You may specify `recast()` within a `plotopts()` or `plot#opts()` option. It is better, however, to specify it as documented here, outside those options. When specified outside those options, you have greater access to the plot-specific rendition options of your specified *plottype*.

CI plot

`ciopts(`*rcap_options*`)` affects the rendition of all confidence-interval plots; see [G-3] ***rcap_options***.

These settings may be overridden for specific confidence-interval plots with the `ci#opts()` option.

`ci#opts(`*rcap_options*`)` affects the rendition of the #th confidence interval; see [G-3] ***rcap_options***.

`recastci(`*plottype*`)` specifies that confidence intervals be plotted using *plottype*. *plottype* may be `rarea`, `rbar`, `rspike`, `rcap`, `rcapsym`, `rline`, `rconnected`, or `rscatter`; see [G-2] **graph twoway**. When `recastci()` is specified, the plot-rendition options appropriate to the specified *plottype* may be used in lieu of *rcap_options*. For details on those options, follow the appropriate link from [G-2] **graph twoway**.

For an example using `recastci()`, see *Continuous covariates*.

You may specify `recastci()` within a `ciopts()` or `ci#opts()` option. It is better, however, to specify it as documented here, outside those options. When specified outside those options, you have greater access to the plot-specific rendition options of your specified *plottype*.

Pairwise

These options have an effect only when the `pwcompare` option was specified on the preceding `margins` command.

`unique` specifies that only unique pairwise comparisons be plotted. The default is to plot all pairwise comparisons, including those that are mirror images of each other—"male" versus "female" and "female" versus "male". `margins` reports only the unique pairwise comparisons. `unique` also changes the default `xdimension()` for graphs of pairwise comparisons from the reference categories (`_pw0`) to the comparisons of each pairwise category (`_pw`).

Unique comparisons are often preferred with horizontal graphs that put all pairwise comparisons on the x axis, whereas including the full matrix of comparisons is preferred for charts showing the reference groups on an axis and the comparison groups as plots; see *Pairwise comparisons* and *Horizontal is sometimes better*.

`csort` specifies that comparison categories are sorted first, and then reference categories are sorted within comparison category. The default is to sort reference categories first, and then sort comparison categories within reference categories. This option has an observable effect only when `_pw` is also specified in one of the dimension options. It then determines the order of the labeling in the dimension where `_pw` is specified.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

For an example using `addplot()`, see *Adding scatterplots of the data*.

If multiple graphs are drawn by a single `marginsplot` command or if *plot* specifies plots with multiple y variables, for example, `scatter y1 y2 x`, then the graph's legend will not clearly identify all the plots and will require customization using the `legend()` option; see [G-3] ***legend_options***.

Y axis, X axis, Titles, Legend, Overall, By

twoway_options are any of the options documented in [G-3] ***twoway_options***. These include options for titling the graph (see [G-3] ***title_options***); for saving the graph to disk (see [G-3] ***saving_option***); for controlling the labeling and look of the axes (see [G-3] ***axis_options***); for controlling the look, contents, position, and organization of the legend (see [G-3] ***legend_options***); for adding lines (see [G-3] ***added_line_options***) and text (see [G-3] ***added_text_options***); and for controlling other aspects of the graph's appearance (see [G-3] ***twoway_options***).

The `label()` suboption of the `legend()` option has no effect on `marginsplot`. Use the `order()` suboption instead.

`byopts(`*byopts*`)` affects the appearance of the combined graph when `bydimension()` is specified or when the default graph has subgraphs, including the overall graph title, the position of the legend, and the organization of subgraphs. See [G-3] ***by_option***.

Remarks

Remarks are presented under the following headings:

Introduction
Dataset
Profile plots
Interaction plots
Contrasts of margins—effects (discrete marginal effects)
Three-way interactions
Continuous covariates
Plots at every value of a continuous covariate
Contrasts of at() groups—discrete effects
Controlling the graph's dimensions
Pairwise comparisons
Horizontal is sometimes better
Marginal effects
Plotting a subset of the results from margins
Advanced usage
Plots with multiple terms
Plots with multiple at() options
Adding scatterplots of the data

Introduction

`marginsplot` is a post-`margins` command. It graphs the results of the `margins` command, whether those results are marginal means, predictive margins, marginal effects, contrasts, pairwise comparisons, or other statistics; see [R] **margins**.

By default, the margins are plotted on the y axis, and all continuous and factor covariates specified in the `margins` command will usually be placed on the x axis or used to identify plots. Exceptions are discussed in the following sections and in *Addendum: Advanced uses of dimlist* below.

`marginsplot` produces classic plots, such as profile plots and interaction plots. Beyond that, anything that `margins` can compute, `marginsplot` can graph.

We will be using some relatively complicated `margins` commands with little explanation of the syntax. We will also avoid lengthy interpretations of the results of margins. See [R] **margins** for the complete syntax of `margins` and discussions of its results.

All graphs in this entry were drawn using the `s2gmanual` scheme; see [G-4] **scheme s2**.

Dataset

For continuity, we will use one dataset for most examples—the Second National Health and Nutrition Examination Survey (NHANES II) (McDowell et al. 1981). NHANES II is part of a study to assess the health and nutritional status of adults and children in the United States. It is designed to be a nationally representative sample of the U.S. population. This particular sample is from 1976 to 1980.

The survey nature of the dataset—weights, strata, and sampling units—will be ignored in our analyses. We are discussing graphing, not survey statistics. If you would like to see the results with the appropriate adjustments for the survey design, just add `svy:` before each estimation command, and if you wish, add `vce(unconditional)` as an option to each `margins` command. See [R] **margins**, particularly the discussion and examples under *Obtaining margins with survey data and representative samples*, for reasons why you probably would want to add `vce(unconditional)` when analyzing survey data. For the most part, adjusting for survey design produces moderately larger confidence intervals and relatively small changes in point estimates.

Profile plots

What does my estimation say about how my response varies as one (or more) of my covariates changes? That is the question that is answered by profile plots. Profile plots are also referred to as plots of estimated (or expected, or least-squares) means, though that is unnecessarily restrictive when considering models of binary, count, and ordered outcomes. In the latter cases, we might prefer to say they plot conditional expectations of responses, where a response might be a probability.

What we do with the other covariates depends on the questions we wish to answer. Sometimes we wish to hold other covariates at fixed values, and sometimes we wish to average the response over their values. `margins` can do either, so you can graph either.

We can fit a fully factorial two-way ANOVA of systolic blood pressure on age group and sex using the NHANES II data.

```
. use http://www.stata-press.com/data/r12/nhanes2
. anova bpsystol agegrp##sex
```

```
                   Number of obs =   10351     R-squared     =  0.2497
                   Root MSE      = 20.2209     Adj R-squared =  0.2489

      Source |  Partial SS    df       MS           F     Prob > F
-------------+----------------------------------------------------
       Model |  1407229.28    11  127929.935     312.88     0.0000

      agegrp |  1243037.82     5  248607.565     608.02     0.0000
         sex |  27728.3794     1  27728.3794      67.81     0.0000
agegrp#sex |   88675.043     5  17735.0086      43.37     0.0000

    Residual |  4227440.75 10339  408.882943
-------------+----------------------------------------------------
       Total |  5634670.03 10350  544.412563
```

If you are more comfortable with regression than ANOVA, then type

```
. regress bpsystol agegrp##sex
```

The `anova` and `regress` commands fit identical models. The output from `anova` displays all the terms in the model and thus tends to be more conducive to exploration with `margins` and `marginsplot`.

We estimate the predictive margins of systolic blood pressure for each age group using `margins`.

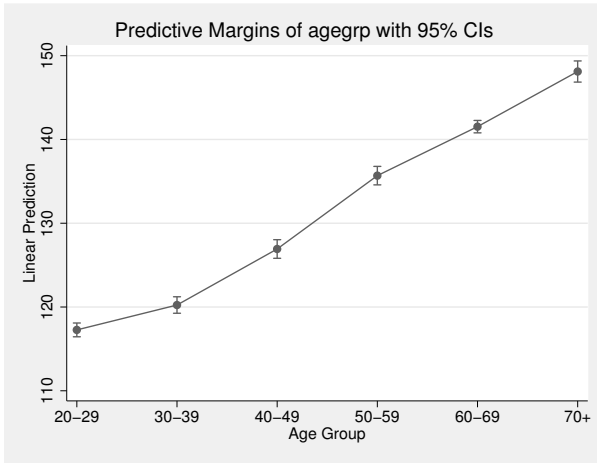
```
. margins agegrp
Predictive margins                              Number of obs   =      10351
Expression   : Linear prediction, predict()
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
agegrp						
1	117.2684	.419845	279.31	0.000	116.4455	118.0913
2	120.2383	.5020813	239.48	0.000	119.2542	121.2224
3	126.9255	.56699	223.86	0.000	125.8142	128.0368
4	135.682	.5628593	241.06	0.000	134.5788	136.7852
5	141.5285	.3781197	374.30	0.000	140.7874	142.2696
6	148.1096	.6445073	229.80	0.000	146.8464	149.3728

The six predictive margins are just the averages of the predictions over the estimation sample, holding `agegrp` to each of its six levels. If this were a designed experiment rather than survey data, we might wish to assume the cells are balanced—that they have the same number of observations—and thus estimate what are often called expected means or least-squares means. To do that, we would simply add the `asbalanced` option to the `margins` command. The NHANES II data are decidedly unbalanced over `sex#agegrp` cells. So much so that it is unreasonable to assume the cells are balanced.

We graph the results:

```
. marginsplot
```



Profile plots are often drawn without confidence intervals (CIs). The CIs may be removed by adding the `noci` option. We prefer to see the CIs.

Disciplines vary widely in their use of the term profile plot. Some disciplines consider any connected plot of a response over values of other variables to be a profile plot. By that definition, most graphs in this entry are profile plots.

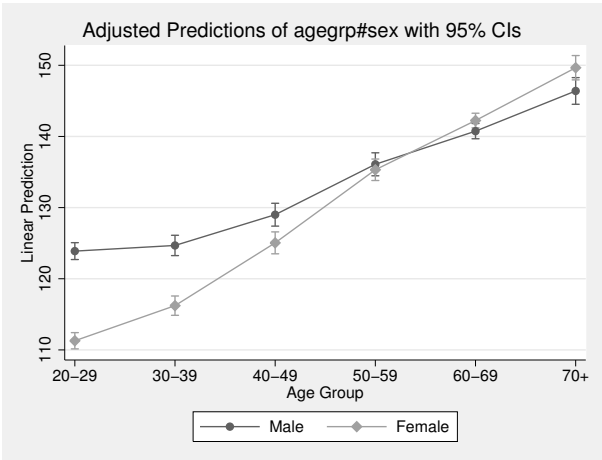
Interaction plots

Interaction plots are often used to explore the form of an interaction. The interaction term in our ANOVA results is highly significant. Are the interaction effects also large enough to matter? What form do they take? We can answer these questions by fixing `agegrp` and `sex` to each possible combination of the two covariates and estimating the margins for those cells.

```
. margins agegrp#sex
```

Then we can graph the results:

```
. marginsplot
```



It is clear that the effect of age differs by sex—there is an interaction. If there were no interaction, then the two lines would be parallel.

While males start out with higher systolic blood pressure, females catch up to the males as age increases and may even surpass males in the upper age groups. We say "may" because we cannot tell if the differences are statistically significant. The CIs overlap for the top three age groups. It is tempting to conclude from this overlap that the differences are not statistically significant. Do not fall into this trap. Likewise, do not fall into the trap that the first three age groups are different because their CIs do not overlap. The CIs are for the point estimates, not the differences. There is a covariance between the differences that we must consider if we are to make statements about those differences.

Contrasts of margins—effects (discrete marginal effects)

To assess the differences, all we need do is ask `margins` to contrast the sets of effects that we just estimated; see [R] **margins, contrast**. With only two groups in sex, it does not matter much which contrast operator we choose. We will use the reference contrast. It will compare the difference between males and females, with males (the first category) as the reference category.

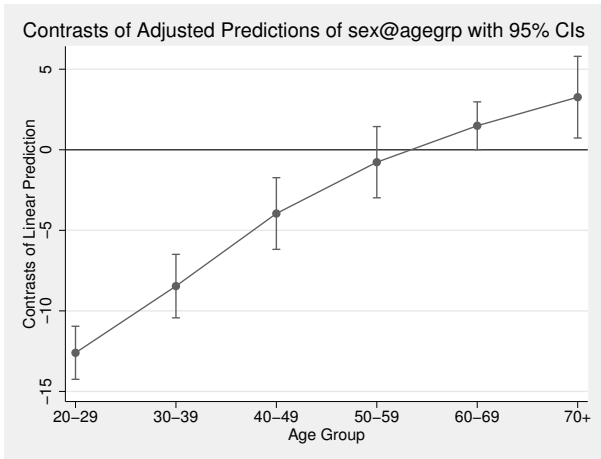
```
. margins r.sex@agegrp
Contrasts of adjusted predictions
Expression   : Linear prediction, predict()
```

	df	chi2	P>chi2
sex@agegrp			
(2 vs 1) 1	1	224.92	0.0000
(2 vs 1) 2	1	70.82	0.0000
(2 vs 1) 3	1	12.15	0.0005
(2 vs 1) 4	1	0.47	0.4949
(2 vs 1) 5	1	3.88	0.0488
(2 vs 1) 6	1	6.37	0.0116
Joint	6	318.62	0.0000

	Contrast	Delta-method Std. Err.	[95% Conf.	Interval]
sex@agegrp				
(2 vs 1) 1	-12.60132	.8402299	-14.24814	-10.9545
(2 vs 1) 2	-8.461161	1.005448	-10.4318	-6.490518
(2 vs 1) 3	-3.956451	1.134878	-6.180771	-1.732131
(2 vs 1) 4	-.7699782	1.128119	-2.98105	1.441094
(2 vs 1) 5	1.491684	.756906	.0081759	2.975193
(2 vs 1) 6	3.264762	1.293325	.7298908	5.799633

Because we are looking for effects that are different from 0, we will add a reference line at 0 to our graph.

```
. marginsplot, yline(0)
```



We can now say that females' systolic blood pressure is substantially and significantly lower than males' in the first three age groups but is significantly higher in the last two age groups. Despite the overlapping CIs for the last two age groups in the interaction graph, the effect of sex is significant in these age groups.

The terminology for what we just estimated and graphed varies widely across disciplines. Those versed in design of experiments refer to these values as contrasts or effects. Economists and some other

social scientists call them marginal or partial effects. The latter groups might be more comfortable if we avoided the whole concept of contrasts and instead estimated the effects by typing

```
. margins agegrp, dydx(sex)
```

This will produce estimates that are identical to those shown above, and we can graph them by typing `marginsplot`.

The advantage of using the contrast notation and thinking in contrasts is most evident when we take marginal effects with respect to a categorical covariate with more than two levels. Marginal effects for each level of the covariate will be taken with respect to a specified base level. Contrasts are much more flexible. Using the `r.` operator, we can reproduce the marginal-effects results by taking derivatives with respect to a reference level (as we saw above.) We can also estimate the marginal effect of first moving from level 1 to level 2, then from level 2 to level 3, then from level 3 to level 4, ... using the `ar.` or "reverse adjacent" operator. Adjacent effects (marginal effects) can be valuable when evaluating an ordinal covariate, such as `agegrp` in our current model. For a discussion of contrasts, see [R] **contrast** and [R] **margins, contrast**.

Three-way interactions

`marginsplot` can handle any number of covariates in your `margins` command. Consider the three-way ANOVA model that results from adding an indicator for whether an individual has been diagnosed with diabetes. We will fully interact the new covariate with the others in the model.

```
. anova bpsystol agegrp##sex##diabetes
                          Number of obs =   10349     R-squared     =  0.2572
                          Root MSE      =  20.131     Adj R-squared =  0.2556
```

Source	Partial SS	df	MS	F	Prob > F
Model	1448983.17	23	62999.2681	155.45	0.0000
agegrp	107963.582	5	21592.7164	53.28	0.0000
sex	1232.79267	1	1232.79267	3.04	0.0812
agegrp#sex	11679.5925	5	2335.91849	5.76	0.0000
diabetes	7324.98924	1	7324.98924	18.07	0.0000
agegrp#diabetes	5484.54623	5	1096.90925	2.71	0.0189
sex#diabetes	102.988239	1	102.988239	0.25	0.6142
agegrp#sex#diabetes	4863.14971	5	972.629943	2.40	0.0349
Residual	4184296.88	10325	405.258778		
Total	5633280.05	10348	544.38346		

The three-way interaction is significant, as is the main effect of `diabetes` and its interaction with `agegrp`.

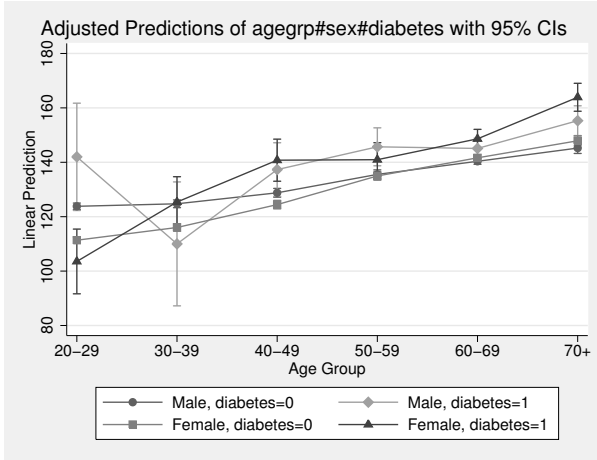
Again, if you are more comfortable with regression than ANOVA, you may type

```
. regress bpsystol agegrp##sex##diabetes
```

The `margins` and `marginsplot` results will be the same.

We estimate the expected cell means for each combination of `agegrp`, `sex`, and `diabetes`, and then graph the results by typing

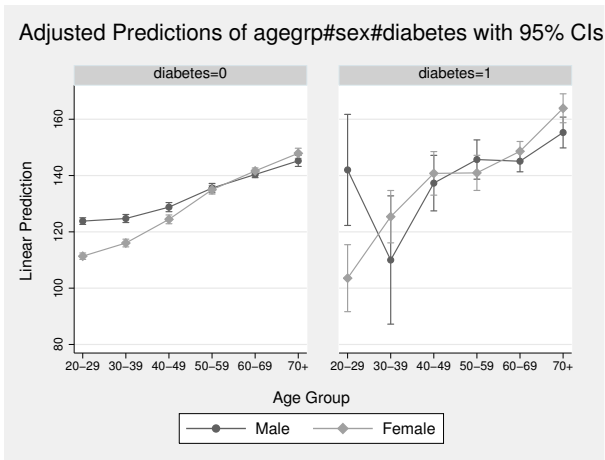
```
. margins agegrp#sex#diabetes
(output omitted)
. marginsplot
```



The graph is busy and difficult to interpret.

We can make it better by putting those with diabetes on one subgraph and those without on another:

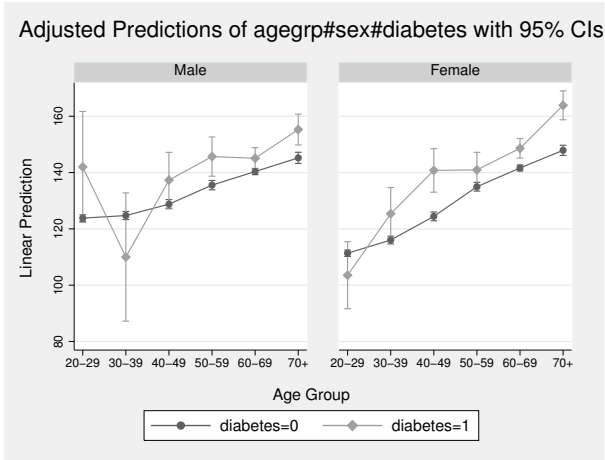
```
. marginsplot, by(diabetes)
```



We notice much larger CIs for diabetics. That is not surprising because our sample contains only 499 diabetics compared with 9,850 nondiabetics.

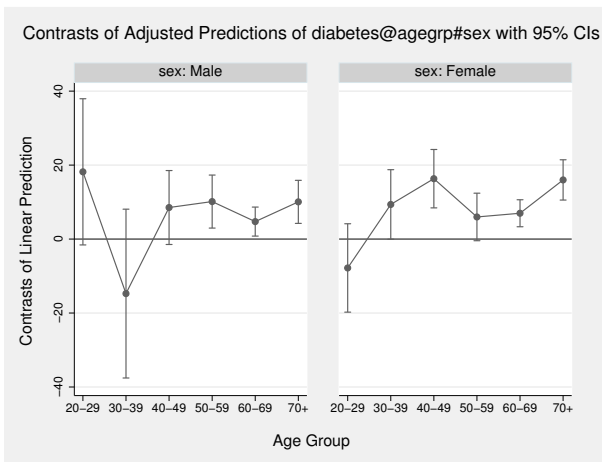
A more interesting way to arrange the plots is by grouping the subgraphs on `sex`:

```
. marginsplot, by(sex)
```



Aside from increased systolic blood pressure in the upper-age groups, which we saw earlier, it appears that those with diabetes are at greater risk of higher systolic blood pressure for many upper-age groups. We can check that by having `margins` estimate the differences between diabetics and nondiabetics, and graphing the results.

```
. margins r.diabetes@agegrp#sex
(output omitted)
. marginsplot, by(sex) yline(0)
```



With CIs above 0 for six of eight age groups over 40, this graph provides evidence that diabetes is related to higher blood pressure in those over 40.

Continuous covariates

margins and marginsplot are just as useful with continuous covariates as they are with factor variables. As a variation on our ANOVA/regression models, let's move to a logistic regression, using as our dependent variable an indicator for whether a person has high blood pressure. We introduce a continuous covariate—body mass index (BMI), a measure of weight relative to height. High BMI is often associated with high blood pressure. We will allow the effect of BMI to vary across sexes, age groups, and sex/age combinations by fully interacting the covariates.

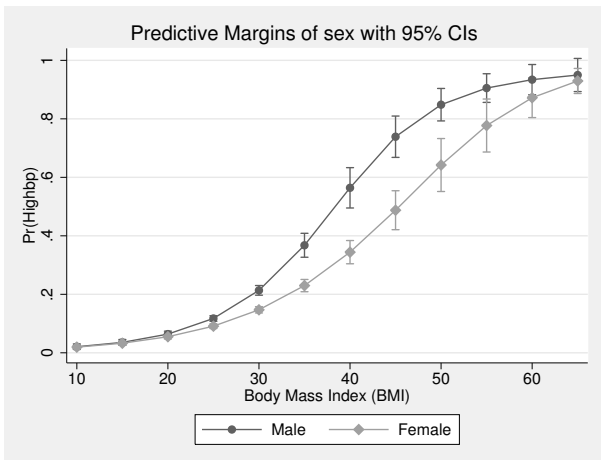
```
. logistic highbp sex##agegrp##c.bmi
```

If we wished, we could perform all the analyses above on this model. Instead of estimating margins, contrasts, and marginal effects on the level of systolic blood pressure, we would be estimating margins, contrasts, and marginal effects on the probability of having high blood pressure. You can see those results by repeating any of the prior commands that involve sex and agegrp. In this section, we will focus on the continuous covariate bmi.

With continuous covariates, rather than specify them in the *marginlist* of margins, we specify the specific values at which we want the covariate evaluated in an at() option. at() options are very flexible, and there are many ways to specify values; see *Syntax of at()* in [R] **margins**.

BMI in our sample ranges from 12.4 to 61.2. Let's estimate the predictive margins for males and females at levels of BMI from 10 through 65 at intervals of 5 and graph the results:

```
. margins sex, at(bmi=(10(5)65))
(output omitted)
. marginsplot, xlabel(10(10)60)
```

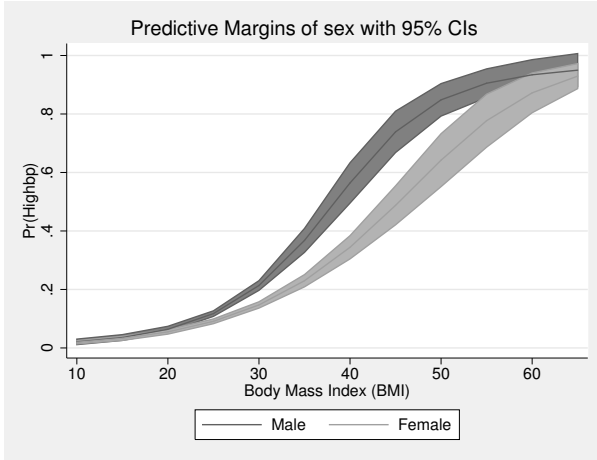


We added the xlabel(10(10)60) option to improve the labeling of the x axis. You may add any *twoway_options* (see [G-3] ***twoway_options***) to the marginsplot command.

For a given BMI, males are generally more susceptible to high blood pressure, though the effect is attenuated by the logistic response when the probabilities approach 0 or 1.

Because bmi is continuous, we might prefer to see the response graphed using a line. We might also prefer that the CIs be plotted as areas. We change the plottype of the response by using the recast() option and the plottype of the CI by using the recastci() option:

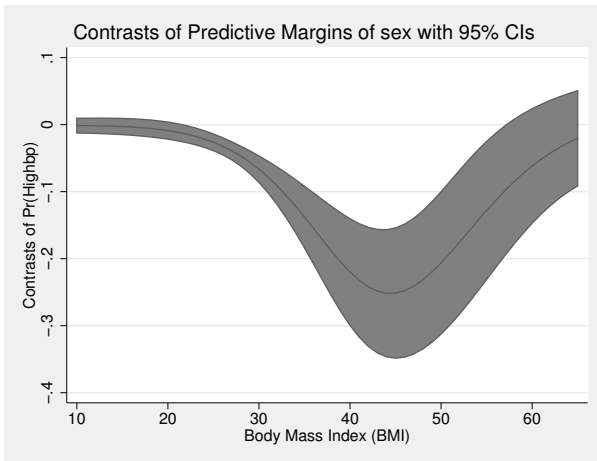
```
. marginsplot, xlabel(10(10)60) recast(line) recastci(rarea)
```



The CIs are a little dark for our tastes. You can dim them a bit by reducing the intensity of their color. Adding `ciopts(color(*.8))` to our `marginsplot` command will do that. Any plot option accepted by `twoway rarea` (see [G-2] **graph twoway rarea**) may be specified in a `ciopts()` option.

Given their confidence regions, the male and female profiles appear to be statistically different over most of the range of BMI. As with the profiles of categorical covariates, we can check that assertion by contrasting the two profiles on `sex` and graphing the results. Let's improve the smoothness of the response by specifying intervals of 1 instead of 5.

```
. margins r.sex, at(bmi=(10(1)65))
```
(*output omitted*)
```
. marginsplot, xlabel(10(10)60) recast(line) recastci(rarea)
```



We see that the difference between the sexes is largest at a BMI of about 45 and that the sexes respond more similarly with very high and very low BMI. This shape is largely determined by the response of the logistic function, which is attenuated near probabilities 0 and 1, combined with the fact that the lowest measured BMIs are associated with extremely low probabilities of high blood pressure and the highest measured BMIs are associated with high probabilities of high blood pressure.

As when we contrasted profiles of categorical variables, different disciplines will think of this graph differently. Those familiar with designed experiments will be comfortable with the terms used above—this is a contrast of profiles, or a profile of effects, or a profile of a contrast. Many social scientists will prefer to think of this as a graph of marginal or partial effects. For them, this is a plot of the discrete marginal effect of being female for various levels of BMI. They can obtain an identical graph, with labeling more appropriate for the marginal effect's interpretation, by typing

```
. margins, at(bmi=(10(1)65)) dydx(sex)
. marginsplot, xlabel(10(10)60) recast(line) recastci(rarea)
```

We can also plot profiles of the response of BMI by levels of another continuous covariate (rather than by the categorical variable `sex`). To do so, we will need another continuous variable in our model. We have been using age groups as a covariate to emphasize the treatment of categorical variables and to allow the effect of age to be flexible. Our dataset also has age recorded in integer years. We replace `agegrp` with continuous `age` in our logistic regression.

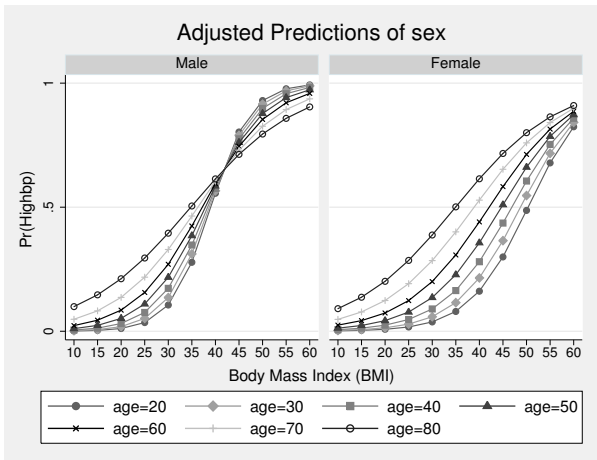
```
. logistic highbp sex##c.age##c.bmi
```

We can now obtain profiles of BMI for different ages by specifying ranges for both `bmi` and `age` in a single `at()` option on the `margins` command:

```
. margins sex, at(bmi=(10(5)60) age=(20(10)80))
```

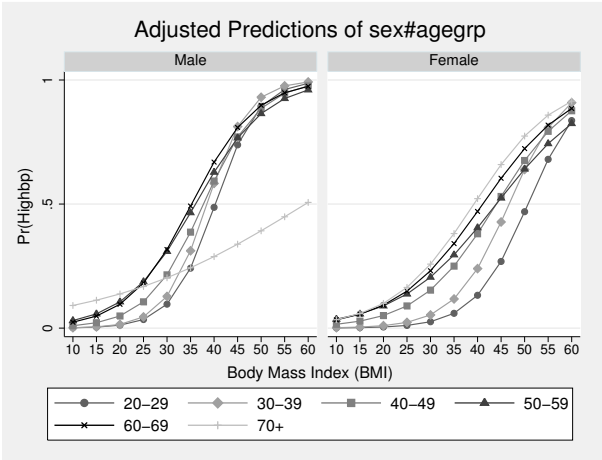
With seven ages specified, we have many profiles, so we will dispense with the CIs by adding the `noci` option and also tidy up the graph by asking for four columns in the legend:

```
. marginsplot, noci by(sex) legend(cols(4))
```



Our model seems to indicate that males have a much sharper reaction to body mass indices than do females. Likewise, younger subjects display a sharper response, while older subjects have a more gradual response with earlier onset. That interpretation might be a result of our parametric treatment of `age`. As it turns out, the interpretation holds if we allow age to take more flexible forms or return to our use of age groups, which allows each of seven age groups to have unique BMI profiles. Here are the commands to perform that analysis:

```
. logistic highbp sex##agegrp##c.bmi
  (output omitted)
. margins sex#agegrp, at(bmi=(10(5)60))
  (output omitted)
. marginsplot, noci by(sex) legend(cols(4))
```



Plots at every value of a continuous covariate

In some cases, the specific values of a continuous covariate are important, and we want to plot the response at those specific values. Return to our logistic example with age treated as a continuous covariate.

```
. logistic highbp sex##c.age##c.bmi
```

We can use a programming trick to extract all the values of age and then supply them in an `at()` option, just as we would any list of values.

```
. levelsof age
. margins sex, at(age=(`r(levels)'))
```

See [P] **levelsof** for a discussion of the `levelsof` command. `levelsof` returns in `r(levels)` the sorted list of unique values of the specified *varlist*, in our case, `age`.

We can then plot the results using `marginsplot`.

This is not a very interesting trick when using our `age` variable, which is recorded as integers from 20 to 74, but the approach will work with almost any continuous variable. In our model, `bmi` might seem more interesting, but there are 9,941 unique values of `bmi` in our dataset. A graph cannot resolve so many different values. For that reason, we usually recommend against plotting at every value of a covariate. Instead, graph at reasonable values over the range of the covariate by using the `at()` option, as we did earlier. This trick is best reserved for variables with a few, or at most a few dozen, unique values.

Contrasts of at() groups—discrete effects

We have previously contrasted across the values of factor variables in our model. Put another way, we have estimated the discrete marginal effects of factor variables. We can do the same for the levels of variables in `at()` specifications and across separate `at()` specifications.

Returning to one of our logistic models and its margins, we earlier estimated the predictive margins of BMI at 5-unit intervals for both sexes. These are the commands we typed:

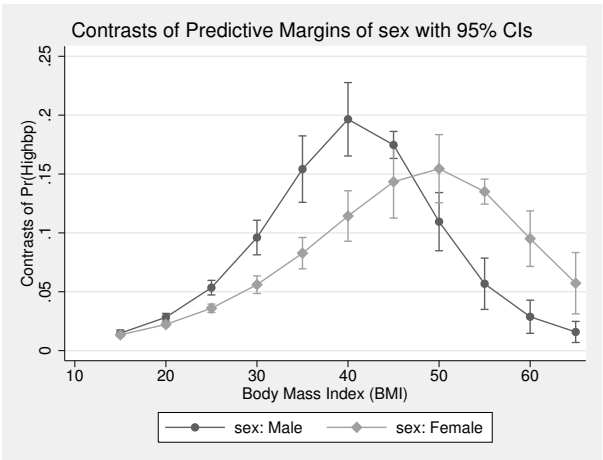
```
. logistic highbp sex##agegrp##c.bmi
. margins sex, at(bmi=(10(5)65))
. marginsplot, xlabel(10(10)60)
```

We can estimate the discrete effects by `sex` of `bmi` moving from 10 to 15, then from 15 to 20, ..., and then from 60 to 65 by contrasting the levels of the `at()` groups using the reverse-adjacent contrast operator (`ar.`). We specify the operator within the `atcontrast()` suboption of the `contrast()` option. We need to specify one other option. By default, `margins, contrast` will apply a contrast to all variables in its *marginlist* when a contrast has been requested. In this case, we do not want to contrast across sexes but rather to contrast across the levels of BMI within each sex. To prevent `margins` from contrasting across the sexes, we specify the `marginswithin` option. Our `margins` command is

```
. margins sex, at(bmi=(10(5)65)) contrast(atcontrast(ar._at) marginswithin)
```

And we graph the results using `marginsplot`:

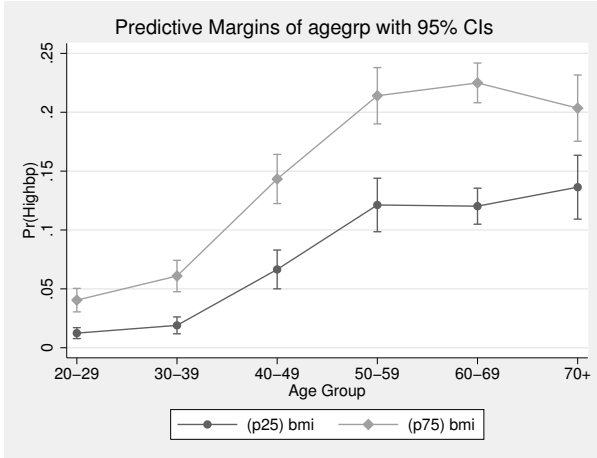
```
. marginsplot
```



The graph shows the contrasts (or if you prefer, discrete changes) in the probability of high blood pressure by sex as one increases BMI in 5-unit increments.

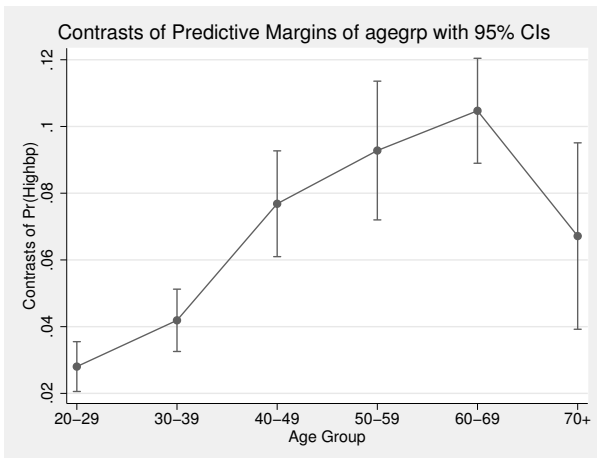
We can even estimate contrasts (discrete effects) across `at()` options. To start, let's compare the age-group profiles of the probability of high blood pressure for those in the 25th and 75th percentile of BMI.

```
. margins agegrp, at((p25) bmi) at((p75) bmi)
  (output omitted)
. marginsplot
```



For each age group, people whose BMI is at the 75th percentile have a much higher probability of high blood pressure than those at the 25th percentile. What is that difference in probability and its CI? To contrast across the percentiles of BMI within age groups, we again specify a contrast operator on the `at()` groups using `atcontrast()`, and we also tell `margins` to perform that contrast within the levels of the *marginlist* by using the `marginswithin` option.

```
. margins agegrp, at((p25) bmi) at((p75) bmi)
> contrast(atcontrast(r._at) marginswithin)
  (output omitted)
. marginsplot
```



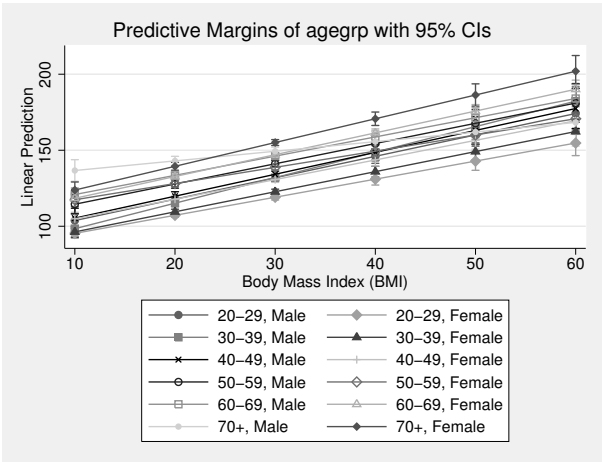
The differences in probability between 25th and 75th BMI percentiles are clearly significantly greater than 0 and appear to be larger for those in higher age groups. The point estimate for those over 70 drops but has a large CI.

Controlling the graph's dimensions

Thus far, `marginsplot` has miraculously done almost exactly what we want in most cases. The things we want on the x axis have been there, the choice of plots has made sense, etc. Some of that luck sprang from the relatively simple analyses we were performing, and some was from careful specification of our `margins` command. Sometimes, we will not be so lucky.

Consider the following `regress`, `margins`, and `marginsplot` commands:

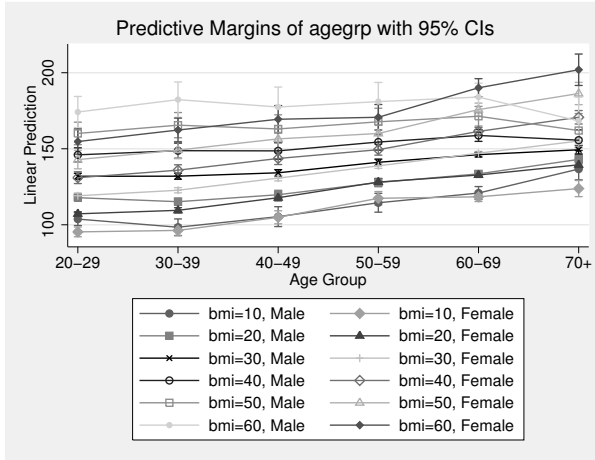
```
. regress bpsystol agegrp##sex##c.bmi
(output omitted)
. margins agegrp, over(sex) at(bmi=(10(10)60))
(output omitted)
. marginsplot
```



By default, `marginsplot` places the levels of the first multilevel `at()` specification on the x axis, and then usually plots the levels of all remaining variables as connected lines. That is what we see in the graph above—`bmi`, the `at()` variable, is on the x axis, and each combination of `agegrp` and `sex` is plotted as a separate connected line. If there is no multilevel `at()` specification, then the first variable in *marginlist* becomes the x axis. There are many more rules, but it is usually best to simply type `marginsplot` and see what happens. If you do not like `marginsplot`'s choices, change them.

What if we wanted `agegrp` on the x axis instead of BMI? We tell `marginsplot` to make that change by specifying `agegrp` in the `xdimension()` option:

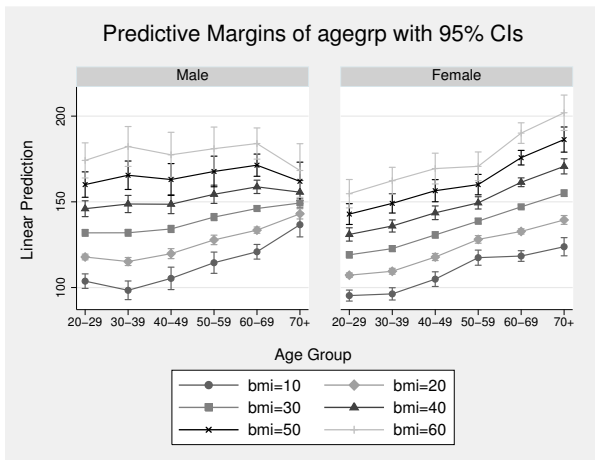
```
. marginsplot, xdimension(agegrp)
  Variables that uniquely identify margins: bmi agegrp sex
```



We have been suppressing the Results window output for `marginsplot`, but that output is helpful if we want to change how things are plotted. You may specify any variable used in your `margins` command in any of the dimension options—`xdimension()`, `plotdimension()`, `bydimension()`, and `graphdimension()`. (In fact, there are some pseudovariables that you may also specify in some cases; see *Addendum: Advanced uses of dimlist* for details.) `marginsplot` tries to help you narrow your choices by listing a set of variables that uniquely identify all your margins. You are not restricted to this list.

We have a different x axis and a different set of plots, but our graph is still busy and difficult to read. We can make it better by creating separate graph panels for each sex. We do that by adding a `bydimension()` option with `sex` as the argument.

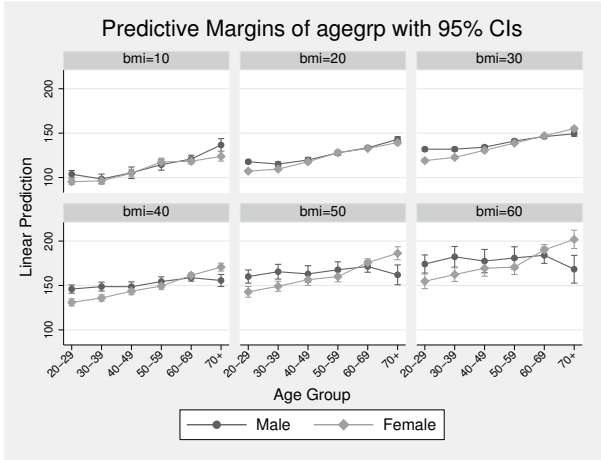
```
. marginsplot, xdimension(agegrp) bydimension(sex)
```



The patterns and the differences between males and females are now easier to see.

If our interest is in comparing males and females, we might even choose to create a separate panel for each level of BMI:

```
. marginsplot, xdimension(agegrp) bydimension(bmi) xlabel(, angle(45))
```



The x-axis labels did not fit, so we angled them.

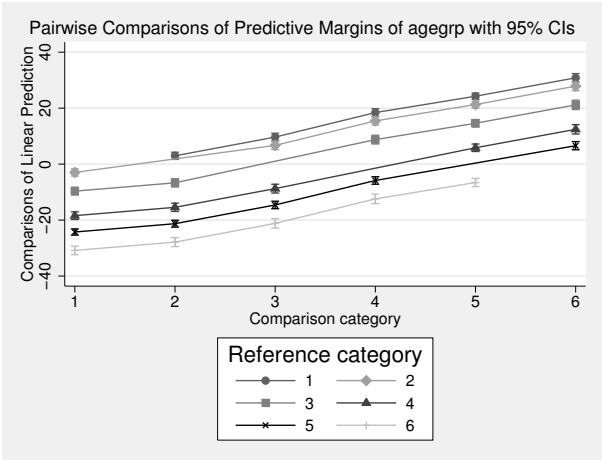
We leave you to explore the use of the `graphdimension()` option. It is much like `bydimension()` but creates separate graphs rather than separate panels. Operationally, the `plotdimension()` option is rarely used. All variables not in the x dimension and not specified elsewhere become the plotted connected lines.

You will likely use the dimension options frequently. This is one of the rare cases where we recommend using the minimal abbreviations of the options—`x()` for `xdimension()`, `plot()` for `plotdimension()`, `by()` for `bydimension()`, and `graph()` for `graphdimension()`. The abbreviations are easy to read and just as meaningful as the full option names. The full names exist to reinforce the relationship between the dimension options.

Pairwise comparisons

`marginsplot` can graph the results of `margins, pwcompare`; see [R] **margins, pwcompare**. We return to one of our ANOVA examples. Here we request pairwise comparisons with the `pwcompare` option of `margins`, and we request Bonferroni-adjusted CIs with the `mcompare()` option:

```
. anova bpsystol agegrp##sex
  (output omitted)
. margins agegrp, pwcompare mcompare(bonferroni)
  (output omitted)
. marginsplot
```



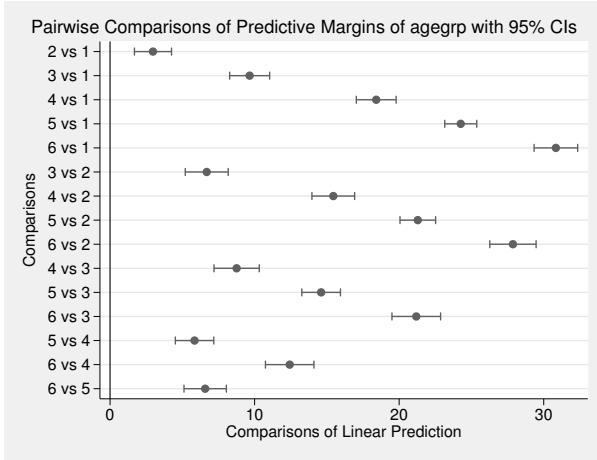
Each connected line plot in the graph represents a reference age-group category for the pairwise comparison. The ticks on the x axis represent comparison age-group categories. So, each plot is a profile for a reference category showing its comparison to each other category.

Horizontal is sometimes better

Another interesting way to graph pairwise comparisons is to simply plot each comparison and label the two categories being compared. This type of graph works better if it is oriented horizontally rather than vertically.

Continuing with the example above, we will switch the graph to horizontal. We will also make several changes to display the graph better. We specify that only `unique` comparisons be plotted. The graph above plotted both 1 versus 2 and 2 versus 1, which are the same comparison with opposite signs. We add a reference line at 0 because we are interested in comparisons that differ from 0. This graph looks better without the connecting lines, so we add the option `recast(scatter)`. We also reverse the y scale so that the smallest levels of age group appear at the top of the axis.

```
. marginsplot, horizontal unique xline(0) recast(scatter) yscale(reverse)
```



All the comparisons differ from 0, so all our age groups are statistically different from each other.

The `horizontal` option can be useful outside of pairwise comparisons. Profile plots are usually oriented vertically. However, when your covariates have long labels or there are many levels at which the margins are being evaluated, the graph may be easier to read when rendered horizontally.

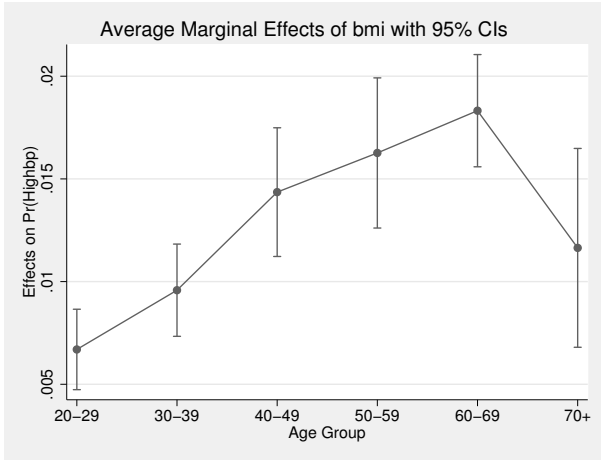
Marginal effects

We have seen how to graph discrete effects for factor variables and continuous variables by using contrasts, and optionally by using the `dydx()` option of `margins`: *Contrasts of margins—effects (discrete marginal effects)* and *Continuous covariates*. Let's now consider graphing instantaneous marginal effects for continuous covariates. Begin by refitting our logistic model of high blood pressure as a function of sex, age, and BMI:

```
. logistic highbp sex##agegrp##c.bmi
```

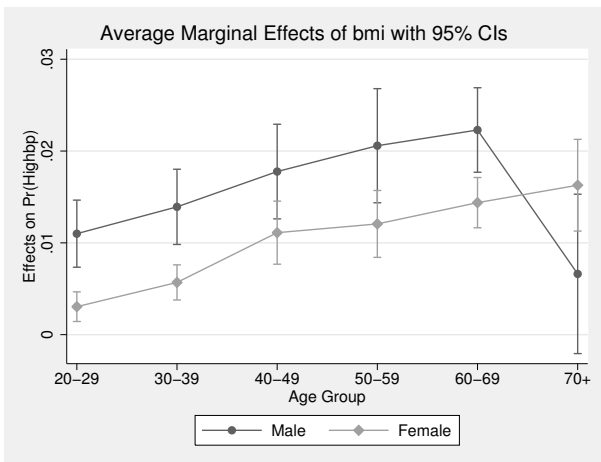
We estimate the average marginal effect of BMI on the probability of high blood pressure for each age group and then graph the results by typing

```
. margins agegrp, dydx(bmi)
(output omitted)
. marginsplot
```



These are the conditional expectations of the marginal effects treating everyone in the sample as though they were in each age group. We can estimate fully conditional marginal effects that do not depend on averaging over the sample by also margining on our one remaining covariate—`sex`.

```
. margins agegrp#sex, dydx(bmi)
(output omitted)
. marginsplot
```



The effect of BMI on the probability of high blood pressure looks to increase with age and is also higher for males than for females.

You may want to confirm that assertion by contrasting across sexes within `agegrp`:

```
. margins r.sex@agegrp, dydx(bmi)
```

Plotting a subset of the results from margins

marginsplot plots all the margins produced by the preceding margins command. If you want a graph that does not include all the margins, then enter a margins command that produces a reduced set of margins. Obvious ways to reduce the number of margins include not specifying some factors or interactions in the *marginlist* of margins, not specifying some at() or over() options, or reducing the values specified in an at() option. A less obvious technique uses selection lists in factor operators to select specific sets of levels from factor variables specified in the *marginlist*.

Instead of typing

```
. margins agegrp
```

which will give you margins for all six age groups in our sample, type

```
. margins i(2/4).agegrp
```

which will give you only three margins—those for groups 2, 3, and 4. See [U] **11.4.3.4 Selecting levels**.

Advanced usage

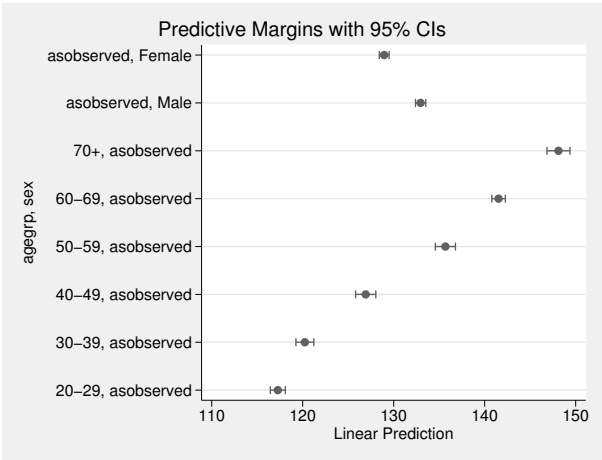
margins is incredibly flexible in the statistics it can estimate and in the grouping of those estimates. Many of the estimates that margins can produce do not make convincing graphs. marginsplot plots the results of any margins command, regardless of whether the resulting graph is easily interpreted. Here we demonstrate some options that can make complicated margins into graphs that are somewhat more useful than those produced by marginsplot's defaults. Others may find truly useful applications for these approaches.

Plots with multiple terms

Margins plots are rarely interesting when you specify multiple terms on your margins command, for example, margins a b. Such plots often compare things that are not comparable. The defaults for marginsplot rarely produce useful plots with multiple terms. Perhaps the most interesting graph in such cases puts all the levels of all the terms together on the vertical axis and plots their margins on the horizontal axis. We do that by including the *marginlist* from margins in an xdimension() option on marginsplot. The long labels on such graphs look better with a horizontal orientation, and there is no need to connect the margin estimates, so we specify the recast(scatter) option.

Using one of our ANOVA examples from earlier,

```
. anova bpsystol agegrp##sex
(output omitted)
. margins agegrp sex
(output omitted)
. marginsplot, xdimension(agegrp sex) horizontal recast(scatter)
```



The "asobserved" notations in the y-axis labels are informing us that, for example, when the margin for females is evaluated, the values of age group are taken as they are observed in the dataset. The margin is computed as an average over those values.

Plots with multiple at() options

Some disciplines like to compute margins at the means of other covariates in their model and others like to compute the response for each observation and then take the means of the response. These correspond to the `margins` options `at((mean) _all)` and `at((asobserved) _all)`. For responses that are linear functions of the coefficients, such as `predict` after `regress`, the two computations yield identical results. For responses that are nonlinear functions of the coefficients, the two computations estimate different things.

Using one of our logistic models of high blood pressure,

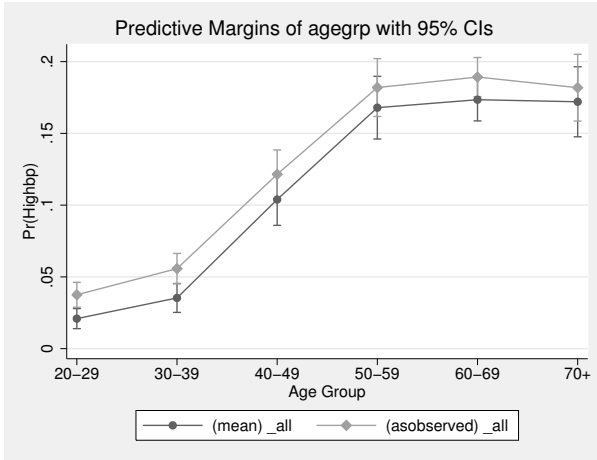
```
. logistic highbp sex##agegrp##c.bmi
```

and computing both sets of margins for each age group,

```
. margins agegrp, at((mean) _all) at((asobserved) _all)
```

we can use `marginsplot` to compare the approaches:

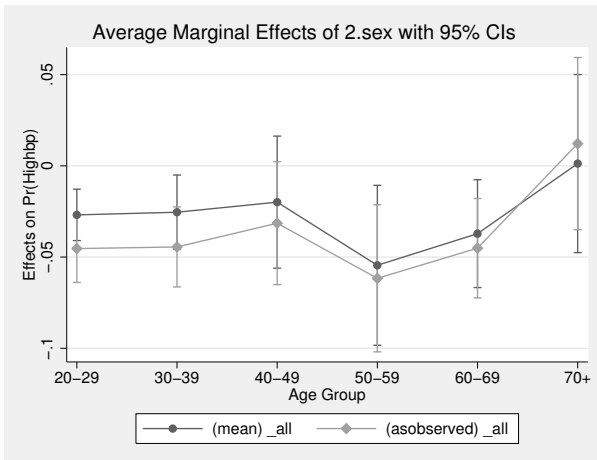
```
. marginsplot
```



In this case, the probabilities of high blood pressure are lower for each age group at the means of `sex` and `bpi` than are the mean probabilities of high blood pressure averaged over the observed values of `sex` and `bpi`.

Such comparisons come up even more frequently when evaluating marginal effects. We can estimate the marginal effects of `sex` at each age group and graph the results by adding `dydx(sex)` to our `margins` command:

```
. margins agegrp, at((mean) _all) at((asobserved) _all) dydx(sex)
  (output omitted)
. marginsplot
```



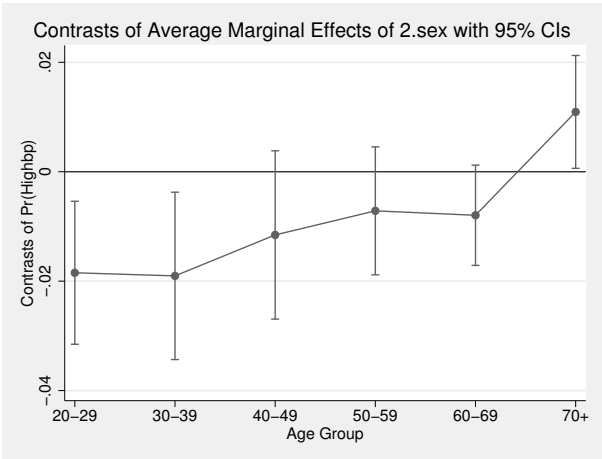
The average marginal effect is smaller for most age groups, but the CIs for both sets of estimates are wide. Can we tell the difference between the estimates? To answer that, we use the now-familiar tactic of taking the contrast of our estimated marginal-effects profiles. That means adding `contrast(atjoint`

`marginswithin`) to our `margins` command. We will also add `mcompare(bonferroni)` to account for the fact that we will be comparing six contrasts.

```
. margins agegrp, at((mean) _all) at((asobserved) _all) dydx(sex)
> contrast(atjoint marginswithin) mcompare(bonferroni)
```

We will also add the familiar reference line at 0 to our graph of the contrasts.

```
. marginsplot, yline(0)
```



While the difference in the estimates of marginal effects is not large, we can distinguish the estimates for three of the six age groups.

The `at()` option of `margins` provides far more flexibility than demonstrated above. It can be used to evaluate a response or marginal effect at almost any point of interest or combinations of such points. See *Syntax of at()* in [R] **margins**.

Adding scatterplots of the data

We can add scatterplots of the observed data to our plots of the margins. The NHANES II dataset is too large for this to be interesting, so for this example, we will use `auto.dta`. We fit mileage on whether the care is foreign and on a quadratic in the weight of the car. We convert the weight into tons (U.S. definition) to improve the scaling, and we format the new `tons` variable to improve its labels on the graph. For our graph, we create separate variables for mileage of domestic and of foreign cars. We fit a fully interacted model so that the effect of weight on mileage can be different for foreign and for domestic cars.

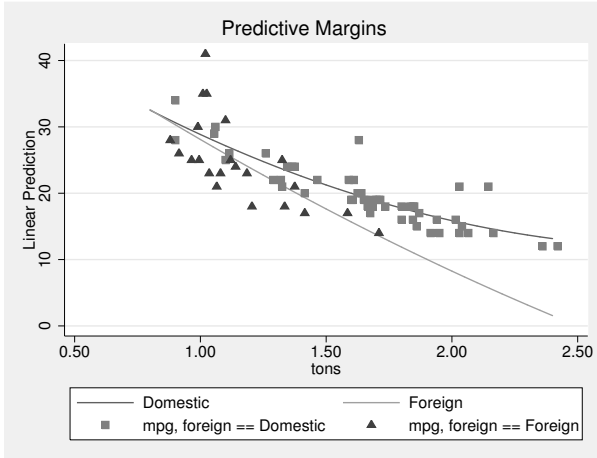
```
. use http://www.stata-press.com/data/r12/auto
. generate tons = weight/2000
. format tons %6.2f
. separate mpg, by(foreign)
. regress mpg foreign##c.tons##c.tons
```

We then estimate the margins over the range of tons, using the option `over(foreign)` to obtain separate estimates for foreign and domestic cars.

```
. margins, at(tons=(.8(.05)2.4)) over(foreign)
```

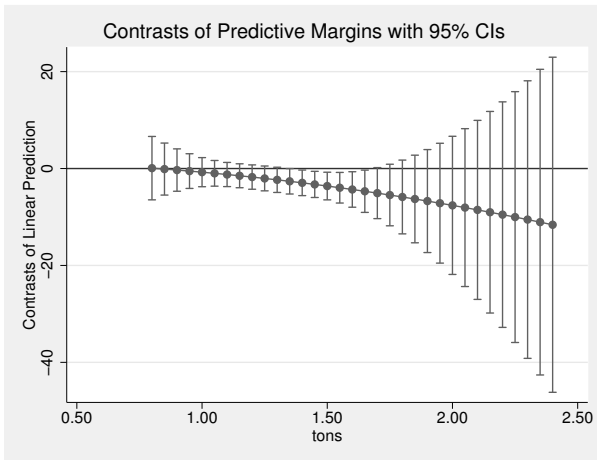
Adding scatterplots of mileage for domestic and foreign cars is easy. We insert into an `addplot()` option of `marginsplot` the same scatterplot syntax for `twoway` that we would type to produce a scatterplot of the data:

```
. marginsplot, addplot(scatter mpg0 tons || scatter mpg1 tons) recast(line) noci
```



Many will be surprised that the mileage profile is higher in 1978 for domestic (U.S. built) cars. Is the difference significant?

```
. margins, at(tons=(.8(.05)2.4)) over(r.for)
  (output omitted)
. marginsplot, yline(0)
```



As we did earlier, we contrast the two profiles. We can discern some difference between the two profiles for midweight vehicles, but otherwise there is insufficient information to believe mileage differs across domestic and foreign cars.

Addendum: Advanced uses of dimlist

dimlist specifies the dimensions from the immediately preceding `margins` command that are to be used for the `marginsplot`'s x axis, plots, subgraphs, and graphs. *dimlist* may contain:

dim	Description
varname	Any variable referenced in the preceding `margins` command.
`at(`*varname*`)`	If a variable is specified in both the *marginlist* or the `over()` option and in the `at()` option of `margins`, then the two uses can be distinguished in `marginsplot` by typing the `at()` variables as `at(`*varname*`)` in *dimlist*.
`_deriv`	If the preceding `margins` command included a `dydx()`, `eyex()`, `dyex()`, or `eydx()` option, *dimlist* may also contain `_deriv` to specify all the variables over which derivatives were taken.
`_term`	If the preceding `margins` command included multiple terms (for example, `margins a b`), then *dimlist* may contain `_term` to enumerate those terms.
`_atopt`	If the preceding `margins` command included multiple `at()` options, then *dimlist* may contain `_atopt` to enumerate those `at()` options.

When the `pairwise` option is specified on `margins`, you may specify dimensions that enumerate the pairwise comparisons.

`_pw`	enumerates all the pairwise comparisons
`_pw0`	enumerates the reference categories of the comparisons
`_pw1`	enumerates the comparison categories of the comparisons

Methods and formulas

`marginsplot` is implemented as an ado-file.

Acknowledgments

StataCorp thanks Phil Ender for consultations and for his programs that demonstrated what could be done in this area. We also thank Michael Mitchell for his generous advice and comprehensive insight into the application of margins and their plots.

Reference

McDowell, A., A. Engel, J. T. Massey, and K. Maurer. 1981. Plan and operation of the Second National Health and Nutrition Examination Survey, 1976–1980. *Vital and Health Statistics* 1(15): 1–144.

Also see

[R] **margins** — Marginal means, predictive margins, and marginal effects

[R] **margins, contrast** — Contrasts of margins

[R] **margins, pwcompare** — Pairwise comparisons of margins

[R] **margins postestimation** — Postestimation tools for margins

Title

matsize — Set the maximum number of variables in a model

Syntax

```
set matsize # [ , permanently ]
```

where 10 ≤ # ≤ 11000 for Stata/MP and Stata/SE and where 10 ≤ # ≤ 800 for Stata/IC.

Description

`set matsize` sets the maximum number of variables that can be included in any of Stata's estimation commands.

For Stata/MP and Stata/SE, the default value is 400, but it may be changed upward or downward. The upper limit is 11,000.

For Stata/IC, the initial value is 400, but it may be changed upward or downward. The upper limit is 800.

This command may not be used with Small Stata; `matsize` is permanently frozen at 100.

Changing `matsize` has no effect on Mata.

Option

`permanently` specifies that, in addition to making the change right now, the `matsize` setting be remembered and become the default setting when you invoke Stata.

Remarks

`set matsize` controls the internal size of matrices that Stata uses. The default of 400 for Stata/IC, for instance, means that linear regression models are limited to 198 independent variables—198 because the constant uses one position and the dependent variable another, making a total of 200.

You may change `matsize` with data in memory, but increasing `matsize` increases the amount of memory consumed by Stata, increasing the probability of page faults and thus of making Stata run more slowly.

▷ Example 1

We wish to fit a model of `y` on the variables `x1` through `x400`. Without thinking, we type

```
. regress y x1-x400
matsize too small
    You have attempted to create a matrix with more than 400 rows or columns
    or to fit a model with more than 400 variables plus ancillary parameters.
    You need to increase matsize by using the set matsize command; see help
    matsize.
r(908);
```

We realize that we need to increase `matsize`, so we type

```
. set matsize 450
. regress y x1-x400
  (output omitted)
```

◁

Programmers should note that the current setting of `matsize` is stored as the c-class value `c(matsize)`; see [P] **creturn**.

Also see

[R] **query** — Display system parameters

[D] **memory** — Memory management

[U] **6 Managing memory**

Title

maximize — Details of iterative maximization

Syntax

Maximum likelihood optimization

mle_cmd ... [, *options*]

Set default maximum iterations

set maxiter # [, permanently]

options	Description
difficult	use a different stepping algorithm in nonconcave regions
technique(*algorithm_spec*)	maximization technique
iterate(#)	perform maximum of # iterations; default is iterate(16000)
[no]log	display an iteration log of the log likelihood; typically, the default
trace	display current parameter vector in iteration log
gradient	display current gradient vector in iteration log
showstep	report steps within an iteration in iteration log
hessian	display current negative Hessian matrix in iteration log
showtolerance	report the calculated result that is compared to the effective convergence criterion
tolerance(#)	tolerance for the coefficient vector; see *Options* for the defaults
ltolerance(#)	tolerance for the log likelihood; see *Options* for the defaults
nrtolerance(#)	tolerance for the scaled gradient; see *Options* for the defaults
qtolerance(#)	when specified with algorithms bhhh, dfp, or bfgs, the $\mathbf{q} - \mathbf{H}$ matrix is used as the final check for convergence rather than nrtolerance() and the $\mathbf{H}$ matrix; seldom used
nonrtolerance	ignore the nrtolerance() option
from(*init_specs*)	initial values for the coefficients

where *algorithm_spec* is

algorithm [# [*algorithm* [#]]...]

algorithm is { nr | bhhh | dfp | bfgs }

and *init_specs* is one of

matname [, skip copy]

{ [*eqname*:]*name* = # | /*eqname* = # } [...]

[# ...], copy

Description

All Stata commands maximize likelihood functions using `moptimize()` and `optimize()`; see *Methods and formulas* below. Commands use the Newton–Raphson method with step halving and special fixups when they encounter nonconcave regions of the likelihood. For details, see [M-5] **moptimize( )** and [M-5] **optimize( )**. For more information about programming maximum likelihood estimators in ado-files and Mata, see [R] **ml** and the fourth edition of *Maximum Likelihood Estimation with Stata* (Gould, Pitblado, and Poi 2010).

`set maxiter` specifies the default maximum number of iterations for estimation commands that iterate. The initial value is `16000`, and # can be `0` to `16000`. To change the maximum number of iterations performed by a particular estimation command, you need not reset `maxiter`; you can specify the `iterate(#)` option. When `iterate(#)` is not specified, the `maxiter` value is used.

Maximization options

`difficult` specifies that the likelihood function is likely to be difficult to maximize because of nonconcave regions. When the message "not concave" appears repeatedly, `ml`'s standard stepping algorithm may not be working well. `difficult` specifies that a different stepping algorithm be used in nonconcave regions. There is no guarantee that `difficult` will work better than the default; sometimes it is better and sometimes it is worse. You should use the `difficult` option only when the default stepper declares convergence and the last iteration is "not concave" or when the default stepper is repeatedly issuing "not concave" messages and producing only tiny improvements in the log likelihood.

`technique(`*algorithm_spec*`)` specifies how the likelihood function is to be maximized. The following algorithms are allowed. For details, see Gould, Pitblado, and Poi (2010).

`technique(nr)` specifies Stata's modified Newton–Raphson (NR) algorithm.

`technique(bhhh)` specifies the Berndt–Hall–Hall–Hausman (BHHH) algorithm.

`technique(dfp)` specifies the Davidon–Fletcher–Powell (DFP) algorithm.

`technique(bfgs)` specifies the Broyden–Fletcher–Goldfarb–Shanno (BFGS) algorithm.

The default is `technique(nr)`.

You can switch between algorithms by specifying more than one in the `technique()` option. By default, an algorithm is used for five iterations before switching to the next algorithm. To specify a different number of iterations, include the number after the technique in the option. For example, specifying `technique(bhhh 10 nr 1000)` requests that `ml` perform 10 iterations with the BHHH algorithm followed by 1000 iterations with the NR algorithm, and then switch back to BHHH for 10 iterations, and so on. The process continues until convergence or until the maximum number of iterations is reached.

`iterate(#)` specifies the maximum number of iterations. When the number of iterations equals `iterate()`, the optimizer stops and presents the current results. If convergence is declared before this threshold is reached, it will stop when convergence is declared. Specifying `iterate(0)` is useful for viewing results evaluated at the initial value of the coefficient vector. Specifying `iterate(0)` and `from()` together allows you to view results evaluated at a specified coefficient vector; however, not all commands allow the `from()` option. The default value of `iterate(#)` for both estimators programmed internally and estimators programmed with `ml` is the current value of `set maxiter`, which is `iterate(16000)` by default.

`log` and `nolog` specify whether an iteration log showing the progress of the log likelihood is to be displayed. For most commands, the log is displayed by default, and `nolog` suppresses it. For a

few commands (such as the svy maximum likelihood estimators), you must specify log to see the log.

trace adds to the iteration log a display of the current parameter vector.

gradient adds to the iteration log a display of the current gradient vector.

showstep adds to the iteration log a report on the steps within an iteration. This option was added so that developers at StataCorp could view the stepping when they were improving the ml optimizer code. At this point, it mainly provides entertainment.

hessian adds to the iteration log a display of the current negative Hessian matrix.

showtolerance adds to the iteration log the calculated value that is compared with the effective convergence criterion at the end of each iteration. Until convergence is achieved, the smallest calculated value is reported.

shownrtolerance is a synonym of showtolerance.

Below we describe the three convergence tolerances. Convergence is declared when the nrtolerance() criterion is met and either the tolerance() or the ltolerance() criterion is also met.

tolerance(#) specifies the tolerance for the coefficient vector. When the relative change in the coefficient vector from one iteration to the next is less than or equal to tolerance(), the tolerance() convergence criterion is satisfied.

tolerance(1e-4) is the default for estimators programmed with ml.

tolerance(1e-6) is the default.

ltolerance(#) specifies the tolerance for the log likelihood. When the relative change in the log likelihood from one iteration to the next is less than or equal to ltolerance(), the ltolerance() convergence is satisfied.

ltolerance(0) is the default for estimators programmed with ml.

ltolerance(1e-7) is the default.

nrtolerance(#) specifies the tolerance for the scaled gradient. Convergence is declared when $\mathbf{g}\mathbf{H}^{-1}\mathbf{g}' <$ nrtolerance(). The default is nrtolerance(1e-5).

qtolerance(#) when specified with algorithms bhhh, dfp, or bfgs uses the $\mathbf{q} - \mathbf{H}$ matrix as the final check for convergence rather than nrtolerance() and the $\mathbf{H}$ matrix.

Beginning with Stata 12, by default, Stata now computes the $\mathbf{H}$ matrix when the $\mathbf{q}-\mathbf{H}$ matrix passes the convergence tolerance, and Stata requires that $\mathbf{H}$ be concave and pass the nrtolerance() criterion before concluding convergence has occurred.

qtolerance() provides a way for the user to obtain Stata's earlier behavior.

nonrtolerance specifies that the default nrtolerance() criterion be turned off.

---

from() specifies initial values for the coefficients. Not all estimators in Stata support this option. You can specify the initial values in one of three ways: by specifying the name of a vector containing the initial values (for example, from(b0), where b0 is a properly labeled vector); by specifying coefficient names with the values (for example, from(age=2.1 /sigma=7.4)); or by specifying a list of values (for example, from(2.1 7.4, copy)). from() is intended for use when doing bootstraps (see [R] **bootstrap**) and in other special situations (for example, with iterate(0)).

Even when the values specified in `from()` are close to the values that maximize the likelihood, only a few iterations may be saved. Poor values in `from()` may lead to convergence problems.

`skip` specifies that any parameters found in the specified initialization vector that are not also found in the model be ignored. The default action is to issue an error message.

`copy` specifies that the list of values or the initialization vector be copied into the initial-value vector by position rather than by name.

Option for set maxiter

`permanently` specifies that, in addition to making the change right now, the `maxiter` setting be remembered and become the default setting when you invoke Stata.

Remarks

Only in rare circumstances would you ever need to specify any of these options, except `nolog`. The `nolog` option is useful for reducing the amount of output appearing in log files.

The following is an example of an iteration log:

```
Iteration 0:   log likelihood = -3791.0251
Iteration 1:   log likelihood =  -3761.738
Iteration 2:   log likelihood = -3758.0632  (not concave)
Iteration 3:   log likelihood = -3758.0447
Iteration 4:   log likelihood = -3757.5861
Iteration 5:   log likelihood =  -3757.474
Iteration 6:   log likelihood = -3757.4613
Iteration 7:   log likelihood = -3757.4606
Iteration 8:   log likelihood = -3757.4606
  (table of results omitted)
```

At iteration 8, the model converged. The message "not concave" at the second iteration is notable. This example was produced using the `heckman` command; its likelihood is not globally concave, so it is not surprising that this message sometimes appears. The other message that is occasionally seen is "backed up". Neither of these messages should be of any concern unless they appear at the final iteration.

If a "not concave" message appears at the last step, there are two possibilities. One is that the result is valid, but there is collinearity in the model that the command did not otherwise catch. Stata checks for obvious collinearity among the independent variables before performing the maximization, but strange collinearities or near collinearities can sometimes arise between coefficients and ancillary parameters. The second, more likely cause for a "not concave" message at the final step is that the optimizer entered a flat region of the likelihood and prematurely declared convergence.

If a "backed up" message appears at the last step, there are also two possibilities. One is that Stata found a perfect maximum and could not step to a better point; if this is the case, all is fine, but this is a highly unlikely occurrence. The second is that the optimizer worked itself into a bad concave spot where the computed gradient and Hessian gave a bad direction for stepping.

If either of these messages appears at the last step, perform the maximization again with the `gradient` option. If the gradient goes to zero, the optimizer has found a maximum that may not be unique but is a maximum. From the standpoint of maximum likelihood estimation, this is a valid result. If the gradient is not zero, it is not a valid result, and you should try tightening up the convergence criterion, or try `ltol(0) tol(1e-7)` to see if the optimizer can work its way out of the bad region.

If you get repeated "not concave" steps with little progress being made at each step, try specifying the `difficult` option. Sometimes `difficult` works wonderfully, reducing the number of iterations and producing convergence at a good (that is, concave) point. Other times, `difficult` works poorly, taking much longer to converge than the default stepper.

Saved results

Maximum likelihood estimators save the following in `e()`:

Scalars

`e(N)`	number of observations	always saved
`e(k)`	number of parameters	always saved
`e(k_eq)`	number of equations in `e(b)`	usually saved
`e(k_eq_model)`	number of equations in overall model test	usually saved
`e(k_dv)`	number of dependent variables	usually saved
`e(df_m)`	model degrees of freedom	always saved
`e(r2_p)`	pseudo-R-squared	sometimes saved
`e(ll)`	log likelihood	always saved
`e(ll_0)`	log likelihood, constant-only model	saved when constant-only model is fit
`e(N_clust)`	number of clusters	saved when `vce(cluster` *clustvar*`)` is specified; see [U] **20.20 Obtaining robust variance estimates**
`e(chi2)`	χ^2	usually saved
`e(p)`	significance of model of test	usually saved
`e(rank)`	rank of `e(V)`	always saved
`e(rank0)`	rank of `e(V)` for constant-only model	saved when constant-only model is fit
`e(ic)`	number of iterations	usually saved
`e(rc)`	return code	usually saved
`e(converged)`	`1` if converged, `0` otherwise	usually saved

Macros		
`e(cmd)`	name of command	always saved
`e(cmdline)`	command as typed	always saved
`e(depvar)`	names of dependent variables	always saved
`e(wtype)`	weight type	saved when weights are specified or implied
`e(wexp)`	weight expression	saved when weights are specified or implied
`e(title)`	title in estimation output	usually saved by commands using `ml`
`e(clustvar)`	name of cluster variable	saved when `vce(cluster` *clustvar*`)` is specified; see [U] **20.20 Obtaining robust variance estimates**
`e(chi2type)`	`Wald` or `LR`; type of model χ^2 test	usually saved
`e(vce)`	*vcetype* specified in `vce()`	saved when command allows (`vce()`)
`e(vcetype)`	title used to label Std. Err.	sometimes saved
`e(opt)`	type of optimization	always saved
`e(which)`	`max` or `min`; whether optimizer is to perform maximization or minimization	always saved
`e(ml_method)`	type of `ml` method	always saved by commands using `ml`
`e(user)`	name of likelihood-evaluator program	always saved
`e(technique)`	from `technique()` option	sometimes saved
`e(singularHmethod)`	`m-marquardt` or `hybrid`; method used when Hessian is singular	sometimes saved[1]
`e(crittype)`	optimization criterion	always saved[1]
`e(properties)`	estimator properties	always saved
`e(predict)`	program used to implement `predict`	usually saved
Matrices		
`e(b)`	coefficient vector	always saved
`e(Cns)`	constraints matrix	sometimes saved
`e(ilog)`	iteration log (up to 20 iterations)	usually saved
`e(gradient)`	gradient vector	usually saved
`e(V)`	variance–covariance matrix of the estimators	always saved
`e(V_modelbased)`	model-based variance	only saved when `e(V)` is neither the OIM nor OPG variance
Functions		
`e(sample)`	marks estimation sample	always saved

1. Type `ereturn list, all` to view these results; see [P] **return**.

See *Saved results* in the manual entry for any maximum likelihood estimator for a list of returned results.

Methods and formulas

Optimization is currently performed by `moptimize()` and `optimize()`, with the former implemented in terms of the latter; see [M-5] **moptimize( )** and [M-5] **optimize( )**. Some estimators use `moptimize()` and `optimize()` directly, and others use the `ml` ado-file interface to `moptimize()`.

Prior to Stata 11, Stata had three separate optimization engines: an internal one used by estimation commands implemented in C code; `ml` implemented in ado-code separately from `moptimize()` and used by most estimators; and `moptimize()` and `optimize()` used by a few recently written

estimators. These days, the internal optimizer and the old version of `ml` are used only under version control. In addition, `arch` and `arima` (see [TS] **arch** and [TS] **arima**) are currently implemented using the old `ml`.

Let L_1 be the log likelihood of the full model (that is, the log-likelihood value shown on the output), and let L_0 be the log likelihood of the "constant-only" model. The likelihood-ratio χ^2 model test is defined as $2(L_1 - L_0)$. The pseudo-R^2 (McFadden 1974) is defined as $1 - L_1/L_0$. This is simply the log likelihood on a scale where 0 corresponds to the "constant-only" model and 1 corresponds to perfect prediction for a discrete model (in which case the overall log likelihood is 0).

Some maximum likelihood routines can report coefficients in an exponentiated form, for example, odds ratios in `logistic`. Let b be the unexponentiated coefficient, s its standard error, and b_0 and b_1 the reported confidence interval for b. In exponentiated form, the point estimate is e^b, the standard error $e^b s$, and the confidence interval e^{b_0} and e^{b_1}. The displayed Z (or t) statistics and p-values are the same as those for the unexponentiated results. This is justified because $e^b = 1$ and $b = 0$ are equivalent hypotheses, and normality is more likely to hold in the b metric.

References

Gould, W. W., J. S. Pitblado, and B. P. Poi. 2010. *Maximum Likelihood Estimation with Stata*. 4th ed. College Station, TX: Stata Press.

McFadden, D. L. 1974. Conditional logit analysis of qualitative choice behavior. In *Frontiers in Econometrics*, ed. P. Zarembka, 105–142. New York: Academic Press.

Also see

[R] **ml** — Maximum likelihood estimation

[SVY] **ml for svy** — Maximum pseudolikelihood estimation for survey data

[M-5] **moptimize( )** — Model optimization

[M-5] **optimize( )** — Function optimization

Title

mean — Estimate means

Syntax

`mean` *varlist* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`stdize(`*varname*`)`	variable identifying strata for standardization
`stdweight(`*varname*`)`	weight variable for standardization
`nostdrescale`	do not rescale the standard weight variable
if/in/over	
`over(`*varlist*[`, nolabel`]`)`	group over subpopulations defined by *varlist*; optionally, suppress group labels
SE/Cluster	
`vce(`*vcetype*`)`	*vcetype* may be `analytic`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noheader`	suppress table header
`nolegend`	suppress table legend
display_options	control column formats and line width
`coeflegend`	display legend instead of statistics

`bootstrap`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `aweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Means

Description

`mean` produces estimates of means, along with standard errors.

Options

Model

`stdize(`*varname*`)` specifies that the point estimates be adjusted by direct standardization across the strata identified by *varname*. This option requires the `stdweight()` option.

`stdweight(`*varname*`)` specifies the weight variable associated with the standard strata identified in the `stdize()` option. The standardization weights must be constant within the standard strata.

`nostdrescale` prevents the standardization weights from being rescaled within the `over()` groups. This option requires `stdize()` but is ignored if the `over()` option is not specified.

if/in/over

`over(`*varlist* [`, nolabel`]`)` specifies that estimates be computed for multiple subpopulations, which are identified by the different values of the variables in *varlist*.

When this option is supplied with one variable name, such as `over(`*varname*`)`, the value labels of *varname* are used to identify the subpopulations. If *varname* does not have labeled values (or there are unlabeled values), the values themselves are used, provided that they are nonnegative integers. Noninteger values, negative values, and labels that are not valid Stata names are substituted with a default identifier.

When `over()` is supplied with multiple variable names, each subpopulation is assigned a unique default identifier.

`nolabel` requests that value labels attached to the variables identifying the subpopulations be ignored.

SE/Cluster

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(analytic)`, the default, uses the analytically derived variance estimator associated with the sample mean.

Reporting

`level(#)`; see [R] **estimation options**.

`noheader` prevents the table header from being displayed. This option implies `nolegend`.

`nolegend` prevents the table legend identifying the subpopulations from being displayed.

display_options: `cformat(%`*fmt*`)` and `nolstretch`; see [R] **estimation options**.

The following option is available with `mean` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Example 1

Using the fuel data from example 2 of [R] **ttest**, we estimate the average mileage of the cars without the fuel treatment (mpg1) and those with the fuel treatment (mpg2).

```
. use http://www.stata-press.com/data/r12/fuel
. mean mpg1 mpg2
Mean estimation                     Number of obs    =      12
```

	Mean	Std. Err.	[95% Conf.	Interval]
mpg1	21	.7881701	19.26525	22.73475
mpg2	22.75	.9384465	20.68449	24.81551

Using these results, we can test the equality of the mileage between the two groups of cars.

```
. test mpg1 = mpg2
 ( 1)  mpg1 - mpg2 = 0
       F(  1,    11) =    5.04
            Prob > F =    0.0463
```

Example 2

In example 1, the joint observations of mpg1 and mpg2 were used to estimate a covariance between their means.

```
. matrix list e(V)
symmetric e(V)[2,2]
            mpg1        mpg2
mpg1   .62121212
mpg2    .4469697   .88068182
```

If the data were organized this way out of convenience but the two variables represent independent samples of cars (coincidentally of the same sample size), we should reshape the data and use the over() option to ensure that the covariance between the means is zero.

```
. use http://www.stata-press.com/data/r12/fuel
. stack mpg1 mpg2, into(mpg) clear
. mean mpg, over(_stack)
Mean estimation                     Number of obs    =      24
            1: _stack = 1
            2: _stack = 2
```

Over	Mean	Std. Err.	[95% Conf.	Interval]
mpg				
1	21	.7881701	19.36955	22.63045
2	22.75	.9384465	20.80868	24.69132

```
. matrix list e(V)
symmetric e(V)[2,2]
             mpg:       mpg:
               1          2
mpg:1  .62121212
mpg:2          0  .88068182
```

Now we can test the equality of the mileage between the two independent groups of cars.

```
. test [mpg]1 = [mpg]2
 ( 1)  [mpg]1 - [mpg]2 = 0
       F(  1,    23) =    2.04
            Prob > F =    0.1667
```

◁

▷ Example 3: standardized means

Suppose that we collected the blood pressure data from example 2 of [R] **dstdize**, and we wish to obtain standardized high blood pressure rates for each city in 1990 and 1992, using, as the standard, the age, sex, and race distribution of the four cities and two years combined. Our rate is really the mean of a variable that indicates whether a sampled individual has high blood pressure. First, we generate the strata and weight variables from our standard distribution, and then use `mean` to compute the rates.

```
. use http://www.stata-press.com/data/r12/hbp, clear
. egen strata = group(age race sex) if inlist(year, 1990, 1992)
(675 missing values generated)
. by strata, sort: gen stdw = _N
. mean hbp, over(city year) stdize(strata) stdweight(stdw)
Mean estimation
N. of std strata =      24          Number of obs    =     455
         Over: city year
    _subpop_1: 1 1990
    _subpop_2: 1 1992
    _subpop_3: 2 1990
    _subpop_4: 2 1992
    _subpop_5: 3 1990
    _subpop_6: 3 1992
    _subpop_7: 5 1990
    _subpop_8: 5 1992
```

Over	Mean	Std. Err.	[95% Conf.	Interval]
hbp				
_subpop_1	.058642	.0296273	.0004182	.1168657
_subpop_2	.0117647	.0113187	-.0104789	.0340083
_subpop_3	.0488722	.0238958	.0019121	.0958322
_subpop_4	.014574	.007342	.0001455	.0290025
_subpop_5	.1011211	.0268566	.0483425	.1538998
_subpop_6	.0810577	.0227021	.0364435	.1256719
_subpop_7	.0277778	.0155121	-.0027066	.0582622
_subpop_8	.0548926	.	.	.

The standard error of the high blood pressure rate estimate is missing for city 5 in 1992 because there was only one individual with high blood pressure; that individual was the only person observed in the stratum of white males 30–35 years old.

By default, mean rescales the standard weights within the over() groups. In the following, we use the nostdrescale option to prevent this, thus reproducing the results in [R] **dstdize**.

```
. mean hbp, over(city year) nolegend stdize(strata) stdweight(stdw)
> nostdrescale
Mean estimation
N. of std strata =      24          Number of obs    =     455
```

Over	Mean	Std. Err.	[95% Conf.	Interval]
hbp				
_subpop_1	.0073302	.0037034	.0000523	.0146082
_subpop_2	.0015432	.0014847	-.0013745	.004461
_subpop_3	.0078814	.0038536	.0003084	.0154544
_subpop_4	.0025077	.0012633	.000025	.0049904
_subpop_5	.0155271	.0041238	.007423	.0236312
_subpop_6	.0081308	.0022772	.0036556	.012606
_subpop_7	.0039223	.0021904	-.0003822	.0082268
_subpop_8	.0088735	0	.	.

Saved results

mean saves the following in e():

Scalars

e(N)	number of observations
e(N_over)	number of subpopulations
e(N_stdize)	number of standard strata
e(N_clust)	number of clusters
e(k_eq)	number of equations in e(b)
e(df_r)	sample degrees of freedom
e(rank)	rank of e(V)

Macros

e(cmd)	mean
e(cmdline)	command as typed
e(varlist)	*varlist*
e(stdize)	*varname* from stdize()
e(stdweight)	*varname* from stdweight()
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(cluster)	name of cluster variable
e(over)	*varlist* from over()
e(over_labels)	labels from over() variables
e(over_namelist)	names from e(over_labels)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	vector of mean estimates
e(V)	(co)variance estimates
e(_N)	vector of numbers of nonmissing observations
e(_N_stdsum)	number of nonmissing observations within the standard strata
e(_p_stdize)	standardizing proportions
e(error)	error code corresponding to e(b)

Functions

e(sample)	marks estimation sample

Methods and formulas

`mean` is implemented as an ado-file.

Methods and formulas are presented under the following headings:

The mean estimator
Survey data
The survey mean estimator
The standardized mean estimator
The poststratified mean estimator
The standardized poststratified mean estimator
Subpopulation estimation

The mean estimator

Let y be the variable on which we want to calculate the mean and y_j an individual observation on y, where $j = 1, \ldots, n$ and n is the sample size. Let w_j be the weight, and if no weight is specified, define $w_j = 1$ for all j. For `aweights`, the w_j are normalized to sum to n. See *The survey mean estimator* for `pweighted` data.

Let W be the sum of the weights

$$W = \sum_{j=1}^{n} w_j$$

The mean is defined as

$$\overline{y} = \frac{1}{W} \sum_{j=1}^{n} w_j y_j$$

The default variance estimator for the mean is

$$\widehat{V}(\overline{y}) = \frac{1}{W(W-1)} \sum_{j=1}^{n} w_j (y_j - \overline{y})^2$$

The standard error of the mean is the square root of the variance.

If x, x_j, and $\overline{x}$ are similarly defined for another variable (observed jointly with y), the covariance estimator between $\overline{x}$ and $\overline{y}$ is

$$\widehat{\mathrm{Cov}}(\overline{x}, \overline{y}) = \frac{1}{W(W-1)} \sum_{j=1}^{n} w_j (x_j - \overline{x})(y_j - \overline{y})$$

Survey data

See [SVY] **variance estimation**, [SVY] **direct standardization**, and [SVY] **poststratification** for discussions that provide background information for the following formulas. The following formulas are derived from the fact that the mean is a special case of the ratio estimator where the denominator variable is one, $x_j = 1$; see [R] **ratio**.

The survey mean estimator

Let Y_j be a survey item for the jth individual in the population, where $j = 1, \ldots, M$ and M is the size of the population. The associated population mean for the item of interest is $\overline{Y} = Y/M$ where

$$Y = \sum_{j=1}^{M} Y_j$$

Let y_j be the survey item for the jth sampled individual from the population, where $j = 1, \ldots, m$ and m is the number of observations in the sample.

The estimator for the mean is $\overline{y} = \widehat{Y}/\widehat{M}$, where

$$\widehat{Y} = \sum_{j=1}^{m} w_j y_j \qquad \text{and} \qquad \widehat{M} = \sum_{j=1}^{m} w_j$$

and w_j is a sampling weight. The score variable for the mean estimator is

$$z_j(\overline{y}) = \frac{y_j - \overline{y}}{\widehat{M}} = \frac{\widehat{M} y_j - \widehat{Y}}{\widehat{M}^2}$$

The standardized mean estimator

Let D_g denote the set of sampled observations that belong to the gth standard stratum and define $I_{D_g}(j)$ to indicate if the jth observation is a member of the gth standard stratum; where $g = 1, \ldots, L_D$ and L_D is the number of standard strata. Also, let π_g denote the fraction of the population that belongs to the gth standard stratum, thus $\pi_1 + \cdots + \pi_{L_D} = 1$. π_g is derived from the `stdweight()` option.

The estimator for the standardized mean is

$$\overline{y}^D = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g}{\widehat{M}_g}$$

where

$$\widehat{Y}_g = \sum_{j=1}^{m} I_{D_g}(j)\, w_j y_j \qquad \text{and} \qquad \widehat{M}_g = \sum_{j=1}^{m} I_{D_g}(j)\, w_j$$

The score variable for the standardized mean is

$$z_j(\overline{y}^D) = \sum_{g=1}^{L_D} \pi_g I_{D_g}(j) \frac{\widehat{M}_g y_j - \widehat{Y}_g}{\widehat{M}_g^2}$$

The poststratified mean estimator

Let P_k denote the set of sampled observations that belong to poststratum k and define $I_{P_k}(j)$ to indicate if the jth observation is a member of poststratum k; where $k = 1, \ldots, L_P$ and L_P is the number of poststrata. Also let M_k denote the population size for poststratum k. P_k and M_k are identified by specifying the `poststrata()` and `postweight()` options on `svyset`; see [SVY] **svyset**.

The estimator for the poststratified mean is

$$\overline{y}^P = \frac{\widehat{Y}^P}{\widehat{M}^P} = \frac{\widehat{Y}^P}{M}$$

where

$$\widehat{Y}^P = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{Y}_k = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j)\, w_j y_j$$

and

$$\widehat{M}^P = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{M}_k = \sum_{k=1}^{L_P} M_k = M$$

The score variable for the poststratified mean is

$$z_j(\overline{y}^P) = \frac{z_j(\widehat{Y}^P)}{M} = \frac{1}{M} \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left(y_j - \frac{\widehat{Y}_k}{\widehat{M}_k} \right)$$

The standardized poststratified mean estimator

The estimator for the standardized poststratified mean is

$$\overline{y}^{DP} = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g^P}{\widehat{M}_g^P}$$

where

$$\widehat{Y}_g^P = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \widehat{Y}_{g,k} = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{D_g}(j) I_{P_k}(j)\, w_j y_j$$

and

$$\widehat{M}_g^P = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \widehat{M}_{g,k} = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{D_g}(j) I_{P_k}(j)\, w_j$$

The score variable for the standardized poststratified mean is

$$z_j(\overline{y}^{DP}) = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{M}_g^P z_j(\widehat{Y}_g^P) - \widehat{Y}_g^P z_j(\widehat{M}_g^P)}{(\widehat{M}_g^P)^2}$$

where

$$z_j(\widehat{Y}_g^P) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_{D_g}(j) y_j - \frac{\widehat{Y}_{g,k}}{\widehat{M}_k} \right\}$$

and

$$z_j(\widehat{M}_g^P) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_{D_g}(j) - \frac{\widehat{M}_{g,k}}{\widehat{M}_k} \right\}$$

Subpopulation estimation

Let S denote the set of sampled observations that belong to the subpopulation of interest, and define $I_S(j)$ to indicate if the jth observation falls within the subpopulation.

The estimator for the subpopulation mean is $\overline{y}^S = \widehat{Y}^S / \widehat{M}^S$, where

$$\widehat{Y}^S = \sum_{j=1}^{m} I_S(j)\, w_j y_j \qquad \text{and} \qquad \widehat{M}^S = \sum_{j=1}^{m} I_S(j)\, w_j$$

Its score variable is

$$z_j(\overline{y}^S) = I_S(j)\frac{y_j - \overline{y}^S}{\widehat{M}^S} = I_S(j)\frac{\widehat{M}^S y_j - \widehat{Y}^S}{(\widehat{M}^S)^2}$$

The estimator for the standardized subpopulation mean is

$$\overline{y}^{DS} = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g^S}{\widehat{M}_g^S}$$

where

$$\widehat{Y}_g^S = \sum_{j=1}^{m} I_{D_g}(j) I_S(j)\, w_j y_j \qquad \text{and} \qquad \widehat{M}_g^S = \sum_{j=1}^{m} I_{D_g}(j) I_S(j)\, w_j$$

Its score variable is

$$z_j(\overline{y}^{DS}) = \sum_{g=1}^{L_D} \pi_g I_{D_g}(j) I_S(j) \frac{\widehat{M}_g^S y_j - \widehat{Y}_g^S}{(\widehat{M}_g^S)^2}$$

The estimator for the poststratified subpopulation mean is

$$\overline{y}^{PS} = \frac{\widehat{Y}^{PS}}{\widehat{M}^{PS}}$$

where

$$\widehat{Y}^{PS} = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{Y}_k^S = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j) I_S(j)\, w_j y_j$$

and

$$\widehat{M}^{PS} = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{M}_k^S = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j) I_S(j)\, w_j$$

Its score variable is

$$z_j(\overline{y}^{PS}) = \frac{\widehat{M}^{PS} z_j(\widehat{Y}^{PS}) - \widehat{Y}^{PS} z_j(\widehat{M}^{PS})}{(\widehat{M}^{PS})^2}$$

where

$$z_j(\widehat{Y}^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_S(j)\, y_j - \frac{\widehat{Y}_k^S}{\widehat{M}_k} \right\}$$

and

$$z_j(\widehat{M}^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j)\frac{M_k}{\widehat{M}_k}\left\{I_S(j) - \frac{\widehat{M}_k^S}{\widehat{M}_k}\right\}$$

The estimator for the standardized poststratified subpopulation mean is

$$\overline{y}^{DPS} = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g^{PS}}{\widehat{M}_g^{PS}}$$

where

$$\widehat{Y}_g^{PS} = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k}\widehat{Y}_{g,k}^S = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{D_g}(j) I_{P_k}(j) I_S(j)\, w_j y_j$$

and

$$\widehat{M}_g^{PS} = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k}\widehat{M}_{g,k}^S = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{D_g}(j) I_{P_k}(j) I_S(j)\, w_j$$

Its score variable is

$$z_j(\overline{y}^{DPS}) = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{M}_g^{PS} z_j(\widehat{Y}_g^{PS}) - \widehat{Y}_g^{PS} z_j(\widehat{M}_g^{PS})}{(\widehat{M}_g^{PS})^2}$$

where

$$z_j(\widehat{Y}_g^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j)\frac{M_k}{\widehat{M}_k}\left\{I_{D_g}(j) I_S(j)\, y_j - \frac{\widehat{Y}_{g,k}^S}{\widehat{M}_k}\right\}$$

and

$$z_j(\widehat{M}_g^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j)\frac{M_k}{\widehat{M}_k}\left\{I_{D_g}(j) I_S(j) - \frac{\widehat{M}_{g,k}^S}{\widehat{M}_k}\right\}$$

References

Bakker, A. 2003. The early history of average values and implications for education. *Journal of Statistics Education* 11(1). http://www.amstat.org/publications/jse/v11n1/bakker.html.

Cochran, W. G. 1977. *Sampling Techniques*. 3rd ed. New York: Wiley.

Stuart, A., and J. K. Ord. 1994. *Kendall's Advanced Theory of Statistics: Distribution Theory, Vol I*. 6th ed. London: Arnold.

Also see

[R] **mean postestimation** — Postestimation tools for mean

[R] **ameans** — Arithmetic, geometric, and harmonic means

[R] **proportion** — Estimate proportions

[R] **ratio** — Estimate ratios

[R] **summarize** — Summary statistics

[R] **total** — Estimate totals

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **poststratification** — Poststratification for survey data

[SVY] **subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **variance estimation** — Variance estimation for survey data

[U] **20 Estimation and postestimation commands**

Title

mean postestimation — Postestimation tools for mean

Description

The following postestimation commands are available after `mean`:

Command	Description
`estat`	VCE
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Remarks

▷ Example 1

We have a dataset with monthly rates of returns on the Dow and NASDAQ stock indices. We can use `mean` to compute the average quarterly rates of return for the two indices separately;

```
. use http://www.stata-press.com/data/r12/rates
. mean dow nasdaq
Mean estimation                   Number of obs    =       357
```

	Mean	Std. Err.	[95% Conf.	Interval]
dow	.2489137	6.524386	-12.58227	13.0801
nasdaq	10.78477	4.160821	2.601887	18.96765

If you chose just one of the indices for your portfolio, you either did rather well or rather poorly, depending on which one you picked. However, as we now show with the postestimation command `lincom`, if you diversified your portfolio, you would have earned a respectable 5.5% rate of return without having to guess which index would be the better performer.

```
. lincom .5*dow + .5*nasdaq
 ( 1)  .5 dow + .5 nasdaq = 0
```

	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	5.51684	4.262673	1.29	0.196	-2.866347	13.90003

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **mean** — Estimate means

[SVY] **svy postestimation** — Postestimation tools for svy

Title

meta — Meta-analysis

Remarks

Stata does not have a meta-analysis command. Stata users, however, have developed an excellent suite of commands for performing meta-analysis, including commands for performing standard and cumulative meta-analysis, commands for producing forest plots and contour-enhanced funnel plots, and commands for nonparametric analysis of publication bias.

Many articles describing these commands have been published in the *Stata Technical Bulletin* and the *Stata Journal*. These articles were updated and published in a cohesive collection: *Meta-Analysis in Stata: An Updated Collection from the Stata Journal*.

In this collection, editor Jonathan Sterne discusses how these articles relate to each other and how they fit in the overall literature of meta-analysis. Sterne has organized the collection into four areas: classic meta-analysis; meta-regression; graphical and analytic tools for detecting bias; and recent advances such as meta-analysis for dose–response curves, diagnostic accuracy, multivariate analysis, and studies containing missing values.

All meta-analysis commands discussed in this collection may be downloaded by visiting http://www.stata-press.com/books/mais.html.

We highly recommend that Stata users interested in meta-analysis read this book. Since the publication of the meta-analysis collection, Kontopantelis and Reeves (2010) published an article in the *Stata Journal* describing a new command `metaan` that performs fixed- or random-effects meta-analysis.

Please also see the following FAQ on the Stata website:

What meta-analysis features are available in Stata?
http://www.stata.com/support/faqs/stat/meta.html

References

Borenstein, M., L. V. Hedges, J. P. T. Higgins, and H. R. Rothstein. 2009. *Introduction to Meta-Analysis*. Chichester, UK: Wiley.

Egger, M., G. Davey Smith, and D. G. Altman, ed. 2001. *Systematic Reviews in Health Care: Meta-analysis in Context*. 2nd ed. London: BMJ Books.

Kontopantelis, E., and D. Reeves. 2010. metaan: Random-effects meta-analysis. *Stata Journal* 10: 395–407.

Sterne, J. A. C., ed. 2009. *Meta-Analysis in Stata: An Updated Collection from the Stata Journal*. College Station, TX: Stata Press.

Sutton, A. J., K. R. Abrams, D. R. Jones, T. A. Sheldon, and F. Song. 2000. *Methods for Meta-Analysis in Medical Research*. New York: Wiley.

Title

mfp — Multivariable fractional polynomial models

Syntax

```
mfp [ , options ] : regression_cmd [ yvar1 [ yvar2 ] ] xvarlist [ if ] [ in ] [ weight ]
    [ , regression_cmd_options ]
```

options	Description
Model 2	
`sequential`	use the Royston and Altman model-selection algorithm; default uses closed-test procedure
`cycles(#)`	maximum number of iteration cycles; default is `cycles(5)`
`dfdefault(#)`	default maximum degrees of freedom; default is `dfdefault(4)`
`center(`*cent_list*`)`	specification of centering for the independent variables
`alpha(`*alpha_list*`)`	*p*-values for testing between FP models; default is `alpha(0.05)`
`df(`*df_list*`)`	degrees of freedom for each predictor
`powers(`*numlist*`)`	list of FP powers to use; default is `powers(-2 -1(.5)1 2 3)`
Adv. model	
`xorder(+|-|n)`	order of entry into model-selection algorithm; default is `xorder(+)`
`select(`*select_list*`)`	nominal *p*-values for selection on each predictor
`xpowers(`*xp_list*`)`	FP powers for each predictor
`zero(`*varlist*`)`	treat nonpositive values of specified predictors as zero when FP transformed
`catzero(`*varlist*`)`	add indicator variable for specified predictors
`all`	include out-of-sample observations in generated variables
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats and line width

regression_cmd_options	Description
Adv. model	
regression_cmd_options	options appropriate to the regression command in use

All weight types supported by *regression_cmd* are allowed; see [U] **11.1.6 weight**.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

`fracgen` may be used to create new variables containing fractional polynomial powers. See [R] **fracpoly**.

where

regression_cmd may be clogit, glm, intreg, logistic, logit, mlogit, nbreg, ologit, oprobit, poisson, probit, qreg, regress, rreg, stcox, stcrreg, streg, or xtgee.

$yvar_1$ is not allowed for streg, stcrreg, and stcox. For these commands, you must first stset your data.

$yvar_1$ and $yvar_2$ must both be specified when *regression_cmd* is intreg.

xvarlist has elements of type *varlist* and/or (*varlist*), for example, x1 x2 (x3 x4 x5)
Elements enclosed in parentheses are tested jointly for inclusion in the model and are not eligible for fractional polynomial transformation.

Menu

Statistics > Linear models and related > Fractional polynomials > Multivariable fractional polynomial models

Description

mfp selects the multivariable fractional polynomial (MFP) model that best predicts the outcome variable from the right-hand-side variables in *xvarlist*.

Options

Model 2

sequential chooses the sequential fractional polynomial (FP) selection algorithm (see *Methods of FP model selection*).

cycles(#) sets the maximum number of iteration cycles permitted. cycles(5) is the default.

dfdefault(#) determines the default maximum degrees of freedom (df) for a predictor. The default is dfdefault(4) (second-degree FP).

center(*cent_list*) defines the centering of the covariates $xvar_1$, $xvar_2$, ... of *xvarlist*. The default is center(mean), except for binary covariates, where it is center(#), with # being the lower of the two distinct values of the covariate. A typical item in *cent_list* is *varlist*:{mean|#|no}. Items are separated by commas. The first item is special in that *varlist* is optional, and if it is omitted, the default is reset to the specified value (mean, #, or no). For example, center(no, age:mean) sets the default to no (that is, no centering) and the centering of age to mean.

alpha(*alpha_list*) sets the significance levels for testing between FP models of different degrees. The rules for *alpha_list* are the same as those for *df_list* in the df() option (see below). The default nominal p-value (significance level, selection level) is 0.05 for all variables.

Example: alpha(0.01) specifies that all variables have an FP selection level of 1%.

Example: alpha(0.05, weight:0.1) specifies that all variables except weight have an FP selection level of 5%; weight has a level of 10%.

df(*df_list*) sets the df for each predictor. The df (not counting the regression constant, _cons) is twice the degree of the FP, so, for example, an *xvar* fit as a second-degree FP (FP2) has 4 df. The first item in *df_list* may be either # or *varlist*:#. Subsequent items must be *varlist*:#. Items are separated by commas, and *varlist* is specified in the usual way for variables. With the first type of item, the df for all predictors is taken to be #. With the second type of item, all members of *varlist* (which must be a subset of *xvarlist*) have # df.

The default number of degrees of freedom for a predictor of type *varlist* specified in *xvarlist* but not in *df_list* is assigned according to the number of distinct (unique) values of the predictor, as follows:

# of distinct values	Default df
1	(invalid predictor)
2–3	1
4–5	min(2, `dfdefault()`)
≥ 6	`dfdefault()`

Example: `df(4)`
All variables have 4 df.

Example: `df(2, weight displ:4)`
`weight` and `displ` have 4 df; all other variables have 2 df.

Example: `df(weight displ:4, mpg:2)`
`weight` and `displ` have 4 df, `mpg` has 2 df; all other variables have default df.

`powers(`*numlist*`)` is the set of FP powers to be used. The default set is -2, -1, -0.5, 0, 0.5, 1, 2, 3 (0 means log).

Adv. model

`xorder(+|-|n)` determines the order of entry of the covariates into the model-selection algorithm. The default is `xorder(+)`, which enters them in decreasing order of significance in a multiple linear regression (most significant first). `xorder(-)` places them in reverse significance order, whereas `xorder(n)` respects the original order in *xvarlist*.

`select(`*select_list*`)` sets the nominal p-values (significance levels) for variable selection by backward elimination. A variable is dropped if its removal causes a nonsignificant increase in deviance. The rules for *select_list* are the same as those for *df_list* in the `df()` option (see above). Using the default selection level of 1 for all variables forces them all into the model. Setting the nominal p-value to be 1 for a given variable forces it into the model, leaving others to be selected or not. The nominal p-value for elements of *xvarlist* bound by parentheses is specified by including (*varlist*) in *select_list*.

Example: `select(0.05)`
All variables have a nominal p-value of 5%.

Example: `select(0.05, weight:1)`
All variables except `weight` have a nominal p-value of 5%; `weight` is forced into the model.

Example: `select(a (b c):0.05)`
All variables except `a`, `b`, and `c` are forced into the model. `b` and `c` are tested jointly with 2 df at the 5% level, and `a` is tested singly at the 5% level.

`xpowers(`*xp_list*`)` sets the permitted FP powers for covariates individually. The rules for *xp_list* are the same as for *df_list* in the `df()` option. The default selection is the same as that for the `powers()` option.

Example: `xpowers(-1 0 1)`
All variables have powers -1, 0, 1.

Example: `xpowers(x5:-1 0 1)`
All variables except `x5` have default powers; `x5` has powers -1, 0, 1.

`zero(`*varlist*`)` treats negative and zero values of members of *varlist* as zero when FP transformations are applied. By default, such variables are subjected to a preliminary linear transformation to avoid negative and zero values (see [R] **fracpoly**). *varlist* must be part of *xvarlist*.

`catzero(`*varlist*`)` is a variation on `zero()`; see *Zeros and zero categories* below. *varlist* must be part of *xvarlist*.

regression_cmd_options may be any of the options appropriate to *regression_cmd*.

`all` includes out-of-sample observations when generating the FP variables. By default, the generated FP variables contain missing values outside the estimation sample.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Iteration report
Estimation algorithm
Methods of FP model selection
Zeros and zero categories

For elements in *xvarlist* not enclosed in parentheses, `mfp` leaves variables in the data named I*xvar*__1, I*xvar*__2, ..., where *xvar* represents the first four letters of the name of $xvar_1$, and so on, for $xvar_2$, $xvar_3$, etc. The new variables contain the best-fitting FP powers of $xvar_1$, $xvar_2$, ...

Iteration report

By default, for each continuous predictor, *x*, `mfp` compares null, linear, and FP1 models for *x* with an FP2 model. The deviance for each of these nested submodels is given in the column labeled "Deviance". The line labeled "Final" gives the deviance for the selected model and its powers. All the other predictors currently selected are included, with their transformations (if any). For models specified as having 1 df, the only choice is whether the variable enters the model.

Estimation algorithm

The estimation algorithm in `mfp` processes the *xvars* in turn. Initially, `mfp` silently arranges *xvarlist* in order of increasing *p*-value (that is, of decreasing statistical significance) for omitting each predictor from the model comprising *xvarlist*, with each term linear. The aim is to model relatively important variables before unimportant ones. This approach may help to reduce potential model-fitting difficulties caused by collinearity or, more generally, "concurvity" among the predictors. See the `xorder()` option above for details on how to change the ordering.

At the initial cycle, the best-fitting FP function for $xvar_1$ (the first of *xvarlist*) is determined, with all the other variables assumed to be linear. Either the default or the alternative procedure is used (see *Methods of FP model selection* below). The functional form (but not the estimated regression coefficients) for $xvar_1$ is kept, and the process is repeated for $xvar_2$, $xvar_3$, etc. The first iteration concludes when all the variables have been processed in this way. The next cycle is similar, except that the functional forms from the initial cycle are retained for all variables except the one currently being processed.

A variable whose functional form is prespecified to be linear (that is, to have 1 df) is tested for exclusion within the above procedure when its nominal p-value (selection level) according to `select()` is less than 1; otherwise, it is included.

Updating of FP functions and candidate variables continues until the functions and variables included in the overall model do not change (convergence). Convergence is usually achieved within 1–4 cycles.

Methods of FP model selection

`mfp` includes two algorithms for FP model selection, both of which combine backward elimination with the selection of an FP function. For each continuous variable in turn, they start from a most-complex permitted FP model and attempt to simplify the model by reducing the degree. The default algorithm resembles a closed-test procedure, a sequence of tests maintaining the overall type I error rate at a prespecified nominal level, such as 5%. All significance tests are approximate; therefore, the algorithm is not precisely a closed-test procedure (Royston and Sauerbrei 2008, chap. 6).

The closed-test algorithm for choosing an FP model with maximum permitted degree $m = 2$ (that is, an FP2 model with 4 df) for one continuous predictor, x, is as follows:

1. Inclusion: Test FP2 against the null model for x on 4 df at the significance level determined by `select()`. If x is significant, continue; otherwise, drop x from the model.
2. Nonlinearity: Test FP2 against a straight line in x on 3 df at the significance level determined by `alpha()`. If significant, continue; otherwise, stop, with the chosen model for x being a straight line.
3. Simplification: Test FP2 against FP1 on 2 df at the significance level determined by `alpha()`. If significant, the final model is FP2; otherwise, it is FP1.

The first step is omitted if x is to be retained in the model, that is, if its nominal p-value, according to the `select()` option, is 1.

An alternative algorithm is available with the `sequential` option, as originally suggested by Royston and Altman (1994):

1. Test FP2 against FP1 on 2 df at the `alpha()` significance level. If significant, the final model is FP2; otherwise, continue.
2. Test FP1 against a straight line on 1 df at the `alpha()` level. If significant, the final model is FP1; otherwise, continue.
3. Test a straight line against omitting x on 1 df at the `select()` level. If significant, the final model is a straight line; otherwise, drop x.

The final step is omitted if x is to be retained in the model, that is, if its nominal p-value, according to the `select()` option, is 1.

If x is uninfluential, the overall type I error rate of this procedure is about double that of the closed-test procedure, for which the rate is close to the nominal value. This inflated type I error rate confers increased apparent power to detect nonlinear relationships.

Zeros and zero categories

The `zero()` option permits fitting an FP model to the positive values of a covariate, taking nonpositive values as zero. An application is the assessment of the effect of cigarette smoking as a risk factor in an epidemiological study. Nonsmokers may be qualitatively different from smokers, so the effect of smoking (regarded as a continuous variable) may not be continuous between one and

zero cigarettes. To allow for this, the risk may be modeled as constant for the nonsmokers and as an FP function of the number of cigarettes for the smokers:

```
. generate byte nonsmokr = cond(n_cigs==0, 1, 0) if n_cigs != .
. mfp, zero(n_cigs) df(4, nonsmokr:1): logit case n_cigs nonsmokr age
```

Omission of `zero(n_cigs)` would cause `n_cigs` to be transformed before analysis by the addition of a suitable constant, probably 1.

A closely related approach involves the `catzero()` option. The command

```
. mfp, catzero(n_cigs): logit case n_cigs age
```

would achieve a similar result to the previous command but with important differences. First, `mfp` would create the equivalent of the binary variable `nonsmokr` automatically and include it in the model. Second, the two smoking variables would be treated as one predictor in the model. With the `select()` option active, the two variables would be tested jointly for inclusion in the model. A modified version is described in Royston and Sauerbrei (2008, sec. 4.15).

▷ Example 1

We illustrate two of the analyses performed by Sauerbrei and Royston (1999). We use `brcancer.dta`, which contains prognostic factors data from the German Breast Cancer Study Group of patients with node-positive breast cancer. The response variable is recurrence-free survival time (`rectime`), and the censoring variable is `censrec`. There are 686 patients with 299 events. We use Cox regression to predict the log hazard of recurrence from prognostic factors, of which five are continuous (`x1`, `x3`, `x5`, `x6`, `x7`) and three are binary (`x2`, `x4a`, `x4b`). Hormonal therapy (`hormon`) is known to reduce recurrence rates and is forced into the model. We use `mfp` to build a model from the initial set of eight predictors by using the backfitting model-selection algorithm. We set the nominal p-value for variable and FP selection to 0.05 for all variables except `hormon`, for which it is set to 1:

```
. use http://www.stata-press.com/data/r12/brcancer
(German breast cancer data)
. stset rectime, fail(censrec)
  (output omitted)
. mfp, alpha(.05) select(.05, hormon:1): stcox x1 x2 x3 x4a x4b x5 x6 x7 hormon,
> nohr
Deviance for model with all terms untransformed =  3471.637, 686 observations
Variable     Model (vs.)   Deviance  Dev diff.   P      Powers   (vs.)
─────────────────────────────────────────────────────────────────────
x5           null   FP2    3503.610    61.366  0.000*   .         .5 3
             lin.          3471.637    29.393  0.000+   1
             FP1           3449.203     6.959  0.031+   0
             Final         3442.244                     .5 3
x6           null   FP2    3464.113    29.917  0.000*   .         -2 .5
             lin.          3442.244     8.048  0.045+   1
             FP1           3435.550     1.354  0.508    .5
             Final         3435.550                     .5
[hormon included with 1 df in model]
x4a          null   lin.   3440.749     5.199  0.023*   .         1
             Final         3435.550                     1
x3           null   FP2    3436.832     3.560  0.469    .         -2 3
             Final         3436.832                     .
x2           null   lin.   3437.589     0.756  0.384    .         1
             Final         3437.589                     .
x4b          null   lin.   3437.848     0.259  0.611    .         1
```

```
             Final         3437.848                      .
x1           null   FP2    3437.893    18.085  0.001*    .          -2 -.5
             lin.          3437.848    18.040  0.000+    1
             FP1           3433.628    13.820  0.001+    -2
             Final         3419.808                      -2 -.5
x7           null   FP2    3420.805     3.715  0.446     .          -.5 3
             Final         3420.805                      .
-------------------------------------------------------------------------------
End of Cycle 1: deviance =    3420.805
-------------------------------------------------------------------------------
x5           null   FP2    3494.867    74.143  0.000*    .          -2 -1
             lin.          3451.795    31.071  0.000+    1
             FP1           3428.023     7.299  0.026+    0
             Final         3420.724                      -2 -1
x6           null   FP2    3452.093    32.704  0.000*    .          0 0
             lin.          3427.703     8.313  0.040+    1
             FP1           3420.724     1.334  0.513     .5
             Final         3420.724                      .5
[hormon included with 1 df in model]
x4a          null   lin.   3425.310     4.586  0.032*    .          1
             Final         3420.724                      1
x3           null   FP2    3420.724     5.305  0.257     .          -.5 0
             Final         3420.724                      .
x2           null   lin.   3420.724     0.214  0.644     .          1
             Final         3420.724                      .
x4b          null   lin.   3420.724     0.145  0.703     .          1
             Final         3420.724                      .
x1           null   FP2    3440.057    19.333  0.001*    .          -2 -.5
             lin.          3440.038    19.314  0.000+    1
             FP1           3436.949    16.225  0.000+    -2
             Final         3420.724                      -2 -.5
x7           null   FP2    3420.724     2.152  0.708     .          -1 3
             Final         3420.724                      .
Fractional polynomial fitting algorithm converged after 2 cycles.
Transformations of covariates:
-> gen double Ix1__1 = X^-2-.0355294635 if e(sample)
-> gen double Ix1__2 = X^-.5-.4341573547 if e(sample)
   (where: X = x1/10)
-> gen double Ix5__1 = X^-2-3.983723313 if e(sample)
-> gen double Ix5__2 = X^-1-1.99592668 if e(sample)
   (where: X = x5/10)
-> gen double Ix6__1 = X^.5-.3331600619 if e(sample)
   (where: X = (x6+1)/1000)
Final multivariable fractional polynomial model for _t
```

Variable	Initial			Final		
	df	Select	Alpha	Status	df	Powers
x1	4	0.0500	0.0500	in	4	-2 -.5
x2	1	0.0500	0.0500	out	0	
x3	4	0.0500	0.0500	out	0	
x4a	1	0.0500	0.0500	in	1	1
x4b	1	0.0500	0.0500	out	0	
x5	4	0.0500	0.0500	in	4	-2 -1
x6	4	0.0500	0.0500	in	2	.5
x7	4	0.0500	0.0500	out	0	
hormon	1	1.0000	0.0500	in	1	1

```
Cox regression -- Breslow method for ties
Entry time _t0                                  Number of obs    =        686
                                                LR chi2(7)       =     155.62
                                                Prob > chi2      =     0.0000
Log likelihood = -1710.3619                     Pseudo R2        =     0.0435

------------------------------------------------------------------------------
          _t |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      Ix1__1 |   44.73377   8.256682     5.42   0.000     28.55097    60.91657
      Ix1__2 |  -17.92302   3.909611    -4.58   0.000    -25.58571   -10.26032
         x4a |   .5006982   .2496324     2.01   0.045     .0114276    .9899687
      Ix5__1 |   .0387904   .0076972     5.04   0.000     .0237041    .0538767
      Ix5__2 |  -.5490645   .0864255    -6.35   0.000    -.7184554   -.3796736
      Ix6__1 |  -1.806966   .3506314    -5.15   0.000    -2.494191   -1.119741
      hormon |  -.4024169   .1280843    -3.14   0.002    -.6534575   -.1513763
------------------------------------------------------------------------------
Deviance: 3420.724.
```

Some explanation of the output from the model-selection algorithm is desirable. Consider the first few lines of output in the iteration log:

```
1. Deviance for model with all terms untransformed =  3471.637, 686 observations
   Variable     Model (vs.)   Deviance  Dev diff.   P      Powers    (vs.)
------------------------------------------------------------------------------
2. x5           null   FP2    3503.610    61.366  0.000*   .          .5 3
3.              lin.          3471.637    29.393  0.000+   1
4.              FP1           3449.203     6.959  0.031+   0
5.              Final         3442.244                     .5 3
```

Line 1 gives the deviance ($-2 \times$ log partial likelihood) for the Cox model with all terms linear, the place where the algorithm starts. The model is modified variable by variable in subsequent steps. The most significant linear term turns out to be `x5`, which is therefore processed first. Line 2 compares the best-fitting FP2 for `x5` with a model omitting `x5`. The FP has powers (0.5, 3), and the test for inclusion of `x5` is highly significant. The reported deviance of 3,503.610 is of the null model, not for the FP2 model. The deviance for the FP2 model may be calculated by subtracting the deviance difference (`Dev diff.`) from the reported deviance, giving $3{,}503.610 - 61.366 = 3{,}442.244$. Line 3 shows that the FP2 model is also a significantly better fit than a straight line (`lin.`) and line 4 that FP2 is also somewhat better than FP1 ($p = 0.031$). Thus at this stage in the model-selection procedure, the final model for `x5` (line 5) is FP2 with powers (0.5, 3). The overall model with an FP2 for `x5` and all other terms linear has a deviance of 3,442.244.

After all the variables have been processed (cycle 1) and reprocessed (cycle 2) in this way, convergence is achieved because the functional forms (FP powers and variables included) after cycle 2 are the same as they were after cycle 1. The model finally chosen is Model II as given in tables 3 and 4 of Sauerbrei and Royston (1999). Because of scaling of variables, the regression coefficients reported there are different, but the model and its deviance are identical. The model includes `x1` with powers $(-2, -0.5)$, `x4a`, `x5` with powers $(-2, -1)$, and `x6` with power 0.5. There is strong evidence of nonlinearity for `x1` and for `x5`, the deviance differences for comparison with a straight-line model (`FP2 vs lin.`) being, respectively, 19.3 and 31.1 at convergence (cycle 2). Predictors `x2`, `x3`, `x4b`, and `x7` are dropped, as may be seen from their status `out` in the table `Final multivariable fractional polynomial model for _t` (the assumed *depvar* when using `stcox`).

All predictors except `x4a` and `hormon`, which are binary, have been centered on the mean of the original variable. For example, the mean of `x1` (age) is 53.05 years. The first FP-transformed variable for `x1` is `x1^-2` and is created by the expression `gen double Ix1__1 = X^-2-.0355 if e(sample)`. The value 0.0355 is obtained from $(53.05/10)^{-2}$. The division by 10 is applied automatically to improve the scaling of the regression coefficient for `Ix1__1`.

According to Sauerbrei and Royston (1999), medical knowledge dictates that the estimated risk function for x5 (number of positive nodes), which was based on the above FP with powers $(-2, -1)$, should be monotonic, but it was not. They improved Model II by estimating a preliminary exponential transformation, x5e $= \exp(-0.12 \cdot$ x5$)$, for x5 and fitting a degree 1 FP for x5e, thus obtaining a monotonic risk function. The value of -0.12 was estimated univariately using nonlinear Cox regression with the ado-file boxtid (Royston and Ambler 1999b, 1999d). To ensure a negative exponent, Sauerbrei and Royston (1999) restricted the powers for x5e to be positive. Their Model III may be fit by using the following command:

```
. mfp, alpha(.05) select(.05, hormon:1) df(x5e:2) xpowers(x5e:0.5 1 2 3):
> stcox x1 x2 x3 x4a x4b x5e x6 x7 hormon
```

Other than the customization for x5e, the command is the same as it was before. The resulting model is as reported in table 4 of Sauerbrei and Royston (1999):

```
. use http://www.stata-press.com/data/r12/brcancer, clear
(German breast cancer data)
. stset rectime, fail(censrec)
  (output omitted)
. mfp, alpha(.05) select(.05, hormon:1) df(x5e:2) xpowers(x5e:0.5 1 2 3):
> stcox x1 x2 x3 x4a x4b x5e x6 x7 hormon, nohr
  (output omitted)
Final multivariable fractional polynomial model for _t
```

Variable	Initial df	Initial Select	Initial Alpha	Final Status	Final df	Final Powers
x1	4	0.0500	0.0500	in	4	-2 -.5
x2	1	0.0500	0.0500	out	0	
x3	4	0.0500	0.0500	out	0	
x4a	1	0.0500	0.0500	in	1	1
x4b	1	0.0500	0.0500	out	0	
x5e	2	0.0500	0.0500	in	1	1
x6	4	0.0500	0.0500	in	2	.5
x7	4	0.0500	0.0500	out	0	
hormon	1	1.0000	0.0500	in	1	1

```
Cox regression -- Breslow method for ties
Entry time _t0                                  Number of obs    =       686
                                                LR chi2(6)       =    153.11
                                                Prob > chi2      =    0.0000
Log likelihood = -1711.6186                     Pseudo R2        =    0.0428
```

_t	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Ix1__1	43.55382	8.253433	5.28	0.000	27.37738	59.73025
Ix1__2	-17.48136	3.911882	-4.47	0.000	-25.14851	-9.814212
x4a	.5174351	.2493739	2.07	0.038	.0286713	1.006199
Ix5e__1	-1.981213	.2268903	-8.73	0.000	-2.425909	-1.536516
Ix6__1	-1.84008	.3508432	-5.24	0.000	-2.52772	-1.15244
hormon	-.3944998	.128097	-3.08	0.002	-.6455654	-.1434342

```
Deviance: 3423.237.
```

◁

Saved results

In addition to what *regression_cmd* saves, `mfp` saves the following in `e()`:

Scalars

`e(fp_nx)`	number of predictors in *xvarlist*
`e(fp_dev)`	deviance of final model fit
`e(Fp_id#)`	initial degrees of freedom for the #th element of *xvarlist*
`e(Fp_fd#)`	final degrees of freedom for the #th element of *xvarlist*
`e(Fp_al#)`	FP selection level for the #th element of *xvarlist*
`e(Fp_se#)`	backward elimination selection level for the #th element of *xvarlist*

Macros

`e(fp_cmd)`	`fracpoly`
`e(fp_cmd2)`	`mfp`
`e(cmdline)`	command as typed
`e(fracpoly)`	command used to fit the selected model using `fracpoly`
`e(fp_fvl)`	variables in final model
`e(fp_depv)`	$yvar_1$ ($yvar_2$)
`e(fp_opts)`	estimation command options
`e(fp_x1)`	first variable in *xvarlist*
`e(fp_x2)`	second variable in *xvarlist*
`...`	
`e(fp_xN)`	last variable in *xvarlist*, N=`e(fp_nx)`
`e(fp_k1)`	power for first variable in *xvarlist* (*)
`e(fp_k2)`	power for second variable in *xvarlist* (*)
`...`	
`e(fp_kN)`	power for last var. in *xvarlist* (*), N=`e(fp_nx)`

Note: (*) contains '`.`' if the variable is not selected in the final model.

Methods and formulas

`mfp` is implemented as an ado-file.

Acknowledgments

`mfp` is an update of `mfracpol` by Royston and Ambler (1998).

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Also see

[R] **mfp postestimation** — Postestimation tools for mfp

[R] **fracpoly** — Fractional polynomial regression

[U] **20 Estimation and postestimation commands**

Title

mfp postestimation — Postestimation tools for mfp

Description

The following postestimation commands are of special interest after `mfp`:

Command	Description
`fracplot`	plot data and fit from most recently fit fractional polynomial model
`fracpred`	create variable containing prediction, deviance residuals, or SEs of fitted values

For `fracplot` and `fracpred`, see [R] **fracpoly postestimation**.

The following standard postestimation commands are also available if available after *regression_cmd*:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`	likelihood-ratio test
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **mfp** — Multivariable fractional polynomial models

[R] **fracpoly postestimation** — Postestimation tools for fracpoly

[U] **20 Estimation and postestimation commands**

Title

misstable — Tabulate missing values

Syntax

Report counts of missing values

```
misstable summarize [varlist] [if] [in] [, summarize_options]
```

Report pattern of missing values

```
misstable patterns [varlist] [if] [in] [, patterns_options]
```

Present a tree view of the pattern of missing values

```
misstable tree [varlist] [if] [in] [, tree_options]
```

List the nesting rules that describe the missing-value pattern

```
misstable nested [varlist] [if] [in] [, nested_options]
```

summarize_options	Description
`all`	show all variables
`showzeros`	show zeros in table
`generate(`*stub* `[, exok])`	generate missing-value indicators

patterns_options	Description
`asis`	use variables in order given
`frequency`	report frequencies instead of percentages
`exok`	treat `.a`, `.b`, ..., `.z` as nonmissing
`replace`	replace data in memory with dataset of patterns
`clear`	okay to `replace` even if original unsaved
`bypatterns`	list by patterns rather than by frequency

tree_options	Description
`asis`	use variables in order given
`frequency`	report frequencies instead of percentages
`exok`	treat `.a`, `.b`, ..., `.z` as nonmissing

nested_options	Description
`exok`	treat `.a`, `.b`, ..., `.z` as nonmissing

In addition, programmer's option nopreserve is allowed with all syntaxes; see [P] **nopreserve option**.

Menu

Statistics > Summaries, tables, and tests > Tables > Tabulate missing values

Description

misstable makes tables that help you understand the pattern of missing values in your data.

Options for misstable summarize

all specifies that the table should include all the variables specified or all the variables in the dataset. The default is to include only numeric variables that contain missing values.

showzeros specifies that zeros in the table should display as 0 rather than being omitted.

generate(*stub* [, exok]) requests that a missing-value indicator *newvar*, a new binary variable containing 0 for complete observations and 1 for incomplete observations, be generated for every numeric variable in *varlist* containing missing values. If the all option is specified, missing-value indicators are created for all the numeric variables specified or for all the numeric variables in the dataset. If exok is specified within generate(), the extended missing values .a, .b, ..., .z are treated as if they do not designate missing.

For each variable in *varlist*, *newvar* is the corresponding variable name *varname* prefixed with *stub*. If the total length of *stub* and *varname* exceeds 32 characters, *newvar* is abbreviated so that its name does not exceed 32 characters.

Options for misstable patterns

asis, frequency, and exok – see *Common options* below.

replace specifies that the data in memory be replaced with a dataset corresponding to the table just displayed; see *misstable patterns* under *Remarks* below.

clear is for use with replace; it specifies that it is okay to change the data in memory even if they have not been saved to disk.

bypatterns specifies the table be ordered by pattern rather than by frequency. That is, bypatterns specifies that patterns containing one incomplete variable be listed first, followed by those for two incomplete variables, and so on. The default is to list the most frequent pattern first, followed by the next most frequent pattern, etc.

Options for misstable tree

asis, frequency, and exok – see *Common options* below.

Option for misstable nested

`exok` – see *Common options* below.

Common options

`asis` specifies that the order of the variables in the table be the same as the order in which they are specified on the `misstable` command. The default is to order the variables by the number of missing values, and within that, by the amount of overlap of missing values.

`frequency` specifies that the table should report frequencies instead of percentages.

`exok` specifies that the extended missing values `.a`, `.b`, ..., `.z` should be treated as if they do not designate missing. Some users use extended missing values to designate values that are missing for a known and valid reason.

`nopreserve` is a programmer's option allowed with all `misstable` commands; see [P] **nopreserve option**.

Remarks

Remarks are presented under the following headings:

misstable summarize
misstable patterns
misstable tree
misstable nested
Execution time of misstable nested

In what follows, we will use data from a 125-observation, fictional, student-satisfaction survey:

```
. use http://www.stata-press.com/data/r12/studentsurvey
(Student Survey)
. summarize
```

Variable	Obs	Mean	Std. Dev.	Min	Max
m1	125	2.456	.8376619	1	4
m2	125	2.472	.8089818	1	4
age	122	18.97541	.8763477	17	21
female	122	.5245902	.5014543	0	1
dept	116	2.491379	1.226488	1	4
offcampus	125	.36	.4819316	0	1
comment	0				

The `m1` and `m2` variables record the student's satisfaction with teaching and with academics. `comment` is a string variable recording any comments the student might have had.

misstable summarize

▷ Example 1

`misstable summarize` reports counts of missing values:

```
. misstable summarize
```

Variable	Obs=.	Obs>.	Obs<.	Obs<. Unique values	Obs<. Min	Obs<. Max
age	3		122	5	17	21
female	3		122	2	0	1
dept	9		116	4	1	4

Stata provides 27 different missing values, namely, `.`, `.a`, `.b`, ..., `.z`. The first of those, `.`, is often called system missing. The remaining missing values are called extended missings. The nonmissing and missing values are ordered *nonmissing* $<$ `.` $<$ `.a` $<$ `.b` $<\cdots<$ `.z`. Thus reported in the column "Obs=." are counts of system missing values; in the column "Obs>.", extended missing values; and in the column "Obs<.", nonmissing values.

The rightmost portion of the table is included to remind you how the variables are encoded.

Our data contain seven variables and yet `misstable` reported only three of them. The omitted variables contain no missing values or are string variables. Even if we specified the varlist explicitly, those variables would not appear in the table unless we specified the `all` option.

We can also create missing-value indicators for each of the variables above using the `generate()` option:

```
. quietly misstable summarize, generate(miss_)
. describe miss_*
```

variable name	storage type	display format	value label	variable label
miss_age	byte	%8.0g		(age>=.)
miss_female	byte	%8.0g		(female>=.)
miss_dept	byte	%8.0g		(dept>=.)

For each variable containing missing values, the `generate()` option creates a new binary variable containing `0` for complete observations and `1` for incomplete observations. In our example, three new missing-value indicators are generated, one for each of the incomplete variables `age`, `female`, and `dept`. The naming convention of `generate()` is to prefix the corresponding variable names with the specified *stub*, which is `miss_` in this example.

Missing-value indicators are useful, for example, for checking whether data are missing completely at random. They are also often used within the multiple-imputation context to identify the observed and imputed data; see [MI] **intro substantive** for a general introduction to multiple imputation. Within Stata's multiple-imputation commands, an incomplete value is identified by the system missing value, a dot. By default, `misstable summarize, generate()` marks the extended missing values as incomplete values, as well. You can use `exok` within `generate()` to treat extended missing values as complete when creating missing-value identifiers.

◁

misstable patterns

▷ Example 2

`misstable patterns` reports the pattern of missing values:

```
. misstable patterns
  Missing-value patterns
                |  Pattern
    Percent     |  1  2  3
----------------+---------
        93%     |  1  1  1
                |
         5      |  1  1  0
         2      |  0  0  0
----------------+---------
        100%    |
  Variables are  (1) age  (2) female  (3) dept
```

There are three patterns in these data: (1,1,1), (1,1,0), and (0,0,0). By default, the rows of the table are ordered by frequency. In larger tables that have more patterns, it is sometimes useful to order the rows by pattern. We could have obtained that by typing `mi misstable patterns, bypatterns`.

In a pattern, 1 indicates that all values of the variable are nonmissing and 0 indicates that all values are missing. Thus pattern (1,1,1) means no missing values, and 93% of our data have that pattern. There are two patterns in which variables are missing, (1,1,0) and (0,0,0). Pattern (1,1,0) means that `age` is nonmissing, `female` is nonmissing, and `dept` is missing. The order of the variables in the patterns appears in the key at the bottom of the table. Five percent of the observations have pattern (1,1,0). The remaining 2% have pattern (0,0,0), meaning that all three variables contain missing.

As with `misstable summarize`, only numeric variables that contain missing are listed, so had we typed `misstable patterns comments age female offcampus dept`, we still would have obtained the same table. Variables that are automatically omitted contain no missing values or are string variables.

The variables in the table are ordered from lowest to highest frequency of missing values, although you cannot see that from the information presented in the table. The variables are ordered this way even if you explicitly specify the varlist with a different ordering. Typing `misstable patterns dept female age` would produce the same table as above. Specify the `asis` option if you want the variables in the order in which you specify them.

You can obtain a dataset of the patterns by specifying the `replace` option:

```
. misstable patterns, replace clear
  Missing-value patterns
                |  Pattern
    Percent     |  1  2  3
----------------+---------
        93%     |  1  1  1
                |
         5      |  1  1  0
         2      |  0  0  0
----------------+---------
        100%    |
  Variables are  (1) age  (2) female  (3) dept
(summary data now in memory)
```

```
. list
```

	_freq	age	female	dept
1.	3	0	0	0
2.	6	1	1	0
3.	116	1	1	1

The differences between the dataset and the printed table are that 1) the dataset always records frequency and 2) the rows are reversed.

◁

misstable tree

▷ Example 3

`misstable tree` presents a tree view of the pattern of missing values:

```
. use http://www.stata-press.com/data/r12/studentsurvey, clear
(Student Survey)
. misstable tree, frequency
```

Nested pattern of missing values

dept	age	female
9	3	3
		0
	6	0
		6
116	0	0
		0
	116	0
		116

(number missing listed first)

In this example, we specified the `frequency` option to see the table in frequency rather than percentage terms. In the table, each column sums to the total number of observations in the data, 125. Variables are ordered from those with the most missing values to those with the least. Start with the first column. The `dept` variable is missing in 9 observations and, farther down, the table reports that it is not missing in 116 observations.

Go back to the first row and read across, but only to the second column. The `dept` variable is missing in 9 observations. Within those 9, `age` is missing in 3 of them and is not missing in the remaining 6. Reading down the second column, within the 116 observations that `dept` is not missing, `age` is missing in 0 and not missing in 116.

Reading straight across the first row again, `dept` is missing in 9 observations, and within the 9, `age` is missing in 3, and within the 3, `female` is also missing in 3. Skipping down just a little, within the 6 observations for which `dept` is missing and `age` is not missing, `female` is not missing, too.

◁

misstable nested

▷ Example 4

`misstable nested` lists the nesting rules that describe the missing-value pattern,

```
. misstable nested
     1.  female(3) <-> age(3) -> dept(9)
```

This line says that in observations in which `female` is missing, so is `age` missing, and vice versa, and in observations in which `age` (or `female`) is missing, so is `dept`. The numbers in parentheses are counts of the missing values. The `female` variable happens to be missing in 3 observations, and the same is true for `age`; the `dept` variable is missing in 9 observations. Thus `dept` is missing in the 3 observations for which `age` and `female` are missing, and in 6 more observations, too.

In these data, it turns out that the missing-value pattern can be summarized in one statement. In a larger dataset, you might see something like this:

```
. misstable nested
     1.  female(50) <-> age(50) -> dept(120)
     2.  female(50) -> m1(58)
     3.  offcampus(11)
```

`misstable nested` accounts for every missing value. In the above, in addition to `female <-> age -> dept`, we have that `female -> m1`, and we have `offcampus`, the last all by itself. The last line says that the 11 missing values in `offcampus` are not themselves nested in the missing value of any other variable, nor do they imply the missing values in another variable. In some datasets, all the statements will be of this last form.

In our data, however, we have one statement:

```
. misstable nested
     1.  female(3) <-> age(3) -> dept(9)
```

When the missing-value pattern can be summarized in one `misstable nested` statement, the pattern of missing values in the data is said to be monotone.

◁

Execution time of misstable nested

The execution time of `misstable nested` is affected little by the number of observations but can grow quickly with the number of variables, depending on the fraction of missing values within variable. The execution time of the example above, which has 3 variables containing missing, is instant. In worst-case scenarios, with 500 variables, the time might be 25 seconds; with 1,000 variables, the execution time might be closer to an hour.

In situations where `misstable nested` takes a long time to complete, it will produce thousands of rules that will defy interpretation. A 523-variable dataset we have seen ran in 20 seconds and produced 8,040 rules. Although we spotted a few rules in the output that did not surprise us, such as the year of the date being missing implied that the month and the day were also missing, mostly the output was not helpful.

If you have such a dataset, we recommend you run `misstable` on groups of variables that you have reason to believe the pattern of missing values might be related.

Saved results

misstable summarize saves the following values of the last variable summarized in r():

Scalars

r(N_eq_dot)	number of observations containing .
r(N_gt_dot)	number of observations containing .a, .b, ..., .z
r(N_lt_dot)	number of observations containing nonmissing
r(K_uniq)	number of unique, nonmissing values
r(min)	variable's minimum value
r(max)	variable's maximum value

Macros

r(vartype)	numeric, string, or none

r(K_uniq) contains . if the number of unique, nonmissing values is greater than 500. r(vartype) contains none if no variables are summarized, and in that case, the value of the scalars are all set to missing (.). Programmers intending to access results after misstable summarize should specify the all option.

misstable patterns saves the following in r():

Scalars

r(N_complete)	number of complete observations
r(N_incomplete)	number of incomplete observations
r(K)	number of patterns

Macros

r(vars)	variables used in order presented

r(N_complete) and r(N_incomplete) are defined with respect to the variables specified if variables were specified and otherwise, defined with respect to all the numeric variables in the dataset. r(N_complete) is the number of observations that contain no missing values.

misstable tree saves the following in r():

Macros

r(vars)	variables used in order presented

misstable nested saves the following in r():

Scalars

r(K)	number of statements

Macros

r(stmt1)	first statement
r(stmt2)	second statement
.	.
.	.
r(stmt`r(K)')	last statement
r(stmt1wc)	r(stmt1) with missing-value counts
r(vars)	variables considered

A statement is encoded "*varname*", "*varname op varname*", or "*varname op varname op varname*", and so on; *op* is either "->" or "<->".

Methods and formulas

misstable is implemented as an ado-file.

Also see

[MI] **mi misstable** — Tabulate pattern of missing values

[R] **summarize** — Summary statistics

[R] **tabulate oneway** — One-way tables of frequencies

[R] **tabulate twoway** — Two-way tables of frequencies

Title

mkspline — Linear and restricted cubic spline construction

Syntax

Linear spline with knots at specified points

```
mkspline newvar1 #1 [newvar2 #2 [...]] newvark = oldvar [if] [in] [, marginal
    displayknots]
```

Linear spline with knots equally spaced or at percentiles of data

```
mkspline stubname # = oldvar [if] [in] [weight] [, marginal pctile
    displayknots]
```

Restricted cubic spline

```
mkspline stubname = oldvar [if] [in] [weight], cubic [nknots(#) knots(numlist)
    displayknots]
```

`fweights` are allowed with the second and third syntax; see [U] **11.1.6 weight**.

Menu

Data > Create or change data > Other variable-creation commands > Linear and cubic spline construction

Description

`mkspline` creates variables containing a linear spline or a restricted cubic spline of *oldvar*.

In the first syntax, `mkspline` creates $newvar_1, \ldots, newvar_k$ containing a linear spline of *oldvar* with knots at the specified $\#_1, \ldots, \#_{k-1}$.

In the second syntax, `mkspline` creates # variables named *stubname*`1`, ..., *stubname*# containing a linear spline of *oldvar*. The knots are equally spaced over the range of *oldvar* or are placed at the percentiles of *oldvar*.

In the third syntax, `mkspline` creates variables containing a restricted cubic spline of *oldvar*. This is also known as a natural spline. The location and spacing of the knots is determined by the specification of the `nknots()` and `knots()` options.

Options

Options

`marginal` is allowed with the first or second syntax. It specifies that the new variables be constructed so that, when used in estimation, the coefficients represent the change in the slope from the preceding interval. The default is to construct the variables so that, when used in estimation, the coefficients measure the slopes for the interval.

`displayknots` displays the values of the knots that were used in creating the linear or restricted cubic spline.

`pctile` is allowed only with the second syntax. It specifies that the knots be placed at percentiles of the data rather than being equally spaced over the range.

`nknots(#)` is allowed only with the third syntax. It specifies the number of knots that are to be used for a restricted cubic spline. This number must be between 3 and 7 unless the knot locations are specified using `knots()`. The default number of knots is 5.

`knots(`*numlist*`)` is allowed only with the third syntax. It specifies the exact location of the knots to be used for a restricted cubic spline. The values of these knots must be given in increasing order. When this option is omitted, the default knot values are based on Harrell's recommended percentiles with the additional restriction that the smallest knot may not be less than the fifth-smallest value of *oldvar* and the largest knot may not be greater than the fifth-largest value of *oldvar*. If both `nknots()` and `knots()` are given, they must specify the same number of knots.

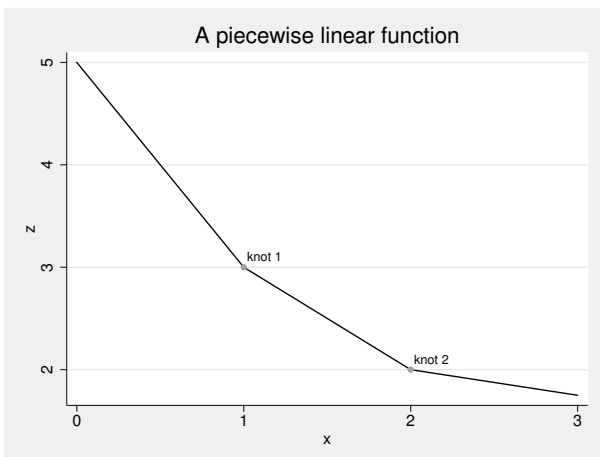
Remarks

Remarks are presented under the following headings:

Linear splines
Restricted cubic splines

Linear splines

Linear splines allow estimating the relationship between y and x as a piecewise linear function, which is a function composed of linear segments—straight lines. One linear segment represents the function for values of x below x_0, another linear segment handles values between x_0 and x_1, and so on. The linear segments are arranged so that they join at x_0, x_1, ..., which are called the knots. An example of a piecewise linear function is shown below.



Example 1

We wish to fit a model of log income on education and age by using a piecewise linear function for age:

$$\texttt{lninc} = b_0 + b_1\,\texttt{educ} + f(\texttt{age}) + u$$

The knots are to be placed at 10-year intervals: 20, 30, 40, 50, and 60.

```
. use http://www.stata-press.com/data/r12/mksp1
. mkspline age1 20 age2 30 age3 40 age4 50 age5 60 age6 = age, marginal
. regress lninc educ age1-age6
```
(*output omitted*)

Because we specified the `marginal` option, we could test whether the age effect is the same in the 30–40 and 40–50 intervals by asking whether the `age4` coefficient is zero. With the `marginal` option, coefficients measure the change in slope from the preceding group. Specifying `marginal` changes only the interpretation of the coefficients; the same model is fit in either case. Without the `marginal` option, the interpretation of the coefficients would have been

$$\frac{dy}{d\texttt{age}} = \begin{cases} a_1 & \text{if } \texttt{age} < 20 \\ a_2 & \text{if } 20 \le \texttt{age} < 30 \\ a_3 & \text{if } 30 \le \texttt{age} < 40 \\ a_4 & \text{if } 40 \le \texttt{age} < 50 \\ a_5 & \text{if } 50 \le \texttt{age} < 60 \\ a_6 & \text{otherwise} \end{cases}$$

With the `marginal` option, the interpretation is

$$\frac{dy}{d\texttt{age}} = \begin{cases} a_1 & \text{if } \texttt{age} < 20 \\ a_1 + a_2 & \text{if } 20 \le \texttt{age} < 30 \\ a_1 + a_2 + a_3 & \text{if } 30 \le \texttt{age} < 40 \\ a_1 + a_2 + a_3 + a_4 & \text{if } 40 \le \texttt{age} < 50 \\ a_1 + a_2 + a_3 + a_4 + a_5 & \text{if } 50 \le \texttt{age} < 60 \\ a_1 + a_2 + a_3 + a_4 + a_5 + a_6 & \text{otherwise} \end{cases}$$

◁

Example 2

Say that we have a binary outcome variable called `outcome`. We are beginning an analysis and wish to parameterize the effect of dosage on outcome. We wish to divide the data into five equal-width groups of dosage for the piecewise linear function.

```
. use http://www.stata-press.com/data/r12/mksp2
. mkspline dose 5 = dosage, displayknots
```

	knot1	knot2	knot3	knot4
dosage	20	40	60	80

```
. logistic outcome dose1-dose5
```
(*output omitted*)

`mkspline dose 5 = dosage` creates five variables—`dose1`, `dose2`, . . . , `dose5`—equally spacing the knots over the range of `dosage`. Because dosage varied between 0 and 100, the `mkspline` command above has the same effect as typing

```
. mkspline dose1 20 dose2 40 dose3 60 dose4 80 dose5 = dosage
```

The `pctile` option sets the knots to divide the data into five equal sample-size groups rather than five equal-width ranges. Typing

```
. mkspline pctdose 5 = dosage, pctile displayknots
```

	knot1	knot2	knot3	knot4
dosage	16	36.4	55.6	82

places the knots at the 20th, 40th, 60th, and 80th percentiles of the data.

◁

Restricted cubic splines

A linear spline can be used to fit many functions well. However, a restricted cubic spline may be a better choice than a linear spline when working with a very curved function. When using a restricted cubic spline, one obtains a continuous smooth function that is linear before the first knot, a piecewise cubic polynomial between adjacent knots, and linear again after the last knot.

▷ Example 3

Returning to the data from example 1, we may feel that a curved function is a better fit. First, we will use the `knots()` option to specify the five knots that we used previously.

```
. use http://www.stata-press.com/data/r12/mksp1, clear
. mkspline agesp = age, cubic knots(20 30 40 50 60)
. regress lninc educ agesp*
```
(*output omitted*)

Harrell (2001, 23) recommends placing knots at equally spaced percentiles of the original variable's marginal distribution. If we do not specify the `knots()` option, variables will be created containing a restricted cubic spline with five knots determined by Harrell's default percentiles.

```
. use http://www.stata-press.com/data/r12/mksp1, clear
. mkspline agesp = age, cubic displayknots
. regress lninc educ agesp*
```
(*output omitted*)

◁

Methods and formulas

`mkspline` is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Linear splines
Restricted cubic splines

Linear splines

Let V_i, $i = 1, \ldots, n$, be the variables to be created; k_i, $i = 1, \ldots, n-1$, be the corresponding knots; and $\mathcal{V}$ be the original variable (the command is `mkspline` V_1 k_1 V_2 k_2 ... V_n `=` $\mathcal{V}$). Then

$$V_1 = \min(\mathcal{V}, k_1)$$
$$V_i = \max\Big\{\min(\mathcal{V}, k_i), k_{i-1}\Big\} - k_{i-1} \quad i = 2, \ldots, n$$

If the `marginal` option is specified, the definitions are

$$V_1 = \mathcal{V}$$
$$V_i = \max(0, \mathcal{V} - k_{i-1}) \quad i = 2, \ldots, n$$

In the second syntax, `mkspline` *stubname* `#` `=` $\mathcal{V}$, so let m and M be the minimum and maximum of $\mathcal{V}$. Without the `pctile` option, knots are set at $m + (M - m)(i/n)$ for $i = 1, \ldots, n-1$. If `pctile` is specified, knots are set at the $100(i/n)$ percentiles, for $i = 1, \ldots, n-1$. Percentiles are calculated by `centile`; see [R] **centile**.

Restricted cubic splines

Let k_i, $i = 1, \ldots, n$, be the knot values; V_i, $i = 1, \ldots, n-1$, be the variables to be created; and $\mathcal{V}$ be the original variable. Then

$$V_1 = \mathcal{V}$$
$$V_{i+1} = \frac{(\mathcal{V} - k_i)_+^3 - (k_n - k_{n-1})^{-1}\{(\mathcal{V} - k_{n-1})_+^3(k_n - k_i) - (\mathcal{V} - k_n)_+^3(k_{n-1} - k_i)\}}{(k_n - k_1)^2}$$
$$i = 1, \ldots, n-2$$

where

$$(u)_+ = \begin{cases} u, \text{ if } & u > 0 \\ 0, \text{ if } & u \leq 0 \end{cases}$$

Without the `knots()` option, the locations of the knots are determined by the percentiles recommended in Harrell (2001, 23). These percentiles are based on the chosen number of knots as follows:

No. of knots	Percentiles						
3	10	50	90				
4	5	35	65	95			
5	5	27.5	50	72.5	95		
6	5	23	41	59	77	95	
7	2.5	18.33	34.17	50	65.83	81.67	97.5

Harrell provides default percentiles when the number of knots is between 3 and 7. When using a number of knots outside this range, the location of the knots must be specified in `knots()`.

Acknowledgment

The restricted cubic spline portion of `mkspline` is based on the `rc_spline` command by William Dupont.

References

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Newson, R. 2000. sg151: B-splines and splines parameterized by their values at reference points on the x-axis. *Stata Technical Bulletin* 57: 20–27. Reprinted in *Stata Technical Bulletin Reprints*, vol. 10, pp. 221–230. College Station, TX: Stata Press.

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Panis, C. 1994. sg24: The piecewise linear spline transformation. *Stata Technical Bulletin* 18: 27–29. Reprinted in *Stata Technical Bulletin Reprints*, vol. 3, pp. 146–149. College Station, TX: Stata Press.

Also see

[R] **fracpoly** — Fractional polynomial regression

Title

ml — Maximum likelihood estimation

Syntax

ml model in interactive mode

`ml model` *method progname eq* [*eq* ...] [*if*] [*in*] [*weight*]
[, *model_options* `svy` *diparm_options*]

`ml model` *method funcname*`()` *eq* [*eq* ...] [*if*] [*in*] [*weight*]
[, *model_options* `svy` *diparm_options*]

ml model in noninteractive mode

`ml model` *method progname eq* [*eq* ...] [*if*] [*in*] [*weight*] , `maximize`
[*model_options* `svy` *diparm_options noninteractive_options*]

`ml model` *method funcname*`()` *eq* [*eq* ...] [*if*] [*in*] [*weight*] , `maximize`
[*model_options* `svy` *diparm_options noninteractive_options*]

Noninteractive mode is invoked by specifying the `maximize` option. Use `maximize` when `ml` will be used as a subroutine of another ado-file or program and you want to carry forth the problem, from definition to posting of results, in one command.

`ml clear`

`ml query`

`ml check`

`ml search` [[`/`]*eqname*[`:`] $\#_{lb}$ $\#_{ub}$] [...] [, *search_options*]

`ml plot` [*eqname*`:`]*name* [# [# [#]]] [, `saving(`*filename*[, `replace`]`)`]

`ml init` { [*eqname*`:`]*name*`=#` | `/`*eqname*`=#` } [...]

`ml init` # [# ...] , `copy`

`ml init` *matname* [, `copy skip`]

`ml report`

`ml trace` { `on` | `off` }

`ml count` [`clear` | `on` | `off`]

`ml maximize` [, *ml_maximize_options display_options eform_option*]

```
ml graph    [#] [, saving(filename[, replace])]

ml display  [, display_options eform_option]

ml footnote

ml score newvar [if] [in] [, equation(eqname) missing]

ml score newvarlist [if] [in] [, missing]

ml score [type] stub* [if] [in] [, missing]
```

where *method* is one of

lf	d0	lf0	gf0
	d1	lf1	
	d1debug	lf1debug	
	d2	lf2	
	d2debug	lf2debug	

or *method* can be specified using one of the longer, more descriptive names

method	Longer name
lf	linearform
d0	derivative0
d1	derivative1
d1debug	derivative1debug
d2	derivative2
d2debug	derivative2debug
lf0	linearform0
lf1	linearform1
lf1debug	linearform1debug
lf2	linearform2
lf2debug	linearform2debug
gf0	generalform0

eq is the equation to be estimated, enclosed in parentheses, and optionally with a name to be given to the equation, preceded by a colon,

(\[*eqname*:\] \[$varlist_y$ =\] \[$varlist_x$\] \[, *eq_options*\])

or *eq* is the name of a parameter, such as sigma, with a slash in front

/*eqname* which is equivalent to (*eqname*:)

and *diparm_options* is one or more `diparm(`*diparm_args*`)` options where *diparm_args* is either `__sep__` or anything accepted by the "undocumented" `_diparm` command; see help `_diparm`.

eq_options	Description
noconstant	do not include an intercept in the equation
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1

model_options	Description
`group(`*varname*`)`	use *varname* to identify groups
`vce(`*vcetype*`)`	*vcetype* may be `robust`, `cluster` *clustvar*, `oim`, or `opg`
`constraints(`*numlist*`)`	constraints by number to be applied
`constraints(`*matname*`)`	matrix that contains the constraints to be applied
`nocnsnotes`	do not display notes when constraints are dropped
`title(`*string*`)`	place a title on the estimation output
`nopreserve`	do not preserve the estimation subsample in memory
`collinear`	keep collinear variables within equations
`missing`	keep observations containing variables with missing values
`lf0(`$\#_k$ $\#_{ll}$`)`	number of parameters and log-likelihood value of the constant-only model
`continue`	specifies that a model has been fit and sets the initial values $\mathbf{b}_0$ for the model to be fit based on those results
`waldtest(#)`	perform a Wald test; see *Options for use with ml model in interactive or noninteractive mode* below
`obs(#)`	number of observations
`crittype(`*string*`)`	describe the criterion optimized by `ml`
`subpop(`*varname*`)`	compute estimates for the single subpopulation
`nosvyadjust`	carry out Wald test as $W/k \sim F(k,d)$
`technique(nr)`	Stata's modified Newton–Raphson (NR) algorithm
`technique(bhhh)`	Berndt–Hall–Hall–Hausman (BHHH) algorithm
`technique(dfp)`	Davidon–Fletcher–Powell (DFP) algorithm
`technique(bfgs)`	Broyden–Fletcher–Goldfarb–Shanno (BFGS) algorithm

noninteractive_options	Description
`init(`*ml_init_args*`)`	set the initial values $\mathbf{b}_0$
`search(on)`	equivalent to `ml search, repeat(0)`; the default
`search(norescale)`	equivalent to `ml search, repeat(0) norescale`
`search(quietly)`	same as `search(on)`, except that output is suppressed
`search(off)`	prevents calling `ml search`
`repeat(#)`	`ml search`'s `repeat()` option; see below
`bounds(`*ml_search_bounds*`)`	specify bounds for `ml search`
`nowarning`	suppress "convergence not achieved" message of `iterate(0)`
`novce`	substitute the zero matrix for the variance matrix
`negh`	indicates that the evaluator returns the negative Hessian matrix
`score(`*newvars*`)`	new variables containing the contribution to the score
maximize_options	control the maximization process; seldom used

search_options	Description
repeat(#)	number of random attempts to find better initial-value vector; default is repeat(10) in interactive mode and repeat(0) in noninteractive mode
restart	use random actions to find starting values; not recommended
norescale	do not rescale to improve parameter vector; not recommended
maximize_options	control the maximization process; seldom used

ml_maximize_options	Description
nowarning	suppress "convergence not achieved" message of iterate(0)
novce	substitute the zero matrix for the variance matrix
negh	indicates that the evaluator returns the negative Hessian matrix
score(*newvars* | *stub**)	new variables containing the contribution to the score
nooutput	suppress display of final results
noclear	do not clear ml problem definition after model has converged
maximize_options	control the maximization process; seldom used

display_options	Description
noheader	suppress header display above the coefficient table
nofootnote	suppress footnote display below the coefficient table
level(#)	set confidence level; default is level(95)
first	display coefficient table reporting results for first equation only
neq(#)	display coefficient table reporting first # equations
showeqns	display equation names in the coefficient table
plus	display coefficient table ending in dashes–plus-sign–dashes
nocnsreport	suppress constraints display above the coefficient table
noomitted	suppress display of omitted variables
vsquish	suppress blank space separating factor-variable terms or time-series–operated variables from other variables
noemptycells	suppress empty cells for interactions of factor variables
baselevels	report base levels of factor variables and interactions
allbaselevels	display all base levels of factor variables and interactions
cformat(%*fmt*)	format the coefficients, standard errors, and confidence limits in the coefficient table
pformat(%*fmt*)	format the p-values in the coefficient table
sformat(%*fmt*)	format the test statistics in the coefficient table
nolstretch	do not automatically widen the coefficient table to accommodate longer variable names
coeflegend	display legend instead of statistics

eform_option	Description
eform(*string*)	display exponentiated coefficients; column title is "*string*"
eform	display exponentiated coefficients; column title is "exp(b)"
hr	report hazard ratios
shr	report subhazard ratios
irr	report incidence-rate ratios
or	report odds ratios
rrr	report relative-risk ratios

fweights, aweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**. With all but method lf, you must write your likelihood-evaluation program carefully if pweights are to be specified, and pweights may not be specified with method d0, d1, d1debug, d2, or d2debug. See Gould, Pitblado, and Poi (2010, chap. 6) for details.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

To redisplay results, type ml display.

Syntax of subroutines for use by evaluator programs

```
mleval      newvar = vecname [ , eq(#) ]
mleval      scalarname = vecname , scalar [ eq(#) ]
mlsum       scalarname_lnf = exp [ if ] [ , noweight ]
mlvecsum    scalarname_lnf rowvecname = exp [ if ] [ , eq(#) ]
mlmatsum    scalarname_lnf matrixname = exp [ if ] [ , eq(#[,#]) ]
mlmatbysum  scalarname_lnf matrixname varname_a varname_b [ varname_c ] [ if ] ,
                by(varname) [ eq(#[,#]) ]
```

Syntax of user-written evaluator

Summary of notation

The log-likelihood function is $\ln L(\theta_{1j}, \theta_{2j}, \ldots, \theta_{Ej})$, where $\theta_{ij} = \mathbf{x}_{ij}\mathbf{b}_i$, $j = 1, \ldots, N$ indexes observations, and $i = 1, \ldots, E$ indexes the linear equations defined by ml model. If the likelihood satisfies the linear-form restrictions, it can be decomposed as $\ln L = \sum_{j=1}^{N} \ln \ell(\theta_{1j}, \theta_{2j}, \ldots, \theta_{Ej})$.

Method-lf evaluators

```
program progname
        version 12
        args lnfj theta1 theta2 ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        quietly gen double `tmp1' = ...
        ...
        quietly replace `lnfj' = ...
end
```

where

`'lnfj'`	variable to be filled in with observation-by-observation values of $\ln\ell_j$
`'theta1'`	variable containing evaluation of first equation $\theta_{1j}=\mathbf{x}_{1j}\mathbf{b}_1$
`'theta2'`	variable containing evaluation of second equation $\theta_{2j}=\mathbf{x}_{2j}\mathbf{b}_2$
`...`	

Method-d0 evaluators

```
program progname
        version 12
        args todo b lnf
        tempvar theta1 theta2 ...
        mleval 'theta1' = 'b', eq(1)
        mleval 'theta2' = 'b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double 'tmp1' = ...
        ...
        mlsum 'lnf' = ...
end
```

where

`'todo'`	always contains `0` (may be ignored)
`'b'`	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`'lnf'`	scalar to be filled in with overall $\ln L$

Method-d1 evaluators

```
program progname
        version 12
        args todo b lnf g
        tempvar theta1 theta2 ...
        mleval 'theta1' = 'b', eq(1)
        mleval 'theta2' = 'b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double 'tmp1' = ...
        ...
        mlsum 'lnf' = ...
        if ('todo'==0 | 'lnf'>=.) exit
        tempname d1 d2 ...
        mlvecsum 'lnf' 'd1' = formula for ∂lnℓj/∂θ1j, eq(1)
        mlvecsum 'lnf' 'd2' = formula for ∂lnℓj/∂θ2j, eq(2)
        ...
        matrix 'g' = ('d1','d2', ... )
end
```

where

`'todo'`	contains `0` or `1` `0`⇒`'lnf'` to be filled in; `1`⇒`'lnf'` and `'g'` to be filled in
`'b'`	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`'lnf'`	scalar to be filled in with overall $\ln L$
`'g'`	row vector to be filled in with overall $\mathbf{g}=\partial\ln L/\partial\mathbf{b}$

Method-d2 evaluators

```
program progname
        version 12
        args todo b lnf g H
        tempvar theta1 theta2 ...
        mleval `theta1' = `b', eq(1)
        mleval `theta2' = `b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double `tmp1' = ...
        ...
        mlsum `lnf' = ...
        if (`todo'==0 | `lnf'>=.) exit
        tempname d1 d2 ...
        mlvecsum `lnf' `d1' = formula for ∂lnℓj/∂θ1j, eq(1)
        mlvecsum `lnf' `d2' = formula for ∂lnℓj/∂θ2j, eq(2)
        ...
        matrix `g' = (`d1',`d2', ... )
        if (`todo'==1 | `lnf'>=.) exit
        tempname d11 d12 d22 ...
        mlmatsum `lnf' `d11' = formula for ∂²lnℓj/∂θ1j², eq(1)
        mlmatsum `lnf' `d12' = formula for ∂²lnℓj/∂θ1j∂θ2j, eq(1,2)
        mlmatsum `lnf' `d22' = formula for ∂²lnℓj/∂θ2j², eq(2)
        ...
        matrix `H' = (`d11',`d12', ... \ `d12'',`d22', ... )
end
```

where

`todo'	contains 0, 1, or 2 0⇒`lnf' to be filled in; 1⇒`lnf' and `g' to be filled in; 2⇒`lnf', `g', and `H' to be filled in
`b'	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`lnf'	scalar to be filled in with overall $\ln L$
`g'	row vector to be filled in with overall $\mathbf{g}=\partial \ln L/\partial \mathbf{b}$
`H'	matrix to be filled in with overall Hessian $\mathbf{H}=\partial^2 \ln L/\partial \mathbf{b}\partial \mathbf{b}'$

Method-lf0 evaluators

```
program progname
        version 12
        args todo b lnfj
        tempvar theta1 theta2 ...
        mleval `theta1' = `b', eq(1)
        mleval `theta2' = `b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double `tmp1' = ...
        ...
        quietly replace `lnfj' = ...
end
```

where

`todo'	always contains 0 (may be ignored)
`b'	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`lnfj'	variable to be filled in with observation-by-observation values of $\ln \ell_j$

Method-lf1 evaluators

```
program progname
        version 12
        args todo b lnfj g1 g2 ...
        tempvar theta1 theta2 ...
        mleval `theta1' = `b', eq(1)
        mleval `theta2' = `b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double `tmp1' = ...
        ...
        quietly replace `lnfj' = ...
        if (`todo'==0) exit
        quietly replace `g1' = formula for ∂ln ℓj/∂θ1j
        quietly replace `g2' = formula for ∂ln ℓj/∂θ2j
        ...
end
```

where

`todo'	contains 0 or 1 0⇒`lnfj'to be filled in; 1⇒`lnfj', `g1', `g2', . . ., to be filled in
`b'	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`lnfj'	variable to be filled in with observation-by-observation values of $\ln\ell_j$
`g1'	variable to be filled in with $\partial\ln\ell_j/\partial\theta_{1j}$
`g2'	variable to be filled in with $\partial\ln\ell_j/\partial\theta_{2j}$
...	

Method-lf2 evaluators

```
program progname
        version 12
        args todo b lnfj g1 g2 ... H
        tempvar theta1 theta2 ...
        mleval `theta1' = `b', eq(1)
        mleval `theta2' = `b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double `tmp1' = ...
        ...
        quietly replace `lnfj' = ...
        if (`todo'==0) exit
        quietly replace `g1' = formula for ∂ln ℓj/∂θ1j
        quietly replace `g2' = formula for ∂ln ℓj/∂θ2j
        ...
        if (`todo'==1) exit
        tempname d11 d12 d22 lnf ...
        mlmatsum `lnf' `d11' = formula for ∂2 ln ℓj/∂θ1j2, eq(1)
        mlmatsum `lnf' `d12' = formula for ∂2 ln ℓj/∂θ1j∂θ2j, eq(1,2)
        mlmatsum `lnf' `d22' = formula for ∂2 ln ℓj/∂θ2j2, eq(2)
        ...
        matrix `H' = (`d11',`d12', ... \ `d12'',`d22', ... )
end
```

where

`'todo'`	contains `0` or `1` `0`⇒`'lnfj'`to be filled in; `1`⇒`'lnfj'`, `'g1'`, `'g2'`, ..., to be filled in `2`⇒`'lnfj'`, `'g1'`, `'g2'`, ..., and `'H'` to be filled in
`'b'`	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`'lnfj'`	scalar to be filled in with observation-by-observation $\ln L$
`'g1'`	variable to be filled in with $\partial \ln\ell_j/\partial\theta_{1j}$
`'g2'`	variable to be filled in with $\partial \ln\ell_j/\partial\theta_{2j}$
...	
`'H'`	matrix to be filled in with overall Hessian $\mathbf{H}=\partial^2 \ln L/\partial\mathbf{b}\partial\mathbf{b}'$

Method-gf0 evaluators

```
program progname
        version 12
        args todo b lnfj
        tempvar theta1 theta2 ...
        mleval 'theta1' = 'b', eq(1)
        mleval 'theta2' = 'b', eq(2) // if there is a θ2
        ...
        // if you need to create any intermediate results:
        tempvar tmp1 tmp2 ...
        gen double 'tmp1' = ...
        ...
        quietly replace 'lnfj' = ...
end
```

where

`'todo'`	always contains `0` (may be ignored)
`'b'`	full parameter row vector $\mathbf{b}=(\mathbf{b}_1,\mathbf{b}_2,...,\mathbf{b}_E)$
`'lnfj'`	variable to be filled in with the values of the log-likelihood $\ln\ell_j$

Global macros for use by all evaluators

`$ML_y1`	name of first dependent variable
`$ML_y2`	name of second dependent variable, if any
...	
`$ML_samp`	variable containing 1 if observation to be used; 0 otherwise
`$ML_w`	variable containing weight associated with observation or 1 if no weights specified

Method-lf evaluators can ignore `$ML_samp`, but restricting calculations to the `$ML_samp==1` subsample will speed execution. Method-lf evaluators must ignore `$ML_w`; application of weights is handled by the method itself.

Methods d0, d1, d2, lf0, lf1, lf2, and gf0 can ignore `$ML_samp` as long as `ml model`'s `nopreserve` option is not specified. These methods will run more quickly if `nopreserve` is specified. These evaluators can ignore `$ML_w` only if they use `mlsum`, `mlvecsum`, `mlmatsum`, and `mlmatbysum` to produce all final results.

Description

`ml model` defines the current problem.

`ml clear` clears the current problem definition. This command is rarely used because when you type `ml model`, any previous problem is automatically cleared.

`ml query` displays a description of the current problem.

`ml check` verifies that the log-likelihood evaluator you have written works. We strongly recommend using this command.

`ml search` searches for (better) initial values. We recommend using this command.

`ml plot` provides a graphical way of searching for (better) initial values.

`ml init` provides a way to specify initial values.

`ml report` reports $\ln L$'s values, gradient, and Hessian at the initial values or current parameter estimates, $\mathbf{b}_0$.

`ml trace` traces the execution of the user-defined log-likelihood evaluation program.

`ml count` counts the number of times the user-defined log-likelihood evaluation program is called; this command is seldom used. `ml count clear` clears the counter. `ml count on` turns on the counter. `ml count` without arguments reports the current values of the counter. `ml count off` stops counting calls.

`ml maximize` maximizes the likelihood function and reports results. Once `ml maximize` has successfully completed, the previously mentioned `ml` commands may no longer be used unless `noclear` is specified. `ml graph` and `ml display` may be used whether or not `noclear` is specified.

`ml graph` graphs the log-likelihood values against the iteration number.

`ml display` redisplays results.

`ml footnote` displays a warning message when the model did not converge within the specified number of iterations.

`ml score` creates new variables containing the equation-level scores. The variables generated by `ml score` are equivalent to those generated by specifying the `score()` option of `ml maximize` (and `ml model ..., ... maximize`).

progname is the name of a Stata program you write to evaluate the log-likelihood function.

funcname`()` is the name of a Mata function you write to evaluate the log-likelihood function.

In this documentation, *progname* and *funcname*`()` are referred to as the user-written evaluator, the likelihood evaluator, or sometimes simply as the evaluator. The program you write is written in the style required by the method you choose. The methods are lf, d0, d1, d2, lf0, lf1, lf2, and gf0. Thus, if you choose to use method lf, your program is called a method-lf evaluator.

Method-lf evaluators are required to evaluate the observation-by-observation log likelihood $\ln \ell_j$, $j = 1, \ldots, N$.

Method-d0 evaluators are required to evaluate the overall log likelihood $\ln L$. Method-d1 evaluators are required to evaluate the overall log likelihood and its gradient vector $\mathbf{g} = \partial \ln L/\partial \mathbf{b}$. Method-d2 evaluators are required to evaluate the overall log likelihood, its gradient, and its Hessian matrix $H = \partial^2 \ln L/\partial \mathbf{b} \partial \mathbf{b}'$.

Method-lf0 evaluators are required to evaluate the observation-by-observation log likelihood $\ln \ell_j$, $j = 1, \ldots, N$. Method-lf1 evaluators are required to evaluate the observation-by-observation log likelihood and its equation-level scores $g_{ji} = \partial \ln \ell/\partial \mathbf{x}_{ji}\mathbf{b}_i$. Method-lf2 evaluators are required to evaluate the observation-by-observation log likelihood, its equation-level scores, and its Hessian matrix $H = \partial^2 \ln \ell/\partial \mathbf{b} \partial \mathbf{b}'$.

Method-gf0 evaluators are required to evaluate the summable pieces of the log likelihood $\ln \ell_k$, $k = 1, \ldots, K$.

`mleval` is a subroutine used by evaluators of methods d0, d1, d2, lf0, lf1, lf2, and gf0 to evaluate the coefficient vector, $\mathbf{b}$, that they are passed.

`mlsum` is a subroutine used by evaluators of methods d0, d1, and d2 to define the value, $\ln L$, that is to be returned.

`mlvecsum` is a subroutine used by evaluators of methods d1 and d2 to define the gradient vector, $\mathbf{g}$, that is to be returned. It is suitable for use only when the likelihood function meets the linear-form restrictions.

`mlmatsum` is a subroutine used by evaluators of methods d2 and lf2 to define the Hessian matrix, $\mathbf{H}$, that is to be returned. It is suitable for use only when the likelihood function meets the linear-form restrictions.

`mlmatbysum` is a subroutine used by evaluator of method d2 to help define the Hessian matrix, $\mathbf{H}$, that is to be returned. It is suitable for use when the likelihood function contains terms made up of grouped sums, such as in panel-data models. For such models, use `mlmatsum` to compute the observation-level outer products and `mlmatbysum` to compute the group-level outer products. `mlmatbysum` requires that the data be sorted by the variable identified in the `by()` option.

Options for use with ml model in interactive or noninteractive mode

`group(`*varname*`)` specifies the numeric variable that identifies groups. This option is typically used to identify panels for panel-data models.

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification, that allow for intragroup correlation, and that are derived from asymptotic theory; see [R] ***vce_option***.

`vce(robust)`, `vce(cluster` *clustvar*`)`, `pweight`, and `svy` will work with evaluators of methods lf, lf0, lf1, lf2, and gf0; all you need do is specify them.

These options will not work with evaluators of methods d0, d1, or d2, and specifying these options will produce an error message.

`constraints(`*numlist* | *matname*`)` specifies the linear constraints to be applied during estimation. `constraints(`*numlist*`)` specifies the constraints by number. Constraints are defined by using the `constraint` command; see [R] **constraint**. `constraint(`*matname*`)` specifies a matrix that contains the constraints.

`nocnsnotes` prevents notes from being displayed when constraints are dropped. A constraint will be dropped if it is inconsistent, contradicts other constraints, or causes some other error when the constraint matrix is being built. Constraints are checked in the order in which they are specified.

`title(`*string*`)` specifies the title for the estimation output when results are complete.

`nopreserve` specifies that `ml` need not ensure that only the estimation subsample is in memory when the user-written likelihood evaluator is called. `nopreserve` is irrelevant when you use method lf.

For the other methods, if `nopreserve` is not specified, `ml` saves the data in a file (preserves the original dataset) and drops the irrelevant observations before calling the user-written evaluator. This way, even if the evaluator does not restrict its attentions to the `$ML_samp==1` subsample, results will still be correct. Later, `ml` automatically restores the original dataset.

`ml` need not go through these machinations for method lf because the user-written evaluator calculates observation-by-observation values, and `ml` itself sums the components.

`ml` goes through these machinations if and only if the estimation sample is a subsample of the data in memory. If the estimation sample includes every observation in memory, `ml` does not preserve the original dataset. Thus programmers must not alter the original dataset unless they `preserve` the data themselves.

We recommend that interactive users of `ml` not specify `nopreserve`; the speed gain is not worth the possibility of getting incorrect results.

We recommend that programmers specify nopreserve, but only after verifying that their evaluator really does restrict its attentions solely to the $ML_samp==1 subsample.

collinear specifies that ml not remove the collinear variables within equations. There is no reason to leave collinear variables in place, but this option is of interest to programmers who, in their code, have already removed collinear variables and do not want ml to waste computer time checking again.

missing specifies that observations containing variables with missing values not be eliminated from the estimation sample. There are two reasons you might want to specify missing:

Programmers may wish to specify missing because, in other parts of their code, they have already eliminated observations with missing values and do not want ml to waste computer time looking again.

You may wish to specify missing if your model explicitly deals with missing values. Stata's heckman command is a good example of this. In such cases, there will be observations where missing values are allowed and other observations where they are not—where their presence should cause the observation to be eliminated. If you specify missing, it is your responsibility to specify an if *exp* that eliminates the irrelevant observations.

lf0($\#_k$ $\#_{ll}$) is typically used by programmers. It specifies the number of parameters and log-likelihood value of the constant-only model so that ml can report a likelihood-ratio test rather than a Wald test. These values may have been analytically determined, or they may have been determined by a previous fitting of the constant-only model on the estimation sample.

Also see the continue option directly below.

If you specify lf0(), it must be safe for you to specify the missing option, too, else how did you calculate the log likelihood for the constant-only model on the same sample? You must have identified the estimation sample, and done so correctly, so there is no reason for ml to waste time rechecking your results. All of which is to say, do not specify lf0() unless you are certain your code identifies the estimation sample correctly.

lf0(), even if specified, is ignored if vce(robust), vce(cluster *clustvar*), pweight, or svy is specified because, in that case, a likelihood-ratio test would be inappropriate.

continue is typically specified by programmers and does two things:

First, it specifies that a model has just been fit by either ml or some other estimation command, such as logit, and that the likelihood value stored in e(ll) and the number of parameters stored in e(b) as of that instant are the relevant values of the constant-only model. The current value of the log likelihood is used to present a likelihood-ratio test unless vce(robust), vce(cluster *clustvar*), pweight, svy, or constraints() is specified. A likelihood-ratio test is inappropriate when vce(robust), vce(cluster *clustvar*), pweight, or svy is specified. We suggest using lrtest when constraints() is specified; see [R] **lrtest**.

Second, continue sets the initial values, $\mathbf{b}_0$, for the model about to be fit according to the e(b) currently stored.

The comments made about specifying missing with lf0() apply equally well here.

waldtest(#) is typically specified by programmers. By default, ml presents a Wald test, but that is overridden if the lf0() or continue option is specified. A Wald test is performed if vce(robust), vce(cluster *clustvar*), or pweight is specified.

waldtest(0) prevents even the Wald test from being reported.

waldtest(-1) is the default. It specifies that a Wald test be performed by constraining all coefficients except the intercept to 0 in the first equation. Remaining equations are to be unconstrained.

A Wald test is performed if neither `lf0()` nor `continue` was specified, and a Wald test is forced if `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweight` was specified.

`waldtest(`k`)` for $k \leq -1$ specifies that a Wald test be performed by constraining all coefficients except intercepts to 0 in the first $|k|$ equations; remaining equations are to be unconstrained. A Wald test is performed if neither `lf0()` nor `continue` was specified, and a Wald test is forced if `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweight` was specified.

`waldtest(`k`)` for $k \geq 1$ works like the options above, except that it forces a Wald test to be reported even if the information to perform the likelihood-ratio test is available and even if none of `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweight` was specified. `waldtest(`k`)`, $k \geq 1$, may not be specified with `lf0()`.

`obs(#)` is used mostly by programmers. It specifies that the number of observations reported and ultimately stored in `e(N)` be `#`. Ordinarily, `ml` works that out for itself. Programmers may want to specify this option when, for the likelihood evaluator to work for N observations, they first had to modify the dataset so that it contained a different number of observations.

`crittype(`*string*`)` is used mostly by programmers. It allows programmers to supply a string (up to 32 characters long) that describes the criterion that is being optimized by `ml`. The default is `"log likelihood"` for nonrobust and `"log pseudolikelihood"` for robust estimation.

`svy` indicates that `ml` is to pick up the `svy` settings set by `svyset` and use the robust variance estimator. This option requires the data to be `svyset`; see [SVY] **svyset**. `svy` may not be specified with `vce()` or *weights*.

`subpop(`*varname*`)` specifies that estimates be computed for the single subpopulation defined by the observations for which *varname* $\neq 0$. Typically, *varname* $= 1$ defines the subpopulation, and *varname* $= 0$ indicates observations not belonging to the subpopulation. For observations whose subpopulation status is uncertain, *varname* should be set to missing (‘`.`’). This option requires the `svy` option.

`nosvyadjust` specifies that the model Wald test be carried out as $W/k \sim F(k, d)$, where W is the Wald test statistic, k is the number of terms in the model excluding the constant term, d is the total number of sampled PSUs minus the total number of strata, and $F(k, d)$ is an F distribution with k numerator degrees of freedom and d denominator degrees of freedom. By default, an adjusted Wald test is conducted: $(d - k + 1)W/(kd) \sim F(k, d - k + 1)$. See Korn and Graubard (1990) for a discussion of the Wald test and the adjustments thereof. This option requires the `svy` option.

`technique(`*algorithm_spec*`)` specifies how the likelihood function is to be maximized. The following algorithms are currently implemented in `ml`. For details, see Gould, Pitblado, and Poi (2010).

`technique(nr)` specifies Stata’s modified Newton–Raphson (NR) algorithm.

`technique(bhhh)` specifies the Berndt–Hall–Hall–Hausman (BHHH) algorithm.

`technique(dfp)` specifies the Davidon–Fletcher–Powell (DFP) algorithm.

`technique(bfgs)` specifies the Broyden–Fletcher–Goldfarb–Shanno (BFGS) algorithm.

The default is `technique(nr)`.

You can switch between algorithms by specifying more than one in the `technique()` option. By default, `ml` will use an algorithm for five iterations before switching to the next algorithm. To specify a different number of iterations, include the number after the technique in the option. For example, `technique(bhhh 10 nr 1000)` requests that `ml` perform 10 iterations using the BHHH algorithm, followed by 1,000 iterations using the NR algorithm, and then switch back to BHHH for 10 iterations, and so on. The process continues until convergence or until reaching the maximum number of iterations.

Options for use with ml model in noninteractive mode

The following extra options are for use with `ml model` in noninteractive mode. Noninteractive mode is for programmers who use `ml` as a subroutine and want to issue one command that will carry forth the estimation from start to finish.

`maximize` is required. It specifies noninteractive mode.

`init(`*ml_init_args*`)` sets the initial values, $\mathbf{b}_0$. *ml_init_args* are whatever you would type after the `ml init` command.

`search(on | norescale | quietly | off)` specifies whether `ml search` is to be used to improve the initial values. `search(on)` is the default and is equivalent to separately running `ml search, repeat(0)`. `search(norescale)` is equivalent to separately running `ml search, repeat(0) norescale`. `search(quietly)` is equivalent to `search(on)`, except that it suppresses `ml search`'s output. `search(off)` prevents calling `ml search`.

`repeat(#)` is `ml search`'s `repeat()` option. `repeat(0)` is the default.

`bounds(`*ml_search_bounds*`)` specifies the search bounds. *ml_search_bounds* is specified as

$$[\,\textit{eqn\_name}\,]\ \textit{lower\_bound upper\_bound}\ \ldots\ [\,\textit{eqn\_name}\,]\ \textit{lower\_bound upper\_bound}$$

for instance, `bounds(100 100 lnsigma 0 10)`. The `ml model` command issues `ml search` *ml_search_bounds*`, repeat(#)`. Specifying search bounds is optional.

`nowarning`, `novce`, `negh`, and `score()` are `ml maximize`'s equivalent options.

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Options for use when specifying equations

`noconstant` specifies that the equation not include an intercept.

`offset(`*varname*$_o$`)` specifies that the equation be $\mathbf{xb} + $ *varname*$_o$—that it include *varname*$_o$ with coefficient constrained to be 1.

`exposure(`*varname*$_e$`)` is an alternative to `offset(`*varname*$_o$`)`; it specifies that the equation be $\mathbf{xb} + \ln($*varname*$_e)$. The equation is to include $\ln($*varname*$_e)$ with coefficient constrained to be 1.

Options for use with ml search

`repeat(#)` specifies the number of random attempts that are to be made to find a better initial-value vector. The default is `repeat(10)`.

`repeat(0)` specifies that no random attempts be made. More precisely, `repeat(0)` specifies that no random attempts be made if the first initial-value vector is a feasible starting point. If it is not, `ml search` will make random attempts, even if you specify `repeat(0)`, because it has no alternative. The `repeat()` option refers to the number of random attempts to be made to improve the initial values. When the initial starting value vector is not feasible, `ml search` will make up to 1,000 random attempts to find starting values. It stops when it finds one set of values that works and then moves into its improve-initial-values logic.

`repeat(`k`)`, $k > 0$, specifies the number of random attempts to be made to improve the initial values.

`restart` specifies that random actions be taken to obtain starting values and that the resulting starting values not be a deterministic function of the current values. Generally, you should not specify this option because, with `restart`, `ml search` intentionally does not produce as good a set of starting values as it could. `restart` is included for use by the optimizer when it gets into serious trouble. The random actions ensure that the optimizer and `ml search`, working together, do not cause an endless loop.

`restart` implies `norescale`, which is why we recommend that you do not specify `restart`. In testing, sometimes `rescale` worked so well that, even after randomization, the rescaler would bring the starting values right back to where they had been the first time and thus defeat the intended randomization.

`norescale` specifies that `ml search` not engage in its rescaling actions to improve the parameter vector. We do not recommend specifying this option because rescaling tends to work so well.

maximize_options: [`no`]`log` and `trace`; see [R] **maximize**. These options are seldom used.

Option for use with ml plot

`saving(`*filename*[`, replace`]`)` specifies that the graph be saved in *filename*`.gph`. See [G-3] ***saving_option***.

Options for use with ml init

`copy` specifies that the list of numbers or the initialization vector be copied into the initial-value vector by position rather than by name.

`skip` specifies that any parameters found in the specified initialization vector that are not also found in the model be ignored. The default action is to issue an error message.

Options for use with ml maximize

`nowarning` is allowed only with `iterate(0)`. `nowarning` suppresses the "convergence not achieved" message. Programmers might specify `iterate(0) nowarning` when they have a vector $\mathbf{b}$ already containing the final estimates and want `ml` to calculate the variance matrix and postestimation results. Then specify `init(b) search(off) iterate(0) nowarning nolog`.

`novce` is allowed only with `iterate(0)`. `novce` substitutes the zero matrix for the variance matrix, which in effect posts estimation results as fixed constants.

`negh` indicates that the evaluator returns the negative Hessian matrix. By default, `ml` assumes d2 and lf2 evaluators return the Hessian matrix.

`score(`*newvars* | *stub*`*)` creates new variables containing the contributions to the score for each equation and ancillary parameter in the model; see [U] **20.21 Obtaining scores**.

If `score(`*newvars*`)` is specified, the *newvars* must contain k new variables. For evaluators of methods lf, lf0, lf1, and lf2, k is the number of equations. For evaluators of method gf0, k is the number of parameters. If `score(`*stub*`*)` is specified, variables named *stub*`1`, *stub*`2`, ..., *stub*`k` are created.

For evaluators of methods lf, lf0, lf1, and lf2, the first variable contains $\partial \ln \ell_j / \partial(\mathbf{x}_{1j}\mathbf{b}_1)$, the second variable contains $\partial \ln \ell_j / \partial(\mathbf{x}_{2j}\mathbf{b}_2)$, and so on.

For evaluators of method gf0, the first variable contains $\partial \ln \ell_j / \partial \mathbf{b}_1$, the second variable contains $\partial \ln \ell_j / \partial \mathbf{b}_2$, and so on.

`nooutput` suppresses display of results. This option is different from prefixing `ml maximize` with `quietly` in that the iteration log is still displayed (assuming that `nolog` is not specified).

`noclear` specifies that the ml problem definition not be cleared after the model has converged. Perhaps you are having convergence problems and intend to run the model to convergence. If so, use `ml search` to see if those values can be improved, and then restart the estimation.

maximize_options: `difficult`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`; see [R] **maximize**. These options are seldom used.

display_options; see *Options for use with ml display* below.

eform_option; see *Options for use with ml display* below.

Option for use with ml graph

`saving(`*filename*`[ , replace])` specifies that the graph be saved in *filename*`.gph`. See [G-3] ***saving_option***.

Options for use with ml display

`noheader` suppresses the header display above the coefficient table that displays the final log-likelihood value, the number of observations, and the model significance test.

`nofootnote` suppresses the footnote display below the coefficient table, which displays a warning if the model fit did not converge within the specified number of iterations. Use `ml footnote` to display the warning if 1) you add to the coefficient table using the `plus` option or 2) you have your own footnotes and want the warning to be last.

`level(#)` is the standard confidence-level option. It specifies the confidence level, as a percentage, for confidence intervals of the coefficients. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`first` displays a coefficient table reporting results for the first equation only, and the report makes it appear that the first equation is the only equation. This option is used by programmers who estimate ancillary parameters in the second and subsequent equations and who wish to report the values of such parameters themselves.

`neq(#)` is an alternative to `first`. `neq(#)` displays a coefficient table reporting results for the first # equations. This option is used by programmers who estimate ancillary parameters in the $\# + 1$ and subsequent equations and who wish to report the values of such parameters themselves.

`showeqns` is a seldom-used option that displays the equation names in the coefficient table. `ml display` uses the numbers stored in `e(k_eq)` and `e(k_aux)` to determine how to display the coefficient table. `e(k_eq)` identifies the number of equations, and `e(k_aux)` identifies how many of these are for ancillary parameters. The `first` option is implied when `showeqns` is not specified and all but the first equation are for ancillary parameters.

`plus` displays the coefficient table, but rather than ending the table in a line of dashes, ends it in dashes–plus-sign–dashes. This is so that programmers can write additional display code to add more results to the table and make it appear as if the combined result is one table. Programmers typically specify `plus` with the `first` or `neq()` options. This option implies `nofootnote`.

`nocnsreport` suppresses the display of constraints above the coefficient table. This option is ignored if constraints were not used to fit the model.

`noomitted` specifies that variables that were omitted because of collinearity not be displayed. The default is to include in the table any variables omitted because of collinearity and to label them as "(omitted)".

`vsquish` specifies that the blank space separating factor-variable terms or time-series–operated variables from other variables in the model be suppressed.

`noemptycells` specifies that empty cells for interactions of factor variables not be displayed. The default is to include in the table interaction cells that do not occur in the estimation sample and to label them as "(empty)".

`baselevels` and `allbaselevels` control whether the base levels of factor variables and interactions are displayed. The default is to exclude from the table all base categories.

`baselevels` specifies that base levels be reported for factor variables and for interactions whose bases cannot be inferred from their component factor variables.

`allbaselevels` specifies that all base levels of factor variables and interactions be reported.

`cformat(%`*fmt*`)` specifies how to format coefficients, standard errors, and confidence limits in the coefficient table.

`pformat(%`*fmt*`)` specifies how to format p-values in the coefficient table.

`sformat(%`*fmt*`)` specifies how to format test statistics in the coefficient table.

`nolstretch` specifies that the width of the coefficient table not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the coefficient table up to the width of the Results window. To change the default, use `set lstretch off`. `nolstretch` is not shown in the dialog box.

`coeflegend` specifies that the legend of the coefficients and how to specify them in an expression be displayed rather than displaying the statistics for the coefficients.

eform_option: `eform(`*string*`)`, `eform`, `hr`, `shr`, `irr`, `or`, and `rrr` display the coefficient table in exponentiated form: for each coefficient, $\exp(b)$ rather than b is displayed, and standard errors and confidence intervals are transformed. *string* is the table header that will be displayed above the transformed coefficients and must be 11 characters or shorter in length—for example, `eform("Odds ratio")`. The options `eform`, `hr`, `shr`, `irr`, `or`, and `rrr` provide a default *string* equivalent to "`exp(b)`", "`Haz. Ratio`", "`SHR`", "`IRR`", "`Odds Ratio`", and "`RRR`", respectively. These options may not be combined.

`ml display` looks at `e(k_eform)` to determine how many equations are affected by an *eform_option*; by default, only the first equation is affected. Type `ereturn list, all` to view `e(k_eform)`; see [P] **ereturn**.

Options for use with mleval

`eq(#)` specifies the equation number, i, for which $\theta_{ij} = \mathbf{x}_{ij}\mathbf{b}_i$ is to be evaluated. `eq(1)` is assumed if `eq()` is not specified.

`scalar` asserts that the ith equation is known to evaluate to a constant, meaning that the equation was specified as `()`, (*name*`:`), or `/`*name* on the `ml model` statement. If you specify this option, the new variable created is created as a scalar. If the ith equation does not evaluate to a scalar, an error message is issued.

Option for use with mlsum

`noweight` specifies that weights (`$ML_w`) be ignored when summing the likelihood function.

Option for use with mlvecsum

`eq(#)` specifies the equation for which a gradient vector $\partial \ln L/\partial \mathbf{b}_i$ is to be constructed. The default is `eq(1)`.

Option for use with mlmatsum

`eq(#[,#])` specifies the equations for which the Hessian matrix is to be constructed. The default is `eq(1)`, which is the same as `eq(1,1)`, which means $\partial^2 \ln L/\partial \mathbf{b}_1 \partial \mathbf{b}_1'$. Specifying `eq(`$i$`,`$j$`)` results in $\partial^2 \ln L/\partial \mathbf{b}_i \partial \mathbf{b}_j'$.

Options for use with mlmatbysum

`by(`*varname*`)` is required and specifies the group variable.

`eq(#[,#])` specifies the equations for which the Hessian matrix is to be constructed. The default is `eq(1)`, which is the same as `eq(1,1)`, which means $\partial^2 \ln L/\partial \mathbf{b}_1 \partial \mathbf{b}_1'$. Specifying `eq(`$i$`,`$j$`)` results in $\partial^2 \ln L/\partial \mathbf{b}_i \partial \mathbf{b}_j'$.

Options for use with ml score

`equation(`*eqname*`)` identifies from which equation the observation scores are to come. This option may be used only when generating one variable.

`missing` specifies that observations containing variables with missing values not be eliminated from the estimation sample.

Remarks

For a thorough discussion of `ml`, see the fourth edition of *Maximum Likelihood Estimation with Stata* (Gould, Pitblado, and Poi 2010). The book provides a tutorial introduction to `ml`, notes on advanced programming issues, and a discourse on maximum likelihood estimation from both theoretical and practical standpoints. See *Survey options and ml* at the end of *Remarks* for examples of the new `svy` options. For more information about survey estimation, see [SVY] **survey**, [SVY] **svy estimation**, and [SVY] **variance estimation**.

`ml` requires that you write a program that evaluates the log-likelihood function and, possibly, its first and second derivatives. The style of the program you write depends upon the method you choose. Methods lf, lf0, d0, and gf0 require that your program evaluate the log likelihood only. Methods d1 and lf1 require that your program evaluate the log likelihood and its first derivatives. Methods d2 and lf2 requires that your program evaluate the log likelihood and its first and second derivatives. Methods lf, lf0, d0, and gf0 differ from each other in that, with methods lf and lf0, your program is required to produce observation-by-observation log-likelihood values $\ln \ell_j$ and it is assumed that $\ln L = \sum_j \ln \ell_j$; with method d0, your program is required to produce only the overall value $\ln L$; and with method gf0, your program is required to produce the summable pieces of the log likelihood, such as those in panel-data models.

Once you have written the program—called an evaluator—you define a model to be fit using `ml model` and obtain estimates using `ml maximize`. You might type

```
. ml model ...
. ml maximize
```

but we recommend that you type

```
. ml model ...
. ml check
. ml search
. ml maximize
```

`ml check` verifies your evaluator has no obvious errors, and `ml search` finds better initial values.

You fill in the `ml model` statement with 1) the method you are using, 2) the name of your program, and 3) the "equations". You write your evaluator in terms of θ_1, θ_2, ..., each of which has a linear equation associated with it. That linear equation might be as simple as $\theta_i = b_0$, it might be $\theta_i = b_1\texttt{mpg} + b_2\texttt{weight} + b_3$, or it might omit the intercept b_3. The equations are specified in parentheses on the `ml model` line.

Suppose that you are using method lf and the name of your evaluator program is `myprog`. The statement

```
. ml model lf myprog (mpg weight)
```

would specify one equation with $\theta_i = b_1\texttt{mpg} + b_2\texttt{weight} + b_3$. If you wanted to omit b_3, you would type

```
. ml model lf myprog (mpg weight, nocons)
```

and if all you wanted was $\theta_i = b_0$, you would type

```
. ml model lf myprog ()
```

With multiple equations, you list the equations one after the other; so, if you typed

```
. ml model lf myprog (mpg weight) ()
```

you would be specifying $\theta_1 = b_1\texttt{mpg} + b_2\texttt{weight} + b_3$ and $\theta_2 = b_4$. You would write your likelihood in terms of θ_1 and θ_2. If the model was linear regression, θ_1 might be the $\mathbf{xb}$ part and θ_2 the variance of the residuals.

When you specify the equations, you also specify any dependent variables. If you typed

```
. ml model lf myprog (price = mpg weight) ()
```

`price` would be the one and only dependent variable, and that would be passed to your program in `$ML_y1`. If your model had two dependent variables, you could type

```
. ml model lf myprog (price displ = mpg weight) ()
```

Then `$ML_y1` would be `price` and `$ML_y2` would be `displ`. You can specify however many dependent variables are necessary and specify them on any equation. It does not matter on which equation you specify them; the first one specified is placed in `$ML_y1`, the second in `$ML_y2`, and so on.

▷ Example 1: Method lf

Using method lf, we want to produce observation-by-observation values of the log likelihood. The probit log-likelihood function is

$$\ln \ell_j = \begin{cases} \ln \Phi(\theta_{1j}) & \text{if } y_j = 1 \\ \ln \Phi(-\theta_{1j}) & \text{if } y_j = 0 \end{cases}$$

$$\theta_{1j} = \mathbf{x}_j \mathbf{b}_1$$

The following is the method-lf evaluator for this likelihood function:

```
program myprobit
        version 12
        args lnf theta1
        quietly replace `lnf' = ln(normal(`theta1')) if $ML_y1==1
        quietly replace `lnf' = ln(normal(-`theta1')) if $ML_y1==0
end
```

If we wanted to fit a model of `foreign` on `mpg` and `weight`, we would type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ml model lf myprobit (foreign = mpg weight)
. ml maximize
```

The '`foreign =`' part specifies that y is `foreign`. The '`mpg weight`' part specifies that $\theta_{1j} = b_1\texttt{mpg}_j + b_2\texttt{weight}_j + b_3$. The result of running this is

```
. ml model lf myprobit (foreign = mpg weight)
. ml maximize
initial:       log likelihood = -51.292891
alternative:   log likelihood = -45.055272
rescale:       log likelihood = -45.055272
Iteration 0:   log likelihood = -45.055272
Iteration 1:   log likelihood = -27.904114
Iteration 2:   log likelihood = -26.858048
Iteration 3:   log likelihood = -26.844198
Iteration 4:   log likelihood = -26.844189
Iteration 5:   log likelihood = -26.844189
                                                Number of obs   =         74
                                                Wald chi2(2)    =      20.75
Log likelihood = -26.844189                     Prob > chi2     =     0.0000
------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         mpg |  -.1039503   .0515689    -2.02   0.044    -.2050235   -.0028772
      weight |  -.0023355   .0005661    -4.13   0.000     -.003445   -.0012261
       _cons |   8.275464   2.554142     3.24   0.001     3.269438    13.28149
------------------------------------------------------------------------------
```

◁

▷ Example 2: Method lf for two-equation, two-dependent-variable model

A two-equation, two-dependent-variable model is a little different. Rather than receiving one θ, our program will receive two. Rather than there being one dependent variable in `$ML_y1`, there will be dependent variables in `$ML_y1` and `$ML_y2`. For instance, the Weibull regression log-likelihood function is

$$\ln \ell_j = -(t_j e^{-\theta_{1j}})^{\exp(\theta_{2j})} + d_j\{\theta_{2j} - \theta_{1j} + (e^{\theta_{2j}} - 1)(\ln t_j - \theta_{1j})\}$$
$$\theta_{1j} = \mathbf{x}_j\mathbf{b}_1$$
$$\theta_{2j} = s$$

where t_j is the time of failure or censoring and $d_j = 1$ if failure and 0 if censored. We can make the log likelihood a little easier to program by introducing some extra variables:

$$p_j = \exp(\theta_{2j})$$
$$M_j = \{t_j \exp(-\theta_{1j})\}^{p_j}$$
$$R_j = \ln t_j - \theta_{1j}$$
$$\ln \ell_j = -M_j + d_j\{\theta_{2j} - \theta_{1j} + (p_j - 1)R_j\}$$

The method-lf evaluator for this is

```
program myweib
        version 12
        args lnf theta1 theta2
        tempvar p M R
        quietly gen double `p' = exp(`theta2')
        quietly gen double `M' = ($ML_y1*exp(-`theta1'))^`p'
        quietly gen double `R' = ln($ML_y1)-`theta1'
        quietly replace `lnf' = -`M' + $ML_y2*(`theta2'-`theta1' + (`p'-1)*`R')
end
```

We can fit a model by typing

```
. ml model lf myweib (studytime died = i.drug age) ()
. ml maximize
```

Note that we specified `()` for the second equation. The second equation corresponds to the Weibull shape parameter s, and the linear combination we want for s contains just an intercept. Alternatively, we could type

```
. ml model lf myweib (studytime died = i.drug age) /s
```

Typing `/s` means the same thing as typing `(s:)`, and both really mean the same thing as `()`. The `s`, either after a slash or in parentheses before a colon, labels the equation. It makes the output look prettier, and that is all:

```
. use http://www.stata-press.com/data/r12/cancer, clear
(Patient Survival in Drug Trial)
. ml model lf myweib (studytime died = i.drug age) /s
. ml maximize
initial:       log likelihood =       -744
alternative:   log likelihood = -356.14276
rescale:       log likelihood = -200.80201
rescale eq:    log likelihood = -136.69232
Iteration 0:   log likelihood = -136.69232  (not concave)
Iteration 1:   log likelihood = -124.11726
Iteration 2:   log likelihood = -113.89828
Iteration 3:   log likelihood = -110.30451
Iteration 4:   log likelihood = -110.26747
Iteration 5:   log likelihood = -110.26736
Iteration 6:   log likelihood = -110.26736
                                                Number of obs   =         48
                                                Wald chi2(3)    =      35.25
Log likelihood = -110.26736                     Prob > chi2     =     0.0000
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
eq1						
drug						
2	1.012966	.2903917	3.49	0.000	.4438086	1.582123
3	1.45917	.2821195	5.17	0.000	.9062261	2.012114
age	-.0671728	.0205688	-3.27	0.001	-.1074868	-.0268587
_cons	6.060723	1.152845	5.26	0.000	3.801188	8.320259
s						
_cons	.5573333	.1402154	3.97	0.000	.2825162	.8321504

◁

▷ Example 3: Method d0

Method-d0 evaluators receive $\mathbf{b} = (\mathbf{b}_1, \mathbf{b_2}, \ldots, \mathbf{b}_E)$, the coefficient vector, rather than the already evaluated $\theta_1, \theta_2, \ldots, \theta_E$, and they are required to evaluate the overall log-likelihood $\ln L$ rather than $\ln \ell_j$, $j = 1, \ldots, N$.

Use `mleval` to produce the thetas from the coefficient vector.

Use `mlsum` to sum the components that enter into $\ln L$.

In the case of Weibull, $\ln L = \sum \ln \ell_j$, and our method-d0 evaluator is

```
program weib0
        version 12
        args todo b lnf
        tempvar theta1 theta2
        mleval `theta1' = `b', eq(1)
        mleval `theta2' = `b', eq(2)
        local t "$ML_y1"           // this is just for readability
        local d "$ML_y2"
        tempvar p M R
        quietly gen double `p' = exp(`theta2')
        quietly gen double `M' = (`t'*exp(-`theta1'))^`p'
        quietly gen double `R' = ln(`t')-`theta1'
        mlsum `lnf' = -`M' + `d'*(`theta2'-`theta1' + (`p'-1)*`R')
end
```

To fit our model using this evaluator, we would type

```
. ml model d0 weib0 (studytime died = i.drug age) /s
. ml maximize
```

◁

❑ Technical note

Method d0 does not require $\ln L = \sum_j \ln \ell_j$, $j = 1, \ldots, N$, as method lf does. Your likelihood function might have independent components only for groups of observations. Panel-data estimators have a log-likelihood value $\ln L = \sum_i \ln L_i$, where i indexes the panels, each of which contains multiple observations. Conditional logistic regression has $\ln L = \sum_k \ln L_k$, where k indexes the risk pools. Cox regression has $\ln L = \sum_{(t)} \ln L_{(t)}$, where (t) denotes the ordered failure times.

To evaluate such likelihood functions, first calculate the within-group log-likelihood contributions. This usually involves `generate` and `replace` statements prefixed with `by`, as in

```
tempvar sumd
by group: gen double `sumd' = sum($ML_y1)
```

Structure your code so that the log-likelihood contributions are recorded in the last observation of each group. Say that a variable is named `'cont'`. To sum the contributions, code

```
tempvar last
quietly by group: gen byte `last' = (_n==_N)
mlsum `lnf' = `cont' if `last'
```

You must inform `mlsum` which observations contain log-likelihood values to be summed. First, you do not want to include intermediate results in the sum. Second, `mlsum` does not skip missing values. Rather, if `mlsum` sees a missing value among the contributions, it sets the overall result, `'lnf'`, to missing. That is how `ml maximize` is informed that the likelihood function could not be evaluated at the particular value of `b`. `ml maximize` will then take action to escape from what it thinks is an infeasible area of the likelihood function.

When the likelihood function violates the linear-form restriction $\ln L = \sum_j \ln \ell_j$, $j = 1, \ldots, N$, with $\ln \ell_j$ being a function solely of values within the jth observation, use method d0. In the following examples, we will demonstrate methods d1 and d2 with likelihood functions that meet this linear-form restriction. The d1 and d2 methods themselves do not require the linear-form restriction, but the utility routines `mlvecsum` and `mlmatsum` do. Using method d1 or d2 when the restriction is violated is difficult; however, `mlmatbysum` may be of some help for method-d2 evaluators. ❑

▷ Example 4: Method d1

Method-d1 evaluators are required to produce the gradient vector $\mathbf{g} = \partial \ln L/\partial \mathbf{b}$, as well as the overall log-likelihood value. Using `mlvecsum`, we can obtain $\partial \ln L/\partial \mathbf{b}$ from $\partial \ln L/\partial \theta_i$, $i = 1, \ldots, E$. The derivatives of the Weibull log-likelihood function are

$$\frac{\partial \ln \ell_j}{\partial \theta_{1j}} = p_j(M_j - d_j)$$
$$\frac{\partial \ln \ell_j}{\partial \theta_{2j}} = d_j - R_j p_j(M_j - d_j)$$

The method-d1 evaluator for this is

```
program weib1
        version 12
        args todo b lnf g                                       // g is new

        tempvar t1 t2
        mleval `t1' = `b', eq(1)
        mleval `t2' = `b', eq(2)

        local t "$ML_y1"
        local d "$ML_y2"

        tempvar p M R
        quietly gen double `p' = exp(`t2')
        quietly gen double `M' = (`t'*exp(-`t1'))^`p'
        quietly gen double `R' = ln(`t')-`t1'

        mlsum `lnf' = -`M' + `d'*(`t2'-`t1' + (`p'-1)*`R')
        if (`todo'==0 | `lnf'>=.) exit                          /* <-- new */

        tempname d1 d2                                          /* <-- new */
        mlvecsum `lnf' `d1' = `p'*(`M'-`d'), eq(1)              /* <-- new */
        mlvecsum `lnf' `d2' = `d' - `R'*`p'*(`M'-`d'), eq(2)    /* <-- new */
        matrix `g' = (`d1',`d2')                                /* <-- new */
end
```

We obtained this code by starting with our method-d0 evaluator and then adding the extra lines that method d1 requires. To fit our model using this evaluator, we could type

```
. ml model d1 weib1 (studytime died = drug2 drug3 age) /s
. ml maximize
```

but we recommend substituting method d1debug for method d1 and typing

```
. ml model d1debug weib1 (studytime died = drug2 drug3 age) /s
. ml maximize
```

Method d1debug will compare the derivatives we calculate with numerical derivatives and thus verify that our program is correct. Once we are certain the program is correct, then we would switch from method d1debug to method d1.

◁

▷ Example 5: Method d2

Method-d2 evaluators are required to produce $\mathbf{H} = \partial^2 \ln L/\partial \mathbf{b} \partial \mathbf{b}'$, the Hessian matrix, as well as the gradient and log-likelihood value. `mlmatsum` will help calculate $\partial^2 \ln L/\partial \mathbf{b} \partial \mathbf{b}'$ from the second derivatives with respect to θ. For the Weibull model, these second derivatives are

$$\frac{\partial^2 \ln \ell_j}{\partial \theta_{1j}^2} = -p_j^2 M_j$$

$$\frac{\partial^2 \ln \ell_j}{\partial \theta_{1j} \partial \theta_{2j}} = p_j(M_j - d_j + R_j p_j M_j)$$

$$\frac{\partial^2 \ln \ell_j}{\partial \theta_{2j}^2} = -p_j R_j(R_j p_j M_j + M_j - d_j)$$

The method-d2 evaluator is

```
program weib2
        version 12
        args todo b lnf g H                         // H added
        tempvar t1 t2
        mleval `t1' = `b', eq(1)
        mleval `t2' = `b', eq(2)
        local t "$ML_y1"
        local d "$ML_y2"
        tempvar p M R
        quietly gen double `p' = exp(`t2')
        quietly gen double `M' = (`t'*exp(-`t1'))^`p'
        quietly gen double `R' = ln(`t')-`t1'
        mlsum `lnf' = -`M' + `d'*(`t2'-`t1' + (`p'-1)*`R')
        if (`todo'==0 | `lnf'>=.) exit
        tempname d1 d2
        mlvecsum `lnf' `d1' = `p'*(`M'-`d'), eq(1)
        mlvecsum `lnf' `d2' = `d' - `R'*`p'*(`M'-`d'), eq(2)
        matrix `g' = (`d1',`d2')
        if (`todo'==1 | `lnf'>=.) exit              // new from here down
        tempname d11 d12 d22
        mlmatsum `lnf' `d11' = -`p'^2 * `M', eq(1)
        mlmatsum `lnf' `d12' = `p'*(`M'-`d' + `R'*`p'*`M'), eq(1,2)
        mlmatsum `lnf' `d22' = -`p'*`R'*(`R'*`p'*`M' + `M' - `d') , eq(2)
        matrix `H' = (`d11',`d12' \ `d12'',`d22')
end
```

We started with our previous method-d1 evaluator and added the lines that method d2 requires. We could now fit a model by typing

```
. ml model d2 weib2 (studytime died = drug2 drug3 age) /s
. ml maximize
```

but we would recommend substituting method d2debug for method d2 and typing

```
. ml model d2debug weib2 (studytime died = drug2 drug3 age) /s
. ml maximize
```

Method d2debug will compare the first and second derivatives we calculate with numerical derivatives and thus verify that our program is correct. Once we are certain the program is correct, then we would switch from method d2debug to method d2. ◁

As we stated earlier, to produce the robust variance estimator with method lf, there is nothing to do except specify `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweight`. For methods d0, d1, and d2, these options do not work. If your likelihood function meets the linear-form restrictions, you can use methods lf0, lf1, and lf2, then these options will work. The equation scores are defined as

$$\frac{\partial \ln \ell_j}{\partial \theta_{1j}}, \quad \frac{\partial \ln \ell_j}{\partial \theta_{2j}}, \quad \ldots$$

Your evaluator will be passed variables, one for each equation, which you fill in with the equation scores. For *both* method lf1 and lf2, these variables are passed in the fourth and subsequent positions of the argument list. That is, you must process the arguments as

```
args todo b lnf g1 g2 ... H
```

Note that for method lf1, the `H` argument is not used and can be ignored.

▷ Example 6: Robust variance estimates

If you have used `mlvecsum` in your evaluator of method d1 or d2, it is easy to turn it into evaluator of method lf1 or lf2 that allows the computation of the robust variance estimator. The expression that you specified on the right-hand side of `mlvecsum` is the equation score.

Here we turn the program that we gave earlier in the method-d1 example into a method-lf1 evaluator that allows `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweight`.

```
program weib1
        version 12
        args todo b lnfj g1 g2          // g1 and g2 are new
        tempvar t1 t2
        mleval `t1' = `b', eq(1)
        mleval `t2' = `b', eq(2)
        local t "$ML_y1"
        local d "$ML_y2"
        tempvar p M R
        quietly gen double `p' = exp(`t2')
        quietly gen double `M' = (`t'*exp(-`t1'))^`p'
        quietly gen double `R' = ln(`t')-`t1'
        quietly replace `lnfj' = -`M' + `d'*(`t2'-`t1' + (`p'-1)*`R')
        if (`todo'==0) exit
        quietly replace `g1' = `p'*(`M'-`d')              /* <-- new     */
        quietly replace `g2' = `d' - `R'*`p'*(`M'-`d')    /* <-- new     */
end
```

To fit our model and get the robust variance estimates, we type

```
. ml model lf1 weib1 (studytime died = drug2 drug3 age) /s, vce(robust)
. ml maximize
```

◁

Survey options and ml

`ml` can handle stratification, poststratification, multiple stages of clustering, and finite population corrections. Specifying the `svy` option implies that the data come from a survey design and also implies that the survey linearized variance estimator is to be used; see [SVY] **variance estimation**.

▷ Example 7

Suppose that we are interested in a probit analysis of data from a survey in which `q1` is the answer to a yes/no question and `x1`, `x2`, `x3` are demographic responses. The following is a lf2 evaluator for the probit model that meets the requirements for `vce(robust)` (linear form and computes the scores).

```
program mylf2probit
        version 12
        args todo b lnfj g1 H
        tempvar z Fz lnf
        mleval `z' = `b'
        quietly gen double `Fz'   = normal( `z')  if $ML_y1 == 1
        quietly replace    `Fz'   = normal(-`z')  if $ML_y1 == 0
        quietly replace    `lnfj' = log(`Fz')
        if (`todo'==0) exit
        quietly replace `g1' =  normalden(`z')/`Fz'  if $ML_y1 == 1
        quietly replace `g1' = -normalden(`z')/`Fz'  if $ML_y1 == 0
        if (`todo'==1) exit
        mlmatsum `lnf' `H' = -`g1'*(`g1'+`z'), eq(1,1)
end
```

To fit a model, we `svyset` the data, then use `svy` with `ml`.

```
. svyset psuid [pw=w], strata(strid)
. ml model lf2 myd2probit (q1 = x1 x2 x3), svy
. ml maximize
```

We could also use the `subpop()` option to make inferences about the subpopulation identified by the variable `sub`:

```
. svyset psuid [pw=w], strata(strid)
. ml model lf2 myd2probit (q1 = x1 x2 x3), svy subpop(sub)
. ml maximize
```

◁

Saved results

For results saved by `ml` without the `svy` option, see [R] **maximize**.

For results saved by `ml` with the `svy` option, see [SVY] **svy**.

Methods and formulas

`ml` is implemented using `moptimize`; see [M-5] **moptimize( )**.

References

Gould, W. W., J. S. Pitblado, and B. P. Poi. 2010. *Maximum Likelihood Estimation with Stata*. 4th ed. College Station, TX: Stata Press.

Korn, E. L., and B. I. Graubard. 1990. Simultaneous testing of regression coefficients with complex survey data: Use of Bonferroni t statistics. *American Statistician* 44: 270–276.

Royston, P. 2007. Profile likelihood for estimation and confidence intervals. *Stata Journal* 7: 376–387.

Also see

[R] **maximize** — Details of iterative maximization

[R] **nl** — Nonlinear least-squares estimation

[M-5] **moptimize( )** — Model optimization

[M-5] **optimize( )** — Function optimization

Title

mlogit — Multinomial (polytomous) logistic regression

Syntax

`mlogit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
`baseoutcome(#)`	value of *depvar* that will be the base outcome
`constraints(`*clist*`)`	apply specified linear constraints; *clist* has the form #[-#] [, #[-#] ...]
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`rrr`	report relative-risk ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

indepvars may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Categorical outcomes > Multinomial logistic regression

Description

`mlogit` fits maximum-likelihood multinomial logit models, also known as polytomous logistic regression. You can define constraints to perform constrained estimation. Some people refer to conditional logistic regression as multinomial logit. If you are one of them, see [R] **clogit**.

See [R] **logistic** for a list of related estimation commands.

Options

Model

`noconstant`; see [R] **estimation options**.

`baseoutcome(#)` specifies the value of *depvar* to be treated as the base outcome. The default is to choose the most frequent outcome.

`constraints(`*clist*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If specifying `vce(bootstrap)` or `vce(jackknife)`, you must also specify `baseoutcome()`.

Reporting

`level(#)`; see [R] **estimation options**.

`rrr` reports the estimated coefficients transformed to relative-risk ratios, that is, e^b rather than b; see *Description of the model* below for an explanation of this concept. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. `rrr` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

The following option is available with `mlogit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Description of the model
Fitting unconstrained models
Fitting constrained models

`mlogit` fits maximum likelihood models with discrete dependent (left-hand-side) variables when the dependent variable takes on more than two outcomes and the outcomes have no natural ordering. If the dependent variable takes on only two outcomes, estimates are identical to those produced by `logistic` or `logit`; see [R] **logistic** or [R] **logit**. If the outcomes are ordered, see [R] **ologit**.

Description of the model

For an introduction to multinomial logit models, see Greene (2012, 763–766), Hosmer and Lemeshow (2000, 260–287), Long (1997, chap. 6), Long and Freese (2006, chap. 6 and 7), and Treiman (2009, 336–341). For a description emphasizing the difference in assumptions and data requirements for conditional and multinomial logit, see Davidson and MacKinnon (1993).

Consider the outcomes 1, 2, 3, ..., m recorded in y, and the explanatory variables X. Assume that there are $m = 3$ outcomes: "buy an American car", "buy a Japanese car", and "buy a European car". The values of y are then said to be "unordered". Even though the outcomes are coded 1, 2, and 3, the numerical values are arbitrary because $1 < 2 < 3$ does not imply that outcome 1 (buy American) is less than outcome 2 (buy Japanese) is less than outcome 3 (buy European). This unordered categorical property of y distinguishes the use of `mlogit` from `regress` (which is appropriate for a continuous dependent variable), from `ologit` (which is appropriate for ordered categorical data), and from `logit` (which is appropriate for two outcomes, which can be thought of as ordered).

In the multinomial logit model, you estimate a set of coefficients, $\beta^{(1)}$, $\beta^{(2)}$, and $\beta^{(3)}$, corresponding to each outcome:

$$\Pr(y=1) = \frac{e^{X\beta^{(1)}}}{e^{X\beta^{(1)}} + e^{X\beta^{(2)}} + e^{X\beta^{(3)}}}$$

$$\Pr(y=2) = \frac{e^{X\beta^{(2)}}}{e^{X\beta^{(1)}} + e^{X\beta^{(2)}} + e^{X\beta^{(3)}}}$$

$$\Pr(y=3) = \frac{e^{X\beta^{(3)}}}{e^{X\beta^{(1)}} + e^{X\beta^{(2)}} + e^{X\beta^{(3)}}}$$

The model, however, is unidentified in the sense that there is more than one solution to $\beta^{(1)}$, $\beta^{(2)}$, and $\beta^{(3)}$ that leads to the same probabilities for $y = 1$, $y = 2$, and $y = 3$. To identify the model, you arbitrarily set one of $\beta^{(1)}$, $\beta^{(2)}$, or $\beta^{(3)}$ to 0—it does not matter which. That is, if you arbitrarily set $\beta^{(1)} = 0$, the remaining coefficients $\beta^{(2)}$ and $\beta^{(3)}$ will measure the change relative to the $y = 1$ group. If you instead set $\beta^{(2)} = 0$, the remaining coefficients $\beta^{(1)}$ and $\beta^{(3)}$ will measure the change relative to the $y = 2$ group. The coefficients will differ because they have different interpretations, but the predicted probabilities for $y = 1$, 2, and 3 will still be the same. Thus either parameterization will be a solution to the same underlying model.

Setting $\beta^{(1)} = 0$, the equations become

$$\Pr(y=1) = \frac{1}{1 + e^{X\beta^{(2)}} + e^{X\beta^{(3)}}}$$

$$\Pr(y=2) = \frac{e^{X\beta^{(2)}}}{1 + e^{X\beta^{(2)}} + e^{X\beta^{(3)}}}$$

$$\Pr(y=3) = \frac{e^{X\beta^{(3)}}}{1 + e^{X\beta^{(2)}} + e^{X\beta^{(3)}}}$$

The relative probability of $y = 2$ to the base outcome is

$$\frac{\Pr(y=2)}{\Pr(y=1)} = e^{X\beta^{(2)}}$$

Let's call this ratio the relative risk, and let's further assume that X and $\beta_k^{(2)}$ are vectors equal to $(x_1, x_2, \ldots, x_k)$ and $(\beta_1^{(2)}, \beta_2^{(2)}, \ldots, \beta_k^{(2)})'$, respectively. The ratio of the relative risk for a one-unit change in x_i is then

$$\frac{e^{\beta_1^{(2)}x_1+\cdots+\beta_i^{(2)}(x_i+1)+\cdots+\beta_k^{(2)}x_k}}{e^{\beta_1^{(2)}x_1+\cdots+\beta_i^{(2)}x_i+\cdots+\beta_k^{(2)}x_k}} = e^{\beta_i^{(2)}}$$

Thus the exponentiated value of a coefficient is the relative-risk ratio for a one-unit change in the corresponding variable (risk is measured as the risk of the outcome relative to the base outcome).

Fitting unconstrained models

▷ Example 1

We have data on the type of health insurance available to 616 psychologically depressed subjects in the United States (Tarlov et al. 1989; Wells et al. 1989). The insurance is categorized as either an indemnity plan (that is, regular fee-for-service insurance, which may have a deductible or coinsurance rate) or a prepaid plan (a fixed up-front payment allowing subsequent unlimited use as provided, for instance, by an HMO). The third possibility is that the subject has no insurance whatsoever. We wish to explore the demographic factors associated with each subject's insurance choice. One of the demographic factors in our data is the race of the participant, coded as white or nonwhite:

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. tabulate insure nonwhite, chi2 col
```

Key
frequency *column percentage*

insure	nonwhite 0	1	Total
Indemnity	251 50.71	43 35.54	294 47.73
Prepaid	208 42.02	69 57.02	277 44.97
Uninsure	36 7.27	9 7.44	45 7.31
Total	495 100.00	121 100.00	616 100.00

Pearson chi2(2) = 9.5599 Pr = 0.008

Although insure appears to take on the values Indemnity, Prepaid, and Uninsure, it actually takes on the values 1, 2, and 3. The words appear because we have associated a value label with the numeric variable insure; see [U] **12.6.3 Value labels**.

When we fit a multinomial logit model, we can tell mlogit which outcome to use as the base outcome, or we can let mlogit choose. To fit a model of insure on nonwhite, letting mlogit choose the base outcome, we type

```
. mlogit insure nonwhite
Iteration 0:   log likelihood = -556.59502
Iteration 1:   log likelihood = -551.78935
Iteration 2:   log likelihood = -551.78348
Iteration 3:   log likelihood = -551.78348
Multinomial logistic regression                 Number of obs   =        616
                                                LR chi2(2)      =       9.62
                                                Prob > chi2     =     0.0081
Log likelihood = -551.78348                     Pseudo R2       =     0.0086
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
nonwhite	.6608212	.2157321	3.06	0.002	.2379942	1.083648
_cons	-.1879149	.0937644	-2.00	0.045	-.3716896	-.0041401
Uninsure						
nonwhite	.3779586	.407589	0.93	0.354	-.4209011	1.176818
_cons	-1.941934	.1782185	-10.90	0.000	-2.291236	-1.592632

mlogit chose the indemnity outcome as the base outcome and presented coefficients for the outcomes prepaid and uninsured. According to the model, the probability of prepaid for whites (nonwhite = 0) is

$$\Pr(\texttt{insure} = \texttt{Prepaid}) = \frac{e^{-.188}}{1 + e^{-.188} + e^{-1.942}} = 0.420$$

Similarly, for nonwhites, the probability of prepaid is

$$\Pr(\texttt{insure} = \texttt{Prepaid}) = \frac{e^{-.188+.661}}{1 + e^{-.188+.661} + e^{-1.942+.378}} = 0.570$$

These results agree with the column percentages presented by tabulate because the mlogit model is fully saturated. That is, there are enough terms in the model to fully explain the column percentage in each cell. The model chi-squared and the tabulate chi-squared are in almost perfect agreement; both test that the column percentages of insure are the same for both values of nonwhite.

◁

▷ Example 2

By specifying the baseoutcome() option, we can control which outcome of the dependent variable is treated as the base. Left to its own, mlogit chose to make outcome 1, indemnity, the base outcome. To make outcome 2, prepaid, the base, we would type

```
. mlogit insure nonwhite, base(2)
Iteration 0:   log likelihood = -556.59502
Iteration 1:   log likelihood = -551.78935
Iteration 2:   log likelihood = -551.78348
Iteration 3:   log likelihood = -551.78348
Multinomial logistic regression                 Number of obs   =        616
                                                LR chi2(2)      =       9.62
                                                Prob > chi2     =     0.0081
Log likelihood = -551.78348                     Pseudo R2       =     0.0086
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity						
nonwhite	-.6608212	.2157321	-3.06	0.002	-1.083648	-.2379942
_cons	.1879149	.0937644	2.00	0.045	.0041401	.3716896
Prepaid	(base outcome)					
Uninsure						
nonwhite	-.2828627	.3977302	-0.71	0.477	-1.0624	.4966742
_cons	-1.754019	.1805145	-9.72	0.000	-2.107821	-1.400217

The `baseoutcome()` option requires that we specify the numeric value of the outcome, so we could not type `base(Prepaid)`.

Although the coefficients now appear to be different, the summary statistics reported at the top are identical. With this parameterization, the probability of prepaid insurance for whites is

$$\Pr(\texttt{insure} = \texttt{Prepaid}) = \frac{1}{1 + e^{.188} + e^{-1.754}} = 0.420$$

This is the same answer we obtained previously. ◁

▷ Example 3

By specifying `rrr`, which we can do at estimation time or when we redisplay results, we see the model in terms of relative-risk ratios:

```
. mlogit, rrr
Multinomial logistic regression                 Number of obs   =        616
                                                LR chi2(2)      =       9.62
                                                Prob > chi2     =     0.0081
Log likelihood = -551.78348                     Pseudo R2       =     0.0086
```

insure	RRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity						
nonwhite	.516427	.1114099	-3.06	0.002	.3383588	.7882073
_cons	1.206731	.1131483	2.00	0.045	1.004149	1.450183
Prepaid	(base outcome)					
Uninsure						
nonwhite	.7536233	.2997387	-0.71	0.477	.3456255	1.643247
_cons	.1730769	.0312429	-9.72	0.000	.1215024	.2465434

Looked at this way, the relative risk of choosing an indemnity over a prepaid plan is 0.516 for nonwhites relative to whites.

To illustrate, from the output and discussions of examples 1 and 2 we find that

$$\Pr(\texttt{insure} = \texttt{Indemnity} \mid \text{white}) = \frac{1}{1 + e^{-.188} + e^{-1.942}} = 0.507$$

and thus the relative risk of choosing indemnity over prepaid (for whites) is

$$\frac{\Pr(\texttt{insure} = \texttt{Indemnity} \mid \text{white})}{\Pr(\texttt{insure} = \texttt{Prepaid} \mid \text{white})} = \frac{0.507}{0.420} = 1.207$$

For nonwhites,

$$\Pr(\texttt{insure} = \texttt{Indemnity} \mid \text{not white}) = \frac{1}{1 + e^{-.188+.661} + e^{-1.942+.378}} = 0.355$$

and thus the relative risk of choosing indemnity over prepaid (for nonwhites) is

$$\frac{\Pr(\texttt{insure} = \texttt{Indemnity} \mid \text{not white})}{\Pr(\texttt{insure} = \texttt{Prepaid} \mid \text{not white})} = \frac{0.355}{0.570} = 0.623$$

The ratio of these two relative risks, hence the name "relative-risk ratio", is $0.623/1.207 = 0.516$, as given in the output under the heading "RRR".

◁

❑ Technical note

In models where only two categories are considered, the `mlogit` model reduces to standard `logit`. Consequently the exponentiated regression coefficients, labeled as `RRR` within `mlogit`, are equal to the odds ratios as given when the `or` option is specified under `logit`; see [R] **logit**.

As such, always referring to `mlogit`'s exponentiated coefficients as odds ratios may be tempting. However, the discussion in example 3 demonstrates that doing so would be incorrect. In general `mlogit` models, the exponentiated coefficients are ratios of relative risks, not ratios of odds.

❑

▷ Example 4

One of the advantages of `mlogit` over `tabulate` is that we can include continuous variables and multiple categorical variables in the model. In examining the data on insurance choice, we decide that we want to control for age, gender, and site of study (the study was conducted in three sites):

```
. mlogit insure age male nonwhite i.site
Iteration 0:   log likelihood = -555.85446
Iteration 1:   log likelihood = -534.67443
Iteration 2:   log likelihood = -534.36284
Iteration 3:   log likelihood = -534.36165
Iteration 4:   log likelihood = -534.36165
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(10)     =      42.99
                                                Prob > chi2     =     0.0000
Log likelihood = -534.36165                     Pseudo R2       =     0.0387
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.011745	.0061946	-1.90	0.058	-.0238862	.0003962
male	.5616934	.2027465	2.77	0.006	.1643175	.9590693
nonwhite	.9747768	.2363213	4.12	0.000	.5115955	1.437958
site						
2	.1130359	.2101903	0.54	0.591	-.2989296	.5250013
3	-.5879879	.2279351	-2.58	0.010	-1.034733	-.1412433
_cons	.2697127	.3284422	0.82	0.412	-.3740222	.9134476
Uninsure						
age	-.0077961	.0114418	-0.68	0.496	-.0302217	.0146294
male	.4518496	.3674867	1.23	0.219	-.268411	1.17211
nonwhite	.2170589	.4256361	0.51	0.610	-.6171725	1.05129
site						
2	-1.211563	.4705127	-2.57	0.010	-2.133751	-.2893747
3	-.2078123	.3662926	-0.57	0.570	-.9257327	.510108
_cons	-1.286943	.5923219	-2.17	0.030	-2.447872	-.1260134

These results suggest that the inclination of nonwhites to choose prepaid care is even stronger than it was without controlling. We also see that subjects in site 2 are less likely to be uninsured.

◁

Fitting constrained models

`mlogit` can fit models with subsets of coefficients constrained to be zero, with subsets of coefficients constrained to be equal both within and across equations, and with subsets of coefficients arbitrarily constrained to equal linear combinations of other estimated coefficients.

Before fitting a constrained model, you define the constraints with the `constraint` command; see [R] **constraint**. Once the constraints are defined, you estimate using `mlogit`, specifying the `constraint()` option. Typing `constraint(4)` would use the constraint you previously saved as 4. Typing `constraint(1,4,6)` would use the previously stored constraints 1, 4, and 6. Typing `constraint(1-4,6)` would use the previously stored constraints 1, 2, 3, 4, and 6.

Sometimes you will not be able to specify the constraints without knowing the omitted outcome. In such cases, assume that the omitted outcome is whatever outcome is convenient for you, and include the `baseoutcome()` option when you specify the `mlogit` command.

▷ Example 5

We can use constraints to test hypotheses, among other things. In our insurance-choice model, let's test the hypothesis that there is no distinction between having indemnity insurance and being uninsured. Indemnity-style insurance was the omitted outcome, so we type

```
. test [Uninsure]
 ( 1)  [Uninsure]age = 0
 ( 2)  [Uninsure]male = 0
 ( 3)  [Uninsure]nonwhite = 0
 ( 4)  [Uninsure]1b.site = 0
 ( 5)  [Uninsure]2.site = 0
 ( 6)  [Uninsure]3.site = 0
       Constraint 4 dropped
           chi2(  5) =    9.31
         Prob > chi2 =    0.0973
```

If indemnity had not been the omitted outcome, we would have typed `test [Uninsure=Indemnity]`.

The results produced by `test` are an approximation based on the estimated covariance matrix of the coefficients. Because the probability of being uninsured is low, the log likelihood may be nonlinear for the uninsured. Conventional statistical wisdom is not to trust the asymptotic answer under these circumstances but to perform a likelihood-ratio test instead.

To use Stata's `lrtest` (likelihood-ratio test) command, we must fit both the unconstrained and constrained models. The unconstrained model is the one we have previously fit. Following the instruction in [R] **lrtest**, we first save the unconstrained model results:

```
. estimates store unconstrained
```

To fit the constrained model, we must refit our model with all the coefficients except the constant set to 0 in the `Uninsure` equation. We define the constraint and then refit:

```
. constraint 1 [Uninsure]
. mlogit insure age male nonwhite i.site, constraints(1)
Iteration 0:   log likelihood = -555.85446
Iteration 1:   log likelihood = -539.80523
Iteration 2:   log likelihood = -539.75644
Iteration 3:   log likelihood = -539.75643
Multinomial logistic regression                 Number of obs   =        615
                                                Wald chi2(5)    =      29.70
Log likelihood = -539.75643                     Prob > chi2     =     0.0000
 ( 1)  [Uninsure]o.age = 0
 ( 2)  [Uninsure]o.male = 0
 ( 3)  [Uninsure]o.nonwhite = 0
 ( 4)  [Uninsure]2o.site = 0
 ( 5)  [Uninsure]3o.site = 0
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.0107025	.0060039	-1.78	0.075	-.0224699	.0010649
male	.4963616	.1939683	2.56	0.010	.1161907	.8765324
nonwhite	.9421369	.2252094	4.18	0.000	.5007346	1.383539
site						
2	.2530912	.2029465	1.25	0.212	-.1446767	.6508591
3	-.5521773	.2187237	-2.52	0.012	-.9808678	-.1234869
_cons	.1792752	.3171372	0.57	0.572	-.4423023	.8008527
Uninsure						
age	0	(omitted)				
male	0	(omitted)				
nonwhite	0	(omitted)				
site						
2	0	(omitted)				
3	0	(omitted)				
_cons	-1.87351	.1601099	-11.70	0.000	-2.18732	-1.5597

We can now perform the likelihood-ratio test:

```
. lrtest unconstrained .
Likelihood-ratio test                           LR chi2(5)  =     10.79
(Assumption: . nested in unconstrained)         Prob > chi2 =    0.0557
```

The likelihood-ratio chi-squared is 10.79 with 5 degrees of freedom—just slightly greater than the magic $p = 0.05$ level—so we should not call this difference significant. ◁

❑ Technical note

In certain circumstances, you should fit a multinomial logit model with conditional logit; see [R] **clogit**. With substantial data manipulation, `clogit` can handle the same class of models with some interesting additions. For example, if we had available the price and deductible of the most competitive insurance plan of each type, `mlogit` could not use this information, but `clogit` could. ❑

Saved results

mlogit saves the following in e():

Scalars

e(N)	number of observations
e(k_out)	number of outcomes
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance
e(k_eq_base)	equation number of the base outcome
e(baseout)	the value of *depvar* to be treated as the base outcome
e(ibaseout)	index of the base outcome
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	mlogit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(eqnames)	names of equations
e(baselab)	value label corresponding to base outcome
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(out)	outcome values
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

mlogit is implemented as an ado-file.

The multinomial logit model is described in Greene (2012, 763–766).

Suppose that there are k categorical outcomes and—without loss of generality—let the base outcome be 1. The probability that the response for the jth observation is equal to the ith outcome is

$$p_{ij} = \Pr(y_j = i) = \begin{cases} \dfrac{1}{1 + \sum_{m=2}^{k} \exp(\mathbf{x}_j \boldsymbol{\beta}_m)}, \text{ if } & i = 1 \\ \dfrac{\exp(\mathbf{x}_j \boldsymbol{\beta}_i)}{1 + \sum_{m=2}^{k} \exp(\mathbf{x}_j \boldsymbol{\beta}_m)}, \text{ if } & i > 1 \end{cases}$$

where $\mathbf{x}_j$ is the row vector of observed values of the independent variables for the jth observation and $\boldsymbol{\beta}_m$ is the coefficient vector for outcome m. The log pseudolikelihood is

$$\ln L = \sum_j w_j \sum_{i=1}^{k} I_i(y_j) \ln p_{ik}$$

where w_j is an optional weight and

$$I_i(y_j) = \begin{cases} 1, \text{ if } y_j = i \\ 0, \text{ otherwise} \end{cases}$$

Newton–Raphson maximum likelihood is used; see [R] **maximize**.

For constrained equations, the set of constraints is orthogonalized, and a subset of maximizable parameters is selected. For example, a parameter that is constrained to zero is not a maximizable parameter. If two parameters are constrained to be equal to each other, only one is a maximizable parameter.

Let $\mathbf{r}$ be the vector of maximizable parameters. $\mathbf{r}$ is physically a subset of the solution parameters, $\mathbf{b}$. A matrix, $\mathbf{T}$, and a vector, $\mathbf{m}$, are defined as

$$\mathbf{b} = \mathbf{T}\mathbf{r} + \mathbf{m}$$

so that

$$\frac{\partial f}{\partial \mathbf{b}} = \frac{\partial f}{\partial \mathbf{r}}\mathbf{T}'$$

$$\frac{\partial^2 f}{\partial \mathbf{b}^2} = \mathbf{T}\frac{\partial^2 f}{\partial \mathbf{r}^2}\mathbf{T}'$$

$\mathbf{T}$ consists of a block form in which one part is a permutation of the identity matrix and the other part describes how to calculate the constrained parameters from the maximizable parameters.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`mlogit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **mlogit postestimation** — Postestimation tools for mlogit

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **mprobit** — Multinomial probit regression

[R] **nlogit** — Nested logit regression

[R] **ologit** — Ordered logistic regression

[R] **rologit** — Rank-ordered logistic regression

[R] **slogit** — Stereotype logistic regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

mlogit postestimation — Postestimation tools for mlogit

Description

The following postestimation commands are available after `mlogit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] {stub* | newvar | newvarlist} [if] [in] [, statistic outcome(outcome)]

predict [type] {stub* | newvarlist} [if] [in], scores
```

statistic	Description
Main	
`pr`	probability of a positive outcome; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction
`stddp`	standard error of the difference in two linear predictions

If you do not specify `outcome()`, `pr` (with one new variable specified), `xb`, and `stdp` assume `outcome(#1)`. You must specify `outcome()` with the `stddp` option.

You specify one or k new variables with `pr`, where k is the number of outcomes.

You specify one new variable with `xb`, `stdp`, and `stddp`.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of each of the categories of the dependent variable or the probability of the level specified in `outcome(`*outcome*`)`. If you specify the `outcome(`*outcome*`)` option, you need to specify only one new variable; otherwise, you must specify a new variable for each category of the dependent variable.

`xb` calculates the linear prediction. You must also specify the `outcome(`*outcome*`)` option.

`stdp` calculates the standard error of the linear prediction. You must also specify the `outcome(`*outcome*`)` option.

`stddp` calculates the standard error of the difference in two linear predictions. You must specify the `outcome(`*outcome*`)` option, and here you specify the two particular outcomes of interest inside the parentheses, for example, `predict sed, stddp outcome(1,3)`.

`outcome(`*outcome*`)` specifies the outcome for which the statistic is to be calculated. `equation()` is a synonym for `outcome()`: it does not matter which you use. `outcome()` or `equation()` can be specified using

`#1`, `#2`, ..., where `#1` means the first category of the dependent variable, `#2` means the second category, etc.;

the values of the dependent variable; or

the value labels of the dependent variable if they exist.

`scores` calculates equation-level score variables. The number of score variables created will be one less than the number of outcomes in the model. If the number of outcomes in the model were k, then

the first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta}_1)$;

the second new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta}_2)$;

...

the $(k-1)$th new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta}_{k-1})$.

Remarks

Remarks are presented under the following headings:

Obtaining predicted values
Calculating marginal effects
Testing hypotheses about coefficients

Obtaining predicted values

▷ Example 1

After estimation, we can use `predict` to obtain predicted probabilities, index values, and standard errors of the index, or differences in the index. For instance, in example 4 of [R] **mlogit**, we fit a model of insurance choice on various characteristics. We can obtain the predicted probabilities for outcome 1 by typing

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. mlogit insure age i.male i.nonwhite i.site
  (output omitted)
. predict p1 if e(sample), outcome(1)
(option pr assumed; predicted probability)
(29 missing values generated)
. summarize p1
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
          p1 |        615    .4764228    .1032279    .1698142     .71939
```

We added the `i.` prefix to the `male`, `nonwhite`, and `site` variables to explicitly identify them as factor variables. That makes no difference in the estimated results, but we will take advantage of it in later examples. We also included `if e(sample)` to restrict the calculation to the estimation sample. In example 4 of [R] **mlogit**, the multinomial logit model was fit on 615 observations, so there must be missing values in our dataset.

Although we typed `outcome(1)`, specifying `1` for the indemnity outcome, we could have typed `outcome(Indemnity)`. For instance, to obtain the probabilities for prepaid, we could type

```
. predict p2 if e(sample), outcome(prepaid)
(option pr assumed; predicted probability)
outcome prepaid not found
r(303);
. predict p2 if e(sample), outcome(Prepaid)
(option pr assumed; predicted probability)
(29 missing values generated)
. summarize p2
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
          p2 |        615    .4504065    .1125962    .1964103    .7885724
```

We must specify the label exactly as it appears in the underlying value label (or how it appears in the `mlogit` output), including capitalization.

Here we have used `predict` to obtain probabilities for the same sample on which we estimated. That is not necessary. We could use another dataset that had the independent variables defined (in our example, `age`, `male`, `nonwhite`, and `site`) and use `predict` to obtain predicted probabilities; here, we would not specify `if e(sample)`.

◁

▷ Example 2

`predict` can also be used to obtain the index values—the $\sum x_i\widehat{\beta}_i^{(k)}$—as well as the probabilities:

```
. predict idx1, outcome(Indemnity) xb
(1 missing value generated)

. summarize idx1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
idx1	643	0	0	0	0

The indemnity outcome was our base outcome—the outcome for which all the coefficients were set to 0—so the index is always 0. For the prepaid and uninsured outcomes, we type

```
. predict idx2, outcome(Prepaid) xb
(1 missing value generated)

. predict idx3, outcome(Uninsure) xb
(1 missing value generated)

. summarize idx2 idx3
```

Variable	Obs	Mean	Std. Dev.	Min	Max
idx2	643	-.0566113	.4962973	-1.298198	1.700719
idx3	643	-1.980747	.6018139	-3.112741	-.8258458

We can obtain the standard error of the index by specifying the `stdp` option:

```
. predict se2, outcome(Prepaid) stdp
(1 missing value generated)

. list p2 idx2 se2 in 1/5
```

	p2	idx2	se2
1.	.3709022	-.4831167	.2437772
2.	.4977667	.055111	.1694686
3.	.4113073	-.1712106	.1793498
4.	.5424927	.3788345	.2513701
5.	.	-.0925817	.1452616

We obtained the probability, `p2`, in the previous example.

Finally, `predict` can calculate the standard error of the difference in the index values between two outcomes with the `stddp` option:

```
. predict se_2_3, outcome(Prepaid,Uninsure) stddp
(1 missing value generated)

. list idx2 idx3 se_2_3 in 1/5
```

	idx2	idx3	se_2_3
1.	-.4831167	-3.073253	.5469354
2.	.055111	-2.715986	.4331918
3.	-.1712106	-1.579621	.3053815
4.	.3788345	-1.462007	.4492552
5.	-.0925817	-2.814022	.4024784

In the first observation, the difference in the indexes is $-0.483 - (-3.073) = 2.59$. The standard error of that difference is 0.547.

◁

▷ Example 3

It is more difficult to interpret the results from `mlogit` than those from `clogit` or `logit` because there are multiple equations. For example, suppose that one of the independent variables in our model takes on the values 0 and 1, and we are attempting to understand the effect of this variable. Assume that the coefficient on this variable for the second outcome, $\beta^{(2)}$, is positive. We might then be tempted to reason that the probability of the second outcome is higher if the variable is 1 rather than 0. Most of the time, that will be true, but occasionally we will be surprised. The probability of some other outcome could increase even more (say, $\beta^{(3)} > \beta^{(2)}$), and thus the probability of outcome 2 would actually fall relative to that outcome. We can use `predict` to help interpret such results.

Continuing with our previously fit insurance-choice model, we wish to describe the model's predictions by race. For this purpose, we can use the method of predictive margins (also known as recycled predictions), in which we vary characteristics of interest across the whole dataset and average the predictions. That is, we have data on both whites and nonwhites, and our individuals have other characteristics as well. We will first pretend that all the people in our data are white but hold their other characteristics constant. We then calculate the probabilities of each outcome. Next we will pretend that all the people in our data are nonwhite, still holding their other characteristics constant. Again we calculate the probabilities of each outcome. The difference in those two sets of calculated probabilities, then, is the difference due to race, holding other characteristics constant.

```
. gen byte nonwhold = nonwhite                  // save real race
. replace nonwhite = 0                          // make everyone white
(126 real changes made)
. predict wpind, outcome(Indemnity)             // predict probabilities
(option pr assumed; predicted probability)
(1 missing value generated)
. predict wpp, outcome(Prepaid)
(option pr assumed; predicted probability)
(1 missing value generated)
. predict wpnoi, outcome(Uninsure)
(option pr assumed; predicted probability)
(1 missing value generated)
. replace nonwhite=1                            // make everyone nonwhite
(644 real changes made)
. predict nwpind, outcome(Indemnity)
(option pr assumed; predicted probability)
(1 missing value generated)
. predict nwpp, outcome(Prepaid)
(option pr assumed; predicted probability)
(1 missing value generated)
. predict nwpnoi, outcome(Uninsure)
(option pr assumed; predicted probability)
(1 missing value generated)
. replace nonwhite=nonwhold                     // restore real race
(518 real changes made)
```

```
. summarize wp* nwp*, sep(3)
```

Variable	Obs	Mean	Std. Dev.	Min	Max
wpind	643	.5141673	.0872679	.3092903	.71939
wpp	643	.4082052	.0993286	.1964103	.6502247
wpnoi	643	.0776275	.0360283	.0273596	.1302816
nwpind	643	.3112809	.0817693	.1511329	.535021
nwpp	643	.630078	.0979976	.3871782	.8278881
nwpnoi	643	.0586411	.0287185	.0209648	.0933874

In example 1 of [R] **mlogit**, we presented a cross-tabulation of insurance type and race. Those values were unadjusted. The means reported above are the values adjusted for age, sex, and site. Combining the results gives

	Unadjusted		Adjusted	
	white	nonwhite	white	nonwhite
Indemnity	0.51	0.36	0.51	0.31
Prepaid	0.42	0.57	0.41	0.63
Uninsured	0.07	0.07	0.08	0.06

We find, for instance, after adjusting for age, sex, and site, that although 57% of nonwhites in our data had prepaid plans, 63% of nonwhites chose prepaid plans.

Computing predictive margins by hand was instructive, but we can compute these values more easily using the `margins` command (see [R] **margins**). The two margins for the indemnity outcome can be estimated by typing

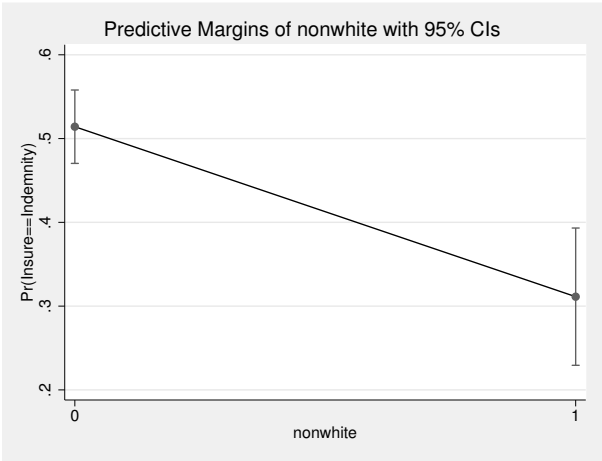
```
. margins nonwhite, predict(outcome(Indemnity)) noesample
Predictive margins                                Number of obs   =        643
Model VCE    : OIM
Expression   : Pr(insure==Indemnity), predict(outcome(Indemnity))
```

	Margin	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
nonwhite						
0	.5141673	.0223485	23.01	0.000	.470365	.5579695
1	.3112809	.0418049	7.45	0.000	.2293448	.393217

`margins` also estimates the standard errors and confidence intervals of the margins. By default, `margins` uses only the estimation sample. We added the `noesample` option so that `margins` would use the entire sample and produce results comparable to our earlier analysis.

We can use `marginsplot` to graph the results from `margins`:

```
. marginsplot
  Variables that uniquely identify margins: nonwhite
```



The margins for the other two outcomes can be computed by typing

```
. margins nonwhite, predict(outcome(Prepaid)) noesample
  (output omitted)
. margins nonwhite, predict(outcome(Uninsure)) noesample
  (output omitted)
```

◁

❑ Technical note

You can use `predict` to classify predicted values and compare them with the observed outcomes to interpret a multinomial logit model. This is a variation on the notions of sensitivity and specificity for logistic regression. Here we will classify indemnity and prepaid as definitely predicting indemnity, definitely predicting prepaid, and ambiguous.

```
. predict indem, outcome(Indemnity) index            // obtain indexes
(1 missing value generated)
. predict prepaid, outcome(Prepaid) index
(1 missing value generated)
. gen diff = prepaid-indem                           // obtain difference
(1 missing value generated)
. predict sediff, outcome(Indemnity,Prepaid) stddp   // & its standard error
(1 missing value generated)
. gen type = 1 if diff/sediff < -1.96                // definitely indemnity
(504 missing values generated)
. replace type = 3 if diff/sediff > 1.96             // definitely prepaid
(100 real changes made)
. replace type = 2 if type>=. & diff/sediff < .      // ambiguous
(404 real changes made)
. label def type 1 "Def Ind" 2 "Ambiguous" 3 "Def Prep"
. label values type type                             // label results
```

```
. tabulate insure type
```

insure	type Def Ind	Ambiguous	Def Prep	Total
Indemnity	78	183	33	294
Prepaid	44	177	56	277
Uninsure	12	28	5	45
Total	134	388	94	616

We can see that the predictive power of this model is modest. There are many misclassifications in both directions, though there are more correctly classified observations than misclassified observations.

Also the uninsured look overwhelmingly as though they might have come from the indemnity system rather than from the prepaid system.

❑

Calculating marginal effects

▷ Example 4

We have already noted that the coefficients from multinomial logit can be difficult to interpret because they are relative to the base outcome. Another way to evaluate the effect of covariates is to examine the marginal effect of changing their values on the probability of observing an outcome.

The `margins` command can be used for this too. We can estimate the marginal effect of each covariate on the probability of observing the first outcome—indemnity insurance—by typing

```
. margins, dydx(*) predict(outcome(Indemnity))
Average marginal effects                        Number of obs   =        615
Model VCE    : OIM
Expression   : Pr(insure==Indemnity), predict(outcome(Indemnity))
dy/dx w.r.t. : age 1.male 1.nonwhite 2.site 3.site
```

	dy/dx	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.0026655	.001399	1.91	0.057	-.0000765	.0054074
1.male	-.1295734	.0450945	-2.87	0.004	-.2179571	-.0411898
1.nonwhite	-.2032404	.0482554	-4.21	0.000	-.2978192	-.1086616
site						
2	.0070995	.0479993	0.15	0.882	-.0869775	.1011765
3	.1216165	.0505833	2.40	0.016	.022475	.220758

```
Note: dy/dx for factor levels is the discrete change from the base level.
```

By default, `margins` estimates the average marginal effect over the estimation sample, and that is what we see above. Being male decreases the average probability of having indemnity insurance by 0.130. We also see, from the note at the bottom of the table, that the marginal effect was computed as a discrete change in the probability of being male rather than female. That is why we made `male` a factor variable when fitting the model.

The `dydx(*)` option requested that `margins` estimate the marginal effect for each regressor, `dydx(age)` would have produced estimates only for the effect of `age`. `margins` has many options for controlling how the marginal effect is computed, including the ability to average over subgroups or to compute estimates for specified values of the regressors; see [R] **margins**.

We could evaluate the marginal effects on the other two outcomes by typing

```
. margins, dydx(*) predict(outcome(Prepaid))
  (output omitted)
. margins, dydx(*) predict(outcome(Uninsure))
  (output omitted)
```

◁

Testing hypotheses about coefficients

▷ Example 5

`test` tests hypotheses about the coefficients just as after any estimation command; see [R] **test**. Note, however, `test`'s syntax for dealing with multiple-equation models. Because `test` bases its results on the estimated covariance matrix, we might prefer a likelihood-ratio test; see example 5 in [R] **mlogit** for an example of `lrtest`.

If we simply list variables after the `test` command, we are testing that the corresponding coefficients are zero across all equations:

```
. test 2.site 3.site
 ( 1)  [Indemnity]2.site = 0
 ( 2)  [Prepaid]2.site = 0
 ( 3)  [Uninsure]2.site = 0
 ( 4)  [Indemnity]3.site = 0
 ( 5)  [Prepaid]3.site = 0
 ( 6)  [Uninsure]3.site = 0
       Constraint 1 dropped
       Constraint 4 dropped
           chi2(  4) =   19.74
         Prob > chi2 =    0.0006
```

We can test that all the coefficients (except the constant) in an equation are zero by simply typing the outcome in square brackets:

```
. test [Uninsure]
 ( 1)  [Uninsure]age = 0
 ( 2)  [Uninsure]0b.male = 0
 ( 3)  [Uninsure]1.male = 0
 ( 4)  [Uninsure]0b.nonwhite = 0
 ( 5)  [Uninsure]1.nonwhite = 0
 ( 6)  [Uninsure]1b.site = 0
 ( 7)  [Uninsure]2.site = 0
 ( 8)  [Uninsure]3.site = 0
       Constraint 2 dropped
       Constraint 4 dropped
       Constraint 6 dropped
           chi2(  5) =    9.31
         Prob > chi2 =    0.0973
```

We specify the outcome just as we do with `predict`; we can specify the label if the outcome variable is labeled, or we can specify the numeric value of the outcome. We would have obtained the same test as above if we had typed `test [3]` because 3 is the value of `insure` for the outcome uninsured.

We can combine the two syntaxes. To test that the coefficients on the site variables are 0 in the equation corresponding to the outcome prepaid, we can type

```
. test [Prepaid]: 2.site 3.site
 ( 1)  [Prepaid]2.site = 0
 ( 2)  [Prepaid]3.site = 0
           chi2(  2) =   10.78
         Prob > chi2 =    0.0046
```

We specified the outcome and then followed that with a colon and the variables we wanted to test.

We can also test that coefficients are equal across equations. To test that all coefficients except the constant are equal for the prepaid and uninsured outcomes, we can type

```
. test [Prepaid=Uninsure]
 ( 1)  [Prepaid]age - [Uninsure]age = 0
 ( 2)  [Prepaid]0b.male - [Uninsure]0b.male = 0
 ( 3)  [Prepaid]1.male - [Uninsure]1.male = 0
 ( 4)  [Prepaid]0b.nonwhite - [Uninsure]0b.nonwhite = 0
 ( 5)  [Prepaid]1.nonwhite - [Uninsure]1.nonwhite = 0
 ( 6)  [Prepaid]1b.site - [Uninsure]1b.site = 0
 ( 7)  [Prepaid]2.site - [Uninsure]2.site = 0
 ( 8)  [Prepaid]3.site - [Uninsure]3.site = 0
       Constraint 2 dropped
       Constraint 4 dropped
       Constraint 6 dropped
           chi2(  5) =   13.80
         Prob > chi2 =    0.0169
```

To test that only the site variables are equal, we can type

```
. test [Prepaid=Uninsure]: 2.site 3.site
 ( 1)  [Prepaid]2.site - [Uninsure]2.site = 0
 ( 2)  [Prepaid]3.site - [Uninsure]3.site = 0
           chi2(  2) =   12.68
         Prob > chi2 =    0.0018
```

Finally, we can test any arbitrary constraint by simply entering the equation and specifying the coefficients as described in [U] **13.5 Accessing coefficients and standard errors**. The following hypothesis is senseless but illustrates the point:

```
. test ([Prepaid]age+[Uninsure]2.site)/2 = 2-[Uninsure]1.nonwhite
 ( 1)  .5*[Prepaid]age + [Uninsure]1.nonwhite + .5*[Uninsure]2.site = 2
           chi2(  1) =   22.45
         Prob > chi2 =    0.0000
```

See [R] **test** for more information about `test`. The information there about combining hypotheses across `test` commands (the `accumulate` option) also applies after `mlogit`.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **mlogit** — Multinomial (polytomous) logistic regression

[U] **20 Estimation and postestimation commands**

Title

more — The —more— message

Syntax

Tell Stata to pause or not pause for —more— messages

```
set more { on | off } [ , permanently ]
```

Set number of lines between —more— messages

```
set pagesize #
```

Description

`set more on`, which is the default, tells Stata to wait until you press a key before continuing when a —more— message is displayed.

`set more off` tells Stata not to pause or display the —more— message.

`set pagesize #` sets the number of lines between —more— messages. The `permanently` option is not allowed with `set pagesize`.

Option

`permanently` specifies that, in addition to making the change right now, the `more` setting be remembered and become the default setting when you invoke Stata.

Remarks

When you see —more— at the bottom of the screen,

Press ...	and Stata ...
letter *l* or *Enter*	displays the next line
letter *q*	acts as if you pressed *Break*
Spacebar or any other key	displays the next screen

You can also click on the **More** button or click on —more— to display the next screen.

—more— is Stata's way of telling you that it has something more to show you but that showing it to you will cause the information on the screen to scroll off.

If you type `set more off`, —more— conditions will never arise, and Stata's output will scroll by at full speed.

If you type `set more on`, —more— conditions will be restored at the appropriate places.

Programmers should see [P] **more** for information on the `more` programming command.

Also see

[R] **query** — Display system parameters

[P] **creturn** — Return c-class values

[P] **more** — Pause until key is pressed

[U] **7 –more– conditions**

Title

mprobit — Multinomial probit regression

Syntax

`mprobit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant terms
`baseoutcome(`*#* | *lbl*`)`	outcome used to normalize location
`probitparam`	use the probit variance parameterization
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(`*#*`)`	set confidence level; default is `level(95)`
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Integration	
`intpoints(`*#*`)`	number of quadrature points
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Categorical outcomes > Independent multinomial probit

Description

`mprobit` fits multinomial probit (MNP) models via maximum likelihood. *depvar* contains the outcome for each observation, and *indepvars* are the associated covariates. The error terms are assumed to be independent, standard normal, random variables. See [R] **asmprobit** for the case where the latent-variable errors are correlated or heteroskedastic and you have alternative-specific variables.

Options

Model

`noconstant` suppresses the $J-1$ constant terms.

`baseoutcome(`*#* | *lbl*`)` specifies the outcome used to normalize the location of the latent variable. The base outcome may be specified as a number or a label. The default is to use the most frequent outcome. The coefficients associated with the base outcome are zero.

`probitparam` specifies to use the probit variance parameterization by fixing the variance of the differenced latent errors between the scale and the base alternatives to be one. The default is to make the variance of the base and scale latent errors one, thereby making the variance of the difference to be two.

`constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If specifying `vce(bootstrap)` or `vce(jackknife)`, you must also specify `baseoutcome()`.

Reporting

`level(#)`; see [R] **estimation options**.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Integration

`intpoints(#)` specifies the number of Gaussian quadrature points to use in approximating the likelihood. The default is 15.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `mprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

The MNP model is used with discrete dependent variables that take on more than two outcomes that do not have a natural ordering. The stochastic error terms for this implementation of the model are assumed to have independent, standard normal distributions. To use `mprobit`, you must have one observation for each decision maker in the sample. See [R] **asmprobit** for another implementation of the MNP model that permits correlated and heteroskedastic errors and is suitable when you have data for each alternative that a decision maker faced.

The MNP model is frequently motivated using a latent-variable framework. The latent variable for the jth alternative, $j = 1, \ldots, J$, is

$$\eta_{ij} = \mathbf{z}_i \boldsymbol{\alpha}_j + \xi_{ij}$$

where the $1 \times q$ row vector $\mathbf{z}_i$ contains the observed independent variables for the ith decision maker. Associated with $\mathbf{z}_i$ are the J vectors of regression coefficients $\boldsymbol{\alpha}_j$. The $\xi_{i,1}, \ldots, \xi_{i,J}$ are distributed independently and identically standard normal. The decision maker chooses the alternative k such that $\eta_{ik} \geq \eta_{im}$ for $m \neq k$.

Suppose that case i chooses alternative k, and take the difference between latent variable η_{ik} and the $J - 1$ others:

$$\begin{aligned} v_{ijk} &= \eta_{ij} - \eta_{ik} \\ &= \mathbf{z}_i(\boldsymbol{\alpha}_j - \boldsymbol{\alpha}_k) + \xi_{ij} - \xi_{ik} \\ &= \mathbf{z}_i \boldsymbol{\gamma}_{j'} + \epsilon_{ij'} \end{aligned} \tag{1}$$

where $j' = j$ if $j < k$ and $j' = j-1$ if $j > k$ so that $j' = 1, \ldots, J-1$. $\mathrm{Var}(\epsilon_{ij'}) = \mathrm{Var}(\xi_{ij} - \xi_{ik}) = 2$ and $\mathrm{Cov}(\epsilon_{ij'}, \epsilon_{il'}) = 1$ for $j' \neq l'$. The probability that alternative k is chosen is

$$\begin{aligned} \Pr(i \text{ chooses } k) &= \Pr(v_{i1k} \leq 0, \ldots, v_{i,J-1,k} \leq 0) \\ &= \Pr(\epsilon_{i1} \leq -\mathbf{z}_i \boldsymbol{\gamma}_1, \ldots, \epsilon_{i,J-1} \leq -\mathbf{z}_i \boldsymbol{\gamma}_{J-1}) \end{aligned}$$

Hence, evaluating the likelihood function involves computing probabilities from the multivariate normal distribution. That all the covariances are equal simplifies the problem somewhat; see *Methods and formulas* for details.

In (1), not all J of the $\boldsymbol{\alpha}_j$ are identifiable. To remove the indeterminacy, $\boldsymbol{\alpha}_l$ is set to the zero vector, where l is the base outcome as specified in the `baseoutcome()` option. That fixes the lth latent variable to zero so that the remaining variables measure the attractiveness of the other alternatives relative to the base.

▷ Example 1

As discussed in example 1 of [R] **mlogit**, we have data on the type of health insurance available to 616 psychologically depressed subjects in the United States (Tarlov et al. 1989; Wells et al. 1989). Patients may have either an indemnity (fee-for-service) plan or a prepaid plan such as an HMO, or the patient may be uninsured. Demographic variables include age, gender, race, and site. Indemnity insurance is the most popular alternative, so `mprobit` will choose it as the base outcome by default.

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. mprobit insure age male nonwhite i.site
Iteration 0:   log likelihood = -535.89424
Iteration 1:   log likelihood = -534.56173
Iteration 2:   log likelihood = -534.52835
Iteration 3:   log likelihood = -534.52833
Multinomial probit regression                     Number of obs   =        615
                                                  Wald chi2(10)   =      40.18
Log likelihood = -534.52833                       Prob > chi2     =     0.0000
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.0098536	.0052688	-1.87	0.061	-.0201802	.000473
male	.4774678	.1718316	2.78	0.005	.1406841	.8142515
nonwhite	.8245003	.1977582	4.17	0.000	.4369013	1.212099
site						
2	.0973956	.1794546	0.54	0.587	-.2543289	.4491201
3	-.495892	.1904984	-2.60	0.009	-.869262	-.1225221
_cons	.22315	.2792424	0.80	0.424	-.324155	.7704549
Uninsure						
age	-.0050814	.0075327	-0.67	0.500	-.0198452	.0096823
male	.3332637	.2432986	1.37	0.171	-.1435929	.8101203
nonwhite	.2485859	.2767734	0.90	0.369	-.29388	.7910518
site						
2	-.6899485	.2804497	-2.46	0.014	-1.23962	-.1402771
3	-.1788447	.2479898	-0.72	0.471	-.6648957	.3072063
_cons	-.9855917	.3891873	-2.53	0.011	-1.748385	-.2227986

◁

The likelihood function for `mprobit` is derived under the assumption that all decision-making units face the same choice set, which is the union of all outcomes observed in the dataset. If that is not true for your model, then an alternative is to use the `asmprobit` command, which does not require this assumption. To do that, you will need to expand the dataset so that each decision maker has k_i observations, where k_i is the number of alternatives in the choice set faced by decision maker i. You will also need to create a binary variable to indicate the choice made by each decision maker. Moreover, you will need to use the `correlation(independent)` and `stddev(homoskedastic)` options with `asmprobit` unless you have alternative-specific variables.

Saved results

mprobit saves the following in e():

Scalars

e(N)	number of observations
e(k_out)	number of outcomes
e(k_points)	number of quadrature points
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_indvars)	number of independent variables
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(ll)	log simulated-likelihood
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance
e(i_base)	base outcome index
e(const)	0 if noconstant is specified, 1 otherwise
e(probitparam)	1 if probitparam is specified, 0 otherwise
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	mprobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(indvars)	independent variables
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(chi2type)	Wald, type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(outeqs)	outcome equations
e(out#)	outcome labels, #=1,...,e(k_out)
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(outcomes)	outcome values
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

mprobit is implemented as an ado-file.

See Cameron and Trivedi (2005, chap. 15) for a discussion of multinomial models, including multinomial probit. Long and Freese (2006, chap. 6) discuss the multinomial logistic, multinomial probit, and stereotype logistic regression models, with examples using Stata.

As discussed in *Remarks*, the latent variables for a J-alternative model are $\eta_{ij} = \mathbf{z}_i\boldsymbol{\alpha}_j + \xi_{ij}$, for $j = 1, \ldots, J$, $i = 1, \ldots, n$, and $\{\xi_{i,1}, \ldots, \xi_{i,\mathrm{J}}\} \sim$ i.i.d.$N(0,1)$. The experimenter observes alternative k for the ith observation if $\eta_{ik} > \eta_{il}$ for $l \neq k$. For $j \neq k$, let

$$\begin{aligned} v_{ij'} &= \eta_{ij} - \eta_{ik} \\ &= \mathbf{z}_i(\boldsymbol{\alpha}_j - \boldsymbol{\alpha}_k) + \xi_{ij} - \xi_{ik} \\ &= \mathbf{z}_i\boldsymbol{\gamma}_{j'} + \epsilon_{ij'} \end{aligned}$$

where $j' = j$ if $j < k$ and $j' = j - 1$ if $j > k$ so that $j' = 1, \ldots, J-1$. $\epsilon_i = (\epsilon_{i1}, \ldots, \epsilon_{i,J-1}) \sim MVN(\mathbf{0}, \boldsymbol{\Sigma})$, where

$$\boldsymbol{\Sigma} = \begin{pmatrix} 2 & 1 & 1 & \ldots & 1 \\ 1 & 2 & 1 & \ldots & 1 \\ 1 & 1 & 2 & \ldots & 1 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & 1 & 1 & \ldots & 2 \end{pmatrix}$$

Denote the deterministic part of the model as $\lambda_{ij'} = \mathbf{z}_i\boldsymbol{\gamma}_{j'}$; the probability that subject i chooses outcome k is

$$\begin{aligned} \Pr(y_i = k) &= \Pr(v_{i1} \leq 0, \ldots, v_{i,J-1} \leq 0) \\ &= \Pr(\epsilon_{i1} \leq -\lambda_{i1}, \ldots, \epsilon_{i,J-1} \leq -\lambda_{i,J-1}) \\ &= \frac{1}{(2\pi)^{(J-1)/2}\,|\boldsymbol{\Sigma}|^{1/2}} \int_{-\infty}^{-\lambda_{i1}} \cdots \int_{-\infty}^{-\lambda_{i,J-1}} \exp\left(-\tfrac{1}{2}\mathbf{z}'\boldsymbol{\Sigma}^{-1}\mathbf{z}\right) d\mathbf{z} \end{aligned}$$

Because of the exchangeable correlation structure of $\boldsymbol{\Sigma}$ ($\rho_{ij} = 1/2$ for all $i \neq j$), we can use Dunnett's (1989) result to reduce the multidimensional integral to one dimension:

$$\Pr(y_i = k) = \frac{1}{\sqrt{\pi}} \int_0^{\infty} \left\{ \prod_{j=1}^{J-1} \Phi\left(-z\sqrt{2} - \lambda_{ij}\right) + \prod_{j=1}^{J-1} \Phi\left(z\sqrt{2} - \lambda_{ij}\right) \right\} e^{-z^2} dz$$

Gaussian quadrature is used to approximate this integral, resulting in the K-point quadrature formula

$$\Pr(y_i = k) \approx \frac{1}{2}\sum_{k=1}^{K} w_k \left\{ \prod_{j=1}^{J-1} \Phi\left(-\sqrt{2x_k} - \lambda_{ij}\right) + \prod_{j=1}^{J-1} \Phi\left(\sqrt{2x_k} - \lambda_{ij}\right) \right\}$$

where w_k and x_k are the weights and roots of the Laguerre polynomial of order K. In `mprobit`, K is specified by the `intpoints()` option.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`mprobit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

Cameron, A. C., and P. K. Trivedi. 2005. *Microeconometrics: Methods and Applications*. New York: Cambridge University Press.

Dunnett, C. W. 1989. Algorithm AS 251: Multivariate normal probability integrals with product correlation structure. *Journal of the Royal Statistical Society, Series C* 38: 564–579.

Haan, P., and A. Uhlendorff. 2006. Estimation of multinomial logit models with unobserved heterogeneity using maximum simulated likelihood. *Stata Journal* 6: 229–245.

Hole, A. R. 2007. Fitting mixed logit models by using maximum simulated likelihood. *Stata Journal* 7: 388–401.

Long, J. S., and J. Freese. 2006. *Regression Models for Categorical Dependent Variables Using Stata*. 2nd ed. College Station, TX: Stata Press.

Tarlov, A. R., J. E. Ware, Jr., S. Greenfield, E. C. Nelson, E. Perrin, and M. Zubkoff. 1989. The medical outcomes study. An application of methods for monitoring the results of medical care. *Journal of the American Medical Association* 262: 925–930.

Wells, K. B., R. D. Hays, M. A. Burnam, W. H. Rogers, S. Greenfield, and J. E. Ware, Jr. 1989. Detection of depressive disorder for patients receiving prepaid or fee-for-service care. Results from the Medical Outcomes Survey. *Journal of the American Medical Association* 262: 3298–3302.

Also see

[R] **mprobit postestimation** — Postestimation tools for mprobit

[R] **asmprobit** — Alternative-specific multinomial probit regression

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **nlogit** — Nested logit regression

[R] **ologit** — Ordered logistic regression

[R] **oprobit** — Ordered probit regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

mprobit postestimation — Postestimation tools for mprobit

Description

The following postestimation commands are available after `mprobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predicted probabilities, linear predictions, and standard errors
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

`predict` [*type*] { *stub*`*` | *newvar* | *newvarlist* } [*if*] [*in*] [`,` *statistic* `outcome(`*outcome*`)`]

`predict` [*type*] { *stub*`*` | *newvarlist* } [*if*] [*in*]`, scores`

statistic	Description
Main	
`pr`	probability of a positive outcome; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction

If you do not specify `outcome()`, `pr` (with one new variable specified), `xb`, and `stdp` assume `outcome(#1)`.
You specify one or k new variables with `pr`, where k is the number of outcomes.

You specify one new variable with `xb` and `stdp`.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of each of the categories of the dependent variable or the probability of the level specified in `outcome(`*outcome*`)`. If you specify the `outcome(`*outcome*`)` option, you need to specify only one new variable; otherwise, you must specify a new variable for each category of the dependent variable.

`xb` calculates the linear prediction, $\mathbf{x}_i\boldsymbol{\alpha}_j$, for alternative j and individual i. The index, j, corresponds to the outcome specified in `outcome()`.

`stdp` calculates the standard error of the linear prediction.

`outcome(`*outcome*`)` specifies the outcome for which the statistic is to be calculated. `equation()` is a synonym for `outcome()`: it does not matter which you use. `outcome()` or `equation()` can be specified using

`#1`, `#2`, ..., where `#1` means the first category of the dependent variable, `#2` means the second category, etc.;

the values of the dependent variable; or

the value labels of the dependent variable if they exist.

`scores` calculates the equation-level score variables. The jth new variable will contain the scores for the jth fitted equation.

Remarks

Once you have fit a multinomial probit model, you can use `predict` to obtain probabilities that an individual will choose each of the alternatives for the estimation sample, as well as other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**.

▷ Example 1

In example 1 of [R] **mprobit**, we fit the multinomial probit model to a dataset containing the type of health insurance available to 616 psychologically depressed subjects in the United States (Tarlov et al. 1989; Wells et al. 1989). We can obtain the predicted probabilities by typing

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. mprobit insure age male nonwhite i.site
  (output omitted)
. predict p1-p3
(option pr assumed; predicted probabilities)
```

```
. list p1-p3 insure in 1/10
```

	p1	p2	p3	insure
1.	.5961306	.3741824	.029687	Indemnity
2.	.4719296	.4972289	.0308415	Prepaid
3.	.4896086	.4121961	.0981953	Indemnity
4.	.3730529	.5416623	.0852848	Prepaid
5.	.5063069	.4629773	.0307158	.
6.	.4768125	.4923548	.0308327	Prepaid
7.	.5035672	.4657016	.0307312	Prepaid
8.	.3326361	.5580404	.1093235	.
9.	.4758165	.4384811	.0857024	Uninsure
10.	.5734057	.3316601	.0949342	Prepaid

`insure` contains a missing value for observations 5 and 8. Because of that, those two observations were not used in the estimation. However, because none of the independent variables is missing, `predict` can still calculate the probabilities. Had we typed

```
. predict p1-p3 if e(sample)
```

`predict` would have filled in missing values for `p1`, `p2`, and `p3` for those observations because they were not used in the estimation.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

References

Tarlov, A. R., J. E. Ware, Jr., S. Greenfield, E. C. Nelson, E. Perrin, and M. Zubkoff. 1989. The medical outcomes study. An application of methods for monitoring the results of medical care. *Journal of the American Medical Association* 262: 925–930.

Wells, K. B., R. D. Hays, M. A. Burnam, W. H. Rogers, S. Greenfield, and J. E. Ware, Jr. 1989. Detection of depressive disorder for patients receiving prepaid or fee-for-service care. Results from the Medical Outcomes Survey. *Journal of the American Medical Association* 262: 3298–3302.

Also see

[R] **mprobit** — Multinomial probit regression

[U] **20 Estimation and postestimation commands**

Title

mvreg — Multivariate regression

Syntax

`mvreg` *depvars* `=` *indepvars* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`corr`	report correlation matrix
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`noheader`	suppress header table from above coefficient table
`notable`	suppress coefficient table
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvars and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`bootstrap`, `by`, `jackknife`, `mi estimate`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.
`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.
`noheader`, `notable`, and `coeflegend` do not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Multiple-equation models > Multivariate regression

Description

`mvreg` fits multivariate regression models.

Options

Model

`noconstant` suppresses the constant term (intercept) in the model.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`corr` displays the correlation matrix of the residuals between the equations.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

The following options are available with mvreg but are not shown in the dialog box:

noheader suppresses display of the table reporting F statistics, R-squared, and root mean squared error above the coefficient table.

notable suppresses display of the coefficient table.

coeflegend; see [R] **estimation options**.

Remarks

Multivariate regression differs from multiple regression in that *several* dependent variables are jointly regressed on the same independent variables. Multivariate regression is related to Zellner's seemingly unrelated regression (see [R] **sureg**), but because the same set of independent variables is used for each dependent variable, the syntax is simpler, and the calculations are faster.

The individual coefficients and standard errors produced by mvreg are identical to those that would be produced by regress estimating each equation separately. The difference is that mvreg, being a joint estimator, also estimates the between-equation covariances, so you can test coefficients across equations and, in fact, the test syntax makes such tests more convenient.

▷ Example 1

Using the automobile data, we fit a multivariate regression for space variables (headroom, trunk, and turn) in terms of a set of other variables, including three performance variables (displacement, gear_ratio, and mpg):

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. mvreg headroom trunk turn = price mpg displ gear_ratio length weight
Equation          Obs  Parms        RMSE    "R-sq"          F        P
------------------------------------------------------------------------
headroom           74      7    .7390205    0.2996   4.777213   0.0004
trunk              74      7    3.052314    0.5326    12.7265   0.0000
turn               74      7    2.132377    0.7844   40.62042   0.0000

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
headroom     |
       price |  -.0000528    .000038    -1.39   0.168    -.0001286    .0000229
         mpg |  -.0093774   .0260463    -0.36   0.720     -.061366    .0426112
displacement |   .0031025   .0024999     1.24   0.219    -.0018873    .0080922
  gear_ratio |   .2108071   .3539588     0.60   0.553    -.4956976    .9173119
      length |    .015886    .012944     1.23   0.224    -.0099504    .0417223
      weight |  -.0000868   .0004724    -0.18   0.855    -.0010296    .0008561
       _cons |  -.4525117   2.170073    -0.21   0.835    -4.783995    3.878972
-------------+----------------------------------------------------------------
trunk        |
       price |   .0000445   .0001567     0.28   0.778    -.0002684    .0003573
         mpg |  -.0220919   .1075767    -0.21   0.838    -.2368159    .1926322
displacement |   .0032118   .0103251     0.31   0.757    -.0173971    .0238207
  gear_ratio |  -.2271321   1.461926    -0.16   0.877    -3.145149    2.690885
      length |    .170811   .0534615     3.20   0.002     .0641014    .2775206
      weight |  -.0015944    .001951    -0.82   0.417    -.0054885    .0022997
       _cons |  -13.28253   8.962868    -1.48   0.143    -31.17249    4.607429
-------------+----------------------------------------------------------------
turn         |
       price |  -.0002647   .0001095    -2.42   0.018    -.0004833   -.0000462
         mpg |  -.0492948   .0751542    -0.66   0.514    -.1993031    .1007136
displacement |   .0036977   .0072132     0.51   0.610    -.0106999    .0180953
  gear_ratio |  -.1048432   1.021316    -0.10   0.919    -2.143399    1.933712
      length |    .072128   .0373487     1.93   0.058    -.0024204    .1466764
      weight |   .0027059    .001363     1.99   0.051    -.0000145    .0054264
       _cons |   20.19157   6.261549     3.22   0.002     7.693467    32.68968
------------------------------------------------------------------------------
```

We should have specified the `corr` option so that we would also see the correlations between the residuals of the equations. We can correct our omission because `mvreg`—like all estimation commands—typed without arguments redisplays results. The `noheader` and `notable` (read "no-table") options suppress redisplaying the output we have already seen:

```
. mvreg, notable noheader corr
Correlation matrix of residuals:

             headroom     trunk      turn
headroom       1.0000
   trunk       0.4986    1.0000
    turn      -0.1090   -0.0628    1.0000

Breusch-Pagan test of independence: chi2(3) =    19.566, Pr = 0.0002
```

The Breusch–Pagan test is significant, so the residuals of these three space variables are not independent of each other.

The three performance variables among our independent variables are `mpg`, `displacement`, and `gear_ratio`. We can jointly test the significance of these three variables in all the equations by typing

```
. test mpg displacement gear_ratio
 ( 1)  [headroom]mpg = 0
 ( 2)  [trunk]mpg = 0
 ( 3)  [turn]mpg = 0
 ( 4)  [headroom]displacement = 0
 ( 5)  [trunk]displacement = 0
 ( 6)  [turn]displacement = 0
 ( 7)  [headroom]gear_ratio = 0
 ( 8)  [trunk]gear_ratio = 0
 ( 9)  [turn]gear_ratio = 0
       F(  9,    67) =    0.33
            Prob > F =    0.9622
```

These three variables are not, as a group, significant. We might have suspected this from their individual significance in the individual regressions, but this multivariate test provides an overall assessment with one p-value.

We can also perform a test for the joint significance of all three equations:

```
. test [headroom]
 (output omitted)
. test [trunk], accum
 (output omitted)
. test [turn], accum
 ( 1)  [headroom]price = 0
 ( 2)  [headroom]mpg = 0
 ( 3)  [headroom]displacement = 0
 ( 4)  [headroom]gear_ratio = 0
 ( 5)  [headroom]length = 0
 ( 6)  [headroom]weight = 0
 ( 7)  [trunk]price = 0
 ( 8)  [trunk]mpg = 0
 ( 9)  [trunk]displacement = 0
 (10)  [trunk]gear_ratio = 0
 (11)  [trunk]length = 0
 (12)  [trunk]weight = 0
 (13)  [turn]price = 0
 (14)  [turn]mpg = 0
 (15)  [turn]displacement = 0
 (16)  [turn]gear_ratio = 0
 (17)  [turn]length = 0
 (18)  [turn]weight = 0
       F( 18,    67) =   19.34
            Prob > F =    0.0000
```

The set of variables as a whole is strongly significant. We might have suspected this, too, from the individual equations.

◁

❑ Technical note

The `mvreg` command provides a good way to deal with multiple comparisons. If we wanted to assess the effect of `length`, we might be dissuaded from interpreting any of its coefficients except that in the `trunk` equation. `[trunk]length`—the coefficient on `length` in the `trunk` equation—has a p-value of 0.002, but in the other two equations, it has p-values of only 0.224 and 0.058.

A conservative statistician might argue that there are 18 tests of significance in `mvreg`'s output (not counting those for the intercept), so p-values more than $0.05/18 = 0.0028$ should be declared

insignificant at the 5% level. A more aggressive but, in our opinion, reasonable approach would be to first note that the three equations are jointly significant, so we are justified in making some interpretation. Then we would work through the individual variables using `test`, possibly using $0.05/6 = 0.0083$ (6 because there are six independent variables) for the 5% significance level. For instance, examining `length`:

```
. test length
 ( 1)  [headroom]length = 0
 ( 2)  [trunk]length = 0
 ( 3)  [turn]length = 0
       F(  3,    67) =    4.94
            Prob > F =    0.0037
```

The reported significance level of 0.0037 is less than 0.0083, so we will declare this variable significant. `[trunk]length` is certainly significant with its p-value of 0.002, but what about in the remaining two equations with p-values 0.224 and 0.058? We perform a joint test:

```
. test [headroom]length [turn]length
 ( 1)  [headroom]length = 0
 ( 2)  [turn]length = 0
       F(  2,    67) =    2.91
            Prob > F =    0.0613
```

At this point, reasonable statisticians could disagree. The 0.06 significance value suggests no interpretation, but these were the two least-significant values out of three, so we would expect the p-value to be a little high. Perhaps an equivocal statement is warranted: there seems to be an effect, but chance cannot be excluded.

❑

Saved results

mvreg saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters in each equation
e(k_eq)	number of equations in e(b)
e(df_r)	residual degrees of freedom
e(chi2)	Breusch–Pagan χ^2 (corr only)
e(df_chi2)	degrees of freedom for Breusch–Pagan χ^2 (corr only)
e(rank)	rank of e(V)

Macros

e(cmd)	mvreg
e(cmdline)	command as typed
e(depvar)	names of dependent variables
e(eqnames)	names of equations
e(wtype)	weight type
e(wexp)	weight expression
e(r2)	R-squared for each equation
e(rmse)	RMSE for each equation
e(F)	F statistic for each equation
e(p_F)	significance of F for each equation
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Sigma)	$\widehat{\mathbf{\Sigma}}$ matrix
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

mvreg is implemented as an ado-file.

Given q equations and p independent variables (including the constant), the parameter estimates are given by the $p \times q$ matrix

$$\mathbf{B} = (\mathbf{X}'\mathbf{W}\mathbf{X})^{-1}\mathbf{X}'\mathbf{W}\mathbf{Y}$$

where $\mathbf{Y}$ is an $n \times q$ matrix of dependent variables and $\mathbf{X}$ is a $n \times p$ matrix of independent variables. $\mathbf{W}$ is a weighting matrix equal to $\mathbf{I}$ if no weights are specified. If weights are specified, let $\mathbf{v}$: $1 \times n$ be the specified weights. If fweight frequency weights are specified, $\mathbf{W} = \text{diag}(\mathbf{v})$. If aweight analytic weights are specified, $\mathbf{W} = \text{diag}\{\mathbf{v}/(\mathbf{1}'\mathbf{v})(\mathbf{1}'\mathbf{1})\}$, meaning that the weights are normalized to sum to the number of observations.

The residual covariance matrix is

$$\mathbf{R} = \{\mathbf{Y}'\mathbf{W}\mathbf{Y} - \mathbf{B}'(\mathbf{X}'\mathbf{W}\mathbf{X})\mathbf{B}\}/(n-p)$$

The estimated covariance matrix of the estimates is $\mathbf{R} \otimes (\mathbf{X}'\mathbf{W}\mathbf{X})^{-1}$. These results are identical to those produced by sureg when the same list of independent variables is specified repeatedly; see [R] **sureg**.

The Breusch and Pagan (1980) χ^2 statistic—a Lagrange multiplier statistic—is given by

$$\lambda = n \sum_{i=1}^{q} \sum_{j=1}^{i-1} r_{ij}^2$$

where r_{ij} is the estimated correlation between the residuals of the equations and n is the number of observations. It is distributed as χ^2 with $q(q-1)/2$ degrees of freedom.

Reference

Breusch, T. S., and A. R. Pagan. 1980. The Lagrange multiplier test and its applications to model specification in econometrics. *Review of Economic Studies* 47: 239–253.

Also see

[R] **mvreg postestimation** — Postestimation tools for mvreg

[MV] **manova** — Multivariate analysis of variance and covariance

[R] **nlsur** — Estimation of nonlinear systems of equations

[R] **reg3** — Three-stage estimation for systems of simultaneous equations

[R] **regress** — Linear regression

[R] **regress postestimation** — Postestimation tools for regress

[R] **sureg** — Zellner's seemingly unrelated regression

[MI] **estimation** — Estimation commands for use with mi estimate

Stata Structural Equation Modeling Reference Manual

[U] **20 Estimation and postestimation commands**

Title

mvreg postestimation — Postestimation tools for mvreg

Description

The following postestimation commands are available after `mvreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	VCE and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` `equation(`*eqno*[`,` *eqno*]`)` *statistic*]

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`residuals`	residuals
`difference`	difference between the linear predictions of two equations
`stddp`	standard error of the difference in linear predictions

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`equation(`*eqno*[`,` *eqno*]`)` specifies the equation to which you are referring.

`equation()` is filled in with one *eqno* for the `xb`, `stdp`, and `residuals` options. `equation(#1)` would mean the calculation is to be made for the first equation, `equation(#2)` would mean the second, and so on. You could also refer to the equations by their names. `equation(income)` would refer to the equation named income and `equation(hours)`, to the equation named hours.

If you do not specify `equation()`, results are the same as if you specified `equation(#1)`.

`difference` and `stddp` refer to between-equation concepts. To use these options, you must specify two equations, for example, `equation(#1,#2)` or `equation(income,hours)`. When two equations must be specified, `equation()` is required. With `equation(#1,#2)`, `difference` computes the prediction of `equation(#1)` minus the prediction of `equation(#2)`.

`xb`, the default, calculates the fitted values—the prediction of $\mathbf{x}_j\mathbf{b}$ for the specified equation.

`stdp` calculates the standard error of the prediction for the specified equation (the standard error of the predicted expected value or mean for the observation's covariate pattern). The standard error of the prediction is also referred to as the standard error of the fitted value.

`residuals` calculates the residuals.

`difference` calculates the difference between the linear predictions of two equations in the system.

`stddp` is allowed only after you have previously fit a multiple-equation model. The standard error of the difference in linear predictions $(\mathbf{x}_{1j}\mathbf{b} - \mathbf{x}_{2j}\mathbf{b})$ between equations 1 and 2 is calculated.

For more information on using `predict` after multiple-equation estimation commands, see [R] **predict**.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **mvreg** — Multivariate regression

[U] **20 Estimation and postestimation commands**

Title

nbreg — Negative binomial regression

Syntax

Negative binomial regression model

`nbreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *nbreg_options*]

Generalized negative binomial model

`gnbreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *gnbreg_options*]

nbreg_options	Description
Model	
`noconstant`	suppress constant term
`dispersion(mean)`	parameterization of dispersion; `dispersion(mean)` is the default
`dispersion(constant)`	constant dispersion for all observations
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nolrtest`	suppress likelihood-ratio test
`irr`	report incidence-rate ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

gnbreg_options	Description
Model	
noconstant	suppress constant term
lnalpha(*varlist*)	dispersion model variables
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
irr	report incidence-rate ratios
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varname*$_e$, and *varname*$_o$ may contain time-series operators (nbreg only); see [U] **11.4.4 Time-series varlists**.

bootstrap, by (nbreg only), fracpoly (nbreg only), jackknife, mfp (nbreg only), mi estimate, nestreg (nbreg only), rolling, statsby, stepwise, and svy are allowed; see [U] **11.1.10 Prefix commands**.

vce(bootstrap) and vce(jackknife) are not allowed with the mi estimate prefix; see [MI] **mi estimate**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

vce() and weights are not allowed with the svy prefix; see [SVY] **svy**.

fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

coeflegend does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

nbreg

Statistics > Count outcomes > Negative binomial regression

gnbreg

Statistics > Count outcomes > Generalized negative binomial regression

Description

`nbreg` fits a negative binomial regression model of *depvar* on *indepvars*, where *depvar* is a nonnegative count variable. In this model, the count variable is believed to be generated by a Poisson-like process, except that the variation is greater than that of a true Poisson. This extra variation is referred to as overdispersion. See [R] **poisson** before reading this entry.

`gnbreg` fits a generalization of the negative binomial mean-dispersion model; the shape parameter α may also be parameterized.

If you have panel data, see [XT] **xtnbreg**.

Options for nbreg

Model

`noconstant`; see [R] **estimation options**.

`dispersion(mean | constant)` specifies the parameterization of the model. `dispersion(mean)`, the default, yields a model with dispersion equal to $1+\alpha\exp(\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j)$; that is, the dispersion is a function of the expected mean: $\exp(\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j)$. `dispersion(constant)` has dispersion equal to $1+\delta$; that is, it is a constant for all observations.

`exposure(`*varname*$_e$`)`, `offset(`*varname*$_o$`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`nolrtest` suppresses fitting the Poisson model. Without this option, a comparison Poisson model is fit, and the likelihood is used in a likelihood-ratio test of the null hypothesis that the dispersion parameter is zero.

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. `irr` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with nbreg but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Options for gnbreg

Model

noconstant; see [R] **estimation options**.

lnalpha(*varlist*) allows you to specify a linear equation for $\ln\alpha$. Specifying lnalpha(male old) means that $\ln\alpha = \gamma_0 + \gamma_1$male $+ \gamma_2$old, where γ_0, γ_1, and γ_2 are parameters to be estimated along with the other model coefficients. If this option is not specified, gnbreg and nbreg will produce the same results because the shape parameter will be parameterized as a constant.

exposure(*varname*$_e$), offset(*varname*$_o$), constraints(*constraints*), collinear; see [R] **estimation options**.

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

level(#); see [R] **estimation options**.

irr reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. irr may be specified at estimation or when replaying previously estimated results.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with gnbreg but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction to negative binomial regression
nbreg
gnbreg

Introduction to negative binomial regression

Negative binomial regression models the number of occurrences (counts) of an event when the event has extra-Poisson variation, that is, when it has overdispersion. The Poisson regression model is

$$y_j \sim \text{Poisson}(\mu_j)$$

where

$$\mu_j = \exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$$

for observed counts y_j with covariates $\mathbf{x}_j$ for the jth observation. One derivation of the negative binomial mean-dispersion model is that individual units follow a Poisson regression model, but there is an omitted variable ν_j, such that e^{ν_j} follows a gamma distribution with mean 1 and variance α:

$$y_j \sim \text{Poisson}(\mu_j^*)$$

where

$$\mu_j^* = \exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j + \nu_j)$$

and

$$e^{\nu_j} \sim \text{Gamma}(1/\alpha, \alpha)$$

With this parameterization, a Gamma(a, b) distribution will have expectation ab and variance ab^2.

We refer to α as the overdispersion parameter. The larger α is, the greater the overdispersion. The Poisson model corresponds to $\alpha = 0$. `nbreg` parameterizes α as $\ln\alpha$. `gnbreg` allows $\ln\alpha$ to be modeled as $\ln\alpha_j = \mathbf{z}_j\boldsymbol{\gamma}$, a linear combination of covariates $\mathbf{z}_j$.

`nbreg` will fit two different parameterizations of the negative binomial model. The default, described above and also given by the `dispersion(mean)` option, has dispersion for the jth observation equal to $1 + \alpha\exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$. This is seen by noting that the above implies that

$$\mu_j^* \sim \text{Gamma}(1/\alpha, \alpha\mu_j)$$

and thus

$$\begin{aligned}\text{Var}(y_j) &= E\left\{\text{Var}(y_j|\mu_j^*)\right\} + \text{Var}\left\{E(y_j|\mu_j^*)\right\} \\ &= E(\mu_j^*) + \text{Var}(\mu_j^*) \\ &= \mu_j(1 + \alpha\mu_j)\end{aligned}$$

The alternative parameterization, given by the `dispersion(constant)` option, has dispersion equal to $1 + \delta$; that is, it is constant for all observations. This is so because the constant-dispersion model assumes instead that

$$\mu_j^* \sim \text{Gamma}(\mu_j/\delta, \delta)$$

and thus $\text{Var}(y_j) = \mu_j(1 + \delta)$. The Poisson model corresponds to $\delta = 0$.

For detailed derivations of both models, see Cameron and Trivedi (1998, 70–77). In particular, note that the mean-dispersion model is known as the NB2 model in their terminology, whereas the constant-dispersion model is referred to as the NB1 model.

See Long and Freese (2006) and Cameron and Trivedi (2010, chap. 17) for a discussion of the negative binomial regression model with Stata examples and for a discussion of other regression models for count data.

Hilbe (2011) provides an extensive review of the negative binomial model and its variations, using Stata examples.

nbreg

It is not uncommon to posit a Poisson regression model and observe a lack of model fit. The following data appeared in Rodríguez (1993):

```
. use http://www.stata-press.com/data/r12/rod93
. list
```

	cohort	age_mos	deaths	exposure
1.	1	0.5	168	278.4
2.	1	2.0	48	538.8
3.	1	4.5	63	794.4
4.	1	9.0	89	1,550.8
5.	1	18.0	102	3,006.0
6.	1	42.0	81	8,743.5
7.	1	90.0	40	14,270.0
8.	2	0.5	197	403.2
9.	2	2.0	48	786.0
10.	2	4.5	62	1,165.3
11.	2	9.0	81	2,294.8
12.	2	18.0	97	4,500.5
13.	2	42.0	103	13,201.5
14.	2	90.0	39	19,525.0
15.	3	0.5	195	495.3
16.	3	2.0	55	956.7
17.	3	4.5	58	1,381.4
18.	3	9.0	85	2,604.5
19.	3	18.0	87	4,618.5
20.	3	42.0	70	9,814.5
21.	3	90.0	10	5,802.5

```
. generate logexp = ln(exposure)
. poisson deaths i.cohort, offset(logexp)
Iteration 0:   log likelihood = -2160.0544
Iteration 1:   log likelihood = -2159.5162
Iteration 2:   log likelihood = -2159.5159
Iteration 3:   log likelihood = -2159.5159
Poisson regression                              Number of obs   =         21
                                                LR chi2(2)      =      49.16
                                                Prob > chi2     =     0.0000
Log likelihood = -2159.5159                     Pseudo R2       =     0.0113
```

deaths	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
cohort						
2	-.3020405	.0573319	-5.27	0.000	-.4144089	-.1896721
3	.0742143	.0589726	1.26	0.208	-.0413698	.1897983
_cons	-3.899488	.0411345	-94.80	0.000	-3.98011	-3.818866
logexp	1	(offset)				

```
. estat gof
        Deviance goodness-of-fit =  4190.689
        Prob > chi2(18)          =    0.0000
        Pearson goodness-of-fit  =  15387.67
        Prob > chi2(18)          =    0.0000
```

The extreme significance of the goodness-of-fit χ^2 indicates that the Poisson regression model is inappropriate, suggesting to us that we should try a negative binomial model:

```
. nbreg deaths i.cohort, offset(logexp) nolog
Negative binomial regression                    Number of obs   =         21
                                                LR chi2(2)      =       0.40
Dispersion     = mean                           Prob > chi2     =     0.8171
Log likelihood = -131.3799                      Pseudo R2       =     0.0015
```

deaths	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
cohort						
2	-.2676187	.7237203	-0.37	0.712	-1.686084	1.150847
3	-.4573957	.7236651	-0.63	0.527	-1.875753	.9609618
_cons	-2.086731	.511856	-4.08	0.000	-3.08995	-1.083511
logexp	1	(offset)				
/lnalpha	.5939963	.2583615			.0876171	1.100376
alpha	1.811212	.4679475			1.09157	3.005295

```
Likelihood-ratio test of alpha=0:  chibar2(01) = 4056.27 Prob>=chibar2 = 0.000
```

Our original Poisson model is a special case of the negative binomial—it corresponds to $\alpha = 0$. `nbreg`, however, estimates α indirectly, estimating instead $\ln\alpha$. In our model, $\ln\alpha = 0.594$, meaning that $\alpha = 1.81$ (`nbreg` undoes the transformation for us at the bottom of the output).

To test $\alpha = 0$ (equivalent to $\ln\alpha = -\infty$), `nbreg` performs a likelihood-ratio test. The staggering χ^2 value of 4,056 asserts that the probability that we would observe these data conditional on $\alpha = 0$ is virtually zero, that is, conditional on the process being Poisson. The data are not Poisson. It is not accidental that this χ^2 value is close to the goodness-of-fit statistic from the Poisson regression itself.

❑ Technical note

The usual Gaussian test of $\alpha = 0$ is omitted because this test occurs on the boundary, invalidating the usual theory associated with such tests. However, the likelihood-ratio test of $\alpha = 0$ has been modified to be valid on the boundary. In particular, the null distribution of the likelihood-ratio test statistic is not the usual χ^2_1, but rather a 50:50 mixture of a χ^2_0 (point mass at zero) and a χ^2_1, denoted as $\overline{\chi}^2_{01}$. See Gutierrez, Carter, and Drukker (2001) for more details. ❑

❑ Technical note

The negative binomial model deals with cases in which there is more variation than would be expected if the process were Poisson. The negative binomial model is not helpful if there is less than Poisson variation—if the variance of the count variable is less than its mean. However, underdispersion is uncommon. Poisson models arise because of independently generated events. Overdispersion comes about if some of the parameters (causes) of the Poisson processes are unknown. To obtain underdispersion, the sequence of events somehow would have to be regulated; that is, events would not be independent but controlled based on past occurrences. ❑

gnbreg

`gnbreg` is a generalization of `nbreg`, `dispersion(mean)`. Whereas in `nbreg`, one $\ln\alpha$ is estimated, `gnbreg` allows $\ln\alpha$ to vary, observation by observation, as a linear combination of another set of covariates: $\ln\alpha_j = \mathbf{z}_j\boldsymbol{\gamma}$.

We will assume that the number of deaths is a function of age, whereas the $\ln\alpha$ parameter is a function of cohort. To fit the model, we type

```
. gnbreg deaths age_mos, lnalpha(i.cohort) offset(logexp)
Fitting constant-only model:
Iteration 0:   log likelihood =   -187.067  (not concave)
Iteration 1:   log likelihood =  -137.4064
Iteration 2:   log likelihood = -134.07766
Iteration 3:   log likelihood = -131.60668
Iteration 4:   log likelihood = -131.57951
Iteration 5:   log likelihood = -131.57948
Iteration 6:   log likelihood = -131.57948
Fitting full model:
Iteration 0:   log likelihood = -124.34327
Iteration 1:   log likelihood = -117.70256
Iteration 2:   log likelihood = -117.56373
Iteration 3:   log likelihood = -117.56164
Iteration 4:   log likelihood = -117.56164
Generalized negative binomial regression          Number of obs   =         21
                                                  LR chi2(1)      =      28.04
                                                  Prob > chi2     =     0.0000
Log likelihood = -117.56164                       Pseudo R2       =     0.1065
------------------------------------------------------------------------------
      deaths |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
deaths       |
     age_mos |  -.0516657   .0051747    -9.98   0.000     -.061808   -.0415233
       _cons |  -1.867225   .2227944    -8.38   0.000    -2.303894   -1.430556
      logexp |          1  (offset)
-------------+----------------------------------------------------------------
lnalpha      |
      cohort |
           2 |   .0939546   .7187747     0.13   0.896    -1.314818    1.502727
           3 |   .0815279   .7365476     0.11   0.912    -1.362079    1.525135
             |
       _cons |  -.4759581   .5156502    -0.92   0.356    -1.486614    .5346978
------------------------------------------------------------------------------
```

We find that age is a significant determinant of the number of deaths. The standard errors for the variables in the $\ln\alpha$ equation suggest that the overdispersion parameter does not vary across cohorts. We can test this assertion by typing

```
. test 2.cohort 3.cohort
 ( 1)  [lnalpha]2.cohort = 0
 ( 2)  [lnalpha]3.cohort = 0
           chi2(  2) =    0.02
         Prob > chi2 =    0.9904
```

There is no evidence of variation by cohort in these data.

❑ Technical note

Note the intentional absence of a likelihood-ratio test for $\alpha = 0$ in gnbreg. The test is affected by the same boundary condition that affects the comparison test in nbreg; however, when α is parameterized by more than a constant term, the null distribution becomes intractable. For this reason, we recommend using nbreg to test for overdispersion and, if you have reason to believe that overdispersion exists, only then modeling the overdispersion using gnbreg.

❑

Saved results

nbreg and gnbreg save the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_aux)	number of auxiliary parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only mode
e(ll_c)	log likelihood, comparison model
e(alpha)	value of alpha
e(delta)	value of delta
e(N_clust)	number of clusters
e(chi2)	χ^2
e(chi2_c)	χ^2 for comparison test
e(p)	significance
e(rank)	rank of e(V)
e(rank0)	rank of e(V) for constant-only model
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	nbreg or gnbreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable (nbreg)
e(offset1)	linear offset variable (gnbreg)
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(dispers)	mean or constant
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

nbreg and gnbreg are implemented as ado-files.

See [R] **poisson** and Johnson, Kemp, and Kotz (2005, chap. 4) for an introduction to the Poisson distribution.

Methods and formulas are presented under the following headings:

Mean-dispersion model
Constant-dispersion model

Mean-dispersion model

A negative binomial distribution can be regarded as a gamma mixture of Poisson random variables. The number of times something occurs, y_j, is distributed as Poisson$(\nu_j\mu_j)$. That is, its conditional likelihood is

$$f(y_j \mid \nu_j) = \frac{(\nu_j\mu_j)^{y_j} e^{-\nu_j\mu_j}}{\Gamma(y_j+1)}$$

where $\mu_j = \exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$ and ν_j is an unobserved parameter with a Gamma$(1/\alpha, \alpha)$ density:

$$g(\nu) = \frac{\nu^{(1-\alpha)/\alpha} e^{-\nu/\alpha}}{\alpha^{1/\alpha}\Gamma(1/\alpha)}$$

This gamma distribution has mean 1 and variance α, where α is our ancillary parameter.

The unconditional likelihood for the jth observation is therefore

$$f(y_j) = \int_0^\infty f(y_j \mid \nu) g(\nu)\, d\nu = \frac{\Gamma(m+y_j)}{\Gamma(y_j+1)\Gamma(m)}\, p_j^m (1-p_j)^{y_j}$$

where $p_j = 1/(1+\alpha\mu_j)$ and $m = 1/\alpha$. Solutions for α are handled by searching for $\ln\alpha$ because α must be greater than zero.

The log likelihood (with weights w_j and offsets) is given by

$$m = 1/\alpha \qquad p_j = 1/(1+\alpha\mu_j) \qquad \mu_j = \exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$$

$$\ln L = \sum_{j=1}^{n} w_j \Big[\ln\{\Gamma(m+y_j)\} - \ln\{\Gamma(y_j+1)\} - \ln\{\Gamma(m)\} + m\ln(p_j) + y_j\ln(1-p_j) \Big]$$

For gnbreg, α can vary across the observations according to the parameterization $\ln\alpha_j = \mathbf{z}_j\boldsymbol{\gamma}$.

Constant-dispersion model

The constant-dispersion model assumes that y_j is conditionally distributed as Poisson(μ_j^*), where $\mu_j^* \sim$ Gamma$(\mu_j/\delta, \delta)$ for some dispersion parameter δ (by contrast, the mean-dispersion model assumes that $\mu_j^* \sim$ Gamma$(1/\alpha, \alpha\mu_j)$). The log likelihood is given by

$$m_j = \mu_j/\delta \qquad p = 1/(1+\delta)$$

$$\ln L = \sum_{j=1}^{n} w_j \Big[\ln\{\Gamma(m_j + y_j)\} - \ln\{\Gamma(y_j + 1)\} - \ln\{\Gamma(m_j)\} + m_j \ln(p) + y_j \ln(1-p) \Big]$$

with everything else defined as before in the calculations for the mean-dispersion model.

`nbreg` and `gnbreg` support the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

These commands also support estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **nbreg postestimation** — Postestimation tools for nbreg and gnbreg

[R] **glm** — Generalized linear models

[R] **poisson** — Poisson regression

[R] **tnbreg** — Truncated negative binomial regression

[R] **zinb** — Zero-inflated negative binomial regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtnbreg** — Fixed-effects, random-effects, & population-averaged negative binomial models

[U] **20 Estimation and postestimation commands**

Title

nbreg postestimation — Postestimation tools for nbreg and gnbreg

Description

The following postestimation commands are available after `nbreg` and `gnbreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat (svy)`.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_disp} [if] [in], scores
```

statistic	Description
Main	
`n`	number of events; the default
`ir`	incidence rate (equivalent to `predict ..., n nooffset`)
`pr(`*n*`)`	probability $\Pr(y_j = n)$
`pr(`*a*`,`*b*`)`	probability $\Pr(a \leq y_j \leq b)$
`xb`	linear prediction
`stdp`	standard error of the linear prediction

In addition, relevant only after gnbreg are the following:

statistic	Description
Main	
alpha	predicted values of α_j
lnalpha	predicted values of $\ln\alpha_j$
stdplna	standard error of predicted $\ln\alpha_j$

These statistics are available both in and out of sample; type predict ... if e(sample) ... if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

n, the default, calculates the predicted number of events, which is $\exp(\mathbf{x}_j\boldsymbol{\beta})$ if neither offset(*varname*$_o$) nor exposure(*varname*$_e$) was specified when the model was fit; $\exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$ if offset() was specified; or $\exp(\mathbf{x}_j\boldsymbol{\beta}) \times \text{exposure}_j$ if exposure() was specified.

ir calculates the incidence rate $\exp(\mathbf{x}_j\boldsymbol{\beta})$, which is the predicted number of events when exposure is 1. This is equivalent to specifying both the n and the nooffset options.

pr(*n*) calculates the probability $\Pr(y_j = n)$, where *n* is a nonnegative integer that may be specified as a number or a variable.

pr(*a*,*b*) calculates the probability $\Pr(a \leq y_j \leq b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b \geq .$) means $+\infty$;
pr(20,.) calculates $\Pr(y_j \geq 20)$;
pr(20,*b*) calculates $\Pr(y_j \geq 20)$ in observations for which $b \geq .$ and calculates $\Pr(20 \leq y_j \leq b)$ elsewhere.

pr(.,*b*) produces a syntax error. A missing value in an observation of the variable *a* causes a missing value in that observation for pr(*a*,*b*).

xb calculates the linear prediction, which is $\mathbf{x}_j\boldsymbol{\beta}$ if neither offset() nor exposure() was specified; $\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$ if offset() was specified; or $\mathbf{x}_j\boldsymbol{\beta} + \ln(\text{exposure}_j)$ if exposure() was specified; see nooffset below.

stdp calculates the standard error of the linear prediction.

alpha, lnalpha, and stdplna are relevant after gnbreg estimation only; they produce the predicted values of α_j, $\ln\alpha_j$, and the standard error of the predicted $\ln\alpha_j$, respectively.

nooffset is relevant only if you specified offset() or exposure() when you fit the model. It modifies the calculations made by predict so that they ignore the offset or exposure variable; the linear prediction is treated as $\mathbf{x}_j\boldsymbol{\beta}$ rather than as $\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$ or $\mathbf{x}_j\boldsymbol{\beta} + \ln(\text{exposure}_j)$. Specifying predict ..., nooffset is equivalent to specifying predict ..., ir.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\ln\alpha_j)$ for `dispersion(mean)` and `gnbreg`.

The second new variable will contain $\partial \ln L/\partial(\ln\delta)$ for `dispersion(constant)`.

Remarks

After `nbreg` and `gnbreg`, `predict` returns the expected number of deaths per cohort and the probability of observing the number of deaths recorded or fewer.

```
. use http://www.stata-press.com/data/r12/rod93
. nbreg deaths i.cohort, nolog
Negative binomial regression                    Number of obs   =         21
                                                LR chi2(2)      =       0.14
Dispersion     = mean                           Prob > chi2     =     0.9307
Log likelihood = -108.48841                     Pseudo R2       =     0.0007

------------------------------------------------------------------------------
      deaths |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      cohort |
           2 |   .0591305   .2978419     0.20   0.843    -.5246289      .64289
           3 |  -.0538792   .2981621    -0.18   0.857    -.6382662     .5305077
             |
       _cons |   4.435906   .2107213    21.05   0.000       4.0229     4.848912
-------------+----------------------------------------------------------------
    /lnalpha |  -1.207379   .3108622                     -1.816657    -.5980999
-------------+----------------------------------------------------------------
       alpha |     .29898   .0929416                      .1625683     .5498555
------------------------------------------------------------------------------
Likelihood-ratio test of alpha=0:  chibar2(01) =  434.62 Prob>=chibar2 = 0.000
. predict count
(option n assumed; predicted number of events)
. predict p, pr(0, deaths)
. summarize deaths count p
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      deaths |         21    84.66667    48.84192        10        197
       count |         21    84.66667     4.00773        80   89.57143
           p |         21    .4991542    .2743702   .0070255   .9801285
```

The expected number of deaths ranges from 80 to 90. The probability $\Pr(y_i \leq \texttt{deaths})$ ranges from 0.007 to 0.98.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

In the following, we use the same notation as in [R] **nbreg**.

Methods and formulas are presented under the following headings:

Mean-dispersion model
Constant-dispersion model

Mean-dispersion model

The equation-level scores are given by

$$\text{score}(\mathbf{x}\boldsymbol{\beta})_j = p_j(y_j - \mu_j)$$
$$\text{score}(\tau)_j = -m\left\{\frac{\alpha_j(\mu_j - y_j)}{1+\alpha_j\mu_j} - \ln(1+\alpha_j\mu_j) + \psi(y_j+m) - \psi(m)\right\}$$

where $\tau_j = \ln\alpha_j$ and $\psi(z)$ is the digamma function.

Constant-dispersion model

The equation-level scores are given by

$$\text{score}(\mathbf{x}\boldsymbol{\beta})_j = m_j\{\psi(y_j+m_j) - \psi(m_j) + \ln(p)\}$$
$$\text{score}(\tau)_j = y_j - (y_j+m_j)(1-p) - \text{score}(\mathbf{x}\boldsymbol{\beta})_j$$

where $\tau_j = \ln\delta_j$.

Also see

[R] **nbreg** — Negative binomial regression

[U] **20 Estimation and postestimation commands**

Title

nestreg — Nested model statistics

Syntax

Standard estimation command syntax

```
nestreg [ , options ]: command_name depvar (varlist) [ (varlist) ... ]
    [ if ] [ in ] [ weight ] [ command_options ]
```

Survey estimation command syntax

```
nestreg [ , options ]: svy [ vcetype ] [ , svy_options ]: command_name depvar
    (varlist) [ (varlist) ... ] [ if ] [ in ] [ , command_options ]
```

options	Description
Reporting	
`waldtable`	report Wald test results; the default
`lrtable`	report likelihood-ratio test results
`quietly`	suppress any output from *command_name*
`store(`*stub*`)`	store nested estimation results in `_est_`*stub#*

`by` is allowed; see [U] **11.1.10 Prefix commands**.

Weights are allowed if *command_name* allows them; see [U] **11.1.6 weight**.

A *varlist* in parentheses indicates that this list of variables is to be considered as a block. Each variable in a *varlist* not bound in parentheses will be treated as its own block.

All postestimation commands behave as they would after *command_name* without the `nestreg` prefix; see the postestimation manual entry for *command_name*.

Menu

Statistics > Other > Nested model statistics

Description

`nestreg` fits nested models by sequentially adding blocks of variables and then reports comparison tests between the nested models.

Options

Reporting

`waldtable` specifies that the table of Wald test results be reported. `waldtable` is the default.

`lrtable` specifies that the table of likelihood-ratio tests be reported. This option is not allowed if `pweights`, the `vce(robust)` option, or the `vce(cluster` *clustvar*`)` option is specified. `lrtable` is also not allowed with the `svy` prefix.

`quietly` suppresses the display of any output from *command_name*.

store(*stub*) specifies that each model fit by nestreg be stored under the name _est_*stub*#, where # is the nesting order from first to last.

Remarks

Remarks are presented under the following headings:

Estimation commands
Wald tests
Likelihood-ratio tests
Programming for nestreg

Estimation commands

nestreg removes collinear predictors and observations with missing values from the estimation sample before calling *command_name*.

The following Stata commands are supported by nestreg:

clogit	nbreg	regress
cloglog	ologit	scobit
glm	oprobit	stcox
intreg	poisson	stcrreg
logistic	probit	streg
logit	qreg	tobit

You do not supply a *depvar* for stcox, stcrreg, or streg; otherwise, *depvar* is required. You must supply two *depvar*s for intreg.

Wald tests

Use nestreg to test the significance of blocks of predictors, building the regression model one block at a time. Using the data from example 1 of [R] **test**, we wish to test the significance of the following predictors of birth rate: medage, medagesq, and region (already partitioned into four indicator variables: reg1, reg2, reg3, and reg4).

```
. use http://www.stata-press.com/data/r12/census4
(birth rate, median age)
. nestreg: regress brate (medage) (medagesq) (reg2-reg4)
Block  1: medage
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  1,    48) =  164.72
       Model |  32675.1044     1  32675.1044            Prob > F      =  0.0000
    Residual |  9521.71561    48  198.369075            R-squared     =  0.7743
-------------+------------------------------           Adj R-squared =  0.7696
       Total |    42196.82    49  861.159592            Root MSE      =  14.084

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      medage |  -15.24893   1.188141   -12.83   0.000    -17.63785   -12.86002
       _cons |   618.3935   35.15416    17.59   0.000     547.7113    689.0756
------------------------------------------------------------------------------
```

```
Block  2: medagesq
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  2,    47) =  158.75
       Model |  36755.8524     2  18377.9262            Prob > F      =  0.0000
    Residual |  5440.96755    47  115.765267            R-squared     =  0.8711
-------------+------------------------------           Adj R-squared =  0.8656
       Total |    42196.82    49  861.159592            Root MSE      =  10.759

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      medage |  -109.8925   15.96663    -6.88   0.000    -142.0132    -77.7718
    medagesq |   1.607332   .2707228     5.94   0.000     1.062708    2.151956
       _cons |   2007.071   235.4316     8.53   0.000     1533.444    2480.698
------------------------------------------------------------------------------

Block  3: reg2 reg3 reg4
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  5,    44) =  100.63
       Model |  38803.419     5  7760.68381            Prob > F      =  0.0000
    Residual |  3393.40095    44  77.1227489            R-squared     =  0.9196
-------------+------------------------------           Adj R-squared =  0.9104
       Total |    42196.82    49  861.159592            Root MSE      =   8.782

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      medage |  -109.0957   13.52452    -8.07   0.000    -136.3526   -81.83886
    medagesq |   1.635208   .2290536     7.14   0.000     1.173581    2.096835
        reg2 |   15.00284   4.252068     3.53   0.001     6.433365    23.57233
        reg3 |   7.366435   3.953336     1.86   0.069    -.6009898    15.33386
        reg4 |   21.39679   4.650602     4.60   0.000     12.02412    30.76946
       _cons |    1947.61   199.8405     9.75   0.000     1544.858    2350.362
------------------------------------------------------------------------------
```

Block	F	Block df	Residual df	Pr > F	R2	Change in R2
1	164.72	1	48	0.0000	0.7743	
2	35.25	1	47	0.0000	0.8711	0.0967
3	8.85	3	44	0.0001	0.9196	0.0485

This single call to `nestreg` ran `regress` three times, adding a block of predictors to the model for each run as in

```
. regress brate medage
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  1,    48) =  164.72
       Model |  32675.1044     1  32675.1044            Prob > F      =  0.0000
    Residual |  9521.71561    48  198.369075            R-squared     =  0.7743
-------------+------------------------------           Adj R-squared =  0.7696
       Total |    42196.82    49  861.159592            Root MSE      =  14.084

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      medage |  -15.24893   1.188141   -12.83   0.000    -17.63785   -12.86002
       _cons |   618.3935   35.15416    17.59   0.000     547.7113    689.0756
------------------------------------------------------------------------------
```

```
. regress brate medage medagesq
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  2,    47) =  158.75
       Model |  36755.8524     2  18377.9262            Prob > F      =  0.0000
    Residual |  5440.96755    47  115.765267            R-squared     =  0.8711
-------------+------------------------------           Adj R-squared =  0.8656
       Total |    42196.82    49  861.159592            Root MSE      =  10.759

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     medage |  -109.8925   15.96663    -6.88   0.000    -142.0132   -77.7718
   medagesq |   1.607332   .2707228     5.94   0.000     1.062708   2.151956
      _cons |   2007.071   235.4316     8.53   0.000     1533.444   2480.698
------------------------------------------------------------------------------

. regress brate medage medagesq reg2-reg4
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  5,    44) =  100.63
       Model |  38803.419     5  7760.68381            Prob > F      =  0.0000
    Residual |  3393.40095    44  77.1227489            R-squared     =  0.9196
-------------+------------------------------           Adj R-squared =  0.9104
       Total |    42196.82    49  861.159592            Root MSE      =   8.782

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     medage |  -109.0957   13.52452    -8.07   0.000    -136.3526   -81.83886
   medagesq |   1.635208   .2290536     7.14   0.000     1.173581    2.096835
       reg2 |   15.00284   4.252068     3.53   0.001     6.433365    23.57233
       reg3 |   7.366435   3.953336     1.86   0.069    -.6009898    15.33386
       reg4 |   21.39679   4.650602     4.60   0.000     12.02412    30.76946
      _cons |    1947.61   199.8405     9.75   0.000     1544.858    2350.362
------------------------------------------------------------------------------
```

`nestreg` collected the F statistic for the corresponding block of predictors and the model R^2 statistic from each model fit.

The F statistic for the first block, 164.72, is for a test of the joint significance of the first block of variables; it is simply the F statistic from the regression of `brate` on `medage`. The F statistic for the second block, 35.25, is for a test of the joint significance of the second block of variables in a regression of both the first and second blocks of variables. In our example, it is an F test of `medagesq` in the regression of `brate` on `medage` and `medagesq`. Similarly, the third block's F statistic of 8.85 corresponds to a joint test of `reg2`, `reg3`, and `reg4` in the final regression.

Likelihood-ratio tests

The `nestreg` command provides a simple syntax for performing likelihood-ratio tests for nested model specifications; also see `lrtest`. Using the data from example 1 of [R] **lrtest**, we wish to jointly test the significance of the following predictors of low birthweight: `age`, `lwt`, `ptl`, and `ht`.

```
. use http://www.stata-press.com/data/r12/lbw
(Hosmer & Lemeshow data)
. xi: nestreg, lr: logistic low (i.race smoke ui) (age lwt ptl ht)
i.race            _Irace_1-3          (naturally coded; _Irace_1 omitted)
Block  1: _Irace_2 _Irace_3 smoke ui
Logistic regression                               Number of obs   =        189
                                                  LR chi2(4)      =      18.80
                                                  Prob > chi2     =     0.0009
Log likelihood = -107.93404                       Pseudo R2       =     0.0801
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_Irace_2	3.052746	1.498087	2.27	0.023	1.166747	7.987382
_Irace_3	2.922593	1.189229	2.64	0.008	1.316457	6.488285
smoke	2.945742	1.101838	2.89	0.004	1.415167	6.131715
ui	2.419131	1.047359	2.04	0.041	1.035459	5.651788
_cons	.1402209	.0512295	-5.38	0.000	.0685216	.2869447

```
Block  2: age lwt ptl ht
Logistic regression                               Number of obs   =        189
                                                  LR chi2(8)      =      33.22
                                                  Prob > chi2     =     0.0001
Log likelihood =   -100.724                       Pseudo R2       =     0.1416
```

low	Odds Ratio	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_Irace_2	3.534767	1.860737	2.40	0.016	1.259736	9.918406
_Irace_3	2.368079	1.039949	1.96	0.050	1.001356	5.600207
smoke	2.517698	1.00916	2.30	0.021	1.147676	5.523162
ui	2.1351	.9808153	1.65	0.099	.8677528	5.2534
age	.9732636	.0354759	-0.74	0.457	.9061578	1.045339
lwt	.9849634	.0068217	-2.19	0.029	.9716834	.9984249
ptl	1.719161	.5952579	1.56	0.118	.8721455	3.388787
ht	6.249602	4.322408	2.65	0.008	1.611152	24.24199
_cons	1.586014	1.910496	0.38	0.702	.1496092	16.8134

Block	LL	LR	df	Pr > LR	AIC	BIC
1	-107.934	18.80	4	0.0009	225.8681	242.0768
2	-100.724	14.42	4	0.0061	219.448	248.6237

The estimation results from the full model are left in `e()`, so we can later use `estat` and other postestimation commands.

```
. estat gof
Logistic model for low, goodness-of-fit test
       number of observations =       189
 number of covariate patterns =       182
           Pearson chi2(173) =       179.24
                 Prob > chi2 =         0.3567
```

Programming for nestreg

If you want your user-written command (*command_name*) to work with `nestreg`, it must follow standard Stata syntax and allow the `if` qualifier. Furthermore, *command_name* must have `sw` or `swml` as a program property; see [P] **program properties**. If *command_name* has `swml` as a property, *command_name* must save the log-likelihood value in `e(ll)` and the model degrees of freedom in `e(df_m)`.

Saved results

`nestreg` saves the following in `r()`:

Matrices

`r(wald)`	matrix corresponding to the Wald table
`r(lr)`	matrix corresponding to the likelihood-ratio table

Methods and formulas

`nestreg` is implemented as an ado-file.

Acknowledgment

We thank Paul H. Bern, Syracuse University, for developing the hierarchical regression command that inspired `nestreg`.

Reference

Acock, A. C. 2010. *A Gentle Introduction to Stata*. 3rd ed. College Station, TX: Stata Press.

Also see

[P] **program properties** — Properties of user-defined programs

Title

net — Install and manage user-written additions from the Internet

Syntax

Set current location for net

```
net from directory_or_url
```

Change to a different net directory

```
net cd path_or_url
```

Change to a different net site

```
net link linkname
```

Search for installed packages

```
net search
```
(see [R] **net search**)

Report current net location

```
net
```

Describe a package

```
net describe pkgname [ , from(directory_or_url) ]
```

Set location where packages will be installed

```
net set ado dirname
```

Set location where ancillary files will be installed

```
net set other dirname
```

Report net 'from', 'ado', and 'other' settings

```
net query
```

Install ado-files and help files from a package

```
net install pkgname [ , all replace force from(directory_or_url) ]
```

Install ancillary files from a package

```
net get pkgname [ , all replace force from(directory_or_url) ]
```

Shortcut to access Stata Journal (SJ) net site

```
net sj vol-issue [insert]
```

Shortcut to access Stata Technical Bulletin (STB) net site

```
net stb issue [insert]
```

List installed packages

```
ado [, find(string) from(dirname)]
ado dir [pkgid] [, find(string) from(dirname)]
```

Describe installed packages

```
ado describe [pkgid] [, find(string) from(dirname)]
```

Uninstall an installed package

```
ado uninstall pkgid [, from(dirname)]
```

where

pkgname	is	name of a package
pkgid	is	name of a package
	or	a number in square brackets: `[#]`
dirname	is	a directory name
	or	`PLUS` (default)
	or	`PERSONAL`
	or	`SITE`

Description

`net` downloads and installs additions to Stata. The additions can be obtained from the Internet or from physical media. The additions can be ado-files (new commands), help files, or even datasets. Collections of files are bound together into *packages*. For instance, the package named zz49 might add the `xyz` command to Stata. At a minimum, such a package would contain `xyz.ado`, the code to implement the new command, and `xyz.sthlp`, the online help to describe it. That the package contains two files is a detail: you use `net` to download the package zz49, regardless of the number of files.

`ado` manages the packages you have installed by using `net`. The `ado` command lets you list and uninstall previously installed packages.

You can also access the `net` and `ado` features by selecting **Help > SJ and User-written Programs**; this is the recommended method to find and install additions to Stata.

Options

`all` is used with `net install` and `net get`. Typing it with either one makes the command equivalent to typing `net install` followed by `net get`.

`replace` is for use with `net install` and `net get`. It specifies that the downloaded files replace existing files if any of the files already exists.

`force` specifies that the downloaded files replace existing files if any of the files already exists, even if Stata thinks all the files are the same. `force` implies `replace`.

`find(`*string*`)` is for use with `ado`, `ado dir`, and `ado describe`. It specifies that the descriptions of the packages installed on your computer be searched, and that the package descriptions containing *string* be listed.

`from(`*dirname*`)`, when used with `ado`, specifies where the packages are installed. The default is `from(PLUS)`. `PLUS` is a code word that Stata understands to correspond to a particular directory on your computer that was set at installation time. On Windows computers, `PLUS` probably means the directory `c:\ado\plus`, but it might mean something else. You can find out what it means by typing `sysdir`, but doing so is irrelevant if you use the defaults.

`from(`*directory_or_url*`)`, when used with `net`, specifies the directory or URL where installable packages may be found. The directory or URL is the same as the one that would have been specified with `net from`.

Remarks

For an introduction to using `net` and `ado`, see [U] **28 Using the Internet to keep up to date**. The purpose of this documentation is

- to briefly, but accurately, describe `net` and `ado` and all their features and
- to provide documentation to those who wish to set up their own sites to distribute additions to Stata.

Remarks are presented under the following headings:

Definition of a package
The purpose of the net and ado commands
Content pages
Package-description pages
Where packages are installed
A summary of the net command
A summary of the ado command
Relationship of net and ado to the point-and-click interface
Creating your own site
Format of content and package-description files
Example 1
Example 2
Additional package directives
SMCL in content and package-description files
Error-free file delivery

Definition of a package

A *package* is a collection of files—typically, `.ado` and `.sthlp` files—that together provide a new feature in Stata. Packages contain additions that you wish had been part of Stata at the outset. We write such additions, and so do other users.

One source of these additions is the *Stata Journal*, a printed and electronic journal with corresponding software. If you want the journal, you must subscribe, but the software is available for free from our website.

The purpose of the net and ado commands

The net command makes it easy to distribute and install packages. The goal is to get you quickly to a package-description page that summarizes the addition, for example,

```
. net describe rte_stat, from(http://www.wemakeitupaswego.edu/faculty/sgazer/)
-------------------------------------------------------------------------------
package rte_stat from http://www.wemakeitupaswego.edu/faculty/sgazer/
-------------------------------------------------------------------------------
TITLE
      rte_stat.  The robust-to-everything statistic; update.
DESCRIPTION/AUTHOR(S)
      S. Gazer, Dept. of Applied Theoretical Mathematics, WMIUAWG Univ.
      Aleph-0 100% confidence intervals proved too conservative for some
      applications; Aleph-1 confidence intervals have been substituted.
      The new robust-to-everything supplants the previous robust-to-
      everything-conceivable statistic.  See "Inference in the absence
      of data" (forthcoming).  After installation, see help rte.
INSTALLATION FILES                                  (type net install rte_stat)
      rte.ado
      rte.sthlp
      nullset.ado
      random.ado
-------------------------------------------------------------------------------
```

If you decide that the addition might prove useful, net makes the installation easy:

```
. net install rte_stat
checking rte_stat consistency and verifying not already installed...
installing into c:\ado\plus\ ...
installation complete.
```

The ado command helps you manage packages installed with net. Perhaps you remember that you installed a package that calculates the robust-to-everything statistic, but you cannot remember the command's name. You could use ado to search what you have previously installed for the rte command,

```
. ado
[1] package sg145 from http://www.stata.com/stb/stb56
      STB-56 sg145. Scalar measures of fit for regression models.
  (output omitted)
[15] package rte_stat from http://www.wemakeitupaswego.edu/faculty/sgazer
      rte_stat.  The robust-to-everything statistic; update.
  (output omitted)
[21] package st0119 from http://www.stata-journal.com/software/sj7-1
      SJ7-1 st0119.  Rasch analysis
```

or you might type

```
. ado, find("robust-to-everything")
[15] package rte_stat from http://www.wemakeitupaswego.edu/faculty/sgazer
      rte_stat.  The robust-to-everything statistic; update.
```

Perhaps you decide that rte, despite the author's claims, is not worth the disk space it occupies. You can use ado to erase it:

```
. ado uninstall rte_stat
package rte_stat from http://www.wemakeitupaswego.edu/faculty/sgazer
      rte_stat.  The robust-to-everything statistic; update.
(package uninstalled)
```

`ado uninstall` is easier than erasing the files by hand because `ado uninstall` erases every file associated with the package, and, moreover, `ado` knows where on your computer `rte_stat` is installed; you would have to hunt for these files.

Content pages

There are two types of pages displayed by `net`: content pages and package-description pages. When you type `net from`, `net cd`, `net link`, or `net` without arguments, Stata goes to the specified place and displays the content page:

```
. net from http://www.stata.com
------------------------------------------------------------------------------
http://www.stata.com/
StataCorp
------------------------------------------------------------------------------

Welcome to StataCorp.

Below we provide links to sites providing additions to Stata, including
the Stata Journal, STB, and Statalist.  These are NOT THE OFFICIAL UPDATES;
you fetch and install the official updates by typing -update-.

PLACES you could -net link- to:
    sj                The Stata Journal

DIRECTORIES you could -net cd- to:
    stb               materials published in the Stata Technical Bulletin
    users             materials written by various people, including StataCorp
                      employees
    meetings          software packages from Stata Users Group meetings
    links             links to other locations providing additions to Stata
------------------------------------------------------------------------------
```

A content page tells you about other content pages and package-description pages. The example above lists other content pages only. Below we follow one of the links for the *Stata Journal*:

```
. net link sj
------------------------------------------------------------------------------
http://www.stata-journal.com/
The Stata Journal
------------------------------------------------------------------------------

The Stata Journal is a refereed, quarterly journal containing articles
of interest to Stata users.  For more details and subscription information,
visit the Stata Journal website at http://www.stata-journal.com.

PLACES you could -net link- to:
    stata             StataCorp website

DIRECTORIES you could -net cd- to:
    production        Files for authors of the Stata Journal
    software          Software associated with Stata Journal articles
------------------------------------------------------------------------------
```

```
. net cd software
-------------------------------------------------------------------------------
http://www.stata-journal.com/software/
The Stata Journal
-------------------------------------------------------------------------------

PLACES you could -net link- to:
    stata             StataCorp website
    stb               Stata Technical Bulletin (STB) software archive
DIRECTORIES you could -net cd- to:
  (output omitted)
    sj7-1             volume 7, issue 1
  (output omitted)
    sj1-1             volume 1, issue 1
-------------------------------------------------------------------------------

. net cd sj7-1
-------------------------------------------------------------------------------
http://www.stata-journal.com/software/sj7-1/
Stata Journal volume 7, issue 1
-------------------------------------------------------------------------------

DIRECTORIES you could -net cd- to:
    ..                Other Stata Journals
PACKAGES you could -net describe-:
    dm0027            File filtering in Stata: handling complex data
                      formats and navigating log files efficiently
    st0119            Rasch analysis
    st0120            Multivariable regression spline models
    st0121            mhbounds - Sensitivity Analysis for Average
                      Treatment Effects
-------------------------------------------------------------------------------
```

`dm0027`, `st0119`, ..., `st0121` are links to package-description pages.

1. When you type `net from`, you follow that with a location to display the location's content page.

   a. The location could be a URL, such as http://www.stata.com. The content page at that location would then be listed.

   b. The location could be `e:` on a Windows computer or a mounted volume on a Mac computer. The content page on that source would be listed. That would work if you had special media obtained from StataCorp or special media prepared by another user.

   c. The location could even be a directory on your computer, but that would work only if that directory contained the right kind of files.

2. Once you have specified a location, typing `net cd` will take you into subdirectories of that location, if there are any. Typing

   ```
   . net from http://www.stata-journal.com
   . net cd software
   ```

   is equivalent to typing

   ```
   . net from http://www.stata-journal.com/software
   ```

   Typing `net cd` displays the content page from that location.

3. Typing `net` without arguments redisplays the current content page, which is the content page last displayed.

4. `net link` is similar to `net cd` in that the result is to change the location, but rather than changing to subdirectories of the current location, `net link` jumps to another location:

```
. net from http://www.stata-journal.com
------------------------------------------------------------------------------
http://www.stata-journal.com/
The Stata Journal
------------------------------------------------------------------------------

The Stata Journal is a refereed, quarterly journal containing articles
of interest to Stata users.  For more details and subscription information,
visit the Stata Journal website at
http://www.stata-journal.com.

PLACES you could -net link- to:
    stata             StataCorp website

DIRECTORIES you could -net cd- to:
    production        Files for authors of the Stata Journal
    software          Software associated with Stata Journal articles
------------------------------------------------------------------------------
```

Typing `net link stata` would jump to http://www.stata.com:

```
. net link stata
------------------------------------------------------------------------------
http://www.stata.com/
StataCorp
------------------------------------------------------------------------------

Welcome to StataCorp.
  (output omitted)
------------------------------------------------------------------------------
```

Package-description pages

Package-description pages describe what could be installed:

```
. net from http://www.stata-journal.com/software/sj7-1
```

```
http://www.stata-journal.com/software/sj7-1/
  (output omitted)
. net describe st0119
```

```
package st0119 from http://www.stata-journal.com/software/sj7-1
```

```
TITLE
      SJ7-1 st0119.  Rasch analysis
DESCRIPTION/AUTHOR(S)
      Rasch analysis
      by Jean-Benoit Hardouin, University of Nantes, France
      Support:  jean-benoit.hardouin@univ-nantes.fr
      After installation, type help gammasym, gausshermite,
          geekel2d, raschtest, and raschtestv7
INSTALLATION FILES                                (type net install st0119)
      st0119/raschtest.ado
      st0119/raschtest.hlp
      st0119/raschtestv7.ado
      st0119/raschtestv7.hlp
      st0119/gammasym.ado
      st0119/gammasym.hlp
      st0119/gausshermite.ado
      st0119/gausshermite.hlp
      st0119/geekel2d.ado
      st0119/geekel2d.hlp
ANCILLARY FILES                                   (type net get st0119)
      st0119/data.dta
      st0119/outrasch.do
```

A package-description page describes the package and tells you how to install the component files. Package-description pages potentially describe two types of files:

1. Installation files: files that you type `net install` to install and that are required to make the addition work.
2. Ancillary files: additional files that you might want to install—you type `net get` to install them—but that you can ignore. Ancillary files are typically datasets that are useful for demonstration purposes. Ancillary files are not really installed in the sense of being copied to an official place for use by Stata itself. They are merely copied into the current directory so that you may use them if you wish.

You install the official files by typing `net install` followed by the package name. For example, to install `st0119`, you would type

```
. net install st0119
checking st0119 consistency and verifying not already installed...
installing into c:\ado\plus\ ...
installation complete.
```

You get the ancillary files—if there are any and if you want them—by typing `net get` followed by the package name:

```
. net get st0119
checking st0119 consistency and verifying not already installed...
copying into current directory...
      copying  data.dta
      copying  outrasch.do
ancillary files successfully copied.
```

Most users ignore the ancillary files.

Once you have installed a package—by typing `net install`—use `ado` to redisplay the package-description page whenever you wish:

```
. ado describe st0119
```

```
[1] package st0119 from http://www.stata-journal.com/software/sj7-1
```

```
TITLE
      SJ7-1 st0119.  Rasch analysis
DESCRIPTION/AUTHOR(S)
      Rasch analysis
      by Jean-Benoit Hardouin, University of Nantes, France
      Support:  jean-benoit.hardouin@univ-nantes.fr
      After installation, type help gammasym, gausshermite,
          geekel2d, raschtest, and raschtestv7
INSTALLATION FILES
      r/raschtest.ado
      r/raschtest.hlp
      r/raschtestv7.ado
      r/raschtestv7.hlp
      g/gammasym.ado
      g/gammasym.hlp
      g/gausshermite.ado
      g/gausshermite.hlp
      g/geekel2d.ado
      g/geekel2d.hlp
INSTALLED ON
      24 Apr 2011
```

The package-description page shown by `ado` includes the location from which we got the package and when we installed it. It does not mention the ancillary files that were originally part of this package because they are not tracked by `ado`.

Where packages are installed

Packages should be installed in `PLUS` or `SITE`, which are code words that Stata understands and that correspond to some real directories on your computer. Typing `sysdir` will tell you where these are, if you care.

```
. sysdir
   STATA:  C:\Program Files\Stata12\
 UPDATES:  C:\Program Files\Stata12\ado\updates\
    BASE:  C:\Program Files\Stata12\ado\base\
    SITE:  C:\Program Files\Stata12\ado\site\
    PLUS:  c:\ado\plus\
PERSONAL:  c:\ado\personal\
OLDPLACE:  c:\ado\
```

If you type `sysdir`, you may obtain different results.

By default, net installs in the PLUS directory, and ado tells you about what is installed there. If you are on a multiple-user system, you may wish to install some packages in the SITE directory. This way, they will be available to other Stata users. To do that, before using net install, type

```
. net set ado SITE
```

and when reviewing what is installed or removing packages, redirect ado to that directory:

```
. ado ..., from(SITE)
```

In both cases, you type SITE because Stata will understand that SITE means the site ado-directory as defined by sysdir. To install into SITE, you must have write access to that directory.

If you reset where net installs and then, in the same session, wish to install into your private ado-directory, type

```
. net set ado PLUS
```

That is how things were originally. If you are confused as to where you are, type net query.

A summary of the net command

The net command displays content pages and package-description pages. Such pages are provided over the Internet, and most users get them there. We recommend that you start at http://www.stata.com and work out from there. We also recommend using net search to find packages of interest to you; see [R] **net search**.

net from moves you to a location and displays the content page.

net cd and net link change from your current location to other locations. net cd enters subdirectories of the original location. net link jumps from one location to another, depending on the code on the content page.

net describe lists a package-description page. Packages are named, and you type net describe *pkgname*.

net install installs a package into your copy of Stata. net get copies any additional files (ancillary files) to your current directory.

net sj and net stb simplify loading files from the *Stata Journal* and its predecessor, the *Stata Technical Bulletin*.

net sj *vol-issue*

is a synonym for typing

net from http://www.stata-journal.com/software/sj*vol-issue*

whereas

net sj *vol-issue insert*

is a synonym for typing

net from http://www.stata-journal.com/software/sj*vol-issue*
net describe *insert*

net set controls where net installs files. By default, net installs in the PLUS directory; see [P] **sysdir**. net set ado SITE would cause subsequent net commands to install in the SITE directory. net set other sets where ancillary files, such as .dta files, are installed. The default is the current directory.

net query displays the current net from, net set ado, and net set other settings.

A summary of the ado command

The ado command lists the package descriptions of previously installed packages.

Typing ado without arguments is the same as typing ado dir. Both list the names and titles of the packages you have installed.

ado describe lists full package-description pages.

ado uninstall removes packages from your computer.

Because you can install packages from a variety of sources, the package names may not always be unique. Thus the packages installed on your computer are numbered sequentially, and you may refer to them by name or by number. For instance, say that you wanted to get rid of the robust-to-everything statistic command you installed. Type

```
. ado, find("robust-to-everything")
[15] package rte_stat from http://www.wemakeitupaswego.edu/faculty/sgazer
     rte_stat.  The robust-to-everything statistic; update.
```

You could then type

```
. ado uninstall rte_stat
```

or

```
. ado uninstall [15]
```

Typing ado uninstall rte_stat would work only if the name rte_stat were unique; otherwise, ado would refuse, and you would have to type the number.

The find() option is allowed with ado dir and ado describe. It searches the package description for the word or phrase you specify, ignoring case (alpha matches Alpha). The complete package description is searched, including the author's name and the name of the files. Thus if rte was the name of a command that you wanted to eliminate, but you could not remember the name of the package, you could type

```
. ado, find(rte)
[15] package rte_stat from http://www.wemakeitupaswego.edu/faculty/sgazer
     rte_stat.  The robust-to-everything statistic; update.
```

Relationship of net and ado to the point-and-click interface

Users may instead select **Help > SJ and User-written Programs**. There are advantages and disadvantages:

1. Flipping through content and package-description pages is easier; it is much like a browser. See [GS] **19 Updating and extending Stata—Internet functionality** (GSM, GSU, or GSW).
2. When browsing a product-description page, note that the .sthlp files are highlighted. You may click on .sthlp files to review them before installing the package.
3. You may not redirect from where ado searches for files.

Creating your own site

The rest of this entry concerns how to create your own site to distribute additions to Stata. The idea is that you have written additions for use with Stata—say, `xyz.ado` and `xyz.sthlp`—and you wish to put them out so that coworkers or researchers at other institutions can easily install them. Or, perhaps you just have a dataset that you and others want to share.

In any case, all you need is a webpage. You place the files that you want to distribute on your webpage (or in a subdirectory), and you add two more files—a content file and a package-description file—and you are done.

Format of content and package-description files

The content file describes the content page. It must be named `stata.toc`:

begin `stata.toc`

```
OFF                                          (to make site unavailable temporarily)
* lines starting with * are comments; they are ignored
* blank lines are ignored, too
* v indicates version—specify v 3, which is the current version of .toc files
v 3
* d lines display description text
* the first d line is the title, and the remaining ones are text
* blank d lines display a blank line
d title
d text
d text
d
...
* l lines display links
l word-to-show path-or-url [description]
l word-to-show path-or-url [description]
...
* t lines display other directories within the site
t path [description]
t path [description]
...
* p lines display packages
p pkgname [description]
p pkgname [description]
...
```

end `stata.toc`

Package files describe packages and are named *pkgname*`.pkg`:

begin *pkgname*.pkg

```
* lines starting with * are comments; they are ignored
* blank lines are ignored, too
* v indicates version—specify v 3, which is the current version of .toc files
v 3
* d lines display package description text
* the first d line is the title, and the remaining ones are text
* blank d lines display a blank line
d title
d text
d Distribution-Date: date
d text
d
...
* f identifies the component files
f [path/]filename [description]
f [path/]filename [description]
...
* e line is optional; it means stop reading
e
```

end *pkgname*.pkg

Note the Distribution-Date description line. This line is optional but recommended. Stata can look for updates to user-written programs with the `adoupdate` command if the package files from which those programs were installed contain a Distribution-Date description line.

Example 1

Say that we want the user to see the following:

```
. net from http://www.university.edu/~me
------------------------------------------------------------------------------
http://www.university.edu/~me
Chris Farrar, Uni University
------------------------------------------------------------------------------

PACKAGES you could -net describe-:
    xyz              interval-truncated survival

. net describe xyz
------------------------------------------------------------------------------
package xyz from http://www.university.edu/~me
------------------------------------------------------------------------------

TITLE
      xyz.  interval-truncated survival.
DESCRIPTION/AUTHOR(S)
      C. Farrar, Uni University.
INSTALLATION FILES                                (type net install xyz)
      xyz.ado
      xyz.sthlp
ANCILLARY FILES                                   (type net get xyz)
      sample.dta
------------------------------------------------------------------------------
```

The files needed to do this would be

begin stata.toc

```
v 3
d Chris Farrar, Uni University
p xyz interval-truncated survival
```

end stata.toc

begin xyz.pkg
```
v 3
d xyz.  interval-truncated survival.
d C. Farrar, Uni University.
f xyz.ado
f xyz.sthlp
f sample.dta
```
end xyz.pkg

On his homepage, Chris would place the following files:

stata.toc	(shown above)
xyz.pkg	(shown above)
xyz.ado	file to be delivered (for use by net install)
xyz.sthlp	file to be delivered (for use by net install)
sample.dta	file to be delivered (for use by net get)

Chris does nothing to distinguish ancillary files from installation files.

Example 2

S. Gazer wants to create a more complex site:

```
. net from http://www.wemakeitupaswego.edu/faculty/sgazer
------------------------------------------------------------------------------
http://www.wemakeitupaswego.edu/faculty/sgazer
Data-free inference materials
------------------------------------------------------------------------------

S. Gazer, Department of Applied Theoretical Mathematics

Also see my homepage for the preprint of "Irrefutable inference".

PLACES you could -net link- to:
    stata             StataCorp website

DIRECTORIES you could -net cd- to:
    ir               irrefutable inference programs (work in progress)

PACKAGES you could -net describe-:
    rtec             Robust-to-everything-conceivable statistic
    rte              Robust-to-everything statistic
```

```
. net describe rte
------------------------------------------------------------------------------
package rte from http://www.wemakeitupaswego.edu/faculty/sgazer/
------------------------------------------------------------------------------

TITLE
      rte.  The robust-to-everything statistic; update.

DESCRIPTION/AUTHOR(S)
      S. Gazer, Dept. of Applied Theoretical Mathematics, WMIUAWG Univ.
      Aleph-0 100% confidence intervals proved too conservative for some
      applications; Aleph-1 confidence intervals have been substituted.
      The new robust-to-everything supplants the previous robust-to-
      everything-conceivable statistic.  See "Inference in the absence
      of data" (forthcoming).  After installation, see help rte.

      Distribution-Date: 20110420

      Support:  email sgazer@wemakeitupaswego.edu

INSTALLATION FILES                                  (type net install rte_stat)
      rte.ado
      rte.sthlp
      nullset.ado
      random.ado

ANCILLARY FILES                                     (type net get rte_stat)
      empty.dta
------------------------------------------------------------------------------
```

The files needed to do this would be

```
------------------------------------------------------------ begin stata.toc -
v 3
d Data-free inference materials
d S. Gazer, Department of Applied Theoretical Mathematics
d
d Also see my homepage for the preprint of "Irrefutable inference".
l stata http://www.stata.com
t ir irrefutable inference programs (work in progress)
p rtec Robust-to-everything-conceivable statistic
p rte  Robust-to-everything statistic
------------------------------------------------------------ end stata.toc -

------------------------------------------------------------ begin rte.pkg -
v 3
d rte.  The robust-to-everything statistic; update.
d {bf:S. Gazer, Dept. of Applied Theoretical Mathematics, WMIUAWG Univ.}
d Aleph-0 100% confidence intervals proved too conservative for some
d applications; Aleph-1 confidence intervals have been substituted.
d The new robust-to-everything supplants the previous robust-to-
d everything-conceivable statistic.  See "Inference in the absence
d of data" (forthcoming).  After installation, see help {bf:rte}.
d
d Distribution-Date: 20110420
d
d Support:  email sgazer@wemakeitupaswego.edu
f rte.ado
f rte.sthlp
f nullset.ado
f random.ado
f empty.dta
------------------------------------------------------------ end rte.pkg -
```

On his homepage, Mr. Gazer would place the following files:

`stata.toc`	(shown above)
`rte.pkg`	(shown above)
`rte.ado`	(file to be delivered)
`rte.sthlp`	(file to be delivered)
`nullset.ado`	(file to be delivered)
`random.ado`	(file to be delivered)
`empty.dta`	(file to be delivered)
`rtec.pkg`	the other package referred to in `stata.toc`
`rtec.ado`	the corresponding files to be delivered
`rtec.sthlp`	
`ir/stata.toc`	the contents file for when the user types `net cd ir`
`ir/...`	whatever other `.pkg` files are referred to
`ir/...`	whatever other files are to be delivered

If Mr. Gazer later updated the `rte` package, he could change the Distribution-Date description line in his package. Then, if someone who had previously installed the `rte` packaged wanted to obtain the latest version, that person could use the `adoupdate` command; see [R] **adoupdate**.

For complex sites, a different structure may prove more convenient:

`stata.toc`	(shown above)
`rte.pkg`	(shown above)
`rtec.pkg`	the other package referred to in `stata.toc`
`rte/`	directory containing rte files to be delivered:
`rte/rte.ado`	(file to be delivered)
`rte/rte.sthlp`	(file to be delivered)
`rte/nullset.ado`	(file to be delivered)
`rte/random.ado`	(file to be delivered)
`rte/empty.dta`	(file to be delivered)
`rtec/`	directory containing rtec files to be delivered:
`rtec/...`	(files to be delivered)
`ir/stata.toc`	the contents file for when the user types `net cd ir`
`ir/*.pkg`	whatever other package files are referred to
`ir/*/...`	whatever other files are to be delivered

If you prefer this structure, it is simply a matter of changing the bottom of the `rte.pkg` from

```
f rte.ado
f rte.sthlp
f nullset.ado
f random.ado
f empty.dta
```

to

```
f rte/rte.ado
f rte/rte.sthlp
f rte/nullset.ado
f rte/random.ado
f rte/empty.dta
```

In writing paths and files, the directory separator forward slash (`/`) is used, regardless of operating system, because this is what the Internet uses.

It does not matter whether the files you put out are in Windows, Mac, or Unix format (how lines end is recorded differently). When Stata reads the files over the Internet, it will figure out the file format on its own and will automatically translate the files to what is appropriate for the receiver.

Additional package directives

F *filename* is similar to f *filename*, except that, when the file is installed, it will always be copied to the system directories (and not the current directory).

With f *filename*, the file is installed into a directory according to the file's suffix. For instance, xyz.ado would be installed in the system directories, whereas xyz.dta would be installed in the current directory.

Coding F xyz.ado would have the same result as coding f xyz.ado.

Coding F xyz.dta, however, would state that xyz.dta is to be installed in the system directories.

g *platformname filename* is also a variation on f *filename*. It specifies that the file be installed only if the user's operating system is of type *platformname*; otherwise, the file is ignored. The platform names are WIN (32-bit x86) and WIN64A (64-bit x86-64) for Windows; MACINTEL (32-bit Intel, GUI), OSX.X86 (32-bit Intel, console), MACINTEL64 (64-bit Intel, GUI), OSX.X8664 (64-bit Intel, console), MAC (32-bit PowerPC), and OSX.PPC (32-bit PowerPC), for Mac; and LINUX (32-bit x86), LINUX64 (64-bit x86-64), SOL64, and SOLX8664 (64-bit x86-64) for Unix.

G *platformname filename* is a variation on F *filename*. The file, if not ignored, is to be installed in the system directories.

g *platformname filename1 filename2* is a more detailed version of g *platformname filename*. In this case, *filename1* is the name of the file on the server (the file to be copied), and *filename2* is to be the name of the file on the user's system; for example, you might code

```
g WIN mydll.forwin mydll.plugin
g LINUX mydll.forlinux mydll.plugin
```

When you specify one *filename*, the result is the same as specifying two identical *filename*s.

G *platformname filename1 filename2* is the install-in-system-directories version of g *platformname filename1 filename2*.

h *filename* asserts that *filename* must be loaded, or this package is not to be installed; for example, you might code

```
g WIN mydll.forwin mydll.plugin
g LINUX mydll.forlinux mydll.plugin
h mydll.plugin
```

if you were offering the plugin mydll.plugin for Windows and Linux only.

SMCL in content and package-description files

The text listed on the second and subsequent d lines in both stata.toc and *pkgname*.pkg may contain SMCL as long as you include v 3; see [P] **smcl**.

Thus, in rte.pkg, S. Gazer coded the third line as

```
d {bf:S. Gazer, Dept. of Applied Theoretical Mathematics, WMIUAWG Univ.}
```

Error-free file delivery

Most people transport files over the Internet and never worry about the file being corrupted in the process because corruption rarely occurs. If, however, the files must be delivered perfectly or not at all, you can include checksum files in the directory.

For instance, say that `big.dta` is included in your package and that it must be sent perfectly. First, use Stata to make the checksum file for `big.dta`

```
. checksum big.dta, save
```

That command creates a small file called `big.sum`; see [D] **checksum**. Then copy both `big.dta` and `big.sum` to your homepage. If `set checksum` is `on` (the default is `off`), whenever Stata reads *filename*`.`*whatever* over the net, it also looks for *filename*`.sum`. If it finds such a file, it uses the information recorded in it to verify that what was copied was error free.

If you do this, be cautious. If you put `big.dta` and `big.sum` on your homepage and then later change `big.dta` without changing `big.sum`, people will think that there are transmission errors when they try to download `big.dta`.

References

Baum, C. F., and N. J. Cox. 1999. ip29: Metadata for user-written contributions to the Stata programming language. *Stata Technical Bulletin* 52: 10–12. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 121–124. College Station, TX: Stata Press.

Cox, N. J., and C. F. Baum. 2000. ip29.1: Metadata for user-written contributions to the Stata programming language. *Stata Technical Bulletin* 54: 21–22. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 124–126. College Station, TX: Stata Press.

Also see

[R] **adoupdate** — Update user-written ado-files

[R] **net search** — Search the Internet for installable packages

[R] **search** — Search Stata documentation

[R] **sj** — Stata Journal and STB installation instructions

[R] **ssc** — Install and uninstall packages from SSC

[D] **checksum** — Calculate checksum of file

[P] **smcl** — Stata Markup and Control Language

[R] **update** — Update Stata

[GSM] **19 Updating and extending Stata—Internet functionality**

[GSU] **19 Updating and extending Stata—Internet functionality**

[GSW] **19 Updating and extending Stata—Internet functionality**

[U] **28 Using the Internet to keep up to date**

Title

net search — Search the Internet for installable packages

Syntax

`net search` *word* [*word* ...] [, *options*]

options	Description
`or`	list packages that contain any of the keywords; default is all
`nosj`	search non-SJ and non-STB sources
`tocpkg`	search both tables of contents and packages; the default
`toc`	search tables of contents only
`pkg`	search packages only
`everywhere`	search packages for match
`filenames`	search filenames associated with package for match
`errnone`	make return code 111 instead of 0 when no matches found

Description

`net search` searches the Internet for user-written additions to Stata, including, but not limited to, user-written additions published in the *Stata Journal* (SJ) and in the *Stata Technical Bulletin* (STB). `net search` lists the available additions that contain the specified keywords.

The user-written materials found are available for immediate download by using the `net` command or by clicking on the link.

In addition to typing `net search`, you may select **Help > Search...** and choose **Search net resources**. This is the recommended way to search for user-written additions to Stata.

Options

`or` is relevant only when multiple keywords are specified. By default, `net search` lists only packages that include all the keywords. `or` changes the command to list packages that contain any of the keywords.

`nosj` specifies that `net search` not list matches that were published in the SJ or in the STB.

`tocpkg`, `toc`, and `pkg` determine what is searched. `tocpkg` is the default, meaning that both tables of contents (tocs) and packages (pkgs) are searched. `toc` restricts the search to tables of contents. `pkg` restricts the search to packages.

`everywhere` and `filenames` determine where in packages `net search` looks for *keywords*. The default is `everywhere`. `filenames` restricts `net search` to search for matches only in the filenames associated with a package. Specifying `everywhere` implies `pkg`.

`errnone` is a programmer's option that causes the return code to be 111 instead of 0 when no matches are found.

Remarks

`net search` searches the Internet for user-written additions to Stata. If you want to search the Stata documentation for a particular topic, command, or author, see [R] **search**. `net search` *word* [*word* ...] (without options) is equivalent to typing `search` *word* [*word* ...]`, net`.

Remarks are presented under the following headings:

Topic searches
Author searches
Command searches
Where does net search look?
How does net search work?

Topic searches

Example: Find what is available about random effects

```
. net search random effect
```

Comments:

- It is best to search using the singular form of a word. `net search random effect` will find both "random effect" and "random effects".
- `net search random effect` will also find "random-effect" because `net search` performs a string search and not a word search.
- `net search random effect` lists all packages containing the words "random" and "effect", not necessarily used together.
- If you wanted all packages containing the word "random" or the word "effect", you would type `net search random effect, or`.

Author searches

Example: Find what is available by author Jeroen Weesie

```
. net search weesie
```

Comments:

- You could type `net search jeroen weesie`, but that might list fewer results because sometimes the last name is used without the first.
- You could type `net search Weesie`, but it would not matter. Capitalization is ignored in the search.

Example: Find what is available by Jeroen Weesie, excluding SJ and STB materials

```
. net search weesie, nosj
```

- The SJ and the STB tend to dominate search results because so much has been published in them. If you know that what you are looking for is not in the SJ or in the STB, specifying the `nosj` option will narrow the search.
- `net search weesie` lists everything that `net search weesie, nosj` lists, and more. If you just type `net search weesie`, look down the list. SJ and STB materials are listed first, and non-SJ and non-STB materials are listed last.

Command searches

Example: Find the user-written command kursus

```
. net search kursus, file
```

- You could just type `net search kursus`, and that will list everything `net search kursus, file` lists, and more. Because you know `kursus` is a command, however, there must be a `kursus.ado` file associated with the package. Typing `net search kursus, file` narrows the search.
- You could also type `net search kursus.ado, file` to narrow the search even more.

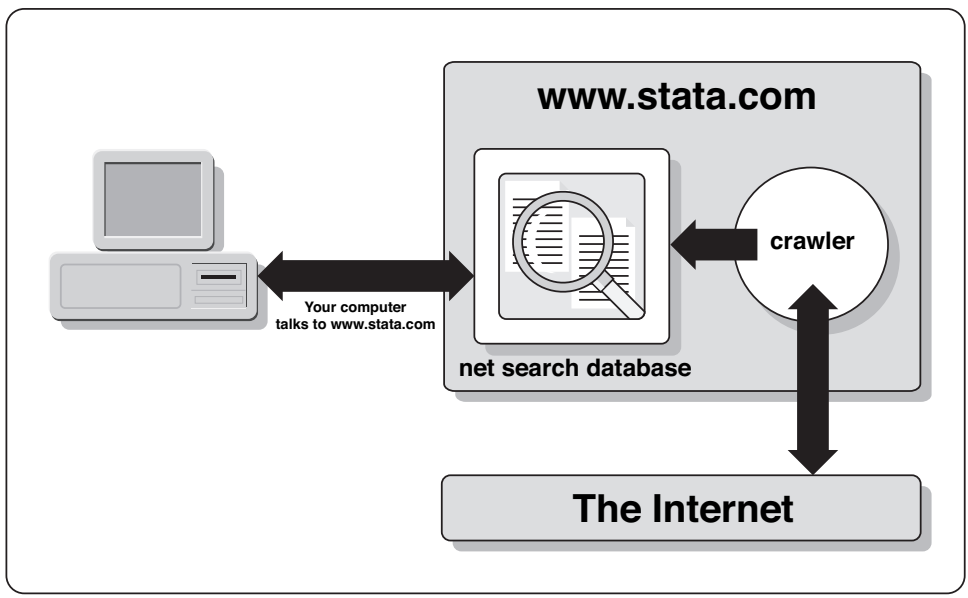
Where does net search look?

`net search` looks everywhere, not just at http://www.stata.com.

`net search` begins by looking at http://www.stata.com, but then follows every link, which takes it to other places, and then follows every link again, which takes it to even more places, and so on.

Authors: Please let us know if you have a site that we should include in our search by sending an email to webmaster@stata.com. We will then link to your site from ours to ensure that `net search` finds your materials. That is not strictly necessary, however, as long as your site is directly or indirectly linked from some site that is linked to ours.

How does net search work?



Our website maintains a database of Stata resources. When you use `net search`, it contacts http://www.stata.com with your request, http://www.stata.com searches its database, and Stata returns the results to you.

Another part of the system is called the crawler, which searches the web for new Stata resources to add to the `net search` database and verifies that the resources already found are still available. When a new resource becomes available, the crawler takes about 2 days to add it to the database, and, similarly, if a resource disappears, the crawler takes roughly 2 days to remove it from the database.

References

Baum, C. F., and N. J. Cox. 1999. ip29: Metadata for user-written contributions to the Stata programming language. *Stata Technical Bulletin* 52: 10–12. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 121–124. College Station, TX: Stata Press.

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Gould, W. W., and A. R. Riley. 2000. stata55: Search web for installable packages. *Stata Technical Bulletin* 54: 4–6. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 10–13. College Station, TX: Stata Press.

Also see

[R] **net** — Install and manage user-written additions from the Internet

[R] **ssc** — Install and uninstall packages from SSC

[R] **sj** — Stata Journal and STB installation instructions

[R] **hsearch** — Search help files

[R] **search** — Search Stata documentation

[R] **adoupdate** — Update user-written ado-files

[R] **update** — Update Stata

Title

netio — Control Internet connections

Syntax

Turn on or off the use of a proxy server

```
set httpproxy {on | off} [, init]
```

Set proxy host name

```
set httpproxyhost ["]name["]
```

Set the proxy port number

```
set httpproxyport #
```

Turn on or off proxy authorization

```
set httpproxyauth {on | off}
```

Set proxy authorization user ID

```
set httpproxyuser ["]name["]
```

Set proxy authorization password

```
set httpproxypw ["]password["]
```

Set time limit for establishing initial connection

```
set timeout1 #seconds [, permanently]
```

Set time limit for data transfer

```
set timeout2 #seconds [, permanently]
```

Description

Several commands (for example, `net`, `news`, and `update`) are designed specifically for use over the Internet. Many other Stata commands that read a file (for example, `copy`, `type`, and `use`) can also read directly from a URL. All these commands will usually work without your ever needing to concern yourself with the `set` commands discussed here. These `set` commands provide control over network system parameters.

If you experience problems when using Stata's network features, ask your system administrator if your site uses a proxy. A proxy is a server between your computer and the rest of the Internet, and your computer may need to communicate with other computers on the Internet through this proxy. If your site uses a proxy, your system administrator can provide you with its host name and the port your computer can use to communicate with it. If your site's proxy requires you to log in to it before it will respond, your system administrator will provide you with a user ID and password.

`set httpproxyhost` sets the name of the host to be used as a proxy server. `set httpproxyport` sets the port number. `set httpproxy` turns on or off the use of a proxy server, leaving the proxy host name and port intact, even when not in use.

Under the Mac and Windows operating systems, when you `set httpproxy on`, Stata will attempt to obtain the values of `httpproxyhost` and `httpproxyport` from the operating system if they have not been previously set. `set httpproxy on, init` attempts to obtain these values from the operating system, even if they have been previously set.

If the proxy requires authorization (user ID and password), set authorization on via `set httpproxyauth on`. The proxy user and proxy password must also be set to the appropriate user ID and password by using `set httpproxyuser` and `set httpproxypw`.

Stata remembers the various proxy settings between sessions and does not need a `permanently` option.

`set timeout1` changes the time limit in seconds that Stata imposes for establishing the initial connection with a remote host. The default value is 30. `set timeout2` changes the time limit in seconds that Stata imposes for subsequent data transfer with the host. The default value is 180. If these time limits are exceeded, a "connection timed out" message and error code 2 are produced. You should seldom need to change these settings.

Options

`init` specifies that `set httpproxy on` attempts to initialize `httpproxyhost` and `httpproxyport` from the operating system (Mac and Windows only).

`permanently` specifies that, in addition to making the change right now, the `timeout1` and `timeout2` settings be remembered and become the default setting when you invoke Stata.

The various `httpproxy` settings do not have a `permanently` option because `permanently` is implied.

Remarks

If you receive an error message, see http://www.stata.com/support/faqs/web/ for the latest information.

1. remote connection failed r(677);

If you see

```
remote connection failed
r(677);
```

then you asked for something to be done over the web, and Stata tried but could not contact the specified host. Stata was able to talk over the network and look up the host but was not able to establish a connection to that host. Perhaps the host is down; try again later.

If all your web accesses result in this message, then perhaps your network connection is through a proxy server. If it is, then you must tell Stata.

Contact your system administrator. Ask for the name and port of the "HTTP proxy server". Say that you are told

> HTTP proxy server: jupiter.myuni.edu
> port number: 8080

In Stata, type

```
. set httpproxyhost jupiter.myuni.edu
. set httpproxyport 8080
. set httpproxy on
```

Your web accesses should then work.

2. connection timed out r(2);

If you see

```
connection timed out
r(2);
```

then an Internet connection has timed out. This can happen when

a. the connection between you and the host is slow, or

b. the connection between you and the host has disappeared, and so it eventually "timed out".

For (b), wait a while (say, 5 minutes) and try again (sometimes pieces of the Internet can break for up to a day, but that is rare). For (a), you can reset the limits for what constitutes "timed out". There are two numbers to set.

The time to establish the initial connection is **timeout1**. By default, Stata waits 30 seconds before declaring a timeout. You can change the limit:

```
. set timeout1 #seconds
```

You might try doubling the usual limit and specify 60; *#seconds* must be between 1 and 32,000.

The time to retrieve data from an open connection is **timeout2**. By default, Stata waits 180 seconds (3 minutes) before declaring a timeout. To change the limit, type

```
. set timeout2 #seconds
```

You might try doubling the usual limit and specify 360; *#seconds* must be between 1 and 32,000.

Also see

[R] **query** — Display system parameters

[P] **creturn** — Return c-class values

[U] **28 Using the Internet to keep up to date**

Title

news — Report Stata news

Syntax

```
news
```

Menu

Help > News

Description

`news` displays a brief listing of recent Stata news and information, which it obtains from Stata's website. `news` requires that your computer be connected to the Internet.

You may also execute `news` by selecting **Help > News**.

Remarks

`news` provides an easy way of displaying a brief list of the latest Stata news:

```
. news

  ___  ____  ____  ____  ____
 /__    /   ____/   /   ____/
___/   /   /___/   /   /___/  News         The latest from http://www.stata.com
_____________________________________________________________________________

8 October 2011.  Official update available for download

    Click here (equivalent to pulling down Help and selecting
    Check for Updates) or type update from http://www.stata.com.

27 July 2011.  Stata 12 available

    Stata 12 -- structural equation models (SEM) -- multiple imputation
    using chained equations -- contrasts and pairwise comparisons --
    autoregressive fractionally integrated moving-average (ARFIMA) models --
    multivariate GARCH -- unobserved-components models -- time-series filters --
    receiver operating characteristic (ROC) regression -- contour plots --
    import Excel -- PDF export -- is now available.
    Visit http://www.stata.com/stata12/ for more information.

21 March 2011.  NetCourse schedule updated

    See http://www.stata.com/netcourse/ for more information.

    (output omitted)

<end>
```

Also see

[U] **28 Using the Internet to keep up to date**

Title

nl — Nonlinear least-squares estimation

Syntax

Interactive version

```
nl (depvar = <sexp>) [if] [in] [weight] [, options]
```

Programmed substitutable expression version

```
nl sexp_prog : depvar [varlist] [if] [in] [weight] [, options]
```

Function evaluator program version

```
nl func_prog @ depvar [varlist] [if] [in] [weight] ,
    { parameters(namelist) | nparameters(#) } [options]
```

where

depvar is the dependent variable;

<sexp> is a substitutable expression;

sexp_prog is a substitutable expression program; and

func_prog is a function evaluator program.

options	Description
Model	
`variables(`*varlist*`)`	variables in model
`initial(`*initial_values*`)`	initial values for parameters
* `parameters(`*namelist*`)`	parameters in model (function evaluator program version only)
* `nparameters(#)`	number of parameters in model (function evaluator program version only)
sexp_options	options for substitutable expression program
func_options	options for function evaluator program
Model 2	
`lnlsq(#)`	use log least-squares where $\ln(depvar - \#)$ is assumed to be normally distributed
`noconstant`	the model has no constant term; seldom used
`hasconstant(`*name*`)`	use *name* as constant term; seldom used
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `gnr`, `robust`, `cluster` *clustvar*, `bootstrap`, `jacknife`, `hac` *kernel*, `hc2`, or `hc3`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`leave`	create variables containing derivative of $E(y)$
`title(`*string*`)`	display *string* as title above the table of parameter estimates
`title2(`*string*`)`	display *string* as subtitle
display_options	control column formats and line width
Optimization	
optimization_options	control the optimization process; seldom used
`eps(#)`	specify # for convergence criterion; default is `eps(1e-5)`
`delta(#)`	specify # for computing derivatives; default is `delta(4e-7)`
`coeflegend`	display legend instead of statistics

* For function evaluator program version, you must specify `parameters(`*namelist*`)` or `nparameters(#)`, or both.
`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.
`vce()`, `leave`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`aweights`, `fweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Nonlinear least squares

Description

nl fits an arbitrary nonlinear regression function by least squares. With the interactive version of the command, you enter the function directly on the command line or in the dialog box by using a *substitutable expression*. If you have a function that you use regularly, you can write a *substitutable expression program* and use the second syntax to avoid having to reenter the function every time. The function evaluator program version gives you the most flexibility in exchange for increased complexity; with this version, your program is given a vector of parameters and a variable list, and your program computes the regression function.

When you write a substitutable expression program or function evaluator program, the first two letters of the name must be nl. *sexp_prog* and *func_prog* refer to the name of the program without the first two letters. For example, if you wrote a function evaluator program named nlregss, you would type nl regss @ ... to estimate the parameters.

Options

Model

variables(*varlist*) specifies the variables in the model. nl ignores observations for which any of these variables have missing values. If you do not specify variables(), then nl issues an error message with return code 480 if the estimation sample contains any missing values.

initial(*initial_values*) specifies the initial values to begin the estimation. You can specify a $1 \times k$ matrix, where k is the number of parameters in the model, or you can specify a parameter name, its initial value, another parameter name, its initial value, and so on. For example, to initialize alpha to 1.23 and delta to 4.57, you would type

```
nl ... , initial(alpha 1.23 delta 4.57) ...
```

Initial values declared using this option override any that are declared within substitutable expressions. If you specify a parameter that does not appear in your model, nl exits with error code 480. If you specify a matrix, the values must be in the same order that the parameters are declared in your model. nl ignores the row and column names of the matrix.

parameters(*namelist*) specifies the names of the parameters in the model. The names of the parameters must adhere to the naming conventions of Stata's variables; see [U] **11.3 Naming conventions**. If you specify both parameters() and nparameters(), the number of names in the former must match the number specified in the latter; if not, nl issues an error message with return code 198.

nparameters(#) specifies the number of parameters in the model. If you do not specify names with the parameters() option, nl names them b1, b2, ..., b#. If you specify both parameters() and nparameters(), the number of names in the former must match the number specified in the latter; if not, nl issues an error message with return code 198.

sexp_options refer to any options allowed by your *sexp_prog*.

func_options refer to any options allowed by your *func_prog*.

Model 2

lnlsq(#) fits the model by using log least-squares, which we define as least squares with shifted lognormal errors. In other words, $\ln(depvar - \#)$ is assumed to be normally distributed. Sums of squares and deviance are adjusted to the same scale as *depvar*.

`noconstant` indicates that the function does not include a constant term. This option is generally not needed, even if there is no constant term in the model, unless the coefficient of variation (over observations) of the partial derivative of the function with respect to a parameter is less than `eps()` and that parameter is not a constant term.

`hasconstant(`*name*`)` indicates that parameter *name* be treated as the constant term in the model and that `nl` should not use its default algorithm to find a constant term. As with `noconstant`, this option is seldom used.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(gnr)`, the default, uses the conventionally derived variance estimator for nonlinear models fit using Gauss–Newton regression.

`nl` also allows the following:

`vce(hac` *kernel* `[`*#*`])` specifies that a heteroskedasticity- and autocorrelation-consistent (HAC) variance estimate be used. HAC refers to the general form for combining weighted matrices to form the variance estimate. There are three kernels available for `nl`:

`nwest` | `gallant` | `anderson`

specifies the number of lags. If *#* is not specified, $N-2$ is assumed.

`vce(hac` *kernel* `[`*#*`])` is not allowed if weights are specified.

`vce(hc2)` and `vce(hc3)` specify alternative bias corrections for the robust variance calculation. `vce(hc2)` and `vce(hc3)` may not be specified with the `svy` prefix. By default, `vce(robust)` uses $\widehat{\sigma}_j^2 = \{n/(n-k)\}u_j^2$ as an estimate of the variance of the jth observation, where u_j is the calculated residual and $n/(n-k)$ is included to improve the overall estimate's small-sample properties.

`vce(hc2)` instead uses $u_j^2/(1-h_{jj})$ as the observation's variance estimate, where h_{jj} is the jth diagonal element of the hat (projection) matrix. This produces an unbiased estimate of the covariance matrix if the model is homoskedastic. `vce(hc2)` tends to produce slightly more conservative confidence intervals than `vce(robust)`.

`vce(hc3)` uses $u_j^2/(1-h_{jj})^2$ as suggested by Davidson and MacKinnon (1993 and 2004), who report that this often produces better results when the model is heteroskedastic. `vce(hc3)` produces confidence intervals that tend to be even more conservative.

See, in particular, Davidson and MacKinnon (2004, 239), who advocate the use of `vce(hc2)` or `vce(hc3)` instead of the plain robust estimator for nonlinear least squares.

Reporting

`level(#)`; see [R] **estimation options**.

`leave` leaves behind after estimation a set of new variables with the same names as the estimated parameters containing the derivatives of $E(y)$ with respect to the parameters. If the dataset contains an existing variable with the same name as a parameter, then using `leave` causes `nl` to issue an error message with return code 110.

`leave` may not be specified with `vce(cluster` *clustvar*`)` or the `svy` prefix.

`title(`*string*`)` specifies an optional title that will be displayed just above the table of parameter estimates.

`title2(`*string*`)` specifies an optional subtitle that will be displayed between the title specified in `title()` and the table of parameter estimates. If `title2()` is specified but `title()` is not, `title2()` has the same effect as `title()`.

display_options: `cformat(`%*fmt*`)`, `pformat(`%*fmt*`)`, `sformat(`%*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Optimization

optimization_options: `iterate(#)`, [`no`]`log`, `trace`. `iterate()` specifies the maximum number of iterations, `log`/`nolog` specifies whether to show the iteration log, and `trace` specifies that the iteration log should include the current parameter vector. These options are seldom used.

`eps(#)` specifies the convergence criterion for successive parameter estimates and for the residual sum of squares. The default is `eps(1e-5)`.

`delta(#)` specifies the relative change in a parameter to be used in computing the numeric derivatives. The derivative for parameter β_i is computed as $\{f(X,\beta_1,\beta_2,\ldots,\beta_i+d,\beta_{i+1},\ldots) - f(X,\beta_1,\beta_2,\ldots,\beta_i,\beta_{i+1},\ldots)\}/d$, where d is $\delta(\beta_i+\delta)$. The default is `delta(4e-7)`.

The following options are available with `nl` but are not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Substitutable expressions
Substitutable expression programs
Built-in functions
Lognormal errors
Other uses
Weights
Potential errors
General comments on fitting nonlinear models
Function evaluator programs

`nl` fits an arbitrary nonlinear function by least squares. The interactive version allows you to enter the function directly on the command line or dialog box using *substitutable expressions*. You can write a *substitutable expression program* for functions that you fit frequently to save yourself time. Finally, *function evaluator programs* give you the most flexibility in defining your nonlinear function, though they are more complicated to use.

The next section explains the substitutable expressions that are used to define the regression function, and the section thereafter explains how to write substitutable expression program files so that you do not need to type in commonly used functions over and over. Later sections highlight other features of `nl`.

The final section discusses function evaluator programs. If you find substitutable expressions adequate to define your nonlinear function, then you can skip that section entirely. Function evaluator programs are generally needed only for complicated problems, such as multistep estimators. The program receives a vector of parameters at which it is to compute the function and a variable into which the results are to be placed.

Substitutable expressions

You define the nonlinear function to be fit by `nl` by using a substitutable expression. Substitutable expressions are just like any other mathematical expressions involving scalars and variables, such as those you would use with Stata's `generate` command, except that the parameters to be estimated are bound in braces. See [U] **13.2 Operators** and [U] **13.3 Functions** for more information on expressions.

For example, suppose that you wish to fit the function

$$y_i = \beta_0(1 - e^{-\beta_1 x_i}) + \epsilon_i$$

where β_0 and β_1 are the parameters to be estimated and ϵ_i is an error term. You would simply type

```
. nl (y = {b0}*(1 - exp(-1*{b1}*x)))
```

You must enclose the entire equation in parentheses. Because `b0` and `b1` are enclosed in braces, `nl` knows that they are parameters in the model. `nl` will initialize `b0` and `b1` to zero by default. To request that `nl` initialize `b0` to 1 and `b1` to 0.25, you would type

```
. nl (y = {b0=1}*(1 - exp(-1*{b1=0.25}*x)))
```

That is, inside the braces denoting a parameter, you put the parameter name followed by an equal sign and the initial value. If a parameter appears in your function multiple times, you need only specify an initial value only once (or never, if you wish to set the initial value to zero). If you do specify more than one initial value for the same parameter, `nl` will use the *last* value given. Parameter names must follow the same conventions as variable names. See [U] **11.3 Naming conventions**.

Frequently, even nonlinear functions contain linear combinations of variables. As an example, suppose that you wish to fit the function

$$y_i = \beta_0 \left\{1 - e^{-(\beta_1 x_{1i} + \beta_2 x_{2i} + \beta_3 x_{3i})}\right\} + \epsilon_i$$

`nl` allows you to declare a linear combination of variables by using the shorthand notation

```
. nl (y = {b0=1}*(1 - exp(-1*{xb: x1 x2 x3})))
```

In the syntax `{xb: x1 x2 x3}`, you are telling `nl` that you are declaring a linear combination named `xb` that is a function of three variables, `x1`, `x2`, and `x3`. `nl` will create three parameters, named `xb_x1`, `xb_x2`, and `xb_x3`, and initialize them to zero. Instead of typing the previous command, you could have typed

```
. nl (y = {b0=1}*(1 - exp(-1*({xb_x1}*x1 + {xb_x2}*x2 + {xb_x3}*x3))))
```

and yielded the same result. You can refer to the parameters created by `nl` in the linear combination later in the function, though you must declare the linear combination first if you intend to do that. When creating linear combinations, `nl` ensures that the parameter names it chooses are unique and have not yet been used in the function.

In general, there are three rules to follow when defining substitutable expressions:

1. Parameters of the model are bound in braces: `{b0}`, `{param}`, etc.
2. Initial values for parameters are given by including an equal sign and the initial value inside the braces: `{b0=1}`, `{param=3.571}`, etc.
3. Linear combinations of variables can be included using the notation {*eqname*`:`*varlist*}, for example, `{xb: mpg price weight}`, `{score: w x z}`, etc. Parameters of linear combinations are initialized to zero.

If you specify initial values by using the `initial()` option, they override whatever initial values are given within the substitutable expression. Substitutable expressions are so named because, once values are assigned to the parameters, the resulting expression can be handled by `generate` and `replace`.

▷ Example 1

We wish to fit the CES production function

$$\ln Q_i = \beta_0 - \frac{1}{\rho}\ln\left\{\delta K_i^{-\rho} + (1-\delta)L_i^{-\rho}\right\} + \epsilon_i \tag{1}$$

where $\ln Q_i$ is the log of output for firm i; K_i and L_i are firm i's capital and labor usage, respectively; and ϵ_i is a regression error term. Because ρ appears in the denominator of a fraction, zero is not a feasible initial value; for a CES production function, $\rho = 1$ is a reasonable choice. Setting $\delta = 0.5$ implies that labor and capital have equal impacts on output, which is also a reasonable choice for an initial value. We type

```
. use http://www.stata-press.com/data/r12/production
. nl (lnoutput = {b0} - 1/{rho=1}*ln({delta=0.5}*capital^(-1*{rho}) +
> (1 - {delta})*labor^(-1*{rho})))
(obs = 100)
Iteration 0:  residual SS =  29.38631
Iteration 1:  residual SS =  29.36637
Iteration 2:  residual SS =  29.36583
Iteration 3:  residual SS =  29.36581
Iteration 4:  residual SS =  29.36581
Iteration 5:  residual SS =  29.36581
Iteration 6:  residual SS =  29.36581
Iteration 7:  residual SS =  29.36581
```

Source	SS	df	MS		
Model	91.1449924	2	45.5724962	Number of obs	100
Residual	29.3658055	97	.302740263	R-squared	0.7563
				Adj R-squared	0.7513
Total	120.510798	99	1.21728079	Root MSE	.5502184
				Res. dev.	161.2538

lnoutput	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
/b0	3.792158	.099682	38.04	0.000	3.594316	3.989999
/rho	1.386993	.472584	2.93	0.004	.4490443	2.324941
/delta	.4823616	.0519791	9.28	0.000	.3791975	.5855258

```
  Parameter b0 taken as constant term in model & ANOVA table
```

`nl` will attempt to find a constant term in the model and, if one is found, mention it at the bottom of the output. `nl` found `b0` to be a constant because the partial derivative $\partial \ln Q_i/\partial$`b0` has a coefficient of variation less than `eps()` in the estimation sample.

The elasticity of substitution for the CES production function is $\sigma = 1/(1+\rho)$; and, having fit the model, we can use `nlcom` to estimate it:

```
. nlcom (1/(1 + _b[/rho]))
       _nl_1:  1/(1 + _b[/rho])
```

lnoutput	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
_nl_1	.4189372	.0829424	5.05	0.000	.2543194	.583555

See [R] **nlcom** and [U] **13.5 Accessing coefficients and standard errors** for more information.

◁

`nl`'s output closely mimics that of `regress`; see [R] **regress** for more information. The R^2, sums of squares, and similar statistics are calculated in the same way that `regress` calculates them. If no "constant" term is specified, the usual caveats apply to the interpretation of the R^2 statistic; see the comments and references in Goldstein (1992). Unlike `regress`, `nl` does not report a model F statistic, because a test of the joint significance of all the parameters except the constant term may not be relevant in a nonlinear model.

Substitutable expression programs

If you fit the same model often or if you want to write an estimator that will operate on whatever variables you specify, then you will want to write a substitutable expression program. That program will return a macro containing a substitutable expression that `nl` can then evaluate, and it may optionally calculate initial values as well. The name of the program must begin with the letters `nl`.

To illustrate, suppose that you use the CES production function often in your work. Instead of typing in the formula each time, you can write a program like this:

```
program nlces, rclass
        version 12
        syntax varlist(min=3 max=3) [if]
        local logout : word 1 of `varlist'
        local capital : word 2 of `varlist'
        local labor : word 3 of `varlist'
        // Initial value for b0 given delta=0.5 and rho=1
        tempvar y
        generate double `y' = `logout' + ln(0.5*`capital'^-1 + 0.5*`labor'^-1)
        summarize `y' `if', meanonly
        local b0val = r(mean)
        // Terms for substitutable expression
        local capterm "{delta=0.5}*`capital'^(-1*{rho})"
        local labterm "(1-{delta})*`labor'^(-1*{rho})"
        local term2   "1/{rho=1}*ln(`capterm' + `labterm')"
        // Return substitutable expression and title
        return local eq "`logout' = {b0=`b0val'} - `term2'"
        return local title "CES ftn., ln Q=`logout', K=`capital', L=`labor'"
end
```

The program accepts three variables for log output, capital, and labor, and it accepts an `if` *exp* qualifier to restrict the estimation sample. All programs that you write to use with `nl` must accept an `if` *exp* qualifier because, when `nl` calls the program, it passes a binary variable that marks the estimation sample (the variable equals one if the observation is in the sample and zero otherwise). When calculating initial values, you will want to restrict your computations to the estimation sample, and you can do so by using `if` with any commands that accept `if` *exp* qualifiers. Even if your program does not calculate initial values or otherwise use the `if` qualifier, the `syntax` statement must still allow it. See [P] **syntax** for more information on the `syntax` command and the use of `if`.

As in the previous example, reasonable initial values for δ and ρ are 0.5 and 1, respectively. Conditional on those values, (1) can be rewritten as

$$\beta_0 = \ln Q_i + \ln(0.5K_i^{-1} + 0.5L_i^{-1}) - \epsilon_i \tag{2}$$

so a good initial value for β_0 is the mean of the right-hand side of (2) ignoring ϵ_i. Lines 7–10 of the function evaluator program calculate that mean and store it in a local macro. Notice the use of `if` in the `summarize` statement so that the mean is calculated only for the estimation sample.

The final part of the program returns two macros. The macro `title` is optional and defines a short description of the model that will be displayed in the output immediately above the table of parameter estimates. The macro `eq` is required and defines the substitutable expression that `nl` will use. If the expression is short, you can define it all at once. However, because the expression used here is somewhat lengthy, defining local macros and then building up the final expression from them is easier.

To verify that there are no errors in your program, you can call it directly and then use `return list`:

```
. use http://www.stata-press.com/data/r12/production
. nlces lnoutput capital labor
  (output omitted)
. return list
macros:
             r(title) : "CES ftn., ln Q=lnoutput, K=capital, L=labor"
                r(eq) : "lnoutput = {b0=3.711606264663641} - 1/{rho=1}*ln({delt
> a=0.5}*capital^(-1*{rho}) + (1-{delta})*labor^(-1*{rho}))"
```

The macro `r(eq)` contains the same substitutable expression that we specified at the command line in the preceding example, except for the initial value for `b0`. In short, an `nl` substitutable expression program should return in `r(eq)` the same substitutable expression you would type at the command line. The only difference is that when writing a substitutable expression program, you do not bind the entire expression inside parentheses.

Having written the program, you can use it by typing

```
. nl ces: lnoutput capital labor
```

(There is a space between `nl` and `ces`.) The output is identical to that shown in example 1, save for the title defined in the function evaluator program that appears immediately above the table of parameter estimates.

❑ Technical note

You will want to store `nlces` as an ado-file called `nlces.ado`. The alternative is to type the code into Stata interactively or to place the code in a do-file. While those alternatives are adequate for occasional use, if you save the program as an ado-file, you can use the function anytime you use Stata without having to redefine the program. When `nl` attempts to execute `nlces`, if the program is not in Stata's memory, Stata will search the disk(s) for an ado-file of the same name and, if found, automatically load it. All you have to do is name the file with the `.ado` suffix and then place it in a directory where Stata will find it. You should put the file in the directory Stata reserves for user-written ado-files, which, depending on your operating system, is `c:\ado\personal` (Windows), `~/ado/personal` (Unix), or `~:ado:personal` (Mac). See [U] **17 Ado-files**. ❑

Sometimes you may want to pass additional options to the substitutable expression program. You can modify the `syntax` statement of your program to accept whatever options you wish. Then when you call `nl` with the syntax

```
. nl func_prog: varlist, options
```

any *options* that are not recognized by `nl` (see the table of options at the beginning of this entry) are passed on to your function evaluator program. The only other restriction is that your program cannot accept an option named `at` because `nl` uses that option with function evaluator programs.

Built-in functions

Some functions are used so often that `nl` has them built in so that you do not need to write them yourself. `nl` automatically chooses initial values for the parameters, though you can use the `initial(...)` option to override them.

Three alternatives are provided for exponential regression with one asymptote:

`exp3`	$y_i = \beta_0 + \beta_1 \beta_2^{x_i} + \epsilon_i$
`exp2`	$y_i = \beta_1 \beta_2^{x_i} + \epsilon_i$
`exp2a`	$y_i = \beta_1 \left(1 - \beta_2^{x_i}\right) + \epsilon_i$

For instance, typing `nl exp3: ras dvl` fits the three-parameter exponential model (parameters β_0, β_1, and β_2) using $y_i =$ `ras` and $x_i =$ `dvl`.

Two alternatives are provided for the logistic function (symmetric sigmoid shape; not to be confused with logistic regression):

`log4`	$y_i = \beta_0 + \beta_1 \Big/ \Big[1 + \exp\big\{-\beta_2(x_i - \beta_3)\big\}\Big] + \epsilon_i$
`log3`	$y_i = \beta_1 \Big/ \Big[1 + \exp\big\{-\beta_2(x_i - \beta_3)\big\}\Big] + \epsilon_i$

Finally, two alternatives are provided for the Gompertz function (asymmetric sigmoid shape):

`gom4`	$y_i = \beta_0 + \beta_1 \exp\Big[-\exp\big\{-\beta_2(x_i - \beta_3)\big\}\Big] + \epsilon_i$
`gom3`	$y_i = \beta_1 \exp\Big[-\exp\big\{-\beta_2(x_i - \beta_3)\big\}\Big] + \epsilon_i$

Lognormal errors

A nonlinear model with errors that are independent and identically distributed normal may be written

$$y_i = f(\mathbf{x}_i, \boldsymbol{\beta}) + u_i, \qquad u_i \sim N(0, \sigma^2) \tag{3}$$

for $i = 1, \ldots, n$. If the y_i are thought to have a k-shifted lognormal instead of a normal distribution—that is, $\ln(y_i - k) \sim N(\zeta_i, \tau^2)$, and the systematic part $f(\mathbf{x}_i, \boldsymbol{\beta})$ of the original model is still thought appropriate for y_i—the model becomes

$$\ln(y_i - k) = \zeta_i + v_i = \ln\big\{f(\mathbf{x}_i, \boldsymbol{\beta}) - k\big\} + v_i, \quad v_i \sim N(0, \tau^2) \tag{4}$$

This model is fit if `lnlsq(`k`)` is specified.

If model (4) is correct, the variance of $(y_i - k)$ is proportional to $\big\{f(\mathbf{x}_i, \boldsymbol{\beta}) - k\big\}^2$. Probably the most common case is $k = 0$, sometimes called "proportional errors" because the standard error of y_i is proportional to its expectation, $f(\mathbf{x}_i, \boldsymbol{\beta})$. Assuming that the value of k is known, (4) is just another nonlinear model in $\boldsymbol{\beta}$, and it may be fit as usual. However, we may wish to compare the fit of (3) with that of (4) using the residual sum of squares (RSS) or the deviance D, $D = -2\times$ log-likelihood, from each model. To do so, we must allow for the change in scale introduced by the log transformation.

Assuming, then, the y_i to be normally distributed, Atkinson (1985, 85–87, 184), by considering the Jacobian $\prod |\partial \ln(y_i - k)/\partial y_i|$, showed that multiplying both sides of (4) by the geometric mean of $y_i - k$, $\dot{y}$, gives residuals on the same scale as those of y_i. The geometric mean is given by

$$\dot{y} = e^{n^{-1} \sum \ln(y_i - k)}$$

which is a constant for a given dataset. The residual deviance for (3) and for (4) may be expressed as

$$D(\widehat{\boldsymbol{\beta}}) = \Big\{1 + \ln(2\pi\widehat{\sigma}^2)\Big\} n \tag{5}$$

where $\widehat{\boldsymbol{\beta}}$ is the maximum likelihood estimate (MLE) of $\boldsymbol{\beta}$ for each model and $n\widehat{\sigma}^2$ is the RSS from (3), or that from (4) multiplied by $\dot{y}^2$.

Because (3) and (4) are models with different error structures but the same functional form, the arithmetic difference in their RSS or deviances is not easily tested for statistical significance. However, if the deviance difference is large (>4, say), we would naturally prefer the model with the smaller deviance. Of course, the residuals for each model should be examined for departures from assumptions (nonconstant variance, nonnormality, serial correlations, etc.) in the usual way.

Alternatively, consider modeling

$$E(y_i) = 1/(C + Ae^{Bx_i}) \tag{6}$$

$$E(1/y_i) = E(y'_i) = C + Ae^{Bx_i} \tag{7}$$

where C, A, and B are parameters to be estimated. Using the data $(y, x) = (0.04, 5)$, $(0.06, 12)$, $(0.08, 25)$, $(0.1, 35)$, $(0.15, 42)$, $(0.2, 48)$, $(0.25, 60)$, $(0.3, 75)$, and $(0.5, 120)$ (Danuso 1991), fitting the models yields

Model	C	A	B	RSS	Deviance
(6)	1.781	25.74	−0.03926	−0.001640	−51.95
(6) with `lnlsq(0)`	1.799	25.45	−0.04051	−0.001431	−53.18
(7)	1.781	25.74	−0.03926	8.197	24.70
(7) with `lnlsq(0)`	1.799	27.45	−0.04051	3.651	17.42

There is little to choose between the two versions of the logistic model (6), whereas for the exponential model (7), the fit using `lnlsq(0)` is much better (a deviance difference of 7.28). The reciprocal transformation has introduced heteroskedasticity into y'_i, which is countered by the proportional errors property of the lognormal distribution implicit in `lnlsq(0)`. The deviances are not comparable between the logistic and exponential models because the change of scale has not been allowed for, although in principle it could be.

Other uses

Even if you are fitting linear regression models, you may find that `nl` can save you some typing. Because you specify the parameters of your model explicitly, you can impose constraints on them directly.

▷ Example 2

In example 2 of [R] **cnsreg**, we showed how to fit the model

$$\texttt{mpg} = \beta_0 + \beta_1\texttt{price} + \beta_2\texttt{weight} + \beta_3\texttt{displ} + \beta_4\texttt{gear\_ratio} + \beta_5\texttt{foreign} + \beta_6\texttt{length} + u$$

subject to the constraints

$$\beta_1 = \beta_2 = \beta_3 = \beta_6$$
$$\beta_4 = -\beta_5 = \beta_0/20$$

An alternative way is to use `nl`:

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. nl (mpg = {b0} + {b1}*price + {b1}*weight + {b1}*displ +
> {b0}/20*gear_ratio - {b0}/20*foreign + {b1}*length)
(obs = 74)
Iteration 0:  residual SS =  1578.522
Iteration 1:  residual SS =  1578.522
```

Source	SS	df	MS		
Model	34429.4777	2	17214.7389	Number of obs =	74
Residual	1578.52226	72	21.9239203	R-squared =	0.9562
				Adj R-squared =	0.9549
Total	36008	74	486.594595	Root MSE =	4.682299
				Res. dev. =	436.4562

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
/b0	26.52229	1.375178	19.29	0.000	23.78092	29.26365
/b1	-.000923	.0001534	-6.02	0.000	-.0012288	-.0006172

The point estimates and standard errors for β_0 and β_1 are identical to those reported in example 2 of [R] **cnsreg**. To get the estimate for β_4, we can use `nlcom`:

```
. nlcom _b[/b0]/20
       _nl_1:  _b[/b0]/20
```

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
_nl_1	1.326114	.0687589	19.29	0.000	1.189046	1.463183

The advantage to using `nl` is that we do not need to use the `constraint` command six times. ◁

`nl` is also a useful tool when doing exploratory data analysis. For example, you may want to run a regression of `y` on a function of `x`, though you have not decided whether to use sqrt(`x`) or ln(`x`). You can use `nl` to run both regressions without having first to generate two new variables:

```
. nl (y = {b0} + {b1}*ln(x))
. nl (y = {b0} + {b1}*sqrt(x))
```

Poi (2008) shows the advantages of using `nl` when marginal effects of transformed variables are desired as well.

Weights

Weights are specified in the usual way—analytic and frequency weights as well as `iweights` are supported; see [U] **20.22 Weighted estimation**. Use of analytic weights implies that the y_i have different variances. Therefore, model (3) may be rewritten as

$$y_i = f(\mathbf{x}_i, \boldsymbol{\beta}) + u_i, \qquad u_i \sim N(0, \sigma^2/w_i) \tag{3a}$$

where w_i are (positive) weights, assumed to be known and normalized such that their sum equals the number of observations. The residual deviance for (3a) is

$$D(\widehat{\boldsymbol{\beta}}) = \{1 + \ln(2\pi\widehat{\sigma}^2)\}n - \sum \ln(w_i) \tag{5a}$$

[compare with (5)], where

$$n\widehat{\sigma}^2 = \text{RSS} = \sum w_i\{y_i - f(\mathbf{x}_i, \widehat{\boldsymbol{\beta}})\}^2$$

Defining and fitting a model equivalent to (4) when weights have been specified as in (3a) is not straightforward and has not been attempted. Thus deviances using and not using the `lnlsq()` option may not be strictly comparable when analytic weights (other than 0 and 1) are used.

You do not need to modify your substitutable expression in any way to use weights. If, however, you write a substitutable expression program, then you should account for weights when obtaining initial values. When `nl` calls your program, it passes whatever weight expression (if any) was specified by the user. Here is an outline of a substitutable expression program that accepts weights:

```
program nl name, rclass
        version 12
        syntax varlist [aw fw iw] if
        ...
        // Obtain initial values allowing weights
        // Use the syntax [‘weight’‘exp’].  For example,
        summarize  varname [‘weight’‘exp’] ‘if’
        regress  depvar  varlist [‘weight’‘exp’] ‘if’
        ...
        // Return substitutable expression
        return local eq "substitutable expression"
        return local title "description of estimator"
end
```

For details on how the `syntax` command processes weight expressions, see [P] **syntax**.

Potential errors

`nl` is reasonably robust to the inability of your nonlinear function to be evaluated at some parameter values. `nl` does assume that your function can be evaluated at the initial values of the parameters. If your function cannot be evaluated at the initial values, an error message is issued with return code 480. Recall that if you do not specify an initial value for a parameter, then `nl` initializes it to zero. Many nonlinear functions cannot be evaluated when some parameters are zero, so in those cases specifying alternative initial values is crucial.

Thereafter, as `nl` changes the parameter values, it monitors your function for unexpected missing values. If these are detected, `nl` backs up. That is, `nl` finds a point between the previous, known-to-be-good parameter vector and the new, known-to-be-bad vector at which the function can be evaluated and continues its iterations from that point.

`nl` requires that once a parameter vector is found where the predictions can be calculated, small changes to the parameter vector be made to calculate numeric derivatives. If a boundary is encountered at this point, an error message is issued with return code 481.

When specifying `lnlsq()`, an attempt to take logarithms of $y_i - k$ when $y_i \leq k$ results in an error message with return code 482.

If `iterate()` iterations are performed and estimates still have not converged, results are presented with a warning, and the return code is set to 430.

If you use the programmed substitutable expression version of `nl` with a function evaluator program, or vice versa, Stata issues an error message. Verify that you are using the syntax appropriate for the program you have.

General comments on fitting nonlinear models

Achieving convergence is often problematic. For example, a unique minimum of the sum-of-squares function may not exist. Much literature exists on different algorithms that have been used, on strategies for obtaining good initial parameter values, and on tricks for parameterizing the model to make its behavior as linear-like as possible. Selected references are Kennedy and Gentle (1980, chap. 10) for computational matters and Ross (1990) and Ratkowsky (1983) for all three aspects. Ratkowsky's book is particularly clear and approachable, with useful discussion on the meaning and practical implications of intrinsic and parameter-effects nonlinearity. An excellent text on nonlinear estimation is Gallant (1987). Also see Davidson and MacKinnon (1993 and 2004).

To enhance the success of `nl`, pay attention to the form of the model fit, along the lines of Ratkowsky and Ross. For example, Ratkowsky (1983, 49–59) analyzes three possible three-parameter yield-density models for plant growth:

$$E(y_i) = \begin{cases} (\alpha + \beta x_i)^{-1/\theta} \\ (\alpha + \beta x_i + \gamma x_i^2)^{-1} \\ (\alpha + \beta x_i^{\phi})^{-1} \end{cases}$$

All three models give similar fits. However, he shows that the second formulation is dramatically more linear-like than the other two and therefore has better convergence properties. In addition, the parameter estimates are virtually unbiased and normally distributed, and the asymptotic approximation to the standard errors, correlations, and confidence intervals is much more accurate than for the other models. Even within a given model, the way the parameters are expressed (for example, ϕ^{x_i} or $e^{\theta x_i}$) affects the degree of linearity and convergence behavior.

Function evaluator programs

Occasionally, a nonlinear function may be so complex that writing a substitutable expression for it is impractical. For example, there could be many parameters in the model. Alternatively, if you are implementing a two-step estimator, writing a substitutable expression may be altogether impossible. Function evaluator programs can be used in these situations.

`nl` will pass to your function evaluator program a list of variables, a weight expression, a variable marking the estimation sample, and a vector of parameters. Your program is to replace the dependent variable, which is the first variable in the variables list, with the values of the nonlinear function evaluated at those parameters. As with substitutable expression programs, the first two letters of the name must be `nl`.

To focus on the mechanics of the function evaluator program, again let's compare the CES production function to the previous examples. The function evaluator program is

```
program nlces2
        version 12
        syntax varlist(min=3 max=3) if, at(name)
        local logout : word 1 of `varlist'
        local capital : word 2 of `varlist'
        local labor : word 3 of `varlist'
        // Retrieve parameters out of at matrix
        tempname b0 rho delta
        scalar `b0' = `at'[1, 1]
        scalar `rho' = `at'[1, 2]
        scalar `delta' = `at'[1, 3]
        tempvar kterm lterm
        generate double `kterm' = `delta'*`capital'^(-1*`rho') `if'
        generate double `lterm' = (1-`delta')*`labor'^(-1*`rho') `if'
        // Fill in dependent variable
        replace `logout' = `b0' - 1/`rho'*ln(`kterm' + `lterm') `if'
end
```

Unlike the previous `nlces` program, this one is not declared to be r-class. The `syntax` statement again accepts three variables: one for log output, one for capital, and one for labor. An `if` *exp* is again required because `nl` will pass a binary variable marking the estimation sample. All function evaluator programs must accept an option named `at()` that takes a `name` as an argument—that is how `nl` passes the parameter vector to your program.

The next part of the program retrieves the output, labor, and capital variables from the variables list. It then breaks up the temporary matrix `at` and retrieves the parameters `b0`, `rho`, and `delta`. Pay careful attention to the order in which the parameters refer to the columns of the `at` matrix because that will affect the syntax you use with `nl`. The temporary names you use inside this program are immaterial, however.

The rest of the program computes the nonlinear function, using some temporary variables to hold intermediate results. The final line of the program then replaces the dependent variable with the values of the function. Notice the use of `'if'` to restrict attention to the estimation sample. `nl` makes a copy of your dependent variable so that when the command is finished your data are left unchanged.

To use the program and fit your model, you type

```
. use http://www.stata-press.com/data/r12/production, clear
. nl ces2 @ lnoutput capital labor, parameters(b0 rho delta)
> initial(b0 0 rho 1 delta 0.5)
```

The output is again identical to that shown in example 1. The order in which the parameters were specified in the `parameters()` option is the same in which they are retrieved from the `at` matrix in the program. To initialize them, you simply list the parameter name, a space, the initial value, and so on.

If you use the `nparameters()` option instead of the `parameters()` option, the parameters are named `b1`, `b2`, ..., `b`k, where k is the number of parameters. Thus you could have typed

```
. nl ces2 @ lnoutput capital labor, nparameters(3) initial(b1 0 b2 1 b3 0.5)
```

With that syntax, the parameters called `b0`, `rho`, and `delta` in the program will be labeled `b1`, `b2`, and `b3`, respectively. In programming situations or if there are many parameters, instead of listing the parameter names and initial values in the `initial()` option, you may find it more convenient to pass a column vector. In those cases, you could type

```
. matrix myvals = (0, 1, 0.5)
. nl ces2 @ lnoutput capital labor, nparameters(3) initial(myvals)
```

In summary, a function evaluator program receives a list of variables, the first of which is the dependent variable that you are to replace with the values of your nonlinear function. Additionally, it must accept an `if` *exp*, as well as an option named `at` that will contain the vector of parameters at which `nl` wants the function evaluated. You are then free to do whatever is necessary to evaluate your function and replace the dependent variable.

If you wish to use weights, your function evaluator program's `syntax` statement must accept them. If your program consists only of, for example, `generate` statements, you need not do anything with the weights passed to your program. However, if in calculating the nonlinear function you use commands such as `summarize` or `regress`, then you will want to use the weights with those commands.

As with substitutable expression programs, `nl` will pass to it any options specified that `nl` does not accept, providing you with a way to pass more information to your function.

❑ Technical note

Before version 9 of Stata, the `nl` command used a different syntax, which required you to write an *nlfcn* program, and it did not have a syntax for interactive use other than the seven functions that were built-in. The old syntax of `nl` still works, and you can still use those *nlfcn* programs. If `nl` does not see a colon, an at sign, or a set of parentheses surrounding the equation in your command, it assumes that the old syntax is being used.

The current version of `nl` uses scalars and matrices to store intermediate calculations instead of local and global macros as the old version did, so the current version produces more accurate results. In practice, however, any discrepancies are likely to be small.

❑

Saved results

nl saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq_model)	number of equations in overall model test; always 0
e(df_m)	model degrees of freedom
e(df_r)	residual degrees of freedom
e(df_t)	total degrees of freedom
e(mss)	model sum of squares
e(rss)	residual sum of squares
e(tss)	total sum of squares
e(mms)	model mean square
e(msr)	residual mean square
e(ll)	log likelihood assuming i.i.d. normal errors
e(r2)	R-squared
e(r2_a)	adjusted R-squared
e(rmse)	root mean squared error
e(dev)	residual deviance
e(N_clust)	number of clusters
e(lnlsq)	value of lnlsq if specified
e(log_t)	1 if lnlsq specified, 0 otherwise
e(gm_2)	square of geometric mean of $(y-k)$ if lnlsq; 1 otherwise
e(cj)	position of constant in e(b) or 0 if no constant
e(delta)	relative change used to compute derivatives
e(rank)	rank of e(V)
e(ic)	number of iterations
e(converge)	1 if converged, 0 otherwise

Macros

e(cmd)	nl
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(title_2)	secondary title in estimation output
e(clustvar)	name of cluster variable
e(hac_kernel)	HAC kernel
e(hac_lag)	HAC lag
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(type)	1 = interactively entered expression 2 = substitutable expression program 3 = function evaluator program
e(sexp)	substitutable expression
e(params)	names of parameters
e(funcprog)	function evaluator program
e(rhs)	contents of variables()
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(init)	initial values vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

`nl` is implemented as an ado-file.

The derivation here is based on Davidson and MacKinnon (2004, chap. 6). Let $\boldsymbol{\beta}$ denote the $k \times 1$ vector of parameters, and write the regression function using matrix notation as $\mathbf{y} = \mathbf{f}(\mathbf{x}, \boldsymbol{\beta}) + \mathbf{u}$ so that the objective function can be written as

$$\text{SSR}(\boldsymbol{\beta}) = \{\mathbf{y} - \mathbf{f}(\mathbf{x}, \boldsymbol{\beta})\}' \, \mathbf{D} \, \{\mathbf{y} - \mathbf{f}(\mathbf{x}, \boldsymbol{\beta})\}$$

The $\mathbf{D}$ matrix contains the weights and is defined in [R] **regress**; if no weights are specified, then $\mathbf{D}$ is the $N \times N$ identity matrix. Taking a second-order Taylor series expansion centered at $\boldsymbol{\beta}_0$ yields

$$\text{SSR}(\boldsymbol{\beta}) \approx \text{SSR}(\boldsymbol{\beta}_0) + \mathbf{g}'(\boldsymbol{\beta}_0)(\boldsymbol{\beta} - \boldsymbol{\beta}_0) + \frac{1}{2}(\boldsymbol{\beta} - \boldsymbol{\beta}_0)'\mathbf{H}(\boldsymbol{\beta}_0)(\boldsymbol{\beta} - \boldsymbol{\beta}_0) \tag{8}$$

where $\mathbf{g}(\boldsymbol{\beta}_0)$ denotes the $k \times 1$ gradient of $\text{SSR}(\boldsymbol{\beta})$ evaluated at $\boldsymbol{\beta}_0$ and $\mathbf{H}(\boldsymbol{\beta}_0)$ denotes the $k \times k$ Hessian of $\text{SSR}(\boldsymbol{\beta})$ evaluated at $\boldsymbol{\beta}_0$. Letting $\mathbf{X}$ denote the $N \times k$ matrix of derivatives of $\mathbf{f}(\mathbf{x}, \boldsymbol{\beta})$ with respect to $\boldsymbol{\beta}$, the gradient $\mathbf{g}(\boldsymbol{\beta})$ is

$$\mathbf{g}(\boldsymbol{\beta}) = -2\mathbf{X}'\mathbf{D}\mathbf{u} \tag{9}$$

$\mathbf{X}$ and $\mathbf{u}$ are obviously functions of $\boldsymbol{\beta}$, though for notational simplicity that dependence is not shown explicitly. The (m, n) element of the Hessian can be written

$$H_{mn}(\boldsymbol{\beta}) = -2 \sum_{i=1}^{i=N} d_{ii} \left[\frac{\partial^2 f_i}{\partial \beta_m \partial \beta_n} u_i - X_{im} X_{in} \right] \tag{10}$$

where d_{ii} is the ith diagonal element of $\mathbf{D}$. As discussed in Davidson and MacKinnon (2004, chap. 6), the first term inside the brackets of (10) has expectation zero, so the Hessian can be approximated as

$$\mathbf{H}(\boldsymbol{\beta}) = 2\mathbf{X}'\mathbf{D}\mathbf{X} \tag{11}$$

Differentiating the Taylor series expansion of $\text{SSR}(\boldsymbol{\beta})$ shown in (8) yields the first-order condition for a minimum

$$\mathbf{g}(\boldsymbol{\beta}_0) + \mathbf{H}(\boldsymbol{\beta}_0)(\boldsymbol{\beta} - \boldsymbol{\beta}_0) = \mathbf{0}$$

which suggests the iterative procedure

$$\boldsymbol{\beta}_{j+1} = \boldsymbol{\beta}_j - \alpha \mathbf{H}^{-1}(\boldsymbol{\beta}_j)\mathbf{g}(\boldsymbol{\beta}_j) \tag{12}$$

where α is a "step size" parameter chosen at each iteration to improve convergence. Using (9) and (11), we can write (12) as

$$\boldsymbol{\beta}_{j+1} = \boldsymbol{\beta}_j + \alpha(\mathbf{X}'\mathbf{D}\mathbf{X})^{-1}\mathbf{X}'\mathbf{D}\mathbf{u} \tag{13}$$

where $\mathbf{X}$ and $\mathbf{u}$ are evaluated at $\boldsymbol{\beta}_j$. Apart from the scalar α, the second term on the right-hand side of (13) can be computed via a (weighted) regression of the columns of $\mathbf{X}$ on the errors. `nl` computes the derivatives numerically and then calls `regress`. At each iteration, α is set to one, and a candidate value $\boldsymbol{\beta}^*_{j+1}$ is computed by (13). If $\text{SSR}(\boldsymbol{\beta}^*_{j+1}) < \text{SSR}(\boldsymbol{\beta}_j)$, then $\boldsymbol{\beta}_{j+1} = \boldsymbol{\beta}^*_{j+1}$ and the iteration is complete. Otherwise, α is halved, a new $\boldsymbol{\beta}^*_{j+1}$ is calculated, and the process is repeated. Convergence is declared when $\alpha|\beta_{j+1,m}| \leq \epsilon(|\beta_{jm}| + \tau)$ for all $m = 1, \ldots, k$. `nl` uses $\tau = 10^{-3}$ and, by default, $\epsilon = 10^{-5}$, though you can specify an alternative value of ϵ with the `eps()` option.

As derived, for example, in Davidson and MacKinnon (2004, chap. 6), an expedient way to obtain the covariance matrix is to compute $\mathbf{u}$ and the columns of $\mathbf{X}$ at the final estimate $\widehat{\boldsymbol{\beta}}$ and then regress that $\mathbf{u}$ on $\mathbf{X}$. The covariance matrix of the estimated parameters of that regression serves as an estimate of $\mathrm{Var}(\widehat{\boldsymbol{\beta}})$. If that regression employs a robust covariance matrix estimator, then the covariance matrix for the parameters of the nonlinear regression will also be robust.

All other statistics are calculated analogously to those in linear regression, except that the nonlinear function $f(\mathbf{x}_i, \boldsymbol{\beta})$ plays the role of the linear function $\mathbf{x}_i'\boldsymbol{\beta}$. See [R] **regress**.

This command supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

Acknowledgments

The original version of `nl` was written by Patrick Royston of the MRC Clinical Trials Unit, London, and published in Royston (1992). Francesco Danuso's menu-driven nonlinear regression program (1991) provided the inspiration.

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Also see

[R] **nl postestimation** — Postestimation tools for nl

[R] **gmm** — Generalized method of moments estimation

[R] **ml** — Maximum likelihood estimation

[R] **nlcom** — Nonlinear combinations of estimators

[R] **nlsur** — Estimation of nonlinear systems of equations

[R] **regress** — Linear regression

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

nl postestimation — Postestimation tools for nl

Description

The following postestimation commands are available after `nl`:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`[2]	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions and residuals
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

[2] You must specify the `variables()` option with `nl`.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic]

predict [type] { stub* | newvar_1 ... newvar_k } [if] [in], scores
```

where k is the number of parameters in the model.

statistic	Description
Main	
`yhat`	fitted values; the default
`residuals`	residuals
`pr(a,b)`	$\Pr(y_j \mid a < y_j < b)$
`e(a,b)`	$E(y_j \mid a < y_j < b)$
`ystar(a,b)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`yhat`, the default, calculates the fitted values.

`residuals` calculates the residuals.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \mid a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated. *a* and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`scores` calculates the scores. The jth new variable created will contain the score for the jth parameter in `e(b)`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **nl** — Nonlinear least-squares estimation

[U] **20 Estimation and postestimation commands**

Title

nlcom — Nonlinear combinations of estimators

Syntax

Nonlinear combination of estimators—one expression

```
nlcom [name:]exp [, options]
```

Nonlinear combinations of estimators—more than one expression

```
nlcom ([name:]exp) [([name:]exp [, options]
```

options	Description
`level(#)`	set confidence level; default is `level(95)`
`iterate(#)`	maximum number of iterations
`post`	post estimation results
display_options	control column formats and line width
`noheader`	suppress output header

`noheader` does not appear in the dialog box.

The second syntax means that if more than one expression is specified, each must be surrounded by parentheses. The optional *name* is any valid Stata name and labels the transformations.

exp is a possibly nonlinear expression containing

```
_b[coef]
_b[eqno:coef]
[eqno]coef
[eqno]_b[coef]
```

eqno is

```
##
name
```

coef identifies a coefficient in the model. *coef* is typically a variable name, a level indicator, an interaction indicator, or an interaction involving continuous variables. Level indicators identify one level of a factor variable and interaction indicators identify one combination of levels of an interaction; see [U] **11.4.3 Factor variables**. *coef* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

Menu

Statistics > Postestimation > Nonlinear combinations of estimates

Description

`nlcom` computes point estimates, standard errors, test statistics, significance levels, and confidence intervals for (possibly) nonlinear combinations of parameter estimates after any Stata estimation command. Results are displayed in the usual table format used for displaying estimation results. Calculations are based on the "delta method", an approximation appropriate in large samples.

`nlcom` can be used with `svy` estimation results; see [SVY] **svy postestimation**.

Options

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`iterate(#)` specifies the maximum number of iterations used to find the optimal step size in calculating numerical derivatives of the transformation(s) with respect to the original parameters. By default, the maximum number of iterations is 100, but convergence is usually achieved after only a few iterations. You should rarely have to use this option.

`post` causes `nlcom` to behave like a Stata estimation (`eclass`) command. When `post` is specified, `nlcom` will post the vector of transformed estimators and its estimated variance–covariance matrix to `e()`. This option, in essence, makes the transformation permanent. Thus you could, after `posting`, treat the transformed estimation results in the same way as you would treat results from other Stata estimation commands. For example, after posting, you could redisplay the results by typing `nlcom` without any arguments, or use `test` to perform simultaneous tests of hypotheses on linear combinations of the transformed estimators; see [R] **test**.

Specifying `post` clears out the previous estimation results, which can be recovered only by refitting the original model or by storing the estimation results before running `nlcom` and then restoring them; see [R] **estimates store**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `nlcom` but is not shown in the dialog box:

`noheader` suppresses the output header.

Remarks

Remarks are presented under the following headings:

Introduction
Basics
Using the post option
Reparameterizing ML estimators for univariate data
nlcom versus eform

Introduction

nlcom and predictnl both use the delta method. They take nonlinear transformations of the estimated parameter vector from some fitted model and apply the delta method to calculate the variance, standard error, Wald test statistic, etc., of the transformations. nlcom is designed for functions of the parameters, and predictnl is designed for functions of the parameters and of the data, that is, for predictions.

nlcom generalizes lincom (see [R] **lincom**) in two ways. First, nlcom allows the transformations to be nonlinear. Second, nlcom can be used to simultaneously estimate many transformations (whether linear or nonlinear) and to obtain the estimated variance–covariance matrix of these transformations.

Basics

In [R] **lincom**, the following regression was performed:

```
. use http://www.stata-press.com/data/r12/regress
. regress y x1 x2 x3
```

Source	SS	df	MS	Number of obs =	148
				F(3, 144) =	96.12
Model	3259.3561	3	1086.45203	Prob > F =	0.0000
Residual	1627.56282	144	11.3025196	R-squared =	0.6670
				Adj R-squared =	0.6600
Total	4886.91892	147	33.2443464	Root MSE =	3.3619

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
x1	1.457113	1.07461	1.36	0.177	-.666934	3.581161
x2	2.221682	.8610358	2.58	0.011	.5197797	3.923583
x3	-.006139	.0005543	-11.08	0.000	-.0072345	-.0050435
_cons	36.10135	4.382693	8.24	0.000	27.43863	44.76407

Then lincom was used to estimate the difference between the coefficients of x1 and x2:

```
. lincom _b[x2] - _b[x1]
 ( 1) - x1 + x2 = 0
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	.7645682	.9950282	0.77	0.444	-1.20218	2.731316

It was noted, however, that nonlinear expressions are not allowed with lincom:

```
. lincom _b[x2]/_b[x1]
not possible with test
r(131);
```

Nonlinear transformations are instead estimated using nlcom:

```
. nlcom _b[x2]/_b[x1]
       _nl_1:  _b[x2]/_b[x1]
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
_nl_1	1.524714	.9812848	1.55	0.122	-.4148688	3.464297

❑ Technical note

The notation _b[*name*] is the standard way in Stata to refer to regression coefficients; see [U] **13.5 Accessing coefficients and standard errors**. Some commands, such as `lincom` and `test`, allow you to drop the _b[] and just refer to the coefficients by *name*. `nlcom`, however, requires the full specification _b[*name*]. ❑

Returning to our linear regression example, `nlcom` also allows simultaneous estimation of more than one combination:

```
. nlcom (_b[x2]/_b[x1]) (_b[x3]/_b[x1]) (_b[x3]/_b[x2])
       _nl_1:  _b[x2]/_b[x1]
       _nl_2:  _b[x3]/_b[x1]
       _nl_3:  _b[x3]/_b[x2]
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
_nl_1	1.524714	.9812848	1.55	0.122	-.4148688	3.464297
_nl_2	-.0042131	.0033483	-1.26	0.210	-.0108313	.002405
_nl_3	-.0027632	.0010695	-2.58	0.011	-.0048772	-.0006493

We can also label the transformations to produce more informative names in the estimation table:

```
. nlcom (ratio21:_b[x2]/_b[x1]) (ratio31:_b[x3]/_b[x1]) (ratio32:_b[x3]/_b[x2])
     ratio21:  _b[x2]/_b[x1]
     ratio31:  _b[x3]/_b[x1]
     ratio32:  _b[x3]/_b[x2]
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
ratio21	1.524714	.9812848	1.55	0.122	-.4148688	3.464297
ratio31	-.0042131	.0033483	-1.26	0.210	-.0108313	.002405
ratio32	-.0027632	.0010695	-2.58	0.011	-.0048772	-.0006493

`nlcom` saves the vector of estimated combinations and its estimated variance–covariance matrix in `r()`.

```
. matrix list r(b)
r(b)[1,3]
       ratio21     ratio31     ratio32
c1   1.5247143  -.00421315  -.00276324
. matrix list r(V)
symmetric r(V)[3,3]
            ratio21     ratio31     ratio32
ratio21   .96291982
ratio31  -.00287781   .00001121
ratio32  -.00014234   2.137e-06   1.144e-06
```

Using the post option

When used with the post option, nlcom saves the estimation vector and variance–covariance matrix in e(), making the transformation permanent:

```
. quietly nlcom (ratio21:_b[x2]/_b[x1]) (ratio31:_b[x3]/_b[x1])
> (ratio32:_b[x3]/_b[x2]), post
. matrix list e(b)
e(b)[1,3]
       ratio21     ratio31     ratio32
y1   1.5247143  -.00421315  -.00276324
. matrix list e(V)
symmetric e(V)[3,3]
            ratio21     ratio31     ratio32
ratio21   .96291982
ratio31  -.00287781   .00001121
ratio32  -.00014234   2.137e-06   1.144e-06
```

After posting, we can proceed as if we had just run a Stata estimation (eclass) command. For instance, we can replay the results,

```
. nlcom
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
ratio21	1.524714	.9812848	1.55	0.122	-.4148688	3.464297
ratio31	-.0042131	.0033483	-1.26	0.210	-.0108313	.002405
ratio32	-.0027632	.0010695	-2.58	0.011	-.0048772	-.0006493

or perform other postestimation tasks in the transformed metric, this time making reference to the new "coefficients":

```
. display _b[ratio31]
-.00421315
. estat vce, correlation
Correlation matrix of coefficients of nlcom model
```

e(V)	ratio21	ratio31	ratio32
ratio21	1.0000		
ratio31	-0.8759	1.0000	
ratio32	-0.1356	0.5969	1.0000

```
. test _b[ratio21] = 1
 ( 1)  ratio21 = 1
       F(  1,   144) =    0.29
            Prob > F =    0.5937
```

We see that testing _b[ratio21]=1 in the transformed metric is equivalent to testing using testnl _b[x2]/_b[x1]=1 in the original metric:

```
. quietly reg y x1 x2 x3
. testnl _b[x2]/_b[x1] = 1
  (1)  _b[x2]/_b[x1] = 1
               F(1, 144) =        0.29
                Prob > F =        0.5937
```

We needed to refit the regression model to recover the original parameter estimates.

❑ Technical note

In a previous technical note, we mentioned that commands such as `lincom` and `test` permit reference to *name* instead of `_b[`*name*`]`. This is not the case when `lincom` and `test` are used after `nlcom, post`. In the above, we used

```
. test _b[ratio21] = 1
```

rather than

```
. test ratio21 = 1
```

which would have returned an error. Consider this a limitation of Stata. For the shorthand notation to work, you need a variable named *name* in the data. In `nlcom`, however, *name* is just a coefficient label that does not necessarily correspond to any variable in the data.

❑

Reparameterizing ML estimators for univariate data

When run using only a response and no covariates, Stata's maximum likelihood (ML) estimation commands will produce ML estimates of the parameters of some assumed univariate distribution for the response. The parameterization, however, is usually not one we are used to dealing with in a nonregression setting. In such cases, `nlcom` can be used to transform the estimation results from a regression model to those from a maximum likelihood estimation of the parameters of a univariate probability distribution in a more familiar metric.

▷ Example 1

Consider the following univariate data on Y = # of traffic accidents at a certain intersection in a given year:

```
. use http://www.stata-press.com/data/r12/trafint
. summarize accidents
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
   accidents |         12    13.83333    14.47778         0         41
```

A quick glance of the output from `summarize` leads us to quickly reject the assumption that Y is distributed as Poisson because the estimated variance of Y is much greater than the estimated mean of Y.

Instead, we choose to model the data as univariate negative binomial, of which a common parameterization is

$$\Pr(Y=y) = \frac{\Gamma(r+y)}{\Gamma(r)\Gamma(y+1)}p^r(1-p)^y \qquad 0 \le p \le 1, \quad r > 0, \quad y = 0, 1, \ldots$$

with

$$E(Y) = \frac{r(1-p)}{p} \qquad \mathrm{Var}(Y) = \frac{r(1-p)}{p^2}$$

There exist no closed-form solutions for the maximum likelihood estimates of p and r, yet they may be estimated by the iterative method of Newton–Raphson. One way to get these estimates would be to write our own Newton–Raphson program for the negative binomial. Another way would be to write our own ML evaluator; see [R] **ml**.

The easiest solution, however, would be to use Stata's existing negative binomial ML regression command, `nbreg`. The only problem with this solution is that `nbreg` estimates a different parameterization of the negative binomial, but we can worry about that later.

```
. nbreg accidents
Fitting Poisson model:
Iteration 0:   log likelihood = -105.05361
Iteration 1:   log likelihood = -105.05361
Fitting constant-only model:
Iteration 0:   log likelihood = -43.948619
Iteration 1:   log likelihood = -43.891483
Iteration 2:   log likelihood =  -43.89144
Iteration 3:   log likelihood =  -43.89144
Fitting full model:
Iteration 0:   log likelihood =  -43.89144
Iteration 1:   log likelihood =  -43.89144
Negative binomial regression                    Number of obs   =         12
                                                LR chi2(0)      =       0.00
Dispersion     = mean                           Prob > chi2     =          .
Log likelihood = -43.89144                      Pseudo R2       =     0.0000
```

accidents	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
_cons	2.627081	.3192233	8.23	0.000	2.001415	3.252747
/lnalpha	.1402425	.4187147			-.6804233	.9609083
alpha	1.150553	.4817534			.5064026	2.61407

```
Likelihood-ratio test of alpha=0:  chibar2(01) =  122.32 Prob>=chibar2 = 0.000
. nbreg, coeflegend
Negative binomial regression                    Number of obs   =         12
                                                LR chi2(0)      =       0.00
Dispersion     = mean                           Prob > chi2     =          .
Log likelihood = -43.89144                      Pseudo R2       =     0.0000
```

accidents	Coef.	Legend
_cons	2.627081	_b[accidents:_cons]
/lnalpha	.1402425	_b[lnalpha:_cons]
alpha	1.150553	

```
Likelihood-ratio test of alpha=0:  chibar2(01) =  122.32 Prob>=chibar2 = 0.000
```

From this output, we see that, when used with univariate data, `nbreg` estimates a regression intercept, β_0, and the logarithm of some parameter α. This parameterization is useful in regression models: β_0 is the intercept meant to be augmented with other terms of the linear predictor, and α is an overdispersion parameter used for comparison with the Poisson regression model.

However, we need to transform $(\beta_0, \ln\alpha)$ to (p, r). Examining *Methods and formulas* of [R] **nbreg** reveals the transformation as

$$p = \{1 + \alpha \exp(\beta_0)\}^{-1} \qquad r = \alpha^{-1}$$

which we apply using `nlcom`:

```
. nlcom (p:1/(1 + exp([lnalpha]_b[_cons] + _b[_cons])))
> (r:exp(-[lnalpha]_b[_cons]))
          p:  1/(1 + exp([lnalpha]_b[_cons] + _b[_cons]))
          r:  exp(-[lnalpha]_b[_cons])
```

accidents	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
p	.0591157	.0292857	2.02	0.044	.0017168	.1165146
r	.8691474	.3639248	2.39	0.017	.1558679	1.582427

Given the invariance of maximum likelihood estimators and the properties of the delta method, the above parameter estimates, standard errors, etc., are precisely those we would have obtained had we instead performed the Newton–Raphson optimization in the (p, r) metric.

◁

❑ Technical note

Note how we referred to the estimate of $\ln\alpha$ above as `[lnalpha]_b[_cons]`. This is not entirely evident from the output of `nbreg`, which is why we redisplayed the results using the `coeflegend` option so that we would know how to refer to the coefficients; [U] **13.5 Accessing coefficients and standard errors**.

❑

nlcom versus eform

Many Stata estimation commands allow you to display exponentiated regression coefficients, some by default, some optionally. Known as "`eform`" in Stata terminology, this reparameterization serves many uses: it gives odds ratios for logistic models, hazard ratios in survival models, incidence-rate ratios in Poisson models, and relative-risk ratios in multinomial logit models, to name a few.

For example, consider the following estimation taken directly from the technical note in [R] **poisson**:

```
. use http://www.stata-press.com/data/r12/airline
. gen lnN = ln(n)
. poisson injuries XYZowned lnN
Iteration 0:   log likelihood = -22.333875
Iteration 1:   log likelihood = -22.332276
Iteration 2:   log likelihood = -22.332276
Poisson regression                              Number of obs   =          9
                                                LR chi2(2)      =      19.15
                                                Prob > chi2     =     0.0001
Log likelihood = -22.332276                     Pseudo R2       =     0.3001
```

injuries	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
XYZowned	.6840667	.3895877	1.76	0.079	-.0795111	1.447645
lnN	1.424169	.3725155	3.82	0.000	.6940517	2.154285
_cons	4.863891	.7090501	6.86	0.000	3.474178	6.253603

When we replay results and specify the `irr` (incidence-rate ratios) option,

```
. poisson, irr
Poisson regression                                Number of obs   =          9
                                                  LR chi2(2)      =      19.15
                                                  Prob > chi2     =     0.0001
Log likelihood = -22.332276                       Pseudo R2       =     0.3001
```

injuries	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
XYZowned	1.981921	.7721322	1.76	0.079	.9235678	4.253085
lnN	4.154402	1.547579	3.82	0.000	2.00181	8.621728
_cons	129.5272	91.84126	6.86	0.000	32.2713	519.8828

we obtain the exponentiated regression coefficients and their estimated standard errors.

Contrast this with what we obtain if we exponentiate the coefficients manually by using `nlcom`:

```
. nlcom (E_XYZowned:exp(_b[XYZowned])) (E_lnN:exp(_b[lnN]))
  E_XYZowned:  exp(_b[XYZowned])
      E_lnN:  exp(_b[lnN])
```

injuries	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
E_XYZowned	1.981921	.7721322	2.57	0.010	.4685701	3.495273
E_lnN	4.154402	1.547579	2.68	0.007	1.121203	7.187602

There are three things to note when comparing `poisson, irr` (and `eform` in general) with `nlcom`:

1. The exponentiated coefficients and standard errors are identical. This is certainly good news.
2. The Wald test statistic (`z`) and level of significance are different. When using `poisson, irr` and other related `eform` options, the Wald test does not change from what you would have obtained without the `eform` option, and you can see this by comparing both versions of the `poisson` output given previously.

   When you use `eform`, Stata knows that what is usually desired is a test of

   $$H_0: \exp(\beta) = 1$$

   and not the uninformative-by-comparison

   $$H_0: \exp(\beta) = 0$$

   The test of $H_0: \exp(\beta) = 1$ is asymptotically equivalent to a test of $H_0: \beta = 0$, the Wald test in the original metric, but the latter has better small-sample properties. Thus if you specify `eform`, you get a test of $H_0: \beta = 0$.

   `nlcom`, however, is general. It does not attempt to infer the test of greatest interest for a given transformation, and so a test of

   $$H_0: \text{transformed coefficient} = 0$$

   is always given, regardless of the transformation.
3. You may be surprised to see that, even though the coefficients and standard errors are identical, the confidence intervals (both 95%) are different.

eform confidence intervals are standard confidence intervals with the endpoints transformed. For example, the confidence interval for the coefficient on lnN is $[0.694, 2.154]$, whereas the confidence interval for the incidence-rate ratio due to lnN is $[\exp(0.694), \exp(2.154)] = [2.002, 8.619]$, which, except for some roundoff error, is what we see from the output of poisson, irr. For exponentiated coefficients, confidence intervals based on transform-the-endpoints methodology generally have better small-sample properties than their asymptotically equivalent counterparts.

The transform-the-endpoints method, however, gives valid coverage only when the transformation is monotonic. nlcom uses a more general and asymptotically equivalent method for calculating confidence intervals, as described in *Methods and formulas*.

Saved results

nlcom saves the following in r():

Scalars

r(N)	number of observations
r(df_r)	residual degrees of freedom

Matrices

r(b)	vector of transformed coefficients
r(V)	estimated variance–covariance matrix of the transformed coefficients

If post is specified, nlcom also saves the following in e():

Scalars

e(N)	number of observations
e(df_r)	residual degrees of freedom
e(N_strata)	number of strata L, if used after svy
e(N_psu)	number of sampled PSUs n, if used after svy
e(rank)	rank of e(V)

Macros

e(cmd)	nlcom
e(predict)	program used to implement predict
e(properties)	b V

Matrices

e(b)	vector of transformed coefficients
e(V)	estimated variance–covariance matrix of the transformed coefficients
e(V_srs)	simple-random-sampling-without-replacement (co)variance $\widehat{V}_{\text{srswor}}$, if svy
e(V_srswr)	simple-random-sampling-with-replacement (co)variance $\widehat{V}_{\text{srswr}}$, if svy and fpc()
e(V_msp)	misspecification (co)variance $\widehat{V}_{\text{msp}}$, if svy and available

Functions

e(sample)	marks estimation sample

Methods and formulas

nlcom is implemented as an ado-file.

Given a $1 \times k$ vector of parameter estimates, $\widehat{\boldsymbol{\theta}} = (\widehat{\theta}_1, \ldots, \widehat{\theta}_k)$, consider the estimated p-dimensional transformation

$$g(\widehat{\boldsymbol{\theta}}) = [g_1(\widehat{\boldsymbol{\theta}}), g_2(\widehat{\boldsymbol{\theta}}), \ldots, g_p(\widehat{\boldsymbol{\theta}})]$$

The estimated variance–covariance of $g(\widehat{\boldsymbol{\theta}})$ is given by

$$\widehat{\text{Var}}\left\{g(\widehat{\boldsymbol{\theta}})\right\} = \mathbf{GVG}'$$

where $\mathbf{G}$ is the $p \times k$ matrix of derivatives for which

$$\mathbf{G}_{ij} = \left.\frac{\partial g_i(\boldsymbol{\theta})}{\partial \theta_j}\right|_{\boldsymbol{\theta}=\widehat{\boldsymbol{\theta}}} \qquad i = 1, \ldots, p \qquad j = 1, \ldots, k$$

and $\mathbf{V}$ is the estimated variance–covariance matrix of $\widehat{\boldsymbol{\theta}}$. Standard errors are obtained as the square roots of the variances.

The Wald test statistic for testing

$$H_0 : g_i(\boldsymbol{\theta}) = 0$$

versus the two-sided alternative is given by

$$Z_i = \frac{g_i(\widehat{\boldsymbol{\theta}})}{\left[\widehat{\mathrm{Var}}_{ii}\left\{g(\widehat{\boldsymbol{\theta}})\right\}\right]^{1/2}}$$

When the variance–covariance matrix of $\widehat{\boldsymbol{\theta}}$ is an asymptotic covariance matrix, Z_i is approximately distributed as Gaussian. For linear regression, Z_i is taken to be approximately distributed as $t_{1,r}$ where r is the residual degrees of freedom from the original fitted model.

A $(1-\alpha) \times 100\%$ confidence interval for $g_i(\boldsymbol{\theta})$ is given by

$$g_i(\widehat{\boldsymbol{\theta}}) \pm z_{\alpha/2}\left[\widehat{\mathrm{Var}}_{ii}\left\{g(\widehat{\boldsymbol{\theta}})\right\}\right]^{1/2}$$

for those cases where Z_i is Gaussian and

$$g_i(\widehat{\boldsymbol{\theta}}) \pm t_{\alpha/2,r}\left[\widehat{\mathrm{Var}}_{ii}\left\{g(\widehat{\boldsymbol{\theta}})\right\}\right]^{1/2}$$

for those cases where Z_i is t distributed. z_p is the $1-p$ quantile of the standard normal distribution, and $t_{p,r}$ is the $1-p$ quantile of the t distribution with r degrees of freedom.

References

Feiveson, A. H. 1999. FAQ: What is the delta method and how is it used to estimate the standard error of a transformed parameter? http://www.stata.com/support/faqs/stat/deltam.html.

Gould, W. W. 1996. crc43: Wald test of nonlinear hypotheses after model estimation. *Stata Technical Bulletin* 29: 2–4. Reprinted in *Stata Technical Bulletin Reprints*, vol. 5, pp. 15–18. College Station, TX: Stata Press.

Oehlert, G. W. 1992. A note on the delta method. *American Statistician* 46: 27–29.

Phillips, P. C. B., and J. Y. Park. 1988. On the formulation of Wald tests of nonlinear restrictions. *Econometrica* 56: 1065–1083.

Also see

[R] **lincom** — Linear combinations of estimators

[R] **predictnl** — Obtain nonlinear predictions, standard errors, etc., after estimation

[R] **test** — Test linear hypotheses after estimation

[R] **testnl** — Test nonlinear hypotheses after estimation

[U] **20 Estimation and postestimation commands**

Title

nlogit — Nested logit regression

Syntax

Nested logit regression

```
nlogit depvar [indepvars] [if] [in] [weight] [|| lev1_equation
    [|| lev2_equation ...]] || altvar: [byaltvarlist], case(varname) [options]
```

where the syntax of *lev#_equation* is

```
altvar: [byaltvarlist] [, base(# | lbl) estconst]
```

Create variable based on specification of branches

```
nlogitgen newaltvar = altvar (branchlist) [, nolog]
```

where *branchlist* is

```
branch, branch [, branch ...]
```

and *branch* is

```
[label:] alternative [| alternative [| alternative ...]]
```

Display tree structure

```
nlogittree altvarlist [if] [in] [weight] [, choice(depvar) nolabel nobranches]
```

options	Description
Model	
* `case(`*varname*`)`	use *varname* to identify cases
`base(#` | *lbl*`)`	use the specified level or label of *altvar* as the base alternative for the bottom level
`noconstant`	suppress the constant terms for the bottom-level alternatives
`nonnormalized`	use the nonnormalized parameterization
`altwise`	use alternativewise deletion instead of casewise deletion
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`notree`	suppress display of tree-structure output; see also `nolabel` and `nobranches`
`nocnsreport`	do not display constraints
display_options	control column formats and line width
Maximization	
maximize_options	control the maximization process; seldom used

* `case(`*varname*`)` is required.

`bootstrap`, `by`, `jackknife`, `statsby`, and `xi` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`fweights`, `iweights`, and `pweights` are allowed with `nlogit`, and `fweights` are allowed with `nlogittree`; see [U] **11.1.6 weight**. Weights for `nlogit` must be constant within case.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

nlogit

Statistics > Categorical outcomes > Nested logit regression

nlogitgen

Statistics > Categorical outcomes > Setup for nested logit regression

nlogittree

Statistics > Categorical outcomes > Display nested logit tree structure

Description

`nlogit` performs full information maximum-likelihood estimation for nested logit models. These models relax the assumption of independently distributed errors and the independence of irrelevant alternatives inherent in conditional and multinomial logit models by clustering similar alternatives into nests.

By default, `nlogit` uses a parameterization that is consistent with random utility maximization (RUM). Before version 10 of Stata, a nonnormalized version of the nested logit model was fit, which you can request by specifying the `nonnormalized` option.

You must use `nlogitgen` to generate a new categorical variable to specify the branches of the decision tree before calling `nlogit`.

Options

Specification and options for lev#_equation

altvar is a variable identifying alternatives at this level of the hierarchy.

byaltvarlist specifies the variables to be used to compute the by-alternative regression coefficients for that level. For each variable specified in the variable list, there will be one regression coefficient for each alternative of that level of the hierarchy. If the variable is constant across each alternative (a case-specific variable), the regression coefficient associated with the base alternative is not identifiable. These regression coefficients are labeled as (base) in the regression table. If the variable varies among the alternatives, a regression coefficient is estimated for each alternative.

`base(`*#* | *lbl*`)` can be specified in each level equation where it identifies the base alternative to be used at that level. The default is the alternative that has the highest frequency.

If `vce(bootstrap)` or `vce(jackknife)` is specified, you must specify the base alternative for each level that has a *byaltvarlist* or if the constants will be estimated. Doing so ensures that the same model is fit with each call to `nlogit`.

`estconst` applies to all the level equations except the bottom-level equation. Specifying `estconst` requests that constants for each alternative (except the base alternative) be estimated. By default, no constant is estimated at these levels. Constants can be estimated in only one level of the tree hierarchy. If you specify `estconst` for one of the level equations, you must specify `noconstant` for the bottom-level equation.

Options for nlogit

Model

`case(`*varname*`)` specifies the variable that identifies each case. `case()` is required.

`base(`*#* | *lbl*`)` can be specified in each level equation where it identifies the base alternative to be used at that level. The default is the alternative that has the highest frequency.

If `vce(bootstrap)` or `vce(jackknife)` is specified, you must specify the base alternative for each level that has a *byaltvarlist* or if the constants will be estimated. Doing so ensures that the same model is fit with each call to `nlogit`.

`noconstant` applies only to the equation defining the bottom level of the hierarchy. By default, constants are estimated for each alternative of *altvar*, less the base alternative. To suppress the constant terms for this level, specify `noconstant`. If you do not specify `noconstant`, you cannot specify `estconst` for the higher-level equations.

`nonnormalized` requests a nonnormalized parameterization of the model that does not scale the inclusive values by the degree of dissimilarity of the alternatives within each nest. Use this option to replicate results from older versions of Stata. The default is to use the RUM–consistent parameterization.

`altwise` specifies that alternativewise deletion be used when marking out observations because of missing values in your variables. The default is to use casewise deletion. This option does not apply to observations that are marked out by the `if` or `in` qualifier or the `by` prefix.

`constraints(`*constraints*`)`; see [R] **estimation options**.

The inclusive-valued/dissimilarity parameters are parameterized as `ml` ancillary parameters. They are labeled as [*alternative*`_tau`]`_const`, where *alternative* is one of the alternatives defining a branch in the tree. To constrain the inclusive-valued/dissimilarity parameter for alternative `a1` to be, say, equal to alternative `a2`, you would use the following syntax:

```
. constraint 1 [a1_tau]_cons = [a2_tau]_cons
. nlogit ..., constraints(1)
```

`collinear` prevents collinear variables from being dropped. Use this option when you know that you have collinear variables and you are applying `constraints()` to handle the rank reduction. See [R] **estimation options** for details on using `collinear` with `constraints()`.

`nlogit` will not allow you to specify an independent variable in more than one level equation. Specifying the `collinear` option will allow execution to proceed in this case, but it is your responsibility to ensure that the parameters are identified.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If `vce(robust)` or `vce(cluster` *clustvar*`)` is specified, the likelihood-ratio test for the independence of irrelevant alternatives (IIA) is not computed.

Reporting

`level(#)`; see [R] **estimation options**.

`notree` specifies that the tree structure of the nested logit model not be displayed. See also `nolabel` and `nobranches` below for when `notree` is not specified.

`nocnsreport`; see [R] **estimation options**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, [`no`]`log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

The `technique(bhhh)` option is not allowed.

Specification and options for nlogitgen

newaltvar and *altvar* are variables identifying alternatives at each level of the hierarchy.

label defines a label to associate with the branch. If no label is given, a numeric value is used.

alternative specifies an alternative, of *altvar* specified in the syntax, to be included in the branch. It is either a numeric value or the label associated with that value. An example of `nlogitgen` is

```
. nlogitgen type = restaurant(fast: 1 | 2,
> family: CafeEccell | LosNortenos | WingsNmore, fancy: 6 | 7)
```

`nolog` suppresses the display of the iteration log.

Specification and options for nlogittree

Main

altvarlist is a list of alternative variables that define the tree hierarchy. The first variable must define bottom-level alternatives, and the order continues to the variable defining the top-level alternatives.

`choice(`*depvar*`)` defines the choice indicator variable and forces `nlogittree` to compute and display choice frequencies for each bottom-level alternative.

`nolabel` forces `nlogittree` to suppress value labels in tree-structure output.

`nobranches` forces `nlogittree` to suppress drawing branches in the tree-structure output.

Remarks

Remarks are presented under the following headings:

Introduction
Data setup and the tree structure
Estimation
Testing for the IIA
Nonnormalized model

Introduction

`nlogit` performs full information maximum-likelihood estimation for nested logit models. These models relax the assumption of independently distributed errors and the IIA inherent in conditional and multinomial logit models by clustering similar alternatives into nests. Because the nested logit model is a direct generalization of the alternative-specific conditional logit model (also known as McFadden's choice model), you may want to read [R] **asclogit** before continuing.

By default, `nlogit` uses a parameterization that is consistent with RUM. Before version 10 of Stata, a nonnormalized version of the nested logit model was fit, which you can request by specifying the `nonnormalized` option. We recommend using the RUM-consistent version of the model for new projects because it is based on a sound model of consumer behavior.

McFadden (1977, 1981) showed how this model can be derived from a rational choice framework. Amemiya (1985, chap. 9) contains a nice discussion of how this model can be derived under the assumption of utility maximization. Hensher, Rose, and Greene (2005) provide a lucid introduction to choice models including nested logit.

Throughout this entry, we consider a model of restaurant choice. We begin by introducing the data.

▷ Example 1

We have fictional data on 300 families and their choice of seven local restaurants. Freebirds and Mama's Pizza are fast food restaurants; Café Eccell, Los Norteños, and Wings 'N More are family restaurants; and Christopher's and Mad Cows are fancy restaurants. We want to model the decision of where to eat as a function of household income (`income`, in thousands of dollars), the number

of children in the household (kids), the rating of the restaurant according to a local restaurant guide (rating, coded 0–5), the average meal cost per person (cost), and the distance between the household and the restaurant (distance, in miles). income and kids are attributes of the family, rating is an attribute of the alternative (the restaurant), and cost and distance are attributes of the alternative as perceived by the families—that is, each family has its own cost and distance for each restaurant.

We begin by loading the data and listing some of the variables for the first three families:

```
. use http://www.stata-press.com/data/r12/restaurant
. describe
Contains data from http://www.stata-press.com/data/r12/restaurant.dta
  obs:         2,100
 vars:             8                          10 Mar 2011 01:17
 size:        67,200
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
family_id       float  %9.0g                  family ID
restaurant      float  %12.0g      names      choices of restaurants
income          float  %9.0g                  household income
cost            float  %9.0g                  average meal cost per person
kids            float  %9.0g                  number of kids in the household
rating          float  %9.0g                  ratings in local restaurant
                                                guide
distance        float  %9.0g                  distance between home and
                                                restaurant
chosen          float  %9.0g                  0 no 1 yes
-------------------------------------------------------------------------------
Sorted by:  family_id
```

```
. list family_id restaurant chosen kids rating distance in 1/21, sepby(fam)
> abbrev(10)
```

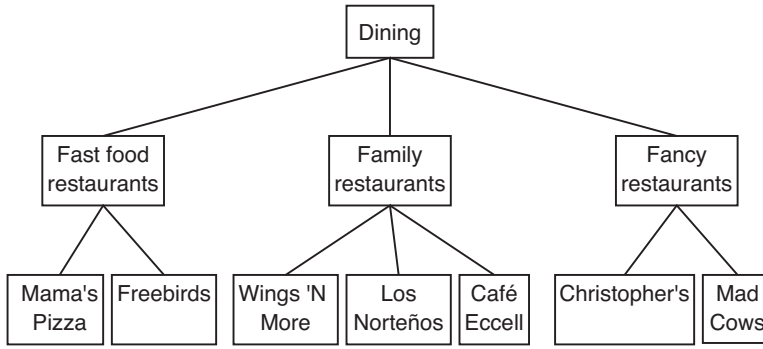
	family_id	restaurant	chosen	kids	rating	distance
1.	1	Freebirds	1	1	0	1.245553
2.	1	MamasPizza	0	1	1	2.82493
3.	1	CafeEccell	0	1	2	4.21293
4.	1	LosNortenos	0	1	3	4.167634
5.	1	WingsNmore	0	1	2	6.330531
6.	1	Christophers	0	1	4	10.19829
7.	1	MadCows	0	1	5	5.601388
8.	2	Freebirds	0	3	0	4.162657
9.	2	MamasPizza	0	3	1	2.865081
10.	2	CafeEccell	0	3	2	5.337799
11.	2	LosNortenos	1	3	3	4.282864
12.	2	WingsNmore	0	3	2	8.133914
13.	2	Christophers	0	3	4	8.664631
14.	2	MadCows	0	3	5	9.119597
15.	3	Freebirds	1	3	0	2.112586
16.	3	MamasPizza	0	3	1	2.215329
17.	3	CafeEccell	0	3	2	6.978715
18.	3	LosNortenos	0	3	3	5.117877
19.	3	WingsNmore	0	3	2	5.312941
20.	3	Christophers	0	3	4	9.551273
21.	3	MadCows	0	3	5	5.539806

Because each family chose among seven restaurants, there are 7 observations in the dataset for each family. The variable `chosen` is coded 0/1, with 1 indicating the chosen restaurant and 0 otherwise. ◁

We could fit a conditional logit model to our data. Because `income` and `kids` are constant within each family, we would use the `asclogit` command instead of `clogit`. However, the conditional logit may be inappropriate. That model assumes that the random errors are independent, and as a result it forces the odds ratio of any two alternatives to be independent of the other alternatives, a property known as the IIA. We will discuss the IIA assumption in more detail later.

Assuming that unobserved shocks influencing a decision maker's attitude toward one alternative have no effect on his attitudes toward the other alternatives may seem innocuous, but often this assumption is too restrictive. Suppose that when a family was deciding which restaurant to visit, they were pressed for time because of plans to attend a movie later. The unobserved shock (being in a hurry) would raise the likelihood that the family goes to either fast food restaurant (Freebirds or Mama's Pizza). Similarly, another family might be choosing a restaurant to celebrate a birthday and therefore be inclined to attend a fancy restaurant (Christopher's or Mad Cows).

Nested logit models relax the independence assumption and allow us to group alternatives for which unobserved shocks may have concomitant effects. Here we suspect that restaurants should be grouped by type (fast, family, or fancy). The tree structure of a family's decision about where to eat might look like this:



At the bottom of the tree are the individual restaurants, indicating that there are some random shocks that affect a family's decision to eat at each restaurant independently. Above the restaurants are the three types of restaurants, indicating that other random shocks affect the type of restaurant chosen. As is customary when drawing decision trees, at the top level is one box, representing the family making the decision.

We use the following terms to describe nested logit models.

level, or decision level, is the level or stage at which a decision is made. The example above has only two levels. In the first level, a type of restaurant is chosen—fast food, family, or fancy—and in the second level, a specific restaurant is chosen.

bottom level is the level where the final decision is made. In our example, this is when we choose a specific restaurant.

alternative set is the set of all possible alternatives at any given decision level.

bottom alternative set is the set of all possible alternatives at the bottom level. This concept is often referred to as the choice set in the economics-choice literature. In our example, the bottom alternative set is all seven of the specific restaurants.

alternative is a specific alternative within an alternative set. In the first level of our example, "fast food" is an alternative. In the second or bottom level, "Mad Cows" is an alternative. Not all alternatives within an alternative set are available to someone making a choice at a specific stage, only those that are nested within all higher-level decisions.

chosen alternative is the alternative from an alternative set that we observe someone having chosen.

❑ Technical note

Although decision trees in nested logit analysis are often interpreted as implying that the highest-level decisions are made first, followed by decisions at lower levels, and finally the decision among alternatives at the bottom level, no such temporal ordering is implied. See Hensher, Rose, and Greene (2005, chap. 13). In our example, we are not assuming that families first choose whether to attend a fast, family, or fancy restaurant and then choose the particular restaurant; we assume merely that they choose one of the seven restaurants.

❑

Data setup and the tree structure

To fit a nested logit model, you must first create a variable that defines the structure of your decision tree.

▷ Example 2

To run `nlogit`, we need to generate a categorical variable that identifies the first-level set of alternatives: fast food, family restaurants, or fancy restaurants. We can do so easily by using `nlogitgen`.

```
. nlogitgen type = restaurant(fast: Freebirds | MamasPizza,
> family: CafeEccell | LosNortenos| WingsNmore, fancy: Christophers | MadCows)
new variable type is generated with 3 groups
label list lb_type
lb_type:
           1 fast
           2 family
           3 fancy
. nlogittree restaurant type, choice(chosen)
tree structure specified for the nested logit model
 type    N      restaurant    N   k
──────────────────────────────────────
 fast   600 ─┬─ Freebirds    300  12
             └─ MamasPizza   300  15
 family 900 ─┬─ CafeEccell   300  78
             ├─ LosNortenos  300  75
             └─ WingsNmore   300  69
 fancy  600 ─┬─ Christophers 300  27
             └─ MadCows      300  24
──────────────────────────────────────
                     total  2100 300
k = number of times alternative is chosen
N = number of observations at each level
```

The new categorical variable is `type`, which takes on value 1 (fast) if `restaurant` is Freebirds or Mama's Pizza; value 2 (family) if `restaurant` is Café Eccell, Los Norteños, or Wings 'N More; and value 3 (fancy) otherwise. `nlogittree` displays the tree structure.

◁

❑ Technical note

We could also use values instead of value labels of `restaurant` in `nlogitgen`. Value labels are optional, and the default value labels for `type` are `type1`, `type2`, and `type3`. The vertical bar is also optional.

```
. use http://www.stata-press.com/data/r12/restaurant, clear
. nlogitgen type = restaurant(1 2, 3 4 5, 6 7)
new variable type is generated with 3 groups
label list lb_type
lb_type:
           1 type1
           2 type2
           3 type3
```

```
. nlogittree restaurant type
tree structure specified for the nested logit model
 type    N      restaurant     N
──────────────────────────────────
 type1 600 ─┬─ Freebirds     300
            └─ MamasPizza    300
 type2 900 ─┬─ CafeEccell    300
            ├─ LosNortenos   300
            └─ WingsNmore    300
 type3 600 ─┬─ Christophers  300
            └─ MadCows       300
──────────────────────────────────
                     total  2100
N = number of observations at each level
```

❑

In our dataset, every family was able to choose among all seven restaurants. However, in other applications some decision makers may not have been able to choose among all possible alternatives. For example, two cases may have choice hierarchies of

```
      case 1                          case 2
type        restaurant          type        restaurant
──────────────────────          ──────────────────────
fast   ─┬─ Freebirds            fast   ─┬─ Freebirds
        └─ MamasPizza                   └─ MamasPizza
family ─┬─ CafeEccell           family ─┬─ LosNortenos
        ├─ LosNortenos                  └─ WingsNmore
        └─ WingsNmore
fancy  ─┬─ Christophers         fancy  ── Christophers
        └─ MadCows
```

where the second case does not have the restaurant alternatives Café Eccell or Mad Cows available to them. The only restriction is that the relationships between higher- and lower-level alternative sets be the same for all decision makers. In this two-level example, Freebirds and Mama's Pizza are classified as fast food restaurants for both cases; Café Eccell, Los Norteños, and Wings 'N More are family restaurants; and Christopher's and Mad Cows are fancy restaurants. `nlogit` requires only that hierarchy be maintained for all cases.

Estimation

▷ Example 3

With our `type` variable created that defines the three types of restaurants, we can now examine how the alternative-specific attributes (`cost`, `rating`, and `distance`) apply to the bottom alternative set (the seven restaurants) and how family-specific attributes (`income` and `kid`) apply to the alternative set at the first decision level (the three types of restaurants).

```
. nlogit chosen cost rating distance || type: income kids, base(family) ||
> restaurant:, noconstant case(family_id)
tree structure specified for the nested logit model
 type    N      restaurant    N   k
──────────────────────────────────────
 fast   600 ─┬─ Freebirds    300  12
             └─ MamasPizza   300  15
 family 900 ─┬─ CafeEccell   300  78
             ├─ LosNortenos  300  75
             └─ WingsNmore   300  69
 fancy  600 ─┬─ Christophers 300  27
             └─ MadCows      300  24
──────────────────────────────────────
                     total  2100 300
k = number of times alternative is chosen
N = number of observations at each level
Iteration 0:   log likelihood = -541.93581
  (output omitted)
Iteration 17:  log likelihood = -485.47331
RUM-consistent nested logit regression          Number of obs      =       2100
Case variable: family_id                        Number of cases    =        300
Alternative variable: restaurant                Alts per case: min =          7
                                                               avg =        7.0
                                                               max =          7
                                                  Wald chi2(7)    =      46.71
Log likelihood = -485.47331                       Prob > chi2     =     0.0000
```

chosen	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
restaurant						
cost	-.1843847	.0933975	-1.97	0.048	-.3674404	-.0013289
rating	.463694	.3264935	1.42	0.156	-.1762215	1.10361
distance	-.3797474	.1003828	-3.78	0.000	-.5764941	-.1830007
type equations						
fast						
income	-.0266038	.0117306	-2.27	0.023	-.0495952	-.0036123
kids	-.0872584	.1385026	-0.63	0.529	-.3587184	.1842016
family						
income	0	(base)				
kids	0	(base)				
fancy						
income	.0461827	.0090936	5.08	0.000	.0283595	.0640059
kids	-.3959413	.1220356	-3.24	0.001	-.6351267	-.1567559
dissimilarity parameters						
type						
/fast_tau	1.712878	1.48685			-1.201295	4.627051
/family_tau	2.505113	.9646351			.614463	4.395763
/fancy_tau	4.099844	2.810123			-1.407896	9.607583

LR test for IIA (tau = 1): chi2(3) = 6.87 Prob > chi2 = 0.0762

First, let's examine how we called `nlogit`. The delimiters (`||`) separate equations. The first equation specifies the dependent variable, `chosen`, and three alternative-specific variables, `cost`,

rating, and distance. We refer to these variables as alternative-specific because they vary among the bottom-level alternatives, the restaurants. We obtain one parameter estimate for each variable. These estimates are listed in the equation subtable labeled restaurant.

For the second equation, we specify the type variable. It identifies the first-level alternatives, the restaurant types. Following the colon after type, we specify two case-specific variables, income and kids. Here we obtain a parameter estimate for each variable for each alternative at this level. That is why we call these variable lists *by-alternative* variables. Because income and kids do not vary within each case, to identify the model one alternative's set of parameters must be set to zero. We specified the base(family) option with this equation to restrict the parameters for the family alternative.

The variable identifying the bottom-level alternatives, restaurant, is specified after the second equation delimiter. We do not specify any variables after the colon delimiter at this level. Had we specified variables here, we would have obtained an estimate for each variable in each equation. As we will see below, these variables parameterize the constant term in the utility equation for each bottom-level alternative. The noconstant option suppresses bottom-level alternative-specific constant terms.

Near the bottom of the output are the dissimilarity parameters, which measure the degree of correlation of random shocks within each of the three types of restaurants. Dissimilarity parameters greater than one imply that the model is inconsistent with RUM; Hensher, Rose, and Greene (2005, sec. 13.6) discuss this in detail. We will ignore the fact that all our dissimilarity parameters exceed one.

The conditional logit model is a special case of nested logit in which all the dissimilarity parameters are equal to one. At the bottom of the output, we find a likelihood-ratio test of this hypothesis. Here we have mixed evidence of the null hypothesis that all the parameters are one. Equivalently, the property known as the IIA imposed by the conditional logit model holds if and only if all dissimilarity parameters are equal to one. We discuss the IIA in more detail now.

◁

Testing for the IIA

The IIA is a property of the multinomial and conditional logit models that forces the odds of choosing one alternative over another to be independent of the other alternatives. For simplicity, suppose that a family was choosing only between Freebirds and Mama's Pizza, and the family was equally likely to choose either of the restaurants. The probability of going to each restaurant is 50%. Now suppose that Bill's Burritos opens up next door to Freebirds, which is also a burrito restaurant. If the IIA holds, then the probability of going to each restaurant must now be 33.33% so that the family remains equally likely to go to Mama's Pizza or Freebirds.

The IIA may sometimes be a plausible assumption. However, a more likely scenario would be for the probability of going to Mama's Pizza to remain at 50% and the probabilities of going to Freebirds and Bill's Burritos to be 25% each, because the two restaurants are next door to each other and serve the same food. Nested logit analysis would allow us to relax the IIA assumption of conditional logit. We could group Bill's Burritos and Freebirds into one nest that encompasses all burrito restaurants and create a second nest for pizzerias.

The IIA is a consequence of assuming that the errors are independent and identically distributed (i.i.d.). Because the errors are i.i.d., they cannot contain any alternative-specific unobserved information, and therefore adding a new alternative cannot affect the relationship between a pair of existing alternatives.

In the previous example, we saw that a joint test that the dissimilarity parameters were equal to one is one way to test for IIA. However, that test required us to specify a decision tree for the

nested logit model, and different specifications could lead to conflicting results of the test. Hausman and McFadden (1984) suggest that if part of the choice set truly is irrelevant with respect to the other alternatives, omitting that subset from the conditional logit model will not lead to inconsistent estimates. Therefore, Hausman's (1978) specification test can be used to test for IIA, and this test will not be sensitive to the tree structure we specify for a nested logit model.

▷ Example 4

We want to test the IIA for the subset of family restaurants against the alternatives of fast food and fancy restaurants. To do so, we need to use Stata's `hausman` command; see [R] **hausman**.

We first run the estimation on the full bottom alternative set, save the results by using `estimates store`, and then run the estimation on the bottom alternative set, excluding the alternatives of family restaurants. We then run the `hausman` test.

```
. generate incFast = (type == 1) * income
. generate incFancy = (type == 3) * income
. generate kidFast = (type == 1) * kids
. generate kidFancy = (type == 3) * kids
. clogit chosen cost rating distance incFast incFancy kidFast kidFancy,
> group(family_id) nolog
Conditional (fixed-effects) logistic regression   Number of obs   =       2100
                                                  LR chi2(7)      =     189.73
                                                  Prob > chi2     =     0.0000
Log likelihood = -488.90834                       Pseudo R2       =     0.1625

------------------------------------------------------------------------------
      chosen |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        cost |  -.1367799   .0358479    -3.82   0.000    -.2070404   -.0665193
      rating |   .3066622   .1418291     2.16   0.031     .0286823    .584642
    distance |  -.1977505   .0471653    -4.19   0.000    -.2901927   -.1053082
     incFast |  -.0390183   .0094018    -4.15   0.000    -.0574455   -.0205911
    incFancy |   .0407053   .0080405     5.06   0.000     .0249462    .0564644
     kidFast |  -.2398757   .1063674    -2.26   0.024     -.448352   -.0313994
    kidFancy |  -.3893862   .1143797    -3.40   0.001    -.6135662   -.1652061
------------------------------------------------------------------------------
. estimates store fullset
. clogit chosen cost rating distance incFast kidFast if type != 2,
> group(family_id) nolog
note: 222 groups (888 obs) dropped because of all positive or
      all negative outcomes.
Conditional (fixed-effects) logistic regression   Number of obs   =        312
                                                  LR chi2(5)      =      44.35
                                                  Prob > chi2     =     0.0000
Log likelihood = -85.955324                       Pseudo R2       =     0.2051

------------------------------------------------------------------------------
      chosen |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        cost |  -.0616621    .067852    -0.91   0.363    -.1946496    .0713254
      rating |   .1659001   .2832041     0.59   0.558    -.3891698     .72097
    distance |   -.244396   .0995056    -2.46   0.014    -.4394234   -.0493687
     incFast |  -.0737506   .0177444    -4.16   0.000     -.108529   -.0389721
     kidFast |   .4105386   .2137051     1.92   0.055    -.0083157    .8293928
------------------------------------------------------------------------------
```

```
. hausman . fullset
                 ---- Coefficients ----
                 (b)          (B)            (b-B)     sqrt(diag(V_b-V_B))
                  .         fullset       Difference          S.E.
-------------------------------------------------------------------------
        cost    -.0616621    -.1367799       .0751178        .0576092
      rating     .1659001     .3066622      -.1407621        .2451308
    distance    -.244396     -.1977505      -.0466456        .0876173
     incFast    -.0737506    -.0390183      -.0347323         .015049
     kidFast     .4105386    -.2398757       .6504143        .1853533
-------------------------------------------------------------------------
                           b = consistent under Ho and Ha; obtained from clogit
        B = inconsistent under Ha, efficient under Ho; obtained from clogit
    Test:  Ho:  difference in coefficients not systematic
                  chi2(5) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                          =       10.70
                Prob>chi2 =      0.0577
                (V_b-V_B is not positive definite)
```

Similar to our findings in example 3, the results of the test of the IIA are mixed. We cannot reject the IIA at the commonly used 5% significance level, but we could at the 10% level. Substantively, a significant test result suggests that the odds of going to one of the fancy restaurants versus going to one of the fast food restaurants changes if we include the family restaurants in the alternative set and that a nested logit specification may be warranted.

◁

Nonnormalized model

Previous versions of Stata fit a nonnormalized nested logit model that is available via the `nonnormalized` option. The nonnormalized version is presented in, for example, Greene (2012, 768–770). Here we outline the differences between the RUM-consistent and nonnormalized models. Our discussion follows Heiss (2002) and assumes the decision tree has two levels, with M alternatives at the upper level and a total of J alternatives at the bottom level.

In a RUM framework, by consuming alternative j, decision maker i obtains utility

$$U_{ij} = V_{ij} + \epsilon_{ij} = \alpha_j + \mathbf{x}_{ij}\boldsymbol{\beta}_j + \mathbf{z}_i\boldsymbol{\gamma}_j + \epsilon_{ij}$$

where V_{ij} is the deterministic part of utility and ϵ_{ij} is the random part. $\mathbf{x}_{ij}$ are alternative-specific variables and $\mathbf{z}_i$ are case-specific variables. The set of errors $\epsilon_{i1}, \ldots, \epsilon_{iJ}$ are assumed to follow the generalized extreme-value (GEV) distribution, which is a generalization of the type 1 extreme-value distribution that allows for alternatives within nests of the tree structure to be correlated. Let ρ_m denote the correlation in nest m, and define the dissimilarity parameter $\tau_m = \sqrt{1-\rho_m}$. $\tau_m = 0$ implies that the alternatives in nest m are perfectly correlated, whereas $\tau_m = 1$ implies independence.

The *inclusive value* for the mth nest corresponds to the expected value of the utility that decision maker i obtains by consuming an alternative in nest m. Denote this value by IV_m:

$$\text{IV}_m = \ln \sum_{j \in B_m} \exp\left(V_k/\tau_m\right) \tag{1}$$

where B_m denotes the set of alternatives in nest m. Given the inclusive values, we can show that the probability that random-utility–maximizing decision maker i chooses alternative j is

$$\Pr_j = \frac{\exp\left\{V_j/\tau(j)\right\}}{\exp\left\{\text{IV}(j)\right\}} \frac{\exp\left\{\tau(j)\text{IV}(j)\right\}}{\sum_m \exp\left(\tau_m \text{IV}_m\right)}$$

where $\tau(j)$ and $\text{IV}(j)$ are the dissimilarity parameter and inclusive value for the nest in which alternative j lies.

In contrast, for the nonnormalized model, we have a latent variable

$$\widetilde{V}_{i,j} = \widetilde{\alpha}_j + \mathbf{x}_{i,j}\widetilde{\boldsymbol{\beta}}_j + \mathbf{z}_i\widetilde{\boldsymbol{\gamma}}_j$$

and corresponding inclusive values

$$\widetilde{\text{IV}}_m = \ln \sum_{j \in B_m} \exp\left(\widetilde{V}_k\right) \tag{2}$$

The probability of choosing alternative j is

$$\Pr_j = \frac{\exp\left(\widetilde{V}_j\right)}{\exp\left\{\widetilde{\text{IV}}(j)\right\}} \frac{\exp\left\{\tau(j)\widetilde{\text{IV}}(j)\right\}}{\sum_m \exp\left(\tau_m \widetilde{\text{IV}}_m\right)}$$

Equations (1) and (2) represent the key difference between the RUM-consistent and nonnormalized models. By scaling the V_{ij} within each nest, the RUM-consistent model allows utilities to be compared across nests. Without the rescaling, utilities can be compared only for goods within the same nest. Moreover, adding a constant to each V_{ij} for consumer i will not affect the probabilities of the RUM-consistent model, but adding a constant to each $\widetilde{V}_{ij}$ will affect the probabilities from the nonnormalized model. Decisions based on utility maximization can depend only on utility differences and not the scale or zero point of the utility function because utility is an ordinal concept, so the nonnormalized model cannot be consistent with utility maximization.

Heiss (2002) showed that the nonnormalized model can be RUM consistent in the special case where all the variables are specified in the bottom-level equation. Then multiplying the nonnormalized coefficients by the respective dissimilarity parameters results in the RUM-consistent coefficients.

❑ Technical note

Degenerate nests occur when there is only one alternative in a branch of the tree hierarchy. The associated dissimilarity parameter of the RUM model is not defined. The inclusive-valued parameter of the nonnormalized model will be identifiable if there are alternative-specific variables specified in (1) of the model specification (the *indepvars* in the model syntax). Numerically, you can skirt the issue of nonidentifiable/undefined parameters by setting constraints on them. For the RUM model constraint, set the dissimilarity parameter to 1. See the description of `constraints()` in *Options* for details on setting constraints on the dissimilarity parameters.

❑

Saved results

nlogit saves the following in e():

Scalars

e(N)	number of observations
e(N_case)	number of cases
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_alt)	number of alternatives for bottom level
e(k_alt*j*)	number of alternatives for *j*th level
e(k_indvars)	number of independent variables
e(k_ind2vars)	number of by-alternative variables for bottom level
e(k_ind2vars*j*)	number of by-alternative variables for *j*th level
e(df_m)	model degrees of freedom
e(df_c)	clogit model degrees of freedom
e(ll)	log likelihood
e(ll_c)	clogit model log likelihood
e(N_clust)	number of clusters
e(chi2)	χ^2
e(chi2_c)	likelihood-ratio test for IIA
e(p)	p-value for model Wald test
e(p_c)	p-value for IIA test
e(i_base)	base index for bottom level
e(i_base*j*)	base index for *j*th level
e(levels)	number of levels
e(alt_min)	minimum number of alternatives
e(alt_avg)	average number of alternatives
e(alt_max)	maximum number of alternatives
e(const)	constant indicator for bottom level
e(const*j*)	constant indicator for *j*th level
e(rum)	1 if RUM model, 0 otherwise
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	nlogit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(indvars)	name of independent variables
e(ind2vars)	by-alternative variables for bottom level
e(ind2vars*j*)	by-alternative variables for *j*th level
e(case)	variable defining cases
e(altvar)	alternative variable for bottom level
e(altvar*j*)	alternative variable for *j*th level
e(alteqs)	equation names for bottom level
e(alteqs*j*)	equation names for *j*th level
e(alt*i*)	*i*th alternative for bottom level
e(alt*j*_*i*)	*i*th alternative for *j*th level
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(chi2type)	Wald, type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(datasignature)	the checksum
e(datasignaturevars)	variables used in calculation of checksum
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(k_altern)	number of alternatives at each level
e(k_branch*j*)	number of branches at each alternative of *j*th level
e(stats)	alternative statistics for bottom level
e(stats*j*)	alternative statistics for *j*th level
e(altidx*j*)	alternative indices for *j*th level
e(alt_ind2vars)	indicators for bottom level estimated by-alternative variable—e(k_alt)×e(k_ind2vars)
e(alt_ind2vars*j*)	indicators for *j*th level estimated by-alternative variable—e(k_alt*j*)×e(k_ind2vars*j*)
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

nlogit, nlogitgen, and nlogittree are implemented as ado-files.

Methods and formulas are presented under the following headings:

Two-level nested logit model
Three-level nested logit model

Two-level nested logit model

Consider our two-level nested logit model for restaurant choice. We define $T = \{1, 2, 3\}$ to be the set of indices denoting the three restaurant types and $R_1 = \{1, 2\}$, $R_2 = \{3, 4, 5\}$, and $R_3 = \{6, 7\}$ to be the set of indices representing each restaurant within type $t \in T$. Let C_1 and C_2 be the random variables that represent the choices made for the first level, restaurant type, and second level, restaurant, of the hierarchy, where we observe the choices $C_1 = t, t \in T$, and $C_2 = j, j \in R_t$. Let $\mathbf{z}_t$ and $\mathbf{x}_{tj}$, for $t \in T$ and $j \in R_t$, refer to the row vectors of explanatory variables for the first-level alternatives and bottom-level alternatives for one case, respectively. We write the utilities (latent variables) as $U_{tj} = \mathbf{z}_t\boldsymbol{\alpha}_t + \mathbf{x}_{tj}\boldsymbol{\beta}_j + \epsilon_{tj} = \boldsymbol{\eta}_{tj} + \epsilon_{tj}$, where $\boldsymbol{\alpha}_t$ and $\boldsymbol{\beta}_j$ are column vectors and the ϵ_{tj} are random disturbances. When the $\mathbf{x}_{tj}$ are alternative specific, we can drop the indices from $\boldsymbol{\beta}$, where we estimate one coefficient for each alternative in R_t, $t \in T$. These variables are specified in the first equation of the `nlogit` syntax (see example 3).

When the random-utility framework is used to describe the choice behavior, the alternative that is chosen is the alternative that has the highest utility. Assume for our restaurant example that we choose restaurant type $t \in T$. For the RUM parameterization of `nlogit`, the conditional distribution of ϵ_{tj} given choice of restaurant type t is a multivariate version of Gumbel's extreme-value distribution,

$$F_{R|T}(\boldsymbol{\epsilon} \,|\, t) = \exp\left[-\left\{\sum_{m \in R_t} \exp(\epsilon_{tm}/\tau_t)\right\}^{\tau_t}\right] \tag{3}$$

where it has been shown that the ϵ_{tj}, $j \in R_t$, are exchangeable with correlation $1 - \tau_t^2$, for $\tau_t \in (0, 1]$ (Kotz and Nadarajah 2000). For example, the probability of choosing Christopher's, $j = 6$ given type $t = 3$, is

$$\begin{aligned}
\Pr(C_2 = 6 \,|\, C_1 = 3) &= \Pr\left(U_{36} - U_{37} > 0\right) \\
&= \Pr\left(\epsilon_{37} \leq \epsilon_{36} + \eta_{36} - \eta_{37}\right) \\
&= \int_{-\infty}^{\infty} \left\{ \int_{-\infty}^{\epsilon_{36}+\eta_{36}-\eta_{37}} f_{R|T}\left(\epsilon_{36}, \epsilon_{37}\right) d\epsilon_{37} \right\} d\epsilon_{36}
\end{aligned}$$

where $f = \dfrac{\partial F}{\partial \epsilon_{36} \partial \epsilon_{37}}$ is the joint density function of $\boldsymbol{\epsilon}$ given t. U_{37} is the utility of eating at Mad Cows, the other fancy ($t = 3$) restaurant. Amemiya (1985) demonstrates that this integral evaluates to the logistic function

$$\begin{aligned}
\Pr(C_2 = 6 \,|\, C_1 = 3) &= \frac{\exp(\boldsymbol{\eta}_{36}/\tau_3)}{\exp(\boldsymbol{\eta}_{36}/\tau_3) + \exp(\boldsymbol{\eta}_{37}/\tau_3)} \\
&= \frac{\exp(\mathbf{x}_{36}\boldsymbol{\beta}_6/\tau_3)}{\exp(\mathbf{x}_{36}\boldsymbol{\beta}_6/\tau_3) + \exp(\mathbf{x}_{37}\boldsymbol{\beta}_7/\tau_3)}
\end{aligned}$$

and in general

$$\Pr(C_2 = j \,|\, C_1 = t) = \frac{\exp(\mathbf{x}_{tj}\boldsymbol{\beta}_j/\tau_t)}{\sum_{m \in R_t} \exp(\mathbf{x}_{tm}\boldsymbol{\beta}_m/\tau_t)} \tag{4}$$

Letting $\tau_t = 1$ in (3) reduces to the product of independent extreme-value distributions, and (4) reduces to the multinomial logistic function.

For the logistic function in (4), we scale the linear predictors by the dissimilarity parameters. Another formulation of the conditional probability of choosing alternative $j \in R_t$ given choice $t \in T$ is the logistic function without this normalization:

$$\Pr(C_2 = j \mid C_1 = t) = \frac{\exp(\mathbf{x}_{tj}\boldsymbol{\beta}_j)}{\sum_{m\in R_t}\exp(\mathbf{x}_{tm}\boldsymbol{\beta}_m)}$$

and this is what is used in `nlogit`'s nonnormalized parameterization.

Amemiya (1985) defines the general form for the joint distribution of the ϵ's as

$$F_{T,R}(\boldsymbol{\epsilon}) = \exp\left\{-\sum_{k\in T}\theta_k\left(\sum_{m\in R_k}\exp(-\epsilon_{km}/\tau_k)\right)^{\tau_k}\right\}$$

from which the probability of choice $t, t \in T$ can be derived as

$$\Pr(C_1 = t) = \frac{\theta_t\left\{\sum_{m\in R_t}\exp(\boldsymbol{\eta}_{tm}/\tau_t)\right\}^{\tau_t}}{\sum_{k\in T}\theta_k\left\{\sum_{m\in R_k}\exp(\boldsymbol{\eta}_{km}/\tau_k)\right\}^{\tau_k}} \tag{5}$$

`nlogit` sets $\theta_t = 1$. Noting that

$$\begin{aligned}\left\{\sum_{m\in R_t}\exp(\boldsymbol{\eta}_{tm}/\tau_t)\right\}^{\tau_t} &= \left\{\sum_{m\in R_t}\exp\left(\frac{\mathbf{z}_t\boldsymbol{\alpha}_t + \mathbf{x}_{tm}\boldsymbol{\beta}_m}{\tau_t}\right)\right\}^{\tau_t}\\ &= \exp(\mathbf{z}_t\boldsymbol{\alpha}_t)\left\{\sum_{m\in R_t}\exp\left(\mathbf{x}_{tm}\boldsymbol{\beta}_m/\tau_t\right)\right\}^{\tau_t}\\ &= \exp(\mathbf{z}_t\boldsymbol{\alpha}_t + \tau_t I_t)\end{aligned}$$

we define the inclusive values I_t as

$$I_t = \ln\left\{\sum_{m\in R_t}\exp(\mathbf{x}_{tm}\boldsymbol{\beta}_m/\tau_t)\right\}$$

and we can view

$$\exp(\tau_t I_t) = \left\{\sum_{m\in R_t}\exp(x_{tm}\boldsymbol{\beta}_m)^{1/\tau_t}\right\}^{\tau_t}$$

as a weighted average of the $\exp(x_{tm}\boldsymbol{\beta}_m)$, for $m \in R_t$. For the `nlogit` RUM parameterization, we can express (5) as

$$\Pr(C_1 = t) = \frac{\exp(\mathbf{z}_t\boldsymbol{\alpha}_t + \tau_t I_t)}{\sum_{k\in T}\exp(\mathbf{z}_k\boldsymbol{\alpha}_k + \tau_k I_k)}$$

Next we define inclusive values for the nonnormalized model to be

$$\widetilde{I}_t = \ln\left\{\sum_{m\in R_t}\exp(\mathbf{x}_{tm}\boldsymbol{\beta}_m)\right\}$$

and we express $\Pr(C_1 = t)$ as

$$\Pr(C_1 = t) = \frac{\exp(\mathbf{z}_t\boldsymbol{\alpha}_t + \tau_t\widetilde{I}_t)}{\sum_{k\in T}\exp(\mathbf{z}_k\boldsymbol{\alpha}_k + \tau_k\widetilde{I}_k)} \tag{6}$$

Equation (5) is consistent with (6) only when $\eta_{ij} = \mathbf{x}_{ij}\boldsymbol{\beta}_j$, so in general the `nlogit` nonnormalized model is not consistent with the RUM model.

Now assume that we have N cases where we add a third subscript, i, to denote case i, $i = 1, \ldots, N$. Denote y_{itj} to be a binary variable indicating the choice made by case i so that for each i only one y_{itj} is 1 and the rest are 0 for all $t \in T$ and $j \in R_t$. The log likelihood for the two-level RUM-consistent model is

$$\begin{aligned}\log \ell &= \sum_{i=1}^{N}\sum_{k\in T}\sum_{m\in R_k} y_{ikm}\log\{\Pr(C_{i1}=i)\Pr(C_{i2}=m|C_{i1}=i)\} \\ &= \sum_{i=1}^{N}\sum_{k\in T}\sum_{m\in R_k} y_{ikm}\left[\mathbf{z}_{ik}\boldsymbol{\alpha}_k + \tau_k I_{ik} - \log\left\{\sum_{l\in T}\exp(\mathbf{z}_{il}\boldsymbol{\alpha}_l + \tau_l I_{il})\right\} + \right. \\ &\qquad \left. \mathbf{x}_{ikm}\boldsymbol{\beta}_m/\tau_k - \log\left\{\sum_{l\in R_k}\exp(\mathbf{x}_{ikl}\boldsymbol{\beta}_l/\tau_k)\right\}\right]\end{aligned}$$

The likelihood for the nonnormalized model has a similar form, replacing I with $\widetilde{I}$ and by not scaling $\mathbf{x}_{ikj}\boldsymbol{\beta}_j$ by τ_k.

Three-level nested logit model

Here we define a three-level nested logit model that can be generalized to the four-level and higher models. As before, let the integer set T be the indices for the first level of choices. Let sets S_t, $t \in T$, be mutually exclusive sets of integers representing the choices of the second level of the hierarchy. Finally, let R_j, $j \in S_t$, be the bottom-level choices. Let $U_{tjk} = \eta_{tjk} + \epsilon_{tjk}$, $k \in R_j$, and the distribution of ϵ_{tjk} be Gumbel's multivariate extreme value of the form

$$F(\boldsymbol{\epsilon}) = \exp\left(-\sum_{t\in T}\left[\sum_{j\in S_t}\left\{\sum_{k\in R_j}\exp(-\eta_{tjk}/\tau_j)\right\}^{\tau_j/\upsilon_t}\right]^{\upsilon_j}\right)$$

Let C_1, C_2, and C_3 represent the choice random variables for levels 1, 2, and the bottom, respectively. Then the set of conditional probabilities is

$$\Pr(C_3 = k \,|\, C_1 = t, C_2 = j) = \frac{\exp(\eta_{tjk}/\tau_j)}{\sum_{l\in R_j}\exp(\eta_{tjl}/\tau_j)}$$

$$\Pr(C_2 = j \,|\, C_1 = t) = \frac{\left\{\sum_{k\in R_j}\exp(\eta_{tjk}/\tau_j)\right\}^{\tau_j/\upsilon_t}}{\sum_{l\in S_t}\left\{\sum_{k\in R_l}\exp(\eta_{tlk}/\tau_l)\right\}^{\tau_l/\upsilon_t}}$$

$$\Pr(C_1 = t) = \frac{\left[\sum_{j\in S_t}\left\{\sum_{k\in R_j}\exp(\eta_{tjk}/\tau_j)\right\}^{\tau_j/\upsilon_t}\right]^{\upsilon_t}}{\sum_{l\in T}\left[\sum_{j\in S_l}\left\{\sum_{k\in R_j}\exp(\eta_{ljk}/\tau_j)\right\}^{\tau_j/\upsilon_l}\right]^{\upsilon_l}}$$

Assume that we can decompose the linear predictor as $\eta_{tjk} = \mathbf{z}_t\boldsymbol{\alpha}_t + \mathbf{u}_{tj}\boldsymbol{\gamma}_j + \mathbf{x}_{tjk}\boldsymbol{\beta}_k$. Here $\mathbf{z}_t$, $\mathbf{u}_{tj}$, and $\mathbf{x}_{tjk}$ are the row vectors of explanatory variables for the first, second, and bottom levels of the hierarchy, respectively, and $\boldsymbol{\alpha}_t$, $\boldsymbol{\gamma}_j$, and $\boldsymbol{\beta}_k$ are the corresponding column vectors of regression coefficients for $t \in T$, $j \in S_t$, and $k \in R_j$. We then can define the inclusive values for the first and second levels as

$$I_{tj} = \log \sum_{k \in R_j} \exp(\mathbf{x}_{tjk}\boldsymbol{\beta}_k/\tau_j)$$

$$J_t = \log \sum_{j \in S_t} \exp(\mathbf{u}_{tj}\boldsymbol{\gamma}_j/\upsilon_t + \frac{\tau_j}{\upsilon_t} I_{tj})$$

and rewrite the probabilities

$$\Pr(C_3 = k \,|\, C_1 = t, C_2 = j) = \frac{\exp(\mathbf{x}_{tjk}\boldsymbol{\beta}_k/\tau_j)}{\sum_{l \in R_j} \exp(\mathbf{x}_{tjl}\boldsymbol{\beta}_l/\tau_j)}$$

$$\Pr(C_2 = j \,|\, C_1 = t) = \frac{\exp(\mathbf{u}_{tj}\boldsymbol{\gamma}_j/\upsilon_t + \frac{\tau_j}{\upsilon_t} I_{tj})}{\sum_{l \in S_t} \exp(\mathbf{u}_{tl}\boldsymbol{\gamma}_l/\upsilon_t + \frac{\tau_l}{\upsilon_t} I_{tl})}$$

$$\Pr(C_1 = t) = \frac{\exp(\mathbf{z}_t\boldsymbol{\alpha}_t + \upsilon_t J_t)}{\sum_{l \in T} \exp(\mathbf{z}_l\boldsymbol{\alpha}_l + \upsilon_l J_l)}$$

We add a fourth index, i, for case and define the indicator variable y_{lijk}, $l = 1, \ldots, N$, to indicate the choice made by case i, $t \in T$, $j \in S_t$, and $k \in R_j$. The log likelihood for the `nlogit` RUM-consistent model is

$$\ell = \sum_{i=1}^{N} \sum_{t \in T} \sum_{j \in S_t} \sum_{k \in R_j} y_{itjk} \left\{ \mathbf{z}_{it}\boldsymbol{\alpha}_t + \upsilon_t J_{it} - \log\left(\sum_{m \in T} \mathbf{z}_{im}\boldsymbol{\alpha}_m + \upsilon_m J_{im} \right) + \right.$$

$$\mathbf{u}_{itj}\boldsymbol{\gamma}_j/\upsilon_t + \frac{\tau_j}{\upsilon_t} I_{itj} - \log\left(\sum_{m \in S_t} \mathbf{u}_{itm}\boldsymbol{\gamma}_m/\upsilon_t + \frac{\tau_m}{\upsilon_t} I_{itm} \right) +$$

$$\left. \mathbf{x}_{itjk}\boldsymbol{\beta}_k/\tau_k - \sum_{m \in R_t} \exp(\mathbf{x}_{itjm}\boldsymbol{\beta}_m/\tau_k) \right\}$$

and for the nonnormalized `nlogit` model the log likelihood is

$$\ell = \sum_{i=1}^{N} \sum_{t \in T} \sum_{j \in S_t} \sum_{k \in R_j} y_{itjk} \left\{ \mathbf{z}_{it}\boldsymbol{\alpha}_t + \upsilon_t J_{it} - \log\left(\sum_{m \in T} \mathbf{z}_{im}\boldsymbol{\alpha}_m + \upsilon_m J_{im} \right) + \right.$$

$$\mathbf{u}_{itj}\boldsymbol{\gamma}_j + \tau_j I_{itj} - \log\left(\sum_{m \in S_t} \mathbf{u}_{itm}\boldsymbol{\gamma}_m + \tau_m I_{itm} \right) +$$

$$\left. \mathbf{x}_{itjk}\boldsymbol{\beta}_k - \sum_{m \in R_t} \exp(\mathbf{x}_{itjm}\boldsymbol{\beta}_m) \right\}$$

Extending the model to more than three levels is straightforward, albeit notationally cumbersome.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

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Also see

[R] **nlogit postestimation** — Postestimation tools for nlogit

[R] **asclogit** — Alternative-specific conditional logit (McFadden's choice) model

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **ologit** — Ordered logistic regression

[R] **rologit** — Rank-ordered logistic regression

[R] **slogit** — Stereotype logistic regression

[U] **20 Estimation and postestimation commands**

Title

nlogit postestimation — Postestimation tools for nlogit

Description

The following postestimation command is of special interest after `nlogit`:

Command	Description
`estat alternatives`	alternative summary statistics

For information about this command, see [R] **asmprobit postestimation**.

The following standard postestimation commands are also available:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`	likelihood-ratio test
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic hlevel(#) altwise]

predict [type] {stub*|newvarlist} [if] [in], scores
```

statistic	Description
Main	
pr	predicted probabilities of choosing the alternatives at all levels of the hierarchy or at level #, where # is specified by `hlevel(#)`; the default
xb	linear predictors for all levels of the hierarchy or at level #, where # is specified by `hlevel(#)`
condp	predicted conditional probabilities at all levels of the hierarchy or at level #, where # is specified by `hlevel(#)`
iv	inclusive values for levels 2, ..., `e(levels)` or for `hlevel(#)`

The inclusive value for the first-level alternatives is not used in estimation; therefore, it is not calculated.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr` calculates the probability of choosing each alternative at each level of the hierarchy. Use the `hlevel(#)` option to compute the alternative probabilities at level #. When `hlevel(#)` is not specified, j new variables must be given, where j is the number of levels, or use the *stub*`*` option to have `predict` generate j variables with the prefix *stub* and numbered from 1 to j. The `pr` option is the default and if one new variable is given, the probability of the bottom-level alternatives are computed. Otherwise, probabilities for all levels are computed and the *stub*`*` option is still valid.

`xb` calculates the linear prediction for each alternative at each level. Use the `hlevel(#)` option to compute the linear predictor at level #. When `hlevel(#)` is not specified, j new variables must be given, where j is the number of levels, or use the *stub*`*` option to have `predict` generate j variables with the prefix *stub* and numbered from 1 to j.

`condp` calculates the conditional probabilities for each alternative at each level. Use the `hlevel(#)` option to compute the conditional probabilities of the alternatives at level #. When `hlevel(#)` is not specified, j new variables must be given, where j is the number of levels, or use the *stub*`*` option to have `predict` generate j variables with the prefix *stub* and numbered from 1 to j.

`iv` calculates the inclusive value for each alternative at each level. Use the `hlevel(#)` option to compute the inclusive value at level #. There is no inclusive value at level 1. If `hlevel(#)` is not used, $j-1$ new variables are required, where j is the number of levels, or use *stub*`*` to have `predict` generate $j-1$ variables with the prefix *stub* and numbered from 2 to j. See *Methods and formulas* in [R] **nlogit** for a definition of the inclusive values.

`hlevel(#)` calculates the prediction only for hierarchy level #.

`altwise` specifies that alternativewise deletion be used when marking out observations due to missing values in your variables. The default is to use casewise deletion. The `xb` option always uses alternativewise deletion.

`scores` calculates the scores for each coefficient in `e(b)`. This option requires a new-variable list of length equal to the number of columns in `e(b)`. Otherwise, use the *stub*`*` option to have `predict` generate enumerated variables with prefix *stub*.

Remarks

`predict` may be used after `nlogit` to obtain the predicted values of the probabilities, the conditional probabilities, the linear predictions, and the inclusive values for each level of the nested logit model. Predicted probabilities for `nlogit` must be interpreted carefully. Probabilities are estimated for each case as a whole and not for individual observations.

▷ Example 1

Continuing with our model in example 3 of [R] **nlogit**, we refit the model and then examine a summary of the alternatives and their frequencies in the estimation sample.

```
. use http://www.stata-press.com/data/r12/restaurant
. nlogitgen type = restaurant(fast: Freebirds | MamasPizza,
> family: CafeEccell | LosNortenos | WingsNmore, fancy: Christophers | MadCows)
```

(*output omitted*)

```
. nlogit chosen cost rating distance || type: income kids, base(family) ||
> restaurant:, noconst case(family_id)
```

(*output omitted*)

```
. estat alternatives
```

Alternatives summary for type

index	Alternative value	label	Cases present	Frequency selected	Percent selected
1	1	fast	600	27	9.00
2	2	family	900	222	74.00
3	3	fancy	600	51	17.00

Alternatives summary for restaurant

index	Alternative value	label	Cases present	Frequency selected	Percent selected
1	1	Freebirds	300	12	4.00
2	2	MamasPizza	300	15	5.00
3	3	CafeEccell	300	78	26.00
4	4	LosNortenos	300	75	25.00
5	5	WingsNmore	300	69	23.00
6	6	Christophers	300	27	9.00
7	7	MadCows	300	24	8.00

Next we predict p2 = Pr(restaurant); p1 = Pr(type); condp = Pr(restaurant | type); xb2, the linear prediction for the bottom-level alternatives; xb1, the linear prediction for the first-level alternatives; and iv, the inclusive values for the bottom-level alternatives.

```
. predict p*
(option pr assumed)
. predict condp, condp hlevel(2)
. sort family_id type restaurant
. list restaurant type chosen p2 p1 condp in 1/14, sepby(family_id) divider
```

	restaurant	type	chosen	p2	p1	condp
1.	Freebirds	fast	1	.0642332	.1189609	.5399519
2.	MamasPizza	fast	0	.0547278	.1189609	.4600481
3.	CafeEccell	family	0	.284409	.7738761	.3675124
4.	LosNortenos	family	0	.3045242	.7738761	.3935051
5.	WingsNmore	family	0	.1849429	.7738761	.2389825
6.	Christophers	fancy	0	.0429508	.107163	.4007991
7.	MadCows	fancy	0	.0642122	.107163	.5992009
8.	Freebirds	fast	0	.0183578	.0488948	.3754559
9.	MamasPizza	fast	0	.030537	.0488948	.6245441
10.	CafeEccell	family	0	.2832149	.756065	.3745907
11.	LosNortenos	family	1	.3038883	.756065	.4019341
12.	WingsNmore	family	0	.1689618	.756065	.2234752
13.	Christophers	fancy	0	.1041277	.1950402	.533878
14.	MadCows	fancy	0	.0909125	.1950402	.466122

```
. predict xb*, xb
. predict iv, iv
. list restaurant type chosen xb* iv in 1/14, sepby(family_id) divider
```

	restaurant	type	chosen	xb1	xb2	iv
1.	Freebirds	fast	1	-1.124805	-1.476914	-.2459659
2.	MamasPizza	fast	0	-1.124805	-1.751229	-.2459659
3.	CafeEccell	family	0	0	-2.181112	.1303341
4.	LosNortenos	family	0	0	-2.00992	.1303341
5.	WingsNmore	family	0	0	-3.259229	.1303341
6.	Christophers	fancy	0	1.405185	-6.804211	-.745332
7.	MadCows	fancy	0	1.405185	-5.155514	-.745332
8.	Freebirds	fast	0	-1.804794	-2.552233	-.5104123
9.	MamasPizza	fast	0	-1.804794	-1.680583	-.5104123
10.	CafeEccell	family	0	0	-2.400434	.0237072
11.	LosNortenos	family	1	0	-2.223939	.0237072
12.	WingsNmore	family	0	0	-3.694409	.0237072
13.	Christophers	fancy	0	1.490775	-5.35932	-.6796131
14.	MadCows	fancy	0	1.490775	-5.915751	-.6796131

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **nlogit** — Nested logit regression

[U] **20 Estimation and postestimation commands**

Title

nlsur — Estimation of nonlinear systems of equations

Syntax

Interactive version

```
nlsur (depvar_1 = <sexp_1>) (depvar_2 = <sexp_2>) ... [if] [in] [weight] [, options]
```

Programmed substitutable expression version

```
nlsur sexp_prog : depvar_1 depvar_2 ... [varlist] [if] [in] [weight] [, options]
```

Function evaluator program version

```
nlsur func_prog @ depvar_1 depvar_2 ... [varlist] [if] [in] [weight] ,
    nequations(#) { parameters(namelist) | nparameters(#) } [options]
```

where

depvar_j is the dependent variable for equation j;

<sexp>_j is the substitutable expression for equation j;

sexp_prog is a substitutable expression program; and

func_prog is a function evaluator program.

options	Description
Model	
`fgnls`	use two-step FGNLS estimator; the default
`ifgnls`	use iterative FGNLS estimator
`nls`	use NLS estimator
`variables(`*varlist*`)`	variables in model
`initial(`*initial_values*`)`	initial values for parameters
`nequations(#)`	number of equations in model (function evaluator program version only)
* `parameters(`*namelist*`)`	parameters in model (function evaluator program version only)
* `nparameters(#)`	number of parameters in model (function evaluator program version only)
sexp_options	options for substitutable expression program
func_options	options for function evaluator program
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `gnr`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`title(`*string*`)`	display *string* as title above the table of parameter estimates
`title2(`*string*`)`	display *string* as subtitle
display_options	control column formats and line width
Optimization	
optimization_options	control the optimization process; seldom used
`eps(#)`	specify # for convergence criteria; default is `eps(1e-5)`
`ifgnlsiterate(#)`	set maximum number of FGNLS iterations
`ifgnlseps(#)`	specify # for FGNLS convergence criterion; default is `ifgnlseps(1e-10)`
`delta(#)`	specify stepsize # for computing derivatives; default is `delta(4e-7)`
`noconstants`	no equations have constant terms
`hasconstants(`*namelist*`)`	use *namelist* as constant terms
`coeflegend`	display legend instead of statistics

* You must specify `parameters(`*namelist*`)`, `nparameters(#)`, or both.

`bootstrap`, `by`, `jackknife`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`aweights`, `fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Multiple-equation models > Nonlinear seemingly unrelated regression

Description

`nlsur` fits a system of nonlinear equations by feasible generalized nonlinear least squares (FGNLS). With the interactive version of the command, you enter the system of equations on the command line or in the dialog box by using *substitutable expressions*. If you have a system that you use regularly, you can write a *substitutable expression program* and use the second syntax to avoid having to reenter the system every time. The function evaluator program version gives you the most flexibility in exchange for increased complexity; with this version, your program is given a vector of parameters and a variable list, and your program computes the system of equations.

When you write a substitutable expression program or a function evaluator program, the first five letters of the name must be `nlsur`. *sexp_prog* and *func_prog* refer to the name of the program without the first five letters. For example, if you wrote a function evaluator program named `nlsurregss`, you would type `nlsur regss @ ...` to estimate the parameters.

Options

Model

`fgnls` requests the two-step FGNLS estimator; this is the default.

`ifgnls` requests the iterative FGNLS estimator. For the nonlinear systems estimator, this is equivalent to maximum likelihood estimation.

`nls` requests the nonlinear least-squares (NLS) estimator.

`variables(`*varlist*`)` specifies the variables in the system. `nlsur` ignores observations for which any of these variables has missing values. If you do not specify `variables()`, `nlsur` issues an error message if the estimation sample contains any missing values.

`initial(`*initial_values*`)` specifies the initial values to begin the estimation. You can specify a $1 \times k$ matrix, where k is the total number of parameters in the system, or you can specify a parameter name, its initial value, another parameter name, its initial value, and so on. For example, to initialize `alpha` to 1.23 and `delta` to 4.57, you would type

```
. nlsur ..., initial(alpha 1.23 delta 4.57) ...
```

Initial values declared using this option override any that are declared within substitutable expressions. If you specify a matrix, the values must be in the same order in which the parameters are declared in your model. `nlsur` ignores the row and column names of the matrix.

`nequations(#)` specifies the number of equations in the system.

`parameters(`*namelist*`)` specifies the names of the parameters in the system. The names of the parameters must adhere to the naming conventions of Stata's variables; see [U] **11.3 Naming conventions**. If you specify both `parameters()` and `nparameters()`, the number of names in the former must match the number specified in the latter.

`nparameters(#)` specifies the number of parameters in the system. If you do not specify names with the `parameters()` options, `nlsur` names them `b1`, `b2`, ..., `b#`. If you specify both `parameters()` and `nparameters()`, the number of names in the former must match the number specified in the latter.

sexp_options refer to any options allowed by your *sexp_prog*.

func_options refer to any options allowed by your *func_prog*.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(gnr)`, the default, uses the conventionally derived variance estimator for nonlinear models fit using Gauss–Newton regression.

Reporting

`level(#)`; see [R] **estimation options**.

`title(`*string*`)` specifies an optional title that will be displayed just above the table of parameter estimates.

`title2(`*string*`)` specifies an optional subtitle that will be displayed between the title specified in `title()` and the table of parameter estimates. If `title2()` is specified but `title()` is not, `title2()` has the same effect as `title()`.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Optimization

optimization_options: `iterate(#)`, [`no`]`log`, `trace`. `iterate()` specifies the maximum number of iterations to use for NLS at each round of FGNLS estimation. This option is different from `ifgnlsiterate()`, which controls the maximum rounds of FGNLS estimation to use when the `ifgnls` option is specified. `log`/`nolog` specifies whether to show the iteration log, and `trace` specifies that the iteration log should include the current parameter vector.

`eps(#)` specifies the convergence criterion for successive parameter estimates and for the residual sum of squares (RSS). The default is `eps(1e-5)` (0.00001). `eps()` also specifies the convergence criterion for successive parameter estimates between rounds of iterative FGNLS estimation when `ifgnls` is specified.

`ifgnlsiterate(#)` specifies the maximum number of FGNLS iterations to perform. The default is the number set using `set maxiter` (see [R] **maximize**), which is 16,000 by default. To use this option, you must also specify the `ifgnls` option.

`ifgnlseps(#)` specifies the convergence criterion for successive estimates of the error covariance matrix during iterative FGNLS estimation. The default is `ifgnlseps(1e-10)`. To use this option, you must also specify the `ifgnls` option.

`delta(#)` specifies the relative change in a parameter, δ, to be used in computing the numeric derivatives. The derivative for parameter β_i is computed as

$$\{f_i(\mathbf{x}_i, \beta_1, \beta_2, \ldots, \beta_i + d, \beta_{i+1}, \ldots) - f_i(\mathbf{x}_i, \beta_1, \beta_2, \ldots, \beta_i, \beta_{i+1}, \ldots)\}/d$$

where $d = \delta(|\beta_i| + \delta)$. The default is `delta(4e-7)`.

`noconstants` indicates that none of the equations in the system includes constant terms. This option is generally not needed, even if there are no constant terms in the system; though in rare cases without this option, `nlsur` may claim that there is one or more constant terms even if there are none.

`hasconstants(`*namelist*`)` indicates the parameters that are to be treated as constant terms in the system of equations. The number of elements of *namelist* must equal the number of equations in

the system. The ith entry of *namelist* specifies the constant term in the ith equation. If an equation does not include a constant term, specify a period (.) instead of a parameter name. This option is seldom needed with the interactive and programmed substitutable expression versions, because in those cases `nlsur` can almost always find the constant terms automatically.

The following options are available with `nlsur` but are not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Substitutable expression programs
Function evaluator programs

Introduction

`nlsur` fits a system of nonlinear equations by FGNLS. It can be viewed as a nonlinear variant of Zellner's seemingly unrelated regression model (Zellner 1962; Zellner and Huang 1962; Zellner 1963) and is therefore commonly called nonlinear SUR or nonlinear SURE. The model is also discussed in textbooks such as Davidson and MacKinnon (1993, 2004) and Greene (2012, 305–306). Formally, the model fit by `nlsur` is

$$\begin{aligned} y_{i1} &= f_1(\mathbf{x}_i, \beta) + u_{i1} \\ y_{i2} &= f_2(\mathbf{x}_i, \beta) + u_{i2} \\ \vdots &= \vdots \\ y_{iM} &= f_M(\mathbf{x}_i, \beta) + u_{iM} \end{aligned}$$

for $i = 1, \ldots, N$ observations and $m = 1, \ldots, M$ equations. The errors for the ith observation, $u_{i1}, u_{i2}, \ldots, u_{iM}$, may be correlated, so fitting the m equations jointly may lead to more efficient estimates. Moreover, fitting the equations jointly allows us to impose cross-equation restrictions on the parameters. Not all elements of the parameter vector β and data vector $\mathbf{x}_i$ must appear in all the equations, though each element of β must appear in at least one equation for β to be identified. For this model, iterative FGNLS estimation is equivalent to maximum likelihood estimation with multivariate normal disturbances.

The syntax you use with `nlsur` closely mirrors that used with `nl`. In particular, you use substitutable expressions with the interactive and programmed substitutable expression versions to define the functions in your system. See [R] **nl** for more information on substitutable expressions. Here we reiterate the three rules that you must follow:

1. Parameters of the model are bound in braces: `{b0}`, `{param}`, etc.
2. Initial values for parameters are given by including an equal sign and the initial value inside the braces: `{b0=1}`, `{param=3.571}`, etc. If you do not specify an initial value, that parameter is initialized to zero. The `initial()` option overrides initial values in substitutable expressions.

3. Linear combinations of variables can be included using the notation {*eqname*:*varlist*}, for example, {xb: mpg price weight}, {score: w x z}, etc. Parameters of linear combinations are initialized to zero.

▷ Example 1: Interactive version using two-step FGNLS estimator

We have data from an experiment in which two closely related types of bacteria were placed in a Petri dish, and the number of each type of bacteria were recorded every hour. We suspect a two-parameter exponential growth model can be used to model each type of bacteria, but because they shared the same dish, we want to allow for correlation in the error terms. We want to fit the system of equations

$$p_1 = \beta_1 {\beta_2}^t + u_1$$
$$p_2 = \gamma_1 {\gamma_2}^t + u_2$$

where p_1 and p_2 are the two populations and t is time, and we want to allow for nonzero correlation between u_1 and u_2. We type

```
. use http://www.stata-press.com/data/r12/petridish
. nlsur (p1 = {b1}*{b2}^t) (p2 = {g1}*{g2}^t)
(obs = 25)
Calculating NLS estimates...
Iteration 0:  Residual SS =  335.5286
Iteration 1:  Residual SS =  333.8583
Iteration 2:  Residual SS =  219.9233
Iteration 3:  Residual SS =  127.9355
Iteration 4:  Residual SS =  14.86765
Iteration 5:  Residual SS =  8.628459
Iteration 6:  Residual SS =  8.281268
Iteration 7:  Residual SS =   8.28098
Iteration 8:  Residual SS =  8.280979
Iteration 9:  Residual SS =  8.280979
Calculating FGNLS estimates...
Iteration 0:  Scaled RSS =  49.99892
Iteration 1:  Scaled RSS =  49.99892
Iteration 2:  Scaled RSS =  49.99892
FGNLS regression
```

Equation		Obs	Parms	RMSE	R-sq	Constant
1	p1	25	2	.4337019	0.9734*	(none)
2	p2	25	2	.3783479	0.9776*	(none)

* Uncentered R-sq

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/b1	.3926631	.064203	6.12	0.000	.2668275	.5184987
/b2	1.119593	.0088999	125.80	0.000	1.102149	1.137036
/g1	.5090441	.0669495	7.60	0.000	.3778256	.6402626
/g2	1.102315	.0072183	152.71	0.000	1.088167	1.116463

The header of the output contains a summary of each equation, including the number of observations and parameters and the root mean squared error of the residuals. `nlsur` checks to see whether each equation contains a constant term, and if an equation does contain a constant term, an R^2 statistic is

presented. If an equation does not have a constant term, an uncentered R^2 is instead reported. The R^2 statistic for each equation measures the percentage of variance explained by the nonlinear function and may be useful for descriptive purposes, though it does not have the same formal interpretation in the context of FGNLS as it does with NLS estimation. As we would expect, β_2 and γ_2 are both greater than one, indicating the two bacterial populations increased in size over time.

◁

The model we fit in the next three examples is in fact linear in the parameters, so it could be fit using the `sureg` command. However, we will fit the model using `nlsur` so that we can focus on the mechanics of using the command. Moreover, using `nlsur` will obviate the need to generate several variables as well as the need to use the `constraint` command to impose parameter restrictions.

▷ Example 2: Interactive version using iterative FGNLS estimator—the translog production function

Greene (1997, sec. 15.6) discusses the transcendental logarithmic (translog) cost function and provides cost and input price data for capital, labor, energy, and materials for the U.S. economy. One way to fit the translog production function to these data is to fit the system of three equations

$$s_k = \beta_k + \delta_{kk} \ln\left(\frac{p_k}{p_m}\right) + \delta_{kl} \ln\left(\frac{p_l}{p_m}\right) + \delta_{ke} \ln\left(\frac{p_e}{p_m}\right) + u_1$$

$$s_l = \beta_l + \delta_{kl} \ln\left(\frac{p_k}{p_m}\right) + \delta_{ll} \ln\left(\frac{p_l}{p_m}\right) + \delta_{le} \ln\left(\frac{p_e}{p_m}\right) + u_2$$

$$s_e = \beta_e + \delta_{ke} \ln\left(\frac{p_k}{p_m}\right) + \delta_{le} \ln\left(\frac{p_l}{p_m}\right) + \delta_{ee} \ln\left(\frac{p_e}{p_m}\right) + u_3$$

where s_k is capital's cost share, s_l is labor's cost share, and s_e is energy's cost share; p_k, p_l, p_e, and p_m are the prices of capital, labor, energy, and materials, respectively; the u's are regression error terms; and the βs and δs are parameters to be estimated. There are three cross-equation restrictions on the parameters: δ_{kl}, δ_{ke}, and δ_{le} each appear in two equations. To fit this model by using the iterative FGNLS estimator, we type

```
. use http://www.stata-press.com/data/r12/mfgcost
. nlsur (s_k = {bk} + {dkk}*ln(pk/pm) + {dkl}*ln(pl/pm) + {dke}*ln(pe/pm))
>       (s_l = {bl} + {dkl}*ln(pk/pm) + {dll}*ln(pl/pm) + {dle}*ln(pe/pm))
>       (s_e = {be} + {dke}*ln(pk/pm) + {dle}*ln(pl/pm) + {dee}*ln(pe/pm)),
>       ifgnls
(obs = 25)
Calculating NLS estimates...
Iteration 0:  Residual SS =  .0009989
Iteration 1:  Residual SS =  .0009989
Calculating FGNLS estimates...
Iteration 0:  Scaled RSS =  65.45197
Iteration 1:  Scaled RSS =  65.45197
  (output omitted)
FGNLS iteration 10...
Iteration 0:  Scaled RSS =        75
Iteration 1:  Scaled RSS =        75
Iteration 2:  Scaled RSS =        75
Parameter change         =  4.076e-06
Covariance matrix change =  6.264e-10
FGNLS regression
```

Equation	Obs	Parms	RMSE	R-sq	Constant
1 s_k	25	4	.0031722	0.4776	bk
2 s_l	25	4	.0053963	0.8171	bl
3 s_e	25	4	.00177	0.6615	be

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/bk	.0568925	.0013454	42.29	0.000	.0542556	.0595294
/dkk	.0294833	.0057956	5.09	0.000	.0181241	.0408425
/dkl	-.0000471	.0038478	-0.01	0.990	-.0075887	.0074945
/dke	-.0106749	.0033882	-3.15	0.002	-.0173157	-.0040341
/bl	.253438	.0020945	121.00	0.000	.2493329	.2575432
/dll	.0754327	.0067572	11.16	0.000	.0621889	.0886766
/dle	-.004756	.002344	-2.03	0.042	-.0093502	-.0001619
/be	.0444099	.0008533	52.04	0.000	.0427374	.0460823
/dee	.0183415	.0049858	3.68	0.000	.0085694	.0281135

We draw your attention to the iteration log at the top of the output. When iterative FGNLS estimation is used, the final scaled RSS will equal the product of the number of observations in the estimation sample and the number of equations; see *Methods and formulas* for details. Because the RSS is scaled by the error covariance matrix during each round of FGNLS estimation, the scaled RSS is not comparable from one FGNLS iteration to the next.

◁

❑ Technical note

You may have noticed that we mentioned having data for four factors of production, yet we fit only three share equations. Because the four shares sum to one, we must drop one of the equations to avoid having a singular error covariance matrix. The iterative FGNLS estimator is equivalent to maximum likelihood estimation, and thus it is invariant to which one of the four equations we choose to drop. The (linearly restricted) parameters of the fourth equation can be obtained using the `lincom` command. Nonlinear functions of the parameters, such as the elasticities of substitution, can be computed using `nlcom`.

❑

Substitutable expression programs

If you fit the same model repeatedly or you want to share code with colleagues, you can write a *substitutable expression program* to define your system of equations and avoid having to retype the system every time. The first five letters of the program's name must be `nlsur`, and the program must set the r-class macro `r(n_eq)` to the number of equations in your system. The first equation's substitutable expression must be returned in `r(eq_1)`, the second equation's in `r(eq_2)`, and so on. You may optionally set `r(title)` to label your output; that has the same effect as specifying the `title()` option.

▷ Example 3: Programmed substitutable expression version

We return to our translog cost function, for which a substitutable expression program is

```
program nlsurtranslog, rclass
     version 12
     syntax varlist(min=7 max=7) [if]
     tokenize ‘varlist’
     args sk sl se pk pl pe pm
     local pkpm ln(‘pk’/‘pm’)
     local plpm ln(‘pl’/‘pm’)
     local pepm ln(‘pe’/‘pm’)
     return scalar n_eq = 3
     return local eq_1 "‘sk’= {bk} + {dkk}*‘pkpm’ + {dkl}*‘plpm’ + {dke}*‘pepm’"
     return local eq_2 "‘sl’= {bl} + {dkl}*‘pkpm’ + {dll}*‘plpm’ + {dle}*‘pepm’"
     return local eq_3 "‘se’= {be} + {dke}*‘pkpm’ + {dle}*‘plpm’ + {dee}*‘pepm’"
     return local title "4-factor translog cost function"
end
```

We made our program accept seven variables, for the three dependent variables s_k, s_l, and s_e, and the four factor prices p_k, p_l, p_m, and p_e. The `tokenize` command assigns to macros `‘1’`, `‘2’`, ..., `‘7’` the seven variables stored in `‘varlist’`, and the `args` command transfers those numbered macros to macros `‘sk’`, `‘sl’`, ..., `‘pm’`. Because we knew our substitutable expressions were going to be somewhat long, we created local macros to hold the log price ratios. These are simply macros that hold strings such as `ln(pk/pm)`, not variables, and they will save us some repetitious typing when we define our substitutable expressions. Our program returns the number of equations in `r(n_eq)`, and we defined our substitutable expressions in `eq_1`, `eq_2`, and `eq_3`. We do not bind the expressions in parentheses as we do with the interactive version of `nlsur`. Finally, we put a title in `r(title)` to label our output.

Our `syntax` command also accepts an `if` clause, and that is how `nlsur` indicates the estimation sample to our program. In this application, we can safely ignore it, because our program does not compute initial values. However, had we used commands such as `summarize` or `regress` to obtain initial values, then we would need to restrict those commands to analyze only the estimation sample. In those cases, typically, you simply need to include `‘if’` with the commands you are using. For example, instead of the command

```
summarize ‘depvar’, meanonly
```

you would use

```
summarize ‘depvar’ ‘if’, meanonly
```

We can check our program by typing

```
. nlsurtranslog s_k s_l s_e pk pl pe pm

. return list

scalars:
              r(n_eq) =  3

macros:
             r(title) : "4-factor translog cost function"
              r(eq_3) : "s_e= {be} + {dke}*ln(pk/pm) + {dle}*ln(pl/pm) + {dee.."
              r(eq_2) : "s_l= {bl} + {dkl}*ln(pk/pm) + {dll}*ln(pl/pm) + {dle.."
              r(eq_1) : "s_k= {bk} + {dkk}*ln(pk/pm) + {dkl}*ln(pl/pm) + {dke.."
```

Now that we know that our program works, we fit our model by typing

```
. nlsur translog: s_k s_l s_e pk pl pe pm, ifgnls
(obs = 25)

Calculating NLS estimates...
Iteration 0:  Residual SS =  .0009989
Iteration 1:  Residual SS =  .0009989
Calculating FGNLS estimates...
Iteration 0:  Scaled RSS =  65.45197
Iteration 1:  Scaled RSS =  65.45197
FGNLS iteration 2...
Iteration 0:  Scaled RSS =  73.28311
Iteration 1:  Scaled RSS =  73.28311
Parameter change         =  6.537e-03
Covariance matrix change =  1.002e-06
  (output omitted)
FGNLS iteration 10...
Iteration 0:  Scaled RSS =        75
Iteration 1:  Scaled RSS =        75
Iteration 2:  Scaled RSS =        75
Parameter change         =  4.076e-06
Covariance matrix change =  6.264e-10

FGNLS regression
```

	Equation	Obs	Parms	RMSE	R-sq	Constant
1	s_k	25	4	.0031722	0.4776	bk
2	s_l	25	4	.0053963	0.8171	bl
3	s_e	25	4	.00177	0.6615	be

4-factor translog cost function

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/bk	.0568925	.0013454	42.29	0.000	.0542556	.0595294
/dkk	.0294833	.0057956	5.09	0.000	.0181241	.0408425
/dkl	-.0000471	.0038478	-0.01	0.990	-.0075887	.0074945
/dke	-.0106749	.0033882	-3.15	0.002	-.0173157	-.0040341
/bl	.253438	.0020945	121.00	0.000	.2493329	.2575432
/dll	.0754327	.0067572	11.16	0.000	.0621889	.0886766
/dle	-.004756	.002344	-2.03	0.042	-.0093502	-.0001619
/be	.0444099	.0008533	52.04	0.000	.0427374	.0460823
/dee	.0183415	.0049858	3.68	0.000	.0085694	.0281135

Because we set `r(title)` in our substitutable expression program, the coefficient table has a title attached to it. The estimates are identical to those we obtained in example 2.

◁

❑ Technical note

nlsur accepts frequency and analytic weights as well as pweights (sampling weights) and iweights (importance weights). You do not need to modify your substitutable expressions in any way to perform weighted estimation, though you must make two changes to your substitutable expression program. The general outline of a *sexp_prog* program is

```
program nlsur name, rclass
    version 12
    syntax varlist [fw aw pw iw] [if]
    // Obtain initial values incorporating weights.  For example,
    summarize varname ['weight''exp'] 'if'
    ...
    // Return n_eqn and substitutable expressions
    return scalar n_eq = #
    return local eq_1 = ...
    ...
end
```

First, we wrote the syntax statement to accept a weight expression. Here we allow all four types of weights, but if you know that your estimator is valid, say, for only frequency weights, then you should modify the syntax line to accept only fweights. Second, if your program computes starting values, then any commands you use must incorporate the weights passed to the program; you do that by including ['weight''exp'] when calling those commands.

❑

Function evaluator programs

Although substitutable expressions are extremely flexible, there are some problems for which the nonlinear system cannot be defined using them. You can use the function evaluator program version of nlsur in these cases. We present two examples, a simple one to illustrate the mechanics of function evaluator programs and a more complicated one to illustrate the power of nlsur.

▷ Example 4: Function evaluator program version

Here we write a function evaluator program to fit the translog cost function used in examples 2 and 3. The function evaluator program is

```
program nlsurtranslog2
        version 12
        syntax varlist(min=7 max=7) [if], at(name)
        tokenize `varlist'
        args sk sl se pk pl pe pm
        tempname bk dkk dkl dke bl dll dle be dee
        scalar `bk'  = `at'[1,1]
        scalar `dkk' = `at'[1,2]
        scalar `dkl' = `at'[1,3]
        scalar `dke' = `at'[1,4]
        scalar `bl'  = `at'[1,5]
        scalar `dll' = `at'[1,6]
        scalar `dle' = `at'[1,7]
        scalar `be'  = `at'[1,8]
        scalar `dee' = `at'[1,9]
        local pkpm ln(`pk'/`pm')
        local plpm ln(`pl'/`pm')
        local pepm ln(`pe'/`pm')
        quietly {
                replace `sk' = `bk' + `dkk'*`pkpm' + `dkl'*`plpm' +    ///
                                      `dke'*`pepm' `if'
                replace `sl' = `bl' + `dkl'*`pkpm' + `dll'*`plpm' +    ///
                                      `dle'*`pepm' `if'
                replace `se' = `be' + `dke'*`pkpm' + `dle'*`plpm' +    ///
                                      `dee'*`pepm' `if'
        }
end
```

Unlike the substitutable expression program we wrote in example 3, `nlsurtranslog2` is not declared as r-class because we will not be returning any saved results. We are again expecting seven variables: three shares and four factor prices, and `nlsur` will again mark the estimation sample with an `if` expression.

Our function evaluator program also accepts an option named `at()`, which will receive a parameter vector at which we are to evaluate the system of equations. All function evaluator programs must accept this option. Our model has nine parameters to estimate, and we created nine temporary scalars to hold the elements of the `` `at' `` matrix.

Because our model has three equations, the first three variables passed to our program are the dependent variables that we are to fill in with the function values. We replaced only the observations in our estimation sample by including the `` `if' `` qualifier in the `replace` statements. Here we could have ignored the `` `if' `` qualifier because `nlsur` will skip over observations not in the estimation sample and we did not perform any computations requiring knowledge of the estimation sample. However, including the `` `if' `` is good practice and may result in a slight speed improvement if the functions of your model are complicated and the estimation sample is much smaller than the dataset in memory.

We could have avoided creating temporary scalars to hold our individual parameters by writing the `replace` statements as, for example,

```
replace `sk' = `at'[1,1] + `at'[1,2]*`pkpm' + `at'[1,3]*`plpm' + `at'[1,4]*`pepm' `if'
```

You can use whichever method you find more appealing, though giving the parameters descriptive names reduces the chance for mistakes and makes debugging easier.

To fit our model by using the function evaluator program version of `nlsur`, we type

```
. nlsur translog2 @ s_k s_l s_e pk pl pe pm, ifgnls nequations(3)
>        parameters(bk dkk dkl dke bl dll dle be dee)
>        hasconstants(bk bl be)
(obs = 25)

Calculating NLS estimates...
Iteration 0:  Residual SS =  .0009989
Iteration 1:  Residual SS =  .0009989
Calculating FGNLS estimates...
Iteration 0:  Scaled RSS =  65.45197
Iteration 1:  Scaled RSS =  65.45197
FGNLS iteration 2...
Iteration 0:  Scaled RSS =  73.28311
Iteration 1:  Scaled RSS =  73.28311
Parameter change         =  6.537e-03
Covariance matrix change =  1.002e-06
FGNLS iteration 3...
Iteration 0:  Scaled RSS =   74.7113
Iteration 1:  Scaled RSS =   74.7113
Parameter change         =  2.577e-03
Covariance matrix change =  3.956e-07
FGNLS iteration 4...
Iteration 0:  Scaled RSS =  74.95356
Iteration 1:  Scaled RSS =  74.95356
Parameter change         =  1.023e-03
Covariance matrix change =  1.571e-07
FGNLS iteration 5...
Iteration 0:  Scaled RSS =  74.99261
Iteration 1:  Scaled RSS =  74.99261
Iteration 2:  Scaled RSS =  74.99261
Iteration 3:  Scaled RSS =  74.99261
Parameter change         =  4.067e-04
Covariance matrix change =  6.250e-08
FGNLS iteration 6...
Iteration 0:  Scaled RSS =  74.99883
Iteration 1:  Scaled RSS =  74.99883
Parameter change         =  1.619e-04
Covariance matrix change =  2.489e-08
FGNLS iteration 7...
Iteration 0:  Scaled RSS =  74.99981
Iteration 1:  Scaled RSS =  74.99981
Parameter change         =  6.449e-05
Covariance matrix change =  9.912e-09
FGNLS iteration 8...
Iteration 0:  Scaled RSS =  74.99997
Iteration 1:  Scaled RSS =  74.99997
Iteration 2:  Scaled RSS =  74.99997
Parameter change         =  2.569e-05
Covariance matrix change =  3.948e-09
FGNLS iteration 9...
Iteration 0:  Scaled RSS =        75
Iteration 1:  Scaled RSS =        75
Iteration 2:  Scaled RSS =        75
Parameter change         =  1.023e-05
Covariance matrix change =  1.573e-09
FGNLS iteration 10...
Iteration 0:  Scaled RSS =        75
Iteration 1:  Scaled RSS =        75
Iteration 2:  Scaled RSS =        75
Parameter change         =  4.076e-06
Covariance matrix change =  6.264e-10
```

```
FGNLS regression
```

Equation		Obs	Parms	RMSE	R-sq	Constant
1	s_k	25	.	.0031722	0.4776	bk
2	s_l	25	.	.0053963	0.8171	bl
3	s_e	25	.	.00177	0.6615	be

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/bk	.0568925	.0013454	42.29	0.000	.0542556	.0595294
/dkk	.0294833	.0057956	5.09	0.000	.0181241	.0408425
/dkl	-.0000471	.0038478	-0.01	0.990	-.0075887	.0074945
/dke	-.0106749	.0033882	-3.15	0.002	-.0173157	-.0040341
/bl	.253438	.0020945	121.00	0.000	.2493329	.2575432
/dll	.0754327	.0067572	11.16	0.000	.0621889	.0886766
/dle	-.004756	.002344	-2.03	0.042	-.0093502	-.0001619
/be	.0444099	.0008533	52.04	0.000	.0427374	.0460823
/dee	.0183415	.0049858	3.68	0.000	.0085694	.0281135

When we use the function evaluator program version, `nlsur` requires us to specify the number of equations in `nequations()`, and it requires us to either specify names for each of our parameters or the number of parameters in the model. Here we used the `parameters()` option to name our parameters; the order in which we specified them in this option is the same as the order in which we extracted them from the `'at'` matrix in our program. Had we instead specified `nparameters(9)`, our parameters would have been labeled `/b1`, `/b2`, ..., `/b9` in the output.

`nlsur` has no way of telling how many parameters appear in each equation, so the `Parms` column in the header contains missing values. Moreover, the function evaluator program version of `nlsur` does not attempt to identify constant terms, so we used the `hasconstant` option to tell `nlsur` which parameter in each equation is a constant term.

The estimates are identical to those we obtained in examples 2 and 3.

◁

❑ Technical note

As with substitutable expression programs, if you intend to do weighted estimation with a function evaluator program, you must modify your *func_prog* program's `syntax` statement to accept weights. Moreover, if you use any statistical commands when computing your nonlinear functions, then you must include the weight expression with those commands.

❑

▷ Example 5: Fitting the basic AIDS model using nlsur

Poi (2002) showed how to fit a quadratic almost ideal demand system (AIDS) by using the `ml` command. Here we show how to fit the basic AIDS model by using `nlsur`. Poi (2008) shows how to fit the quadratic AIDS model using `nlsur`. The dataset `food.dta` contains household expenditures, expenditure shares, and log prices for four broad food groups. For a four-good demand system, we need to fit the following system of three equations:

$$w_1 = \alpha_1 + \gamma_{11}\ln p_1 + \gamma_{12}\ln p_2 + \gamma_{13}\ln p_3 + \beta_1 \ln\left\{\frac{m}{P(\mathbf{p})}\right\} + u_1$$
$$w_2 = \alpha_2 + \gamma_{12}\ln p_1 + \gamma_{22}\ln p_2 + \gamma_{23}\ln p_3 + \beta_2 \ln\left\{\frac{m}{P(\mathbf{p})}\right\} + u_2$$
$$w_3 = \alpha_3 + \gamma_{13}\ln p_1 + \gamma_{23}\ln p_2 + \gamma_{33}\ln p_3 + \beta_3 \ln\left\{\frac{m}{P(\mathbf{p})}\right\} + u_3$$

where w_k denotes a household's fraction of expenditures on good k, $\ln p_k$ denotes the logarithm of the price paid for good k, m denotes a household's total expenditure on all four goods, the u's are regression error terms, and

$$\ln P(\mathbf{p}) = \alpha_0 + \sum_{i=1}^{4}\alpha_i \ln p_i + \frac{1}{2}\sum_{i=1}^{4}\sum_{j=1}^{4}\gamma_{ij}\ln p_i \ln p_j$$

The parameters for the fourth good's share equation can be recovered from the following constraints that are imposed by economic theory:

$$\sum_{i=1}^{4}\alpha_i = 1 \qquad \sum_{i=1}^{4}\beta_i = 0 \qquad \gamma_{ij} = \gamma_{ji} \qquad \text{and} \qquad \sum_{i=1}^{4}\gamma_{ij} = 0 \ \text{ for all } j$$

Our model has a total of 12 unrestricted parameters. We will not estimate α_0 directly. Instead, we will set it equal to 5 as was done in Poi (2002); see Deaton and Muellbauer (1980) for a discussion of why treating α_0 as fixed is acceptable.

Our function evaluator program is

```
program nlsuraids
        version 12
        syntax varlist(min=8 max=8) if, at(name)
        tokenize `varlist'
        args w1 w2 w3 lnp1 lnp2 lnp3 lnp4 lnm
        tempname a1 a2 a3 a4
        scalar `a1' = `at'[1,1]
        scalar `a2' = `at'[1,2]
        scalar `a3' = `at'[1,3]
        scalar `a4' = 1 - `a1' - `a2' - `a3'
        tempname b1 b2 b3
        scalar `b1' = `at'[1,4]
        scalar `b2' = `at'[1,5]
        scalar `b3' = `at'[1,6]
        tempname g11 g12 g13 g14
        tempname g21 g22 g23 g24
        tempname g31 g32 g33 g34
        tempname g41 g42 g43 g44
        scalar `g11' = `at'[1,7]
        scalar `g12' = `at'[1,8]
        scalar `g13' = `at'[1,9]
        scalar `g14' = -`g11'-`g12'-`g13'
        scalar `g21' = `g12'
        scalar `g22' = `at'[1,10]
        scalar `g23' = `at'[1,11]
        scalar `g24' = -`g21'-`g22'-`g23'
        scalar `g31' = `g13'
        scalar `g32' = `g23'
        scalar `g33' = `at'[1,12]
        scalar `g34' = -`g31'-`g32'-`g33'
        scalar `g41' = `g14'
        scalar `g42' = `g24'
        scalar `g43' = `g34'
        scalar `g44' = -`g41'-`g42'-`g43'
        quietly {
                tempvar lnpindex
                gen double `lnpindex' = 5 + `a1'*`lnp1' + `a2'*`lnp2' + ///
                                            `a3'*`lnp3' + `a4'*`lnp4'
                forvalues i = 1/4 {
                        forvalues j = 1/4 {
                                replace `lnpindex' = `lnpindex' + ///
                                        0.5*`g`i''`j''*`lnp`i''*`lnp`j''
                        }
                }
                replace `w1' = `a1' + `g11'*`lnp1' + `g12'*`lnp2' + ///
                                      `g13'*`lnp3' + `g14'*`lnp4' + ///
                                       `b1'*(`lnm' - `lnpindex')
                replace `w2' = `a2' + `g21'*`lnp1' + `g22'*`lnp2' + ///
                                      `g23'*`lnp3' + `g24'*`lnp4' + ///
                                      `b2'*(`lnm' - `lnpindex')
                replace `w3' = `a3' + `g31'*`lnp1' + `g32'*`lnp2' + ///
                                      `g33'*`lnp3' + `g34'*`lnp4' + ///
                                      `b3'*(`lnm' - `lnpindex')
        }
end
```

The `syntax` statement accepts eight variables: three expenditure share variables, all four log-price variables, and a variable for log expenditures ($\ln m$). Most of the code simply extracts the parameters

from the 'at' matrix. Although we are estimating only 12 parameters, to calculate the price index term and the expenditure share equations, we need the restricted parameters as well. Notice how we impose the constraints on the parameters. We then created a temporary variable to hold $\ln P(\mathbf{p})$, and we filled the three dependent variables with the predicted expenditure shares.

To fit our model, we type

```
. use http://www.stata-press.com/data/r12/food

. nlsur aids @ w1 w2 w3 lnp1 lnp2 lnp3 lnp4 lnexp,
>              parameters(a1 a2 a3 b1 b2 b3
>                         g11 g12 g13 g22 g32 g33)
>              neq(3) ifgnls
(obs = 4048)

Calculating NLS estimates...
Iteration 0:  Residual SS =  126.9713
Iteration 1:  Residual SS =   125.669
Iteration 2:  Residual SS =   125.669
Iteration 3:  Residual SS =   125.669
Iteration 4:  Residual SS =   125.669
Calculating FGNLS estimates...
Iteration 0:  Scaled RSS =  12080.14
Iteration 1:  Scaled RSS =  12080.14
Iteration 2:  Scaled RSS =  12080.14
Iteration 3:  Scaled RSS =  12080.14
FGNLS iteration 2...
Iteration 0:  Scaled RSS =  12143.99
Iteration 1:  Scaled RSS =  12143.99
Iteration 2:  Scaled RSS =  12143.99
Parameter change         =  1.972e-04
Covariance matrix change =  2.936e-06
FGNLS iteration 3...
Iteration 0:  Scaled RSS =     12144
Iteration 1:  Scaled RSS =     12144
Parameter change         =  2.178e-06
Covariance matrix change =  3.467e-08

FGNLS regression
```

Equation	Obs	Parms	RMSE	R-sq	Constant
1 w1	4048	.	.1333175	0.9017*	(none)
2 w2	4048	.	.1024166	0.8480*	(none)
3 w3	4048	.	.053777	0.7906*	(none)

* Uncentered R-sq

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
/a1	.3163958	.0073871	42.83	0.000	.3019175	.3308742
/a2	.2712501	.0056938	47.64	0.000	.2600904	.2824097
/a3	.1039898	.0029004	35.85	0.000	.0983051	.1096746
/b1	.0161044	.0034153	4.72	0.000	.0094105	.0227983
/b2	-.0260771	.002623	-9.94	0.000	-.0312181	-.0209361
/b3	.0014538	.0013776	1.06	0.291	-.0012463	.004154
/g11	.1215838	.0057186	21.26	0.000	.1103756	.1327921
/g12	-.0522943	.0039305	-13.30	0.000	-.0599979	-.0445908
/g13	-.0351292	.0021788	-16.12	0.000	-.0393996	-.0308588
/g22	.0644298	.0044587	14.45	0.000	.0556909	.0731687
/g32	-.0011786	.0019767	-0.60	0.551	-.0050528	.0026957
/g33	.0424381	.0017589	24.13	0.000	.0389909	.0458854

To get the restricted parameters for the fourth share equation, we can use `lincom`. For example, to obtain α_4, we type

```
. lincom 1 - [a1]_cons - [a2]_cons - [a3]_cons
 ( 1) - [a1]_cons - [a2]_cons - [a3]_cons = -1
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
(1)	.3083643	.0052611	58.61	0.000	.2980528	.3186758

For more information on `lincom`, see [R] **lincom**.

◁

Saved results

`nlsur` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_#)`	number of parameters for equation #
`e(k_eq)`	number of equation names in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(n_eq)`	number of equations
`e(mss_#)`	model sum of squares for equation #
`e(rss_#)`	RSS for equation #
`e(rmse_#)`	root mean squared error for equation #
`e(r2_#)`	R^2 for equation #
`e(ll)`	Gaussian log likelihood (`iflgs` version only)
`e(N_clust)`	number of clusters
`e(rank)`	rank of `e(V)`
`e(converge)`	`1` if converged, `0` otherwise

Macros

`e(cmd)`	`nlsur`
`e(cmdline)`	command as typed
`e(method)`	`fgnls`, `ifgnls`, or `nls`
`e(depvar)`	names of dependent variables
`e(depvar_#)`	dependent variable for equation #
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(title_2)`	secondary title in estimation output
`e(clustvar)`	name of cluster variable
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used in label Std. Err.
`e(type)`	`1` = interactively entered expression `2` = substitutable expression program `3` = function evaluator program
`e(sexpprog)`	substitutable expression program
`e(sexp_#)`	substitutable expression for equation #
`e(params)`	names of all parameters
`e(params_#)`	parameters in equation #
`e(funcprog)`	function evaluator program
`e(rhs)`	contents of `variables()`
`e(constants)`	identifies constant terms
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`

Matrices

`e(b)`	coefficient vector
`e(init)`	initial values vector
`e(Sigma)`	error covariance matrix ($\widehat{\mathbf{\Sigma}}$)
`e(V)`	variance–covariance matrix of the estimators

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`nlsur` is implemented as an ado-file.

Write the system of equations for the ith observation as

$$\mathbf{y}_i = \mathbf{f}(\mathbf{x}_i, \beta) + \mathbf{u}_i \tag{1}$$

where $\mathbf{y}_i$ and $\mathbf{u}_i$ are $1 \times M$ vectors, for $i = 1, \ldots, N$; $\mathbf{f}$ is a function that returns a $1 \times M$ vector; $\mathbf{x}_i$ represents all the exogenous variables in the system; and β is a $1 \times k$ vector of parameters. The generalized nonlinear least-squares system estimator is defined as

$$\widehat{\beta} \equiv \text{argmin}_\beta \sum_{i=1}^{N} \{\mathbf{y}_i - \mathbf{f}(\mathbf{x}_i, \beta)\} \, \mathbf{\Sigma}^{-1} \, \{\mathbf{y}_i - \mathbf{f}(\mathbf{x}_i, \beta)\}'$$

where $\mathbf{\Sigma} = E(\mathbf{u}_i' \mathbf{u}_i)$ is an $M \times M$ positive-definite weight matrix. Let $\mathbf{T}$ be the Cholesky decomposition of $\mathbf{\Sigma}^{-1}$; that is, $\mathbf{T}\mathbf{T}' = \mathbf{\Sigma}^{-1}$. Postmultiply (1) by $\mathbf{T}$:

$$\mathbf{y}_i \mathbf{T} = \mathbf{f}(\mathbf{x}_i, \beta)\mathbf{T} + \mathbf{u}_i \mathbf{T} \tag{2}$$

Because $E(\mathbf{T}' \mathbf{u}_i' \mathbf{u}_i \mathbf{T}) = \mathbf{I}$, we can "stack" the columns of (2) and write

$$\begin{aligned}
\mathbf{y}_1\mathbf{T}_1 &= \mathbf{f}(\mathbf{x}_1, \beta)\mathbf{T}_1 + \widetilde{u}_{11} \\
\mathbf{y}_1\mathbf{T}_2 &= \mathbf{f}(\mathbf{x}_1, \beta)\mathbf{T}_2 + \widetilde{u}_{12} \\
&\vdots = \vdots \\
\mathbf{y}_1\mathbf{T}_M &= \mathbf{f}(\mathbf{x}_1, \beta)\mathbf{T}_M + \widetilde{u}_{1M} \\
&\vdots = \vdots \\
\mathbf{y}_N\mathbf{T}_1 &= \mathbf{f}(\mathbf{x}_N, \beta)\mathbf{T}_1 + \widetilde{u}_{N1} \\
\mathbf{y}_N\mathbf{T}_2 &= \mathbf{f}(\mathbf{x}_N, \beta)\mathbf{T}_2 + \widetilde{u}_{N2} \\
&\vdots = \vdots \\
\mathbf{y}_N\mathbf{T}_M &= \mathbf{f}(\mathbf{x}_N, \beta)\mathbf{T}_M + \widetilde{u}_{NM}
\end{aligned} \tag{3}$$

where $\mathbf{T}_j$ denotes the jth column of $\mathbf{T}$. By construction, all $\widetilde{u}_{ij}$ are independently distributed with unit variance. As a result, by transforming the model in (1) to that shown in (3), we have reduced the multivariate generalized nonlinear least-squares system estimator to a univariate nonlinear least-squares problem; and the same parameter estimation technique used by `nl` can be used here. See [R] **nl** for the details. Moreover, because the $\widetilde{u}_{ij}$ all have variance 1, the final scaled RSS reported by `nlsur` is equal to NM.

To make the estimator feasible, we require an estimate $\widehat{\mathbf{\Sigma}}$ of $\mathbf{\Sigma}$. `nlsur` first sets $\widehat{\mathbf{\Sigma}} = \mathbf{I}$. Although not efficient, the resulting estimate, $\widehat{\beta}_{\rm NLS}$, is consistent. If the `nls` option is specified, estimation is complete. Otherwise, the residuals

$$\widehat{\mathbf{u}}_i = \mathbf{y}_i - \mathbf{f}(\mathbf{x}_i, \widehat{\beta}_{\rm NLS})$$

are calculated and used to compute

$$\widehat{\mathbf{\Sigma}} = \frac{1}{N}\sum_{i=1}^{N} \widehat{\mathbf{u}}_i' \widehat{\mathbf{u}}_i$$

With $\widehat{\mathbf{\Sigma}}$ in hand, a new estimate $\widehat{\beta}$ is then obtained.

If the `ifgnls` option is specified, the new $\widehat{\beta}$ is used to recompute the residuals and obtain a new estimate of $\widehat{\mathbf{\Sigma}}$, from which $\widehat{\beta}$ can then be reestimated. Iterations stop when the relative change in $\widehat{\beta}$ is less than `eps()`, the relative change in $\widehat{\mathbf{\Sigma}}$ is less than `ifgnlseps()`, or if `ifgnlsiterate()` iterations have been performed.

If the `vce(robust)` and `vce(cluster` *clustvar*`)` options were not specified, then

$$V(\widehat{\beta}) = \left(\sum_{i=1}^{N} \mathbf{X}_i' \widehat{\mathbf{\Sigma}}^{-1} \mathbf{X}_i\right)^{-1}$$

where the $M \times k$ matrix $\mathbf{X}_i$ has typical element X_{ist}, the derivative of the sth element of $\mathbf{f}$ with respect to the tth element of β, evaluated at $\mathbf{x}_i$ and $\widehat{\beta}$. As a practical matter, once the model is written in the form of (3), the variance–covariance matrix can be calculated via a Gauss–Newton regression; see Davidson and MacKinnon (1993, chap. 6).

If `robust` is specified, then

$$V_R(\widehat{\beta}) = \left(\sum_{i=1}^{N} \mathbf{X}_i' \widehat{\mathbf{\Sigma}}^{-1} \mathbf{X}_i\right)^{-1} \sum_{i=1}^{N} \mathbf{X}_i' \widehat{\mathbf{\Sigma}}^{-1} \widehat{\mathbf{u}}_i' \widehat{\mathbf{u}}_i \widehat{\mathbf{\Sigma}}^{-1} \mathbf{X}_i \left(\sum_{i=1}^{N} \mathbf{X}_i' \widehat{\mathbf{\Sigma}}^{-1} \mathbf{X}_i\right)^{-1}$$

The cluster–robust variance matrix is

$$V_C(\widehat{\beta}) = \left(\sum_{i=1}^{N} \mathbf{X}_i' \widehat{\mathbf{\Sigma}}^{-1} \mathbf{X}_i\right)^{-1} \sum_{c=1}^{N_C} \mathbf{w}_c' \mathbf{w}_c \left(\sum_{i=1}^{N} \mathbf{X}_i' \widehat{\mathbf{\Sigma}}^{-1} \mathbf{X}_i\right)^{-1}$$

where N_C is the number of clusters and

$$\mathbf{w}_c = \sum_{j \in C_k} \mathbf{X}_j' \widehat{\mathbf{\Sigma}}^{-1} \widehat{\mathbf{u}}_j'$$

with C_k denoting the set of observations in the kth cluster. In evaluating these formulas, we use the value of $\widehat{\mathbf{\Sigma}}$ used in calculating the final estimate of $\widehat{\beta}$. That is, we do not recalculate $\widehat{\mathbf{\Sigma}}$ after we obtain the final value of $\widehat{\beta}$.

The RSS for the jth equation, RSS_j, is

$$\text{RSS}_j = \sum_{i=1}^{N} (\widehat{y}_{ij} - y_{ij})^2$$

where $\widehat{y}_{ij}$ is the predicted value of the ith observation on the jth dependent variable; the total sum of squares (TSS) for the jth equation, TSS_j, is

$$\text{TSS}_j = \sum_{i=1}^{N} (y_{ij} - \bar{y}_j)^2$$

if there is a constant term in the jth equation, where $\bar{y}_j$ is the sample mean of the jth dependent variable, and

$$\text{TSS}_j = \sum_{i=1}^{N} y_{ij}^2$$

if there is no constant term in the jth equation; and the model sum of squares (MSS) for the jth equation, MSS_j, is $\text{TSS}_j - \text{RSS}_j$.

The R^2 for the jth equation is $\text{MSS}_j/\text{TSS}_j$. If an equation does not have a constant term, then the reported R^2 for that equation is "uncentered" and based on the latter definition of TSS_j.

Under the assumption that the $\mathbf{u}_i$ are independent and identically distributed $N(\mathbf{0}, \widehat{\mathbf{\Sigma}})$, the log likelihood for the model is

$$\ln L = -\frac{MN}{2}\{1 + \ln(2\pi)\} - \frac{N}{2}\ln\left|\widehat{\mathbf{\Sigma}}\right|$$

The log likelihood is reported only when the `ifgnls` option is specified.

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Also see

[R] **nlsur postestimation** — Postestimation tools for nlsur

[R] **nl** — Nonlinear least-squares estimation

[R] **gmm** — Generalized method of moments estimation

[R] **sureg** — Zellner's seemingly unrelated regression

[R] **reg3** — Three-stage estimation for systems of simultaneous equations

[R] **ml** — Maximum likelihood estimation

[U] **20 Estimation and postestimation commands**

Title

nlsur postestimation — Postestimation tools for nlsur

Description

The following postestimation commands are available after `nlsur`:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`	likelihood-ratio test
`margins`[1]	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] You must specify the `variables()` option with `nlsur`.

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` `equation(#`*eqno*`)` `yhat` `residuals`]

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`equation(#`*eqno*`)` specifies to which equation you are referring. `equation(#1)` would mean that the calculation is to be made for the first equation, `equation(#2)` would mean the second, and so on. If you do not specify `equation()`, results are the same as if you had specified `equation(#1)`.

`yhat`, the default, calculates the fitted values for the specified equation.

`residuals` calculates the residuals for the specified equation.

Remarks

▷ Example 1

In example 2 of [R] **nlsur**, we fit a four-factor translog cost function to data for the U.S. economy. The own-price elasticity for a factor measures the percentage change in its usage as a result of a 1% increase in the factor's price, assuming that output is held constant. For the translog production function, the own-price factor elasticities are

$$\eta_i = \frac{\delta_{ii} + s_i(s_i - 1)}{s_i}$$

Here we compute the elasticity for capital at the sample mean of capital's factor share. First, we use `summarize` to get the mean of `s_k` and store that value in a scalar:

```
. summarize s_k
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         s_k |         25    .053488    .0044795      .04602      .06185
. scalar kmean = r(mean)
```

Now we can use `nlcom` to calculate the elasticity:

```
. nlcom (([dkk]_cons + kmean*(kmean-1)) / kmean)
       _nl_1:  ([dkk]_cons + kmean*(kmean-1)) / kmean
------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _nl_1 |  -.3952986   .1083535    -3.65   0.000    -.6076676   -.1829295
------------------------------------------------------------------------------
```

If the price of capital increases by 1%, its usage will decrease by about 0.4%. To maintain its current level of output, a firm would increase its usage of other inputs to compensate for the lower capital usage. The standard error reported by `nlcom` reflects the sampling variance of the estimated parameter $\widehat{\delta_{kk}}$, but `nlcom` treats the sample mean of `s_k` as a fixed parameter that does not contribute to the sampling variance of the estimated elasticity.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **nlsur** — Estimation of nonlinear systems of equations

[U] **20 Estimation and postestimation commands**

Title

nptrend — Test for trend across ordered groups

Syntax

```
nptrend varname [if] [in] , by(groupvar) [nodetail score(scorevar)]
```

Menu

Statistics > Nonparametric analysis > Tests of hypotheses > Trend test across ordered groups

Description

`nptrend` performs a nonparametric test for trend across ordered groups.

Options

Main

`by(`*groupvar*`)` is required; it specifies the group on which the data are to be ordered.

`nodetail` suppresses the listing of group rank sums.

`score(`*scorevar*`)` defines scores for groups. When it is not specified, the values of *groupvar* are used for the scores.

Remarks

`nptrend` performs the nonparametric test for trend across ordered groups developed by Cuzick (1985), which is an extension of the Wilcoxon rank-sum test (see [R] **ranksum**). A correction for ties is incorporated into the test. `nptrend` is a useful adjunct to the Kruskal–Wallis test; see [R] **kwallis**.

If your data are not grouped, you can test for trend with the `signtest` and `spearman` commands; see [R] **signrank** and [R] **spearman**. With `signtest`, you can perform the Cox and Stuart test, a sign test applied to differences between equally spaced observations of *varname*. With `spearman`, you can perform the Daniels test, a test of zero Spearman correlation between *varname* and a time index. See Conover (1999, 169–175, 323) for a discussion of these tests and their asymptotic relative efficiency.

▷ Example 1

The following data (Altman 1991, 217) show ocular exposure to ultraviolet radiation for 32 pairs of sunglasses classified into three groups according to the amount of visible light transmitted.

Group	Transmission of visible light	Ocular exposure to ultraviolet radiation
1	< 25%	1.4 1.4 1.4 1.6 2.3 2.3
2	25 to 35%	0.9 1.0 1.1 1.1 1.2 1.2 1.5 1.9 2.2 2.6 2.6 2.6 2.8 2.8 3.2 3.5 4.3 5.1
3	> 35%	0.8 1.7 1.7 1.7 3.4 7.1 8.9 13.5

Entering these data into Stata, we have

```
. use http://www.stata-press.com/data/r12/sg
. list, sep(6)
```

	group	exposure
1.	1	1.4
2.	1	1.4
3.	1	1.4
4.	1	1.6
5.	1	2.3
6.	1	2.3
7.	2	.9
	(*output omitted*)	
31.	3	8.9
32.	3	13.5

We use `nptrend` to test for a trend of (increasing) exposure across the three groups by typing

```
. nptrend exposure, by(group)
    group     score       obs      sum of ranks
        1         1         6            76
        2         2        18           290
        3         3         8           162

         z  =  1.52
Prob > |z| = 0.129
```

When the groups are given any equally spaced scores (such as -1, 0, 1), we will obtain the same answer as above. To illustrate the effect of changing scores, an analysis of these data with scores 1, 2, and 5 (admittedly not sensible here) produces

```
. gen mysc = cond(group==3,5,group)
. nptrend exposure, by(group) score(mysc)
    group     score       obs      sum of ranks
        1         1         6            76
        2         2        18           290
        3         5         8           162

         z  =  1.46
Prob > |z| = 0.143
```

This example suggests that the analysis is not all that sensitive to the scores chosen.

◁

❑ Technical note

The grouping variable may be either a string variable or a numeric variable. If it is a string variable and no score variable is specified, the natural numbers 1, 2, 3, ... are assigned to the groups in the sort order of the string variable. This may not always be what you expect. For example, the sort order of the strings “one”, “two”, “three” is “one”, “three”, “two”.

❑

Saved results

nptrend saves the following in r():

Scalars

r(N)	number of observations	r(z)	z statistic
r(p)	two-sided p-value	r(T)	test statistic

Methods and formulas

nptrend is implemented as an ado-file.

nptrend is based on a method in Cuzick (1985). The following description of the statistic is from Altman (1991, 215–217). We have k groups of sample sizes n_i ($i = 1, \ldots, k$). The groups are given scores, l_i, which reflect their ordering, such as 1, 2, and 3. The scores do not have to be equally spaced, but they usually are. $N = \sum n_i$ observations are ranked from 1 to N, and the sums of the ranks in each group, R_i, are obtained. L, the weighted sum of all the group scores, is

$$L = \sum_{i=1}^{k} l_i n_i$$

The statistic T is calculated as

$$T = \sum_{i=1}^{k} l_i R_i$$

Under the null hypothesis, the expected value of T is $E(T) = 0.5(N+1)L$, and its standard error is

$$\mathrm{se}(T) = \sqrt{\frac{N+1}{12}\left(N\sum_{i=1}^{k} l_i^2 n_i - L^2\right)}$$

so that the test statistic, z, is given by $z = \{T - E(T)\}/\mathrm{se}(T)$, which has an approximately standard normal distribution when the null hypothesis of no trend is true.

The correction for ties affects the standard error of T. Let $\widetilde{N}$ be the number of unique values of the variable being tested ($\widetilde{N} \leq N$), and let t_j be the number of times the jth unique value of the variable appears in the data. Define

$$a = \frac{\sum_{j=1}^{\widetilde{N}} t_j(t_j^2 - 1)}{N(N^2 - 1)}$$

The corrected standard error of T is $\widetilde{\mathrm{se}}(T) = \sqrt{1-a}\ \mathrm{se}(T)$.

Acknowledgments

nptrend was written by K. A. Stepniewska and D. G. Altman (1992) of the Cancer Research UK.

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Also see

[R] **kwallis** — Kruskal–Wallis equality-of-populations rank test

[R] **signrank** — Equality tests on matched data

[R] **spearman** — Spearman's and Kendall's correlations

[R] **symmetry** — Symmetry and marginal homogeneity tests

[ST] **epitab** — Tables for epidemiologists

[ST] **strate** — Tabulate failure rates and rate ratios

Title

ologit — Ordered logistic regression

Syntax

`ologit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`or`	report odds ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Ordinal outcomes > Ordered logistic regression

Description

`ologit` fits ordered logit models of ordinal variable *depvar* on the independent variables *indepvars*. The actual values taken on by the dependent variable are irrelevant, except that larger values are assumed to correspond to "higher" outcomes.

See [R] **logistic** for a list of related estimation commands.

Options

Model

`offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`or` reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. `or` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

The following option is available with `ologit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Ordered logit models are used to estimate relationships between an ordinal dependent variable and a set of independent variables. An *ordinal* variable is a variable that is categorical and ordered, for instance, "poor", "good", and "excellent", which might indicate a person's current health status or the repair record of a car. If there are only two outcomes, see [R] **logistic**, [R] **logit**, and [R] **probit**. This entry is concerned only with more than two outcomes. If the outcomes cannot be ordered (for example, residency in the north, east, south, or west), see [R] **mlogit**. This entry is concerned only with models in which the outcomes can be ordered.

In ordered logit, an underlying score is estimated as a linear function of the independent variables and a set of cutpoints. The probability of observing outcome i corresponds to the probability that the estimated linear function, plus random error, is within the range of the cutpoints estimated for the outcome:

$$\Pr(\text{outcome}_j = i) = \Pr(\kappa_{i-1} < \beta_1 x_{1j} + \beta_2 x_{2j} + \cdots + \beta_k x_{kj} + u_j \leq \kappa_i)$$

u_j is assumed to be logistically distributed in ordered logit. In either case, we estimate the coefficients β_1, β_2, ..., β_k together with the cutpoints κ_1, κ_2, ..., κ_{k-1}, where k is the number of possible outcomes. κ_0 is taken as $-\infty$, and κ_k is taken as $+\infty$. All of this is a direct generalization of the ordinary two-outcome logit model.

▷ Example 1

We wish to analyze the 1977 repair records of 66 foreign and domestic cars. The data are a variation of the automobile dataset described in [U] **1.2.2 Example datasets**. The 1977 repair records, like those in 1978, take on values "Poor", "Fair", "Average", "Good", and "Excellent". Here is a cross-tabulation of the data:

```
. use http://www.stata-press.com/data/r12/fullauto
(Automobile Models)
. tabulate rep77 foreign, chi2
```

Repair Record 1977	Foreign: Domestic	Foreign	Total
Poor	2	1	3
Fair	10	1	11
Average	20	7	27
Good	13	7	20
Excellent	0	5	5
Total	45	21	66

Pearson chi2(4) = 13.8619 Pr = 0.008

Although it appears that `foreign` takes on the values "`Domestic`" and "`Foreign`", it is actually a numeric variable taking on the values 0 and 1. Similarly, `rep77` takes on the values 1, 2, 3, 4, and 5, corresponding to "`Poor`", "`Fair`", and so on. The more meaningful words appear because we have attached value labels to the data; see [U] **12.6.3 Value labels**.

Because the chi-squared value is significant, we could claim that there is a relationship between `foreign` and `rep77`. Literally, however, we can only claim that the distributions are different; the chi-squared test is not directional. One way to model these data is to model the categorization that took place when the data were created. Cars have a true frequency of repair, which we will assume is given by $S_j = \beta\,\texttt{foreign}_j + u_j$, and a car is categorized as "poor" if $S_j \leq \kappa_0$, as "fair" if $\kappa_0 < S_j \leq \kappa_1$, and so on:

```
. ologit rep77 foreign
Iteration 0:   log likelihood = -89.895098
Iteration 1:   log likelihood = -85.951765
Iteration 2:   log likelihood = -85.908227
Iteration 3:   log likelihood = -85.908161
Iteration 4:   log likelihood = -85.908161
Ordered logistic regression                     Number of obs   =         66
                                                LR chi2(1)      =       7.97
                                                Prob > chi2     =     0.0047
Log likelihood = -85.908161                     Pseudo R2       =     0.0444
```

rep77	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
foreign	1.455878	.5308951	2.74	0.006	.4153425	2.496413
/cut1	-2.765562	.5988208			-3.939229	-1.591895
/cut2	-.9963603	.3217706			-1.627019	-.3657016
/cut3	.9426153	.3136398			.3278925	1.557338
/cut4	3.123351	.5423257			2.060412	4.18629

Our model is $S_j = 1.46\,\texttt{foreign}_j + u_j$; the expected value for foreign cars is 1.46 and, for domestic cars, 0; foreign cars have better repair records.

The estimated cutpoints tell us how to interpret the score. For a foreign car, the probability of a poor record is the probability that $1.46 + u_j \leq -2.77$, or equivalently, $u_j \leq -4.23$. Making this calculation requires familiarity with the logistic distribution: the probability is $1/(1+e^{4.23}) = 0.014$. On the other hand, for domestic cars, the probability of a poor record is the probability $u_j \leq -2.77$, which is 0.059.

This, it seems to us, is a far more reasonable prediction than we would have made based on the table alone. The table showed that 2 of 45 domestic cars had poor records, whereas 1 of 21 foreign cars had poor records—corresponding to probabilities $2/45 = 0.044$ and $1/21 = 0.048$. The predictions from our model imposed a smoothness assumption—foreign cars should not, overall, have better repair records without the difference revealing itself in each category. In our data, the fractions of foreign and domestic cars in the poor category are virtually identical only because of the randomness associated with small samples.

Thus if we were asked to predict the true fractions of foreign and domestic cars that would be classified in the various categories, we would choose the numbers implied by the ordered logit model:

	tabulate		logit	
	Domestic	Foreign	Domestic	Foreign
Poor	0.044	0.048	0.059	0.014
Fair	0.222	0.048	0.210	0.065
Average	0.444	0.333	0.450	0.295
Good	0.289	0.333	0.238	0.467
Excellent	0.000	0.238	0.043	0.159

See [R] **ologit postestimation** for a more complete explanation of how to generate predictions from an ordered logit model.

◁

❑ Technical note

Here ordered logit provides an alternative to ordinary two-outcome logistic models with an arbitrary dichotomization, which might otherwise have been tempting. We could, for instance, have summarized these data by converting the five-outcome `rep77` variable to a two-outcome variable, combining cars in the average, fair, and poor categories to make one outcome and combining cars in the good and excellent categories to make the second.

Another even less appealing alternative would have been to use ordinary regression, arbitrarily labeling "excellent" as 5, "good" as 4, and so on. The problem is that with different but equally valid labelings (say, 10 for "excellent"), we would obtain different estimates. We would have no way of choosing one metric over another. That assertion is not, however, true of `ologit`. The actual values used to label the categories make no difference other than through the order they imply.

In fact, our labeling was 5 for "excellent", 4 for "good", and so on. The words "excellent" and "good" appear in our output because we attached a value label to the variables; see [U] **12.6.3 Value labels**. If we were to now go back and type `replace rep77=10 if rep77==5`, changing all the 5s to 10s, we would still obtain the same results when we refit our model.

❑

▷ Example 2

In the example above, we used ordered logit as a way to model a table. We are not, however, limited to including only one explanatory variable or to including only categorical variables. We can explore the relationship of `rep77` with any of the variables in our data. We might, for instance, model `rep77` not only in terms of the origin of manufacture, but also including `length` (a proxy for size) and `mpg`:

```
. ologit rep77 foreign length mpg
Iteration 0:   log likelihood = -89.895098
Iteration 1:   log likelihood = -78.775147
Iteration 2:   log likelihood = -78.254294
Iteration 3:   log likelihood = -78.250719
Iteration 4:   log likelihood = -78.250719
Ordered logistic regression                     Number of obs   =         66
                                                LR chi2(3)      =      23.29
                                                Prob > chi2     =     0.0000
Log likelihood = -78.250719                     Pseudo R2       =     0.1295
```

rep77	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
foreign	2.896807	.7906411	3.66	0.000	1.347179	4.446435
length	.0828275	.02272	3.65	0.000	.0382972	.1273579
mpg	.2307677	.0704548	3.28	0.001	.0926788	.3688566
/cut1	17.92748	5.551191			7.047344	28.80761
/cut2	19.86506	5.59648			8.896161	30.83396
/cut3	22.10331	5.708936			10.914	33.29262
/cut4	24.69213	5.890754			13.14647	36.2378

`foreign` still plays a role—and an even larger role than previously. We find that larger cars tend to have better repair records, as do cars with better mileage ratings.

◁

Saved results

ologit saves the following in e():

Scalars

e(N)	number of observations
e(N_cd)	number of completely determined observations
e(k_cat)	number of categories
e(k)	number of parameters
e(k_aux)	number of auxiliary parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance of model test
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	ologit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(cat)	category values
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`ologit` is implemented as an ado-file.

See Long and Freese (2006, chap. 5) for a discussion of models for ordinal outcomes and examples that use Stata. Cameron and Trivedi (2005, chap. 15) describe multinomial models, including the model fit by `ologit`. When you have a qualitative dependent variable, several estimation procedures are available. A popular choice is multinomial logistic regression (see [R] **mlogit**), but if you use this procedure when the response variable is ordinal, you are discarding information because multinomial logit ignores the ordered aspect of the outcome. Ordered logit and probit models provide a means to exploit the ordering information.

There is more than one "ordered logit" model. The model fit by `ologit`, which we will call the ordered logit model, is also known as the proportional odds model. Another popular choice, not fit by `ologit`, is known as the stereotype model; see [R] **slogit**. All ordered logit models have been derived by starting with a binary logit/probit model and generalizing it to allow for more than two outcomes.

The proportional-odds ordered logit model is so called because, if we consider the odds $\mathrm{odds}(k) = P(Y \leq k)/P(Y > k)$, then $\mathrm{odds}(k_1)$ and $\mathrm{odds}(k_2)$ have the same ratio for all independent variable combinations. The model is based on the principle that the only effect of combining adjoining categories in ordered categorical regression problems should be a loss of efficiency in estimating the regression parameters (McCullagh 1980). This model was also described by McKelvey and Zavoina (1975) and, previously, by Aitchison and Silvey (1957) in a different algebraic form. Brant (1990) offers a set of diagnostics for the model.

Peterson and Harrell (1990) suggest a model that allows nonproportional odds for a subset of the explanatory variables. `ologit` does not allow this, but a model similar to this was implemented by Fu (1998).

The stereotype model rejects the principle on which the ordered logit model is based. Anderson (1984) argues that there are two distinct types of ordered categorical variables: "grouped continuous", such as income, where the "type a" model applies; and "assessed", such as extent of pain relief, where the stereotype model applies. Greenland (1985) independently developed the same model. The stereotype model starts with a multinomial logistic regression model and imposes constraints on this model.

Goodness of fit for `ologit` can be evaluated by comparing the likelihood value with that obtained by fitting the model with `mlogit`. Let $\ln L_1$ be the log-likelihood value reported by `ologit`, and let $\ln L_0$ be the log-likelihood value reported by `mlogit`. If there are p independent variables (excluding the constant) and k categories, `mlogit` will estimate $p(k-1)$ additional parameters. We can then perform a "likelihood-ratio test", that is, calculate $-2(\ln L_1 - \ln L_0)$, and compare it with $\chi^2\{p(k-2)\}$. This test is suggestive only because the ordered logit model is not nested within the multinomial logit model. A large value of $-2(\ln L_1 - \ln L_0)$ should, however, be taken as evidence of poorness of fit. Marginally large values, on the other hand, should not be taken too seriously.

The coefficients and cutpoints are estimated using maximum likelihood as described in [R] **maximize**. In our parameterization, no constant appears, because the effect is absorbed into the cutpoints.

`ologit` and `oprobit` begin by tabulating the dependent variable. Category $i = 1$ is defined as the minimum value of the variable, $i = 2$ as the next ordered value, and so on, for the empirically determined k categories.

The probability of a given observation for ordered logit is

$$p_{ij} = \Pr(y_j = i) = \Pr\Big(\kappa_{i-1} < \mathbf{x}_j\boldsymbol{\beta} + u \leq \kappa_i\Big)$$
$$= \frac{1}{1+\exp(-\kappa_i + \mathbf{x}_j\boldsymbol{\beta})} - \frac{1}{1+\exp(-\kappa_{i-1} + \mathbf{x}_j\boldsymbol{\beta})}$$

κ_0 is defined as $-\infty$ and κ_k as $+\infty$.

For ordered probit, the probability of a given observation is

$$p_{ij} = \Pr(y_j = i) = \Pr\Big(\kappa_{i-1} < \mathbf{x}_j\boldsymbol{\beta} + u \leq \kappa_i\Big)$$
$$= \Phi\Big(\kappa_i - \mathbf{x}_j\boldsymbol{\beta}\Big) - \Phi\Big(\kappa_{i-1} - \mathbf{x}_j\boldsymbol{\beta}\Big)$$

where $\Phi(\cdot)$ is the standard normal cumulative distribution function.

The log likelihood is

$$\ln L = \sum_{j=1}^{N} w_j \sum_{i=1}^{k} I_i(y_j)\ln p_{ij}$$

where w_j is an optional weight and

$$I_i(y_j) = \begin{cases} 1, \text{ if } y_j = i \\ 0, \text{ otherwise} \end{cases}$$

`ologit` and `oprobit` support the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

These commands also support estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **ologit postestimation** — Postestimation tools for ologit

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **oprobit** — Ordered probit regression

[R] **rologit** — Rank-ordered logistic regression

[R] **slogit** — Stereotype logistic regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

ologit postestimation — Postestimation tools for ologit

Description

The following postestimation commands are available after `ologit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] { stub* | newvar | newvarlist } [if] [in] [, statistic
    outcome(outcome) nooffset]

predict [type] { stub* | newvarlist } [if] [in], scores
```

statistic	Description
Main	
`pr`	predicted probabilities; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction

If you do not specify `outcome()`, `pr` (with one new variable specified) assumes `outcome(#1)`.

You specify one or k new variables with `pr`, where k is the number of outcomes.

You specify one new variable with `xb` and `stdp`.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the predicted probabilities. If you do not also specify the `outcome()` option, you specify k new variables, where k is the number of categories of the dependent variable. Say that you fit a model by typing `ologit result x1 x2`, and `result` takes on three values. Then you could type `predict p1 p2 p3` to obtain all three predicted probabilities. If you specify the `outcome()` option, you must specify one new variable. Say that `result` takes on the values 1, 2, and 3. Typing `predict p1, outcome(1)` would produce the same `p1`.

`xb` calculates the linear prediction. You specify one new variable, for example, `predict linear, xb`. The linear prediction is defined, ignoring the contribution of the estimated cutpoints.

`stdp` calculates the standard error of the linear prediction. You specify one new variable, for example, `predict se, stdp`.

`outcome(`*outcome*`)` specifies for which outcome the predicted probabilities are to be calculated. `outcome()` should contain either one value of the dependent variable or one of `#1`, `#2`, ..., with `#1` meaning the first category of the dependent variable, `#2` meaning the second category, etc.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `ologit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables. The number of score variables created will equal the number of outcomes in the model. If the number of outcomes in the model was k, then

the first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\mathbf{b})$;

the second new variable will contain $\partial \ln L/\partial\kappa_1$;

the third new variable will contain $\partial \ln L/\partial\kappa_2$;

...

and the kth new variable will contain $\partial \ln L/\partial\kappa_{k-1}$, where κ_i refers to the ith cutpoint.

Remarks

See [U] **20 Estimation and postestimation commands** for instructions on obtaining the variance–covariance matrix of the estimators, predicted values, and hypothesis tests. Also see [R] **lrtest** for performing likelihood-ratio tests.

▷ Example 1

In example 2 of [R] **ologit**, we fit the model `ologit rep77 foreign length mpg`. The `predict` command can be used to obtain the predicted probabilities.

We type `predict` followed by the names of the new variables to hold the predicted probabilities, ordering the names from low to high. In our data, the lowest outcome is "poor", and the highest is "excellent". We have five categories, so we must type five names following `predict`; the choice of names is up to us:

```
. predict poor fair avg good exc
(option pr assumed; predicted probabilities)
. list exc good make model rep78 if rep77>=., sep(4) divider
```

	exc	good	make	model	rep78
3.	.0033341	.0393056	AMC	Spirit	.
10.	.0098392	.1070041	Buick	Opel	.
32.	.0023406	.0279497	Ford	Fiesta	Good
44.	.015697	.1594413	Merc.	Monarch	Average
53.	.065272	.4165188	Peugeot	604	.
56.	.005187	.059727	Plym.	Horizon	Average
57.	.0261461	.2371826	Plym.	Sapporo	.
63.	.0294961	.2585825	Pont.	Phoenix	.

The eight cars listed were introduced after 1977, so they do not have 1977 repair records in our data. We predicted what their 1977 repair records might have been using the fitted model. We see that, based on its characteristics, the Peugeot 604 had about a $41.65 + 6.53 \approx 48.2\%$ chance of a good or excellent repair record. The Ford Fiesta, which had only a 3% chance of a good or excellent repair record, in fact, had a good record when it was introduced in the following year.

◁

❑ Technical note

For ordered logit, `predict, xb` produces $S_j = x_{1j}\beta_1 + x_{2j}\beta_2 + \cdots + x_{kj}\beta_k$. The ordered-logit predictions are then the probability that $S_j + u_j$ lies between a pair of cutpoints, κ_{i-1} and κ_i. Some handy formulas are

$$\Pr(S_j + u_j < \kappa) = 1/(1 + e^{S_j - \kappa})$$
$$\Pr(S_j + u_j > \kappa) = 1 - 1/(1 + e^{S_j - \kappa})$$
$$\Pr(\kappa_1 < S_j + u_j < \kappa_2) = 1/(1 + e^{S_j - \kappa_2}) - 1/(1 + e^{S_j - \kappa_1})$$

Rather than using `predict` directly, we could calculate the predicted probabilities by hand. If we wished to obtain the predicted probability that the repair record is excellent and the probability that it is good, we look back at `ologit`'s output to obtain the cutpoints. We find that "good" corresponds to the interval `/cut3` $< S_j + u <$ `/cut4` and "excellent" to the interval $S_j + u >$ `/cut4`:

```
. predict score, xb
. generate probgood = 1/(1+exp(score-_b[/cut4])) - 1/(1+exp(score-_b[/cut3]))
. generate probexc = 1 - 1/(1+exp(score-_b[/cut4]))
```

The results of our calculation will be the same as those produced in the previous example. We refer to the estimated cutpoints just as we would any coefficient, so `_b[/cut3]` refers to the value of the `/cut3` coefficient; see [U] **13.5 Accessing coefficients and standard errors**.

❑

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **ologit** — Ordered logistic regression

[U] **20 Estimation and postestimation commands**

Title

oneway — One-way analysis of variance

Syntax

`oneway` *response_var factor_var* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`bonferroni`	Bonferroni multiple-comparison test
`scheffe`	Scheffé multiple-comparison test
`sidak`	Šidák multiple-comparison test
`tabulate`	produce summary table
[`no`]`means`	include or suppress means; default is `means`
[`no`]`standard`	include or suppress standard deviations; default is `standard`
[`no`]`freq`	include or suppress frequencies; default is `freq`
[`no`]`obs`	include or suppress number of obs; default is `obs` if data are weighted
`noanova`	suppress the ANOVA table
`nolabel`	show numeric codes, not labels
`wrap`	do not break wide tables
`missing`	treat missing values as categories

`by` is allowed; see [D] **by**.

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Linear models and related > ANOVA/MANOVA > One-way ANOVA

Description

The `oneway` command reports one-way analysis-of-variance (ANOVA) models and performs multiple-comparison tests.

If you wish to fit more complicated ANOVA layouts or wish to fit analysis-of-covariance (ANCOVA) models, see [R] **anova**.

See [D] **encode** for examples of fitting ANOVA models on string variables.

See [R] **loneway** for an alternative `oneway` command with slightly different features.

Options

Main

`bonferroni` reports the results of a Bonferroni multiple-comparison test.

`scheffe` reports the results of a Scheffé multiple-comparison test.

`sidak` reports the results of a Šidák multiple-comparison test.

`tabulate` produces a table of summary statistics of the *response_var* by levels of the *factor_var*. The table includes the mean, standard deviation, frequency, and, if the data are weighted, the number of observations. Individual elements of the table may be included or suppressed by using the [`no`]`means`, [`no`]`standard`, [`no`]`freq`, and [`no`]`obs` options. For example, typing

```
oneway response factor, tabulate means standard
```

produces a summary table that contains only the means and standard deviations. You could achieve the same result by typing

```
oneway response factor, tabulate nofreq
```

[`no`]`means` includes or suppresses only the means from the table produced by the `tabulate` option. See `tabulate` above.

[`no`]`standard` includes or suppresses only the standard deviations from the table produced by the `tabulate` option. See `tabulate` above.

[`no`]`freq` includes or suppresses only the frequencies from the table produced by the `tabulate` option. See `tabulate` above.

[`no`]`obs` includes or suppresses only the reported number of observations from the table produced by the `tabulate` option. If the data are not weighted, only the frequency is reported. If the data are weighted, the frequency refers to the sum of the weights. See `tabulate` above.

`noanova` suppresses the display of the ANOVA table.

`nolabel` causes the numeric codes to be displayed rather than the value labels in the ANOVA and multiple-comparison test tables.

`wrap` requests that Stata not break up wide tables to make them more readable.

`missing` requests that missing values of *factor_var* be treated as a category rather than as observations to be omitted from the analysis.

Remarks

Remarks are presented under the following headings:

Introduction
Obtaining observed means
Multiple-comparison tests
Weighted data

Introduction

The `oneway` command reports one-way ANOVA models. To perform a one-way layout of a variable called `endog` on `exog`, type `oneway endog exog`.

▷ Example 1

We run an experiment varying the amount of fertilizer used in growing apple trees. We test four concentrations, using each concentration in three groves of 12 trees each. Later in the year, we measure the average weight of the fruit.

If all had gone well, we would have had 3 observations on the average weight for each of the four concentrations. Instead, two of the groves were mistakenly leveled by a confused man on a large bulldozer. We are left with the following dataset:

```
. use http://www.stata-press.com/data/r12/apple
(Apple trees)

. describe
Contains data from http://www.stata-press.com/data/r12/apple.dta
  obs:            10                          Apple trees
 vars:             2                          16 Jan 2011 11:23
 size:           100
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
treatment       int    %8.0g                  Fertilizer
weight          double %10.0g                 Average weight in grams
-------------------------------------------------------------------------------
Sorted by:

. list, abbreviate(10)

     +-------------------+
     | treatment   weight |
     |-------------------|
  1. |         1    117.5 |
  2. |         1    113.8 |
  3. |         1    104.4 |
  4. |         2     48.9 |
  5. |         2     50.4 |
     |-------------------|
  6. |         2     58.9 |
  7. |         3     70.4 |
  8. |         3     86.9 |
  9. |         4     87.7 |
 10. |         4     67.3 |
     +-------------------+
```

To obtain the one-way ANOVA results, we type

```
. oneway weight treatment
                        Analysis of Variance
    Source              SS         df      MS            F     Prob > F
------------------------------------------------------------------------
Between groups      5295.54433      3   1765.18144     21.46     0.0013
 Within groups      493.591667      6   82.2652778
------------------------------------------------------------------------
    Total             5789.136      9   643.237333
Bartlett's test for equal variances:  chi2(3) =   1.3900  Prob>chi2 = 0.708
```

We find significant (at better than the 1% level) differences among the four concentrations.

◁

❑ Technical note

Rather than using the `oneway` command, we could have performed this analysis by using `anova`. Example 1 in [R] **anova** repeats this same analysis. You may wish to compare the output.

You will find the `oneway` command quicker than the `anova` command, and, as you will learn, `oneway` allows you to perform multiple-comparison tests. On the other hand, `anova` will let you generate predictions, examine the covariance matrix of the estimators, and perform more general hypothesis tests.

❑

❑ Technical note

Although the output is a usual ANOVA table, let's run through it anyway. The between-group sum of squares for the model is 5295.5 with 3 degrees of freedom, resulting in a mean square of $5295.5/3 \approx 1765.2$. The corresponding F statistic is 21.46 and has a significance level of 0.0013. Thus the model appears to be significant at the 0.13% level.

The second line summarizes the within-group (residual) variation. The within-group sum of squares is 493.59 with 6 degrees of freedom, resulting in a mean squared error of 82.27.

The between- and residual-group variations sum to the total sum of squares (TSS), which is reported as 5789.1 in the last line of the table. This is the TSS of `weight` after removal of the mean. Similarly, the between plus residual degrees of freedom sum to the total degrees of freedom, 9. Remember that there are 10 observations. Subtracting 1 for the mean, we are left with 9 total degrees of freedom.

At the bottom of the table, Bartlett's test for equal variances is reported. The value of the statistic is 1.39. The corresponding significance level (χ^2 with 3 degrees of freedom) is 0.708, so we cannot reject the assumption that the variances are homogeneous.

❑

Obtaining observed means

▷ Example 2

We typed `oneway weight treatment` to obtain an ANOVA table of weight of fruit by fertilizer concentration. Although we obtained the table, we obtained no information on which fertilizer seems to work the best. If we add the `tabulate` option, we obtain that additional information:

```
. oneway weight treatment, tabulate
```

Fertilizer	Summary of Average weight in grams Mean	Std. Dev.	Freq.
1	111.9	6.7535176	3
2	52.733333	5.3928966	3
3	78.65	11.667262	2
4	77.5	14.424978	2
Total	80.62	25.362124	10

Analysis of Variance

Source	SS	df	MS	F	Prob > F
Between groups	5295.54433	3	1765.18144	21.46	0.0013
Within groups	493.591667	6	82.2652778		
Total	5789.136	9	643.237333		

```
Bartlett's test for equal variances:  chi2(3) =   1.3900  Prob>chi2 = 0.708
```

We find that the average weight was largest when we used fertilizer concentration 1.

◁

Multiple-comparison tests

▷ Example 3

`oneway` can also perform multiple-comparison tests using either Bonferroni, Scheffé, or Šidák normalizations. For instance, to obtain the Bonferroni multiple-comparison test, we specify the `bonferroni` option:

```
. oneway weight treatment, bonferroni
                        Analysis of Variance
    Source              SS         df      MS            F     Prob > F
------------------------------------------------------------------------
Between groups      5295.54433      3   1765.18144     21.46     0.0013
 Within groups      493.591667      6   82.2652778
------------------------------------------------------------------------
    Total             5789.136      9   643.237333
Bartlett's test for equal variances:  chi2(3) =   1.3900  Prob>chi2 = 0.708
             Comparison of Average weight in grams by Fertilizer
                                (Bonferroni)
Row Mean-
Col Mean |          1          2          3
---------+---------------------------------
       2 |   -59.1667
         |      0.001
         |
       3 |     -33.25    25.9167
         |      0.042      0.122
         |
       4 |      -34.4    24.7667      -1.15
         |      0.036      0.146      1.000
```

The results of the Bonferroni test are presented as a matrix. The first entry, -59.17, represents the difference between fertilizer concentrations 2 and 1 (labeled "`Row Mean - Col Mean`" in the upper stub of the table). Remember that in the previous example we requested the `tabulate` option. Looking back, we find that the means of concentrations 1 and 2 are 111.90 and 52.73, respectively. Thus $52.73 - 111.90 = -59.17$.

Underneath that number is reported "`0.001`". This is the Bonferroni-adjusted significance of the difference. The difference is significant at the 0.1% level. Looking down the column, we see that concentration 3 is also worse than concentration 1 (4.2% level), as is concentration 4 (3.6% level).

On the basis of this evidence, we would use concentration 1 if we grew apple trees.

◁

▷ Example 4

We can just as easily obtain the Scheffé-adjusted significance levels. Rather than specifying the `bonferroni` option, we specify the `scheffe` option.

We will also add the noanova option to prevent Stata from redisplaying the ANOVA table:

```
. oneway weight treatment, noanova scheffe

            Comparison of Average weight in grams by Fertilizer
                                    (Scheffe)
Row Mean-
Col Mean |          1          2          3
---------+------------------------------------
       2 |   -59.1667
         |      0.001
         |
       3 |     -33.25    25.9167
         |       0.039      0.101
         |
       4 |       -34.4    24.7667      -1.15
         |       0.034      0.118      0.999
```

The differences are the same as those we obtained in the Bonferroni output, but the significance levels are not. According to the Bonferroni-adjusted numbers, the significance of the difference between fertilizer concentrations 1 and 3 is 4.2%. The Scheffé-adjusted significance level is 3.9%.

We will leave it to you to decide which results are more accurate.

◁

▷ Example 5

Let's conclude this example by obtaining the Šidák-adjusted multiple-comparison tests. We do this to illustrate Stata's capabilities to calculate these results, because searching across adjustment methods until you find the results you want is not a valid technique for obtaining significance levels.

```
. oneway weight treatment, noanova sidak

            Comparison of Average weight in grams by Fertilizer
                                    (Sidak)
Row Mean-
Col Mean |          1          2          3
---------+------------------------------------
       2 |   -59.1667
         |      0.001
         |
       3 |     -33.25    25.9167
         |       0.041      0.116
         |
       4 |       -34.4    24.7667      -1.15
         |       0.035      0.137      1.000
```

We find results that are similar to the Bonferroni-adjusted numbers.

◁

Henry Scheffé (1907–1977) was born in New York. He studied mathematics at the University of Wisconsin, gaining a doctorate with a dissertation on differential equations. He taught mathematics at Wisconsin, Oregon State University, and Reed College, but his interests changed to statistics and he joined Wilks at Princeton. After periods at Syracuse, UCLA, and Columbia, Scheffé settled in Berkeley from 1953. His research increasingly focused on linear models and particularly ANOVA, on which he produced a celebrated monograph. His death was the result of a bicycle accident.

Weighted data

▷ Example 6

oneway can work with both weighted and unweighted data. Let's assume that we wish to perform a one-way layout of the death rate on the four census regions of the United States using state data. Our data contain three variables, drate (the death rate), region (the region), and pop (the population of the state).

To fit the model, we type oneway drate region [weight=pop], although we typically abbreviate weight as w. We will also add the tabulate option to demonstrate how the table of summary statistics differs for weighted data:

```
. use http://www.stata-press.com/data/r12/census8
(1980 Census data by state)
. oneway drate region [w=pop], tabulate
(analytic weights assumed)
```

Census region	Summary of Death Rate Mean	Std. Dev.	Freq.	Obs.
NE	97.15	5.82	49135283	9
N Cntrl	88.10	5.58	58865670	12
South	87.05	10.40	74734029	16
West	75.65	8.23	43172490	13
Total	87.34	10.43	2.259e+08	50

Analysis of Variance

Source	SS	df	MS	F	Prob > F
Between groups	2360.92281	3	786.974272	12.17	0.0000
Within groups	2974.09635	46	64.6542685		
Total	5335.01916	49	108.877942		

```
Bartlett's test for equal variances:  chi2(3) =   5.4971  Prob>chi2 = 0.139
```

When the data are weighted, the summary table has four columns rather than three. The column labeled "Freq." reports the sum of the weights. The overall frequency is 2.259×10^8, meaning that there are approximately 226 million people in the United States.

The ANOVA table is appropriately weighted. Also see [U] **11.1.6 weight**.

◁

Saved results

oneway saves the following in r():

Scalars

r(N)	number of observations	r(df_m)	between-group degrees of freedom
r(F)	F statistic	r(rss)	within-group sum of squares
r(df_r)	within-group degrees of freedom	r(chi2bart)	Bartlett's χ^2
r(mss)	between-group sum of squares	r(df_bart)	Bartlett's degrees of freedom

Methods and formulas

Methods and formulas are presented under the following headings:

One-way analysis of variance
Bartlett's test
Multiple-comparison tests

One-way analysis of variance

The model of one-way ANOVA is

$$y_{ij} = \mu + \alpha_i + \epsilon_{ij}$$

for levels $i = 1, \ldots, k$ and observations $j = 1, \ldots, n_i$. Define $\overline{y}_i$ as the (weighted) mean of y_{ij} over j and $\overline{y}$ as the overall (weighted) mean of y_{ij}. Define w_{ij} as the weight associated with y_{ij}, which is 1 if the data are unweighted. w_{ij} is normalized to sum to $n = \sum_i n_i$ if `aweights` are used and is otherwise not normalized. w_i refers to $\sum_j w_{ij}$, and w refers to $\sum_i w_i$.

The between-group sum of squares is then

$$S_1 = \sum_i w_i(\overline{y}_i - \overline{y})^2$$

The TSS is

$$S = \sum_i \sum_j w_{ij}(y_{ij} - \overline{y})^2$$

The within-group sum of squares is given by $S_e = S - S_1$.

The between-group mean square is $s_1^2 = S_1/(k-1)$, and the within-group mean square is $s_e^2 = S_e/(w-k)$. The test statistic is $F = s_1^2/s_e^2$. See, for instance, Snedecor and Cochran (1989).

Bartlett's test

Bartlett's test assumes that you have m independent, normal, random samples and tests the hypothesis $\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_m^2$. The test statistic, M, is defined as

$$M = \frac{(T-m)\ln\widehat{\sigma}^2 - \sum(T_i - 1)\ln\widehat{\sigma}_i^2}{1 + \frac{1}{3(m-1)}\left\{\left(\sum \frac{1}{T_i - 1}\right) - \frac{1}{T-m}\right\}}$$

where there are T overall observations, T_i observations in the ith group, and

$$(T_i - 1)\widehat{\sigma}_i^2 = \sum_{j=1}^{T_i}(y_{ij} - \overline{y}_i)^2$$

$$(T-m)\widehat{\sigma}^2 = \sum_{i=1}^{m}(T_i - 1)\widehat{\sigma}_i^2$$

An approximate test of the homogeneity of variance is based on the statistic M with critical values obtained from the χ^2 distribution of $m-1$ degrees of freedom. See Bartlett (1937) or Draper and Smith (1998, 56–57).

Multiple-comparison tests

Let's begin by reviewing the logic behind these adjustments. The "standard" t statistic for the comparison of two means is

$$t = \frac{\overline{y}_i - \overline{y}_j}{s\sqrt{\frac{1}{n_i} + \frac{1}{n_j}}}$$

where s is the overall standard deviation, $\overline{y}_i$ is the measured average of y in group i, and n_i is the number of observations in the group. We perform hypothesis tests by calculating this t statistic. We simultaneously choose a critical level, α, and look up the t statistic corresponding to that level in a table. We reject the hypothesis if our calculated t exceeds the value we looked up. Alternatively, because we have a computer at our disposal, we calculate the significance level e corresponding to our calculated t statistic, and if $e < \alpha$, we reject the hypothesis.

This logic works well when we are performing one test. Now consider what happens when we perform several separate tests, say, n of them. Let's assume, just for discussion, that we set α equal to 0.05 and that we will perform six tests. For each test, we have a 0.05 probability of falsely rejecting the equality-of-means hypothesis. Overall, then, our chances of falsely rejecting *at least one* of the hypotheses is $1 - (1 - 0.05)^6 \approx 0.26$ if the tests are independent.

The idea behind multiple-comparison tests is to control for the fact that we will perform multiple tests and to reduce our overall chances of falsely rejecting each hypothesis to α rather than letting our chances increase with each additional test. (See Miller [1981] and Hochberg and Tamhane [1987] for rather advanced texts on multiple-comparison procedures.)

The Bonferroni adjustment (see Miller [1981]; also see van Belle et al. [2004, 534–537]) does this by (falsely but approximately) asserting that the critical level we should use, a, is the true critical level, α, divided by the number of tests, n; that is, $a = \alpha/n$. For instance, if we are going to perform six tests, each at the 0.05 significance level, we want to adopt a critical level of $0.05/6 \approx 0.00833$.

We can just as easily apply this logic to e, the significance level associated with our t statistic, as to our critical level α. If a comparison has a calculated significance of e, then its "real" significance, adjusted for the fact of n comparisons, is $n \times e$. If a comparison has a significance level of, say, 0.012, and we perform six tests, then its "real" significance is 0.072. If we adopt a critical level of 0.05, we cannot reject the hypothesis. If we adopt a critical level of 0.10, we can reject it.

Of course, this calculation can go above 1, but that just means that there is no $\alpha < 1$ for which we could reject the hypothesis. (This situation arises because of the crude nature of the Bonferroni adjustment.) Stata handles this case by simply calling the significance level 1. Thus the formula for the Bonferroni significance level is

$$e_b = \min(1, en)$$

where $n = k(k-1)/2$ is the number of comparisons.

The Šidák adjustment (Šidák [1967]; also see Winer, Brown, and Michels [1991, 165–166]) is slightly different and provides a tighter bound. It starts with the assertion that

$$a = 1 - (1 - \alpha)^{1/n}$$

Turning this formula around and substituting calculated significance levels, we obtain

$$e_s = \min\left\{1, 1 - (1 - e)^n\right\}$$

For example, if the calculated significance is 0.012 and we perform six tests, the "real" significance is approximately 0.07.

The Scheffé test (Scheffé [1953, 1959]; also see Kuehl [2000, 97–98]) differs in derivation, but it attacks the same problem. Let there be k means for which we want to make all the pairwise tests. Two means are declared significantly different if

$$t \geq \sqrt{(k-1)F(\alpha; k-1, \nu)}$$

where $F(\alpha; k-1, \nu)$ is the α-critical value of the F distribution with $k-1$ numerator and ν denominator degrees of freedom. Scheffé's test has the nicety that it never declares a contrast significant if the overall F test is not significant.

Turning the test around, Stata calculates a significance level

$$\widehat{e} = F\left(\frac{t^2}{k-1}, k-1, \nu\right)$$

For instance, you have a calculated t statistic of 4.0 with 50 degrees of freedom. The simple t test says that the significance level is 0.00021. The F test equivalent, 16 with 1 and 50 degrees of freedom, says the same. If you are comparing three means, however, you calculate an F test of 8.0 with 2 and 50 degrees of freedom, which says that the significance level is 0.0010.

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Also see

[R] **anova** — Analysis of variance and covariance

[R] **loneway** — Large one-way ANOVA, random effects, and reliability

Title

oprobit — Ordered probit regression

Syntax

`oprobit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `fracpoly`, `jackknife`, `mfp`, `mi estimate`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Ordinal outcomes > Ordered probit regression

Description

`oprobit` fits ordered probit models of ordinal variable *depvar* on the independent variables *indepvars*. The actual values taken on by the dependent variable are irrelevant, except that larger values are assumed to correspond to "higher" outcomes.

See [R] **logistic** for a list of related estimation commands.

Options

Model

`offset(`*varname*`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

The following option is available with `oprobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

An ordered probit model is used to estimate relationships between an ordinal dependent variable and a set of independent variables. An *ordinal* variable is a variable that is categorical and ordered, for instance, "poor", "good", and "excellent", which might indicate a person's current health status or the repair record of a car. If there are only two outcomes, see [R] **logistic**, [R] **logit**, and [R] **probit**. This entry is concerned only with more than two outcomes. If the outcomes cannot be ordered (for example, residency in the north, east, south, or west), see [R] **mlogit**. This entry is concerned only with models in which the outcomes can be ordered.

In ordered probit, an underlying score is estimated as a linear function of the independent variables and a set of cutpoints. The probability of observing outcome i corresponds to the probability that the estimated linear function, plus random error, is within the range of the cutpoints estimated for the outcome:

$$\Pr(\text{outcome}_j = i) = \Pr(\kappa_{i-1} < \beta_1 x_{1j} + \beta_2 x_{2j} + \cdots + \beta_k x_{kj} + u_j \leq \kappa_i)$$

u_j is assumed to be normally distributed. In either case, we estimate the coefficients β_1, β_2, …, β_k together with the cutpoints κ_1, κ_2, …, κ_{I-1}, where I is the number of possible outcomes. κ_0 is taken as $-\infty$, and κ_I is taken as $+\infty$. All of this is a direct generalization of the ordinary two-outcome probit model.

Example 1

In example 2 of [R] **ologit**, we use a variation of the automobile dataset (see [U] **1.2.2 Example datasets**) to analyze the 1977 repair records of 66 foreign and domestic cars. We use ordered logit to explore the relationship of `rep77` in terms of `foreign` (origin of manufacture), `length` (a proxy for size), and `mpg`. Here we fit the same model using ordered probit rather than ordered logit:

```
. use http://www.stata-press.com/data/r12/fullauto
(Automobile Models)
. oprobit rep77 foreign length mpg

Iteration 0:   log likelihood = -89.895098
Iteration 1:   log likelihood = -78.106316
Iteration 2:   log likelihood = -78.020086
Iteration 3:   log likelihood = -78.020025
Iteration 4:   log likelihood = -78.020025
Ordered probit regression                       Number of obs   =         66
                                                LR chi2(3)      =      23.75
                                                Prob > chi2     =     0.0000
Log likelihood = -78.020025                     Pseudo R2       =     0.1321

------------------------------------------------------------------------------
       rep77 |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     foreign |   1.704861   .4246796     4.01   0.000     .8725037    2.537217
      length |   .0468675    .012648     3.71   0.000      .022078    .0716571
         mpg |   .1304559   .0378628     3.45   0.001     .0562463    .2046656
-------------+----------------------------------------------------------------
       /cut1 |    10.1589   3.076754                      4.128577    16.18923
       /cut2 |   11.21003   3.107527                      5.119389    17.30067
       /cut3 |   12.54561   3.155233                      6.361467    18.72975
       /cut4 |   13.98059   3.218793                      7.671874    20.28931
------------------------------------------------------------------------------
```

We find that foreign cars have better repair records, as do larger cars and cars with better mileage ratings.

Saved results

oprobit saves the following in e():

Scalars

e(N)	number of observations
e(N_cd)	number of completely determined observations
e(k_cat)	number of categories
e(k)	number of parameters
e(k_aux)	number of auxiliary parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance of model test
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	oprobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(cat)	category values
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

oprobit is implemented as an ado-file.

See *Methods and formulas* of [R] **ologit**.

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Also see

[R] **oprobit postestimation** — Postestimation tools for oprobit

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **mprobit** — Multinomial probit regression

[R] **ologit** — Ordered logistic regression

[R] **probit** — Probit regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

oprobit postestimation — Postestimation tools for oprobit

Description

The following postestimation commands are available after `oprobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] { stub* | newvar | newvarlist } [if] [in] [, statistic
    outcome(outcome) nooffset]

predict [type] { stub* | newvarlist } [if] [in], scores
```

statistic	Description
Main	
`pr`	predicted probabilities; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction

If you do not specify `outcome()`, `pr` (with one new variable specified) assumes `outcome(#1)`.

You specify one or k new variables with `pr`, where k is the number of outcomes.

You specify one new variable with `xb` and `stdp`.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the predicted probabilities. If you do not also specify the `outcome()` option, you specify k new variables, where k is the number of categories of the dependent variable. Say that you fit a model by typing `oprobit result x1 x2`, and `result` takes on three values. Then you could type `predict p1 p2 p3` to obtain all three predicted probabilities. If you specify the `outcome()` option, you must specify one new variable. Say that `result` takes on values 1, 2, and 3. Typing `predict p1, outcome(1)` would produce the same `p1`.

`xb` calculates the linear prediction. You specify one new variable, for example, `predict linear, xb`. The linear prediction is defined ignoring the contribution of the estimated cutpoints.

`stdp` calculates the standard error of the linear prediction. You specify one new variable, for example, `predict se, stdp`.

`outcome(`*outcome*`)` specifies for which outcome the predicted probabilities are to be calculated. `outcome()` should contain either one value of the dependent variable or one of `#1`, `#2`, ..., with `#1` meaning the first category of the dependent variable, `#2` meaning the second category, etc.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `oprobit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables. The number of score variables created will equal the number of outcomes in the model. If the number of outcomes in the model was k, then

the first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\mathbf{b})$;

the second new variable will contain $\partial \ln L/\partial\kappa_1$;

the third new variable will contain $\partial \ln L/\partial\kappa_2$;

...

and the kth new variable will contain $\partial \ln L/\partial\kappa_{k-1}$, where κ_i refers to the ith cutpoint.

Remarks

See [U] **20 Estimation and postestimation commands** for instructions on obtaining the variance–covariance matrix of the estimators, predicted values, and hypothesis tests. Also see [R] **lrtest** for performing likelihood-ratio tests.

▷ Example 1

In example 1 of [R] **oprobit**, we fit the model `oprobit rep77 foreign length mpg`. The `predict` command can be used to obtain the predicted probabilities. We type `predict` followed by the names of the new variables to hold the predicted probabilities, ordering the names from low to high. In our data, the lowest outcome is "poor" and the highest is "excellent". We have five categories, so we must type five names following `predict`; the choice of names is up to us:

```
. predict poor fair avg good exc
(option pr assumed; predicted probabilities)
. list make model exc good if rep77>=., sep(4) divider
```

	make	model	exc	good
3.	AMC	Spirit	.0006044	.0351813
10.	Buick	Opel	.0043803	.1133763
32.	Ford	Fiesta	.0002927	.0222789
44.	Merc.	Monarch	.0093209	.1700846
53.	Peugeot	604	.0734199	.4202766
56.	Plym.	Horizon	.001413	.0590294
57.	Plym.	Sapporo	.0197543	.2466034
63.	Pont.	Phoenix	.0234156	.266771

◁

❑ Technical note

For ordered probit, `predict, xb` produces $S_j = x_{1j}\beta_1 + x_{2j}\beta_2 + \cdots + x_{kj}\beta_k$. Ordered probit is identical to ordered logit, except that we use different distribution functions for calculating probabilities. The ordered-probit predictions are then the probability that $S_j + u_j$ lies between a pair of cutpoints κ_{i-1} and κ_i. The formulas for ordered probit are

$$\Pr(S_j + u < \kappa) = \Phi(\kappa - S_j)$$
$$\Pr(S_j + u > \kappa) = 1 - \Phi(\kappa - S_j) = \Phi(S_j - \kappa)$$
$$\Pr(\kappa_1 < S_j + u < \kappa_2) = \Phi(\kappa_2 - S_j) - \Phi(\kappa_1 - S_j)$$

Rather than using `predict` directly, we could calculate the predicted probabilities by hand.

```
. predict pscore, xb
. generate probexc = normal(pscore-_b[/cut4])
. generate probgood = normal(_b[/cut4]-pscore) - normal(_b[/cut3]-pscore)
```

❑

Methods and formulas

All postestimation tools listed above are implemented as ado-files.

Also see

[R] **oprobit** — Ordered probit regression

[U] **20 Estimation and postestimation commands**

Title

orthog — Orthogonalize variables and compute orthogonal polynomials

Syntax

Orthogonalize variables

```
orthog [varlist] [if] [in] [weight] , generate(newvarlist) [matrix(matname)]
```

Compute orthogonal polynomial

```
orthpoly varname [if] [in] [weight] ,
    { generate(newvarlist) | poly(matname) } [degree(#)]
```

`orthpoly` requires that `generate(`*newvarlist*`)` or `poly(`*matname*`)`, or both, be specified.
varlist may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`iweights`, `fweights`, `pweights`, and `aweights` are allowed, see [U] **11.1.6 weight**.

Menu

orthog

Data > Create or change data > Other variable-creation commands > Orthogonalize variables

orthpoly

Data > Create or change data > Other variable-creation commands > Orthogonal polynomials

Description

`orthog` orthogonalizes a set of variables, creating a new set of orthogonal variables (all of type `double`), using a modified Gram–Schmidt procedure (Golub and Van Loan 1996). The order of the variables determines the orthogonalization; hence, the "most important" variables should be listed first.

Execution time is proportional to the square of the number of variables. With many (>10) variables, `orthog` will be fairly slow.

`orthpoly` computes orthogonal polynomials for one variable.

Options for orthog

Main

`generate(`*newvarlist*`)` is required. `generate()` creates new orthogonal variables of type `double`. For `orthog`, *newvarlist* will contain the orthogonalized *varlist*. If *varlist* contains d variables, then so will *newvarlist*. *newvarlist* can be specified by giving a list of exactly d new variable names, or it can be abbreviated using the styles *newvar*`1-`*newvard* or *newvar*`*`. For these two styles of abbreviation, new variables *newvar*`1`, *newvar*`2`, ..., *newvard* are generated.

`matrix(`*matname*`)` creates a $(d+1) \times (d+1)$ matrix containing the matrix R defined by $X = QR$, where X is the $N \times (d+1)$ matrix representation of *varlist* plus a column of ones and Q is the $N \times (d+1)$ matrix representation of *newvarlist* plus a column of ones (d = number of variables in *varlist*, and N = number of observations).

Options for orthpoly

Main

`generate(`*newvarlist*`)` or `poly()`, or both, must be specified. `generate()` creates new orthogonal variables of type `double`. *newvarlist* will contain orthogonal polynomials of degree 1, 2, ..., d evaluated at *varname*, where d is as specified by `degree(`d`)`. *newvarlist* can be specified by giving a list of exactly d new variable names, or it can be abbreviated using the styles *newvar*`1-`*newvard* or *newvar*`*`. For these two styles of abbreviation, new variables *newvar*`1`, *newvar*`2`, ..., *newvard* are generated.

`poly(`*matname*`)` creates a $(d+1) \times (d+1)$ matrix called *matname* containing the coefficients of the orthogonal polynomials. The orthogonal polynomial of degree $i \leq d$ is

matname`[`i`, `$d+1$`] + `*matname*`[`i`, 1]*`*varname* `+` *matname*`[`i`, 2]*`*varname*^{2} `+` $\cdots$ `+` *matname*`[`i`, `i`]*`*varname*^{i}

The coefficients corresponding to the constant term are placed in the last column of the matrix. The last row of the matrix is all zeros, except for the last column, which corresponds to the constant term.

`degree(#)` specifies the highest-degree polynomial to include. Orthogonal polynomials of degree 1, 2, ..., d = # are computed. The default is $d = 1$.

Remarks

Orthogonal variables are useful for two reasons. The first is numerical accuracy for highly collinear variables. Stata's `regress` and other estimation commands can face much collinearity and still produce accurate results. But, at some point, these commands will drop variables because of collinearity. If you know with certainty that the variables are not perfectly collinear, you may want to retain all their effects in the model. If you use `orthog` or `orthpoly` to produce a set of orthogonal variables, all variables will be present in the estimation results.

Users are more likely to find orthogonal variables useful for the second reason: ease of interpreting results. `orthog` and `orthpoly` create a set of variables such that the "effects" of all the preceding variables have been removed from each variable. For example, if we issue the command

```
. orthog x1 x2 x3, generate(q1 q2 q3)
```

the effect of the constant is removed from `x1` to produce `q1`; the constant and `x1` are removed from `x2` to produce `q2`; and finally the constant, `x1`, and `x2` are removed from `x3` to produce `q3`. Hence,

$$\texttt{q1} = r_{01} + r_{11}\,\texttt{x1}$$
$$\texttt{q2} = r_{02} + r_{12}\,\texttt{x1} + r_{22}\,\texttt{x2}$$
$$\texttt{q3} = r_{03} + r_{13}\,\texttt{x1} + r_{23}\,\texttt{x2} + r_{33}\,\texttt{x3}$$

This effect can be generalized and written in matrix notation as

$$X = QR$$

where X is the $N \times (d+1)$ matrix representation of *varlist* plus a column of ones, and Q is the $N \times (d+1)$ matrix representation of *newvarlist* plus a column of ones (d = number of variables in *varlist* and N = number of observations). The $(d+1) \times (d+1)$ matrix R is a permuted upper-triangular matrix, that is, R would be upper triangular if the constant were first, but the constant is last, so the first row/column has been permuted with the last row/column. Because Stata's estimation commands list the constant term last, this allows R, obtained via the `matrix()` option, to be used to transform estimation results.

▷ Example 1

Consider Stata's `auto.dta` dataset. Suppose that we postulate a model in which `price` depends on the car's `length`, `weight`, `headroom`, and trunk size (`trunk`). These predictors are collinear, but not extremely so—the correlations are not that close to 1:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. correlate length weight headroom trunk
(obs=74)
```

	length	weight	headroom	trunk
length	1.0000			
weight	0.9460	1.0000		
headroom	0.5163	0.4835	1.0000	
trunk	0.7266	0.6722	0.6620	1.0000

`regress` certainly has no trouble fitting this model:

```
. regress price length weight headroom trunk
```

Source	SS	df	MS		
Model	236016580	4	59004145	Number of obs	= 74
Residual	399048816	69	5783316.17	F(4, 69)	= 10.20
				Prob > F	= 0.0000
				R-squared	= 0.3716
				Adj R-squared	= 0.3352
Total	635065396	73	8699525.97	Root MSE	= 2404.9

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
length	-101.7092	42.12534	-2.41	0.018	-185.747	-17.67147
weight	4.753066	1.120054	4.24	0.000	2.518619	6.987512
headroom	-711.5679	445.0204	-1.60	0.114	-1599.359	176.2236
trunk	114.0859	109.9488	1.04	0.303	-105.2559	333.4277
_cons	11488.47	4543.902	2.53	0.014	2423.638	20553.31

However, we may believe a priori that `length` is the most important predictor, followed by `weight`, `headroom`, and `trunk`. We would like to remove the "effect" of `length` from all the other predictors, remove `weight` from `headroom` and `trunk`, and remove `headroom` from `trunk`. We can do this by running `orthog`, and then we fit the model again using the orthogonal variables:

```
. orthog length weight headroom trunk, gen(olength oweight oheadroom otrunk)
> matrix(R)
. regress price olength oweight oheadroom otrunk
```

Source	SS	df	MS	Number of obs =	74
Model	236016580	4	59004145	F(4, 69) =	10.20
Residual	399048816	69	5783316.17	Prob > F =	0.0000
				R-squared =	0.3716
				Adj R-squared =	0.3352
Total	635065396	73	8699525.97	Root MSE =	2404.9

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
olength	1265.049	279.5584	4.53	0.000	707.3454	1822.753
oweight	1175.765	279.5584	4.21	0.000	618.0617	1733.469
oheadroom	-349.9916	279.5584	-1.25	0.215	-907.6955	207.7122
otrunk	290.0776	279.5584	1.04	0.303	-267.6262	847.7815
_cons	6165.257	279.5584	22.05	0.000	5607.553	6722.961

Using the matrix `R`, we can transform the results obtained using the orthogonal predictors back to the metric of original predictors:

```
. matrix b = e(b)*inv(R)'
. matrix list b
b[1,5]
        length      weight    headroom       trunk       _cons
y1  -101.70924   4.7530659  -711.56789   114.08591   11488.475
```

◁

❑ Technical note

The matrix R obtained using the `matrix()` option with `orthog` can also be used to recover X (the original *varlist*) from Q (the orthogonalized *newvarlist*), one variable at a time. Continuing with the previous example, we illustrate how to recover the `trunk` variable:

```
. matrix C = R[1...,"trunk"]'
. matrix score double rtrunk = C
. compare rtrunk trunk
```

	count	difference minimum	difference average	difference maximum
rtrunk>trunk	74	1.42e-14	2.27e-14	3.55e-14
jointly defined	74	1.42e-14	2.27e-14	3.55e-14
total	74			

Here the recovered variable `rtrunk` is almost exactly the same as the original `trunk` variable. When you are orthogonalizing many variables, this procedure can be performed to check the numerical soundness of the orthogonalization. Because of the ordering of the orthogonalization procedure, the last variable and the variables near the end of the *varlist* are the most important ones to check.

❑

The `orthpoly` command effectively does for polynomial terms what the `orthog` command does for an arbitrary set of variables.

▷ Example 2

Again consider the auto.dta dataset. Suppose that we wish to fit the model

$$\texttt{mpg} = \beta_0 + \beta_1\,\texttt{weight} + \beta_2\,\texttt{weight}^2 + \beta_3\,\texttt{weight}^3 + \beta_4\,\texttt{weight}^4 + \epsilon$$

We will first compute the regression with natural polynomials:

```
. gen double w1 = weight
. gen double w2 = w1*w1
. gen double w3 = w2*w1
. gen double w4 = w3*w1
. correlate w1-w4
(obs=74)
```

	w1	w2	w3	w4
w1	1.0000			
w2	0.9915	1.0000		
w3	0.9665	0.9916	1.0000	
w4	0.9279	0.9679	0.9922	1.0000

```
. regress mpg w1-w4
```

Source	SS	df	MS		
Model	1652.73666	4	413.184164	Number of obs =	74
Residual	790.722803	69	11.4597508	F(4, 69) =	36.06
				Prob > F =	0.0000
				R-squared =	0.6764
				Adj R-squared =	0.6576
Total	2443.45946	73	33.4720474	Root MSE =	3.3852

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
w1	.0289302	.1161939	0.25	0.804	-.2028704	.2607307
w2	-.0000229	.0000566	-0.40	0.687	-.0001359	.0000901
w3	5.74e-09	1.19e-08	0.48	0.631	-1.80e-08	2.95e-08
w4	-4.86e-13	9.14e-13	-0.53	0.596	-2.31e-12	1.34e-12
_cons	23.94421	86.60667	0.28	0.783	-148.8314	196.7198

Some of the correlations among the powers of weight are very large, but this does not create any problems for regress. However, we may wish to look at the quadratic trend with the constant removed, the cubic trend with the quadratic and constant removed, etc. orthpoly will generate polynomial terms with this property:

```
. orthpoly weight, generate(pw*) deg(4) poly(P)
. regress mpg pw1-pw4
```

Source	SS	df	MS		
Model	1652.73666	4	413.184164	Number of obs =	74
Residual	790.722803	69	11.4597508	F(4, 69) =	36.06
				Prob > F =	0.0000
				R-squared =	0.6764
				Adj R-squared =	0.6576
Total	2443.45946	73	33.4720474	Root MSE =	3.3852

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
pw1	-4.638252	.3935245	-11.79	0.000	-5.423312	-3.853192
pw2	.8263545	.3935245	2.10	0.039	.0412947	1.611414
pw3	-.3068616	.3935245	-0.78	0.438	-1.091921	.4781982
pw4	-.209457	.3935245	-0.53	0.596	-.9945168	.5756028
_cons	21.2973	.3935245	54.12	0.000	20.51224	22.08236

Compare the p-values of the terms in the natural polynomial regression with those in the orthogonal polynomial regression. With orthogonal polynomials, it is easy to see that the pure cubic and quartic trends are not significant and that the constant, linear, and quadratic terms each have $p < 0.05$.

The matrix `P` obtained with the `poly()` option can be used to transform coefficients for orthogonal polynomials to coefficients for natural polynomials:

```
. orthpoly weight, poly(P) deg(4)
. matrix b = e(b)*P
. matrix list b
b[1,5]
          deg1        deg2        deg3        deg4       _cons
y1   .02893016  -.00002291   5.745e-09  -4.862e-13   23.944212
```

◁

Methods and formulas

`orthog` and `orthpoly` are implemented as ado-files.

`orthog`'s orthogonalization can be written in matrix notation as

$$X = QR$$

where X is the $N \times (d+1)$ matrix representation of *varlist* plus a column of ones and Q is the $N \times (d+1)$ matrix representation of *newvarlist* plus a column of ones ($d =$ number of variables in *varlist*, and $N =$ number of observations). The $(d+1) \times (d+1)$ matrix R is a permuted upper-triangular matrix; that is, R would be upper triangular if the constant were first, but the constant is last, so the first row/column has been permuted with the last row/column.

Q and R are obtained using a modified Gram–Schmidt procedure; see Golub and Van Loan (1996, 218–219) for details. The traditional Gram–Schmidt procedure is notoriously unsound, but the modified procedure is good. `orthog` performs two passes of this procedure.

`orthpoly` uses the Christoffel–Darboux recurrence formula (Abramowitz and Stegun 1972).

Both `orthog` and `orthpoly` normalize the orthogonal variables such that

$$Q'WQ = MI$$

where $W = \text{diag}(w_1, w_2, \ldots, w_N)$ with weights $w_1, w_2, \ldots, w_N$ (all 1 if weights are not specified), and M is the sum of the weights (the number of observations if weights are not specified).

References

Abramowitz, M., and I. A. Stegun, ed. 1972. *Handbook of Mathematical Functions with Formulas, Graphs, and Mathematical Tables*. 10th ed. Washington, DC: National Bureau of Standards.

Golub, G. H., and C. F. Van Loan. 1996. *Matrix Computations*. 3rd ed. Baltimore: Johns Hopkins University Press.

Sribney, W. M. 1995. sg37: Orthogonal polynomials. *Stata Technical Bulletin* 25: 17–18. Reprinted in *Stata Technical Bulletin Reprints*, vol. 5, pp. 96–98. College Station, TX: Stata Press.

Also see

[R] **regress** — Linear regression

Title

pcorr — Partial and semipartial correlation coefficients

Syntax

`pcorr` *varname*$_1$ *varlist* [*if*] [*in*] [*weight*]

varname$_1$ and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`by` is allowed; see [D] **by**.
`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Partial correlations

Description

`pcorr` displays the partial and semipartial correlation coefficients of *varname*$_1$ with each variable in *varlist* after removing the effects of all other variables in *varlist*. The squared correlations and corresponding significance are also reported.

Remarks

Assume that y is determined by x_1, x_2, ..., x_k. The partial correlation between y and x_1 is an attempt to estimate the correlation that would be observed between y and x_1 if the other x's did not vary. The semipartial correlation, also called part correlation, between y and x_1 is an attempt to estimate the correlation that would be observed between y and x_1 after the effects of all other x's are removed from x_1 but not from y.

Both squared correlations estimate the proportion of the variance of y that is explained by each predictor. The squared semipartial correlation between y and x_1 represents the proportion of variance in y that is explained by x_1 only. This squared correlation can also be interpreted as the decrease in the model's R^2 value that results from removing x_1 from the full model. Thus one could use the squared semipartial correlations as criteria for model selection. The squared partial correlation between y and x_1 represents the proportion of variance in y not associated with any other x's that is explained by x_1. Thus the squared partial correlation gives an estimate of how much of the variance of y not explained by the other x's is explained by x_1.

▷ Example 1

Using our automobile dataset (described in [U] **1.2.2 Example datasets**), we can obtain the simple correlations between `price`, `mpg`, `weight`, and `foreign` from `correlate` (see [R] **correlate**):

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. correlate price mpg weight foreign
(obs=74)
```

	price	mpg	weight	foreign
price	1.0000			
mpg	-0.4686	1.0000		
weight	0.5386	-0.8072	1.0000	
foreign	0.0487	0.3934	-0.5928	1.0000

Although `correlate` gave us the full correlation matrix, our interest is in just the first column. We find, for instance, that the higher the `mpg`, the lower the `price`. We obtain the partial and semipartial correlation coefficients by using `pcorr`:

```
. pcorr price mpg weight foreign
(obs=74)
Partial and semipartial correlations of price with
```

Variable	Partial Corr.	Semipartial Corr.	Partial Corr.^2	Semipartial Corr.^2	Significance Value
mpg	0.0352	0.0249	0.0012	0.0006	0.7693
weight	0.5488	0.4644	0.3012	0.2157	0.0000
foreign	0.5402	0.4541	0.2918	0.2062	0.0000

We now find that the partial and semipartial correlations of `price` with `mpg` are near 0. In the simple correlations, we found that `price` and `foreign` were virtually uncorrelated. In the partial and semipartial correlations, we find that `price` and `foreign` are positively correlated. The nonsignificance of `mpg` tells us that the amount in which R^2 decreases by removing `mpg` from the model is not significant. We find that removing either `weight` or `foreign` results in a significant drop in the R^2 of the model.

◁

❑ Technical note

Use caution when interpreting the above results. As we said at the outset, the partial and semipartial correlation coefficients are an *attempt* to estimate the correlation that would be observed if the effects of all other variables were taken out of both y and x or only x. `pcorr` makes it too easy to ignore the fact that we are fitting a model. In the example above, the model is

$$\texttt{price} = \beta_0 + \beta_1\texttt{mpg} + \beta_2\texttt{weight} + \beta_3\texttt{foreign} + \epsilon$$

which is, in all honesty, a rather silly model. Even if we accept the implied economic assumptions of the model—that consumers value `mpg`, `weight`, and `foreign`—do we really believe that consumers place equal value on every extra 1,000 pounds of weight? That is, have we correctly parameterized the model? If we have not, then the estimated partial and semipartial correlation coefficients may not represent what they claim to represent. Partial and semipartial correlation coefficients are a reasonable way to summarize data if we are convinced that the underlying model is reasonable. We should not, however, pretend that there is no underlying model and that these correlation coefficients are unaffected by the assumptions and parameterization.

❑

Saved results

pcorr saves the following in r():

Scalars

r(N)	number of observations
r(df)	degrees of freedom

Matrices

r(p_corr)	partial correlation coefficient vector
r(sp_corr)	semipartial correlation coefficient vector

Methods and formulas

pcorr is implemented as an ado-file.

Results are obtained by fitting a linear regression of *varname*$_1$ on *varlist*; see [R] **regress**. The partial correlation coefficient between *varname*$_1$ and each variable in *varlist* is then calculated as

$$\frac{t}{\sqrt{t^2+n-k}}$$

(Greene 2012, 37), where t is the t statistic, n is the number of observations, and k is the number of independent variables, including the constant but excluding any dropped variables.

The semipartial correlation coefficient between *varname*$_1$ and each variable in *varlist* is calculated as

$$\text{sign}(t)\sqrt{\frac{t^2(1-R^2)}{n-k}}$$

(Cohen et al. 2003, 89), where R^2 is the model R^2 value, and t, n, and k are as described above.

The significance is given by $2\Pr(t_{n-k} > |t|)$, where t_{n-k} follows a Student's t distribution with $n-k$ degrees of freedom.

Acknowledgment

The addition of semipartial correlation coefficients to pcorr is based on the pcorr2 command by Richard Williams, University of Notre Dame.

References

Cohen, J., P. Cohen, S. G. West, and L. S. Aiken. 2003. *Applied Multiple Regression/Correlation Analysis for the Behavioral Sciences*. 3rd ed. Hillsdale, NJ: Erlbaum.

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

Also see

[R] **correlate** — Correlations (covariances) of variables or coefficients

[R] **spearman** — Spearman's and Kendall's correlations

Title

permute — Monte Carlo permutation tests

Syntax

Compute permutation test

`permute` *permvar exp_list* [`,` *options*] `:` *command*

Report saved results

`permute` [*varlist*] [`using` *filename*] [`,` *display_options*]

options	Description
Main	
`reps(#)`	perform # random permutations; default is `reps(100)`
`left` | `right`	compute one-sided p-values; default is two-sided
Options	
`strata(`*varlist*`)`	permute within strata
`saving(`*filename*`, ...)`	save results to *filename*; save statistics in double precision; save results to *filename* every # replications
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noheader`	suppress table header
`nolegend`	suppress table legend
`verbose`	display full table legend
`nodrop`	do not drop observations
`nodots`	suppress replication dots
`noisily`	display any output from *command*
`trace`	trace *command*
`title(`*text*`)`	use *text* as title for permutation results
Advanced	
`eps(#)`	numerical tolerance; seldom used
`nowarn`	do not warn when `e(sample)` is not set
`force`	do not check for *weights* or `svy` commands; seldom used
`reject(`*exp*`)`	identify invalid results
`seed(#)`	set random-number seed to #

weights are not allowed in *command*.

display_options	Description
`left` | `right`	compute one-sided p-values; default is two-sided
`level(#)`	set confidence level; default is `level(95)`
`noheader`	suppress table header
`nolegend`	suppress table legend
`verbose`	display full table legend
`title(`*text*`)`	use *text* as title for results
`eps(#)`	numerical tolerance; seldom used

exp_list contains	(*name*: *elist*)
	elist
	eexp
elist contains	*newvar* = (*exp*)
	(*exp*)
eexp is	*specname*
	[*eqno*]*specname*
specname is	_b
	_b[]
	_se
	_se[]
eqno is	##
	name

exp is a standard Stata expression; see [U] **13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and $[\,]$, which indicate optional arguments.

Menu

Statistics > Resampling > Permutation tests

Description

`permute` estimates p-values for permutation tests on the basis of Monte Carlo simulations. Typing

```
. permute permvar exp_list, reps(#): command
```

randomly permutes the values in *permvar* # times, each time executing *command* and collecting the associated values from the expression in *exp_list*.

These p-value estimates can be one-sided: $\Pr(T^* \leq T)$ or $\Pr(T^* \geq T)$. The default is two-sided: $\Pr(|T^*| \geq |T|)$. Here T^* denotes the value of the statistic from a randomly permuted dataset, and T denotes the statistic as computed on the original data.

permvar identifies the variable whose observed values will be randomly permuted.

command defines the statistical command to be executed. Most Stata commands and user-written programs can be used with `permute`, as long as they follow standard Stata syntax; see [U] **11 Language syntax**. The `by` prefix may not be part of *command*.

exp_list specifies the statistics to be collected from the execution of *command*.

`permute` may be used for replaying results, but this feature is appropriate only when a dataset generated by `permute` is currently in memory or is identified by the `using` option. The variables specified in *varlist* in this context must be present in the respective dataset.

Options

Main

`reps(#)` specifies the number of random permutations to perform. The default is 100.

`left` or `right` requests that one-sided p-values be computed. If `left` is specified, an estimate of $\Pr(T^* \leq T)$ is produced, where T^* is the test statistic and T is its observed value. If `right` is specified, an estimate of $\Pr(T^* \geq T)$ is produced. By default, two-sided p-values are computed; that is, $\Pr(|T^*| \geq |T|)$ is estimated.

Options

`strata(`*varlist*`)` specifies that the permutations be performed within each stratum defined by the values of *varlist*.

`saving(`*filename*`[ , `*suboptions*` ])` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the replicates.

`double` specifies that the results for each replication be stored as `doubles`, meaning 8-byte reals. By default, they are stored as `floats`, meaning 4-byte reals.

`every(#)` specifies that results are to be written to disk every #th replication. `every()` should be specified only in conjunction with `saving()` when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

`replace` specifies that *filename* be overwritten if it exists. This option does not appear in the dialog box.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [R] **level**.

`noheader` suppresses display of the table header. This option implies the `nolegend` option.

`nolegend` suppresses display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

`verbose` requests that the full table legend be displayed. By default, coefficients and standard errors are not displayed.

`nodrop` prevents `permute` from dropping observations outside the `if` and `in` qualifiers. `nodrop` will also cause `permute` to ignore the contents of `e(sample)` if it exists as a result of running *command*. By default, `permute` temporarily drops out-of-sample observations.

`nodots` suppresses display of the replication dots. By default, one dot character is displayed for each successful replication. A red 'x' is displayed if *command* returns an error or if one of the values in *exp_list* is missing.

`noisily` requests that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`title(`*text*`)` specifies a title to be displayed above the table of permutation results; the default title is `Monte Carlo permutation results`.

Advanced

`eps(#)` specifies the numerical tolerance for testing $|T^*| \geq |T|$, $T^* \leq T$, or $T^* \geq T$. These are considered true if, respectively, $|T^*| \geq |T|-\#$, $T^* \leq T+\#$, or $T^* \geq T-\#$. The default is `1e-7`. You will not have to specify `eps()` under normal circumstances.

`nowarn` suppresses the printing of a warning message when *command* does not set `e(sample)`.

`force` suppresses the restriction that *command* may not specify weights or be a `svy` command. `permute` is not suited for weighted estimation, thus `permute` should not be used with weights or `svy`. `permute` reports an error when it encounters weights or `svy` in *command* if the `force` option is not specified. This is a seldom used option, so use it only if you know what you are doing!

`reject(`*exp*`)` identifies an expression that indicates when results should be rejected. When *exp* is true, the resulting values are reset to missing values.

`seed(#)` sets the random-number seed. Specifying this option is equivalent to typing the following command prior to calling `permute`:

```
. set seed #
```

Remarks

Permutation tests determine the significance of the observed value of a test statistic in light of rearranging the order (permuting) of the observed values of a variable.

▷ Example 1

Suppose that we conducted an experiment to determine the effect of a treatment on the development of cells. Further suppose that we are restricted to six experimental units because of the extreme cost of the experiment. Thus three units are to be given a placebo, and three units are given the treatment. The measurement is the number of newly developed healthy cells. The following listing gives the hypothetical data, along with some summary statistics.

```
. input y treatment
            y  treatment
  1. 7 0
  2. 9 0
  3. 11 0
  4. 10 1
  5. 12 1
  6. 14 1
  7. end
. sort treatment
```

```
. summarize y
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
           y |          6        10.5    2.428992         7         14

. by treatment: summarize y

-------------------------------------------------------------------------------
-> treatment = 0
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
           y |          3           9           2         7         11

-------------------------------------------------------------------------------
-> treatment = 1
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
           y |          3          12           2        10         14
```

Clearly, there are more cells in the treatment group than in the placebo group, but a statistical test is needed to conclude that the treatment does affect the development of cells. If the sum of the treatment measures is our test statistic, we can use `permute` to determine the probability of observing 36 or more cells, given the observed data and assuming that there is no effect due to the treatment.

```
. set seed 1234

. permute y sum=r(sum), saving(permdish) right nodrop nowarn: sum y if treatment
(running summarize on estimation sample)

Permutation replications (100)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
..................................................   100

Monte Carlo permutation results                 Number of obs   =          6

      command:  summarize y if treatment
          sum:  r(sum)
  permute var:  y

------------------------------------------------------------------------------
T             |     T(obs)       c       n   p=c/n   SE(p) [95% Conf. Interval]
--------------+---------------------------------------------------------------
          sum |         36      10     100  0.1000  0.0300   .0490047   .1762226
------------------------------------------------------------------------------

Note:  confidence interval is with respect to p=c/n.
Note:  c = #{T >= T(obs)}
```

We see that 10 of the 100 randomly permuted datasets yielded sums from the treatment group larger than or equal to the observed sum of 36. Thus the evidence is not strong enough, at the 5% level, to reject the null hypothesis that there is no effect of the treatment.

Because of the small size of this experiment, we could have calculated the exact permutation p-value from all possible permutations. There are six units, but we want the sum of the treatment units. Thus there are $\binom{6}{3} = 20$ permutation sums from the possible unique permutations.

$$
\begin{array}{cccc}
7+9+10=26 & 7+10+12=29 & 9+10+11=30 & 9+12+14=35 \\
7+9+11=27 & 7+10+14=31 & 9+10+12=31 & 10+11+12=33 \\
7+9+12=28 & 7+11+12=30 & 9+10+14=33 & 10+11+14=35 \\
7+9+14=30 & 7+11+14=32 & 9+11+12=32 & 10+12+14=36 \\
7+10+11=28 & 7+12+14=33 & 9+11+14=34 & 11+12+14=37
\end{array}
$$

Two of the 20 permutation sums are greater than or equal to 36. Thus the exact p-value for this permutation test is 0.1. Tied values will decrease the number of unique permutations.

When the `saving()` option is supplied, `permute` saves the values of the permutation statistic to the indicated file, in our case, `permdish.dta`. This file can be used to replay the result of `permute`. The `level()` option controls the confidence level of the confidence interval for the permutation p-value. This confidence interval is calculated using `cii` with the reported `n` (number of nonmissing replications) and `c` (the counter for events of significance).

```
. permute using permdish, level(80)
Monte Carlo permutation results                 Number of obs    =          6

      command:  summarize y if treatment
          sum:  r(sum)
  permute var:  y
```

T	T(obs)	c	n	p=c/n	SE(p)	[80% Conf.	Interval]
sum	36	10	100	0.1000	0.0300	.0631113	.1498826

```
Note:  confidence interval is with respect to p=c/n.
Note:  c = #{|T| >= |T(obs)|}
```

◁

▷ Example 2

Consider some fictional data from a randomized complete-block design in which we wish to determine the significance of five treatments.

```
. use http://www.stata-press.com/data/r12/permute1, clear
. list y treatment in 1/10, abbrev(10)
```

	y	treatment
1.	4.407557	1
2.	5.693386	1
3.	7.099699	1
4.	3.12132	1
5.	5.242648	1
6.	4.280349	2
7.	4.508785	2
8.	4.079967	2
9.	5.904368	2
10.	3.010556	2

These data may be analyzed using anova.

```
. anova y treatment subject
```

```
                    Number of obs =      50     R-squared     =  0.3544
                    Root MSE      = .914159     Adj R-squared =  0.1213
```

Source	Partial SS	df	MS	F	Prob > F
Model	16.5182188	13	1.27063221	1.52	0.1574
treatment	13.0226706	9	1.44696341	1.73	0.1174
subject	3.49554813	4	.873887032	1.05	0.3973
Residual	30.0847503	36	.835687509		
Total	46.6029691	49	.951081002		

Suppose that we want to compute the significance of the F statistic for treatment by using permute. All we need to do is write a short program that will save the result of this statistic for permute to use. For example,

```
program panova, rclass
        version 12
        args response fac_intrst fac_other
        anova `response' `fac_intrst' `fac_other'
        return scalar Fmodel = e(F)
        test `fac_intrst'
        return scalar F = r(F)
end
```

Now in panova, test saves the F statistic for the factor of interest in r(F). This is different from e(F), which is the overall model F statistic for the model fit by anova that panova saves in r(Fmodel). In the following example, we use the strata() option so that the treatments are randomly rearranged within each subject. It should not be too surprising that the estimated p-values are equal for this example, because the two F statistics are equivalent when controlling for differences between subjects. However, we would not expect to always get the same p-values every time we reran permute.

```
. set seed 1234
. permute treatment treatmentF=r(F) modelF=e(F), reps(1000) strata(subject)
> saving(permanova) nodots: panova y treatment subject
Monte Carlo permutation results
Number of strata =          5                     Number of obs   =         50
      command:  panova y treatment subject
   treatmentF:  r(F)
       modelF:  e(F)
  permute var:  treatment
```

T	T(obs)	c	n	p=c/n	SE(p)	[95% Conf.	Interval]
treatmentF	1.731465	118	1000	0.1180	0.0102	.0986525	.1396277
modelF	1.520463	118	1000	0.1180	0.0102	.0986525	.1396277

```
Note:  confidence intervals are with respect to p=c/n.
Note:  c = #{|T| >= |T(obs)|}
```

◁

▷ Example 3

As a final example, let's consider estimating the p-value of the Z statistic returned by `ranksum`. Suppose that we collected data from some experiment: `y` is some measure we took on 17 individuals, and `group` identifies the group that an individual belongs to.

```
. use http://www.stata-press.com/data/r12/permute2
. list
```

	group	y
1.	1	6
2.	1	11
3.	1	20
4.	1	2
5.	1	9
6.	1	5
7.	0	2
8.	0	1
9.	0	6
10.	0	0
11.	0	2
12.	0	3
13.	0	3
14.	0	12
15.	0	4
16.	0	1
17.	0	5

Next we analyze the data using `ranksum` and notice that the observed value of the test statistic (saved as `r(z)`) is -2.02 with an approximate p-value of 0.0434.

```
. ranksum y, by(group)
Two-sample Wilcoxon rank-sum (Mann-Whitney) test
      group |      obs    rank sum    expected
------------+---------------------------------
          0 |       11          79          99
          1 |        6          74          54
------------+---------------------------------
   combined |       17         153         153
unadjusted variance       99.00
adjustment for ties       -0.97
                        ---------
adjusted variance         98.03
Ho: y(group==0) = y(group==1)
             z =  -2.020
    Prob > |z| =   0.0434
```

The observed value of the rank-sum statistic is 79, with an expected value (under the null hypothesis of no group effect) of 99. There are 17 observations, so the permutation distribution contains $\binom{17}{6} = 12{,}376$ possible values of the rank-sum statistic if we ignore ties. With ties, we have fewer possible values but still too many to want to count them. Thus we use `permute` with 10,000 replications and see that the Monte Carlo permutation test agrees with the result of the test based on the normal approximation.

```
. set seed 18385766
. permute y z=r(z), reps(10000) nowarn nodots: ranksum y, by(group)
Monte Carlo permutation results                 Number of obs    =         17
      command:  ranksum y, by(group)
            z:  r(z)
  permute var:  y
```

T	T(obs)	c	n	p=c/n	SE(p)	[95% Conf.	Interval]
z	-2.020002	468	10000	0.0468	0.0021	.0427429	.0511236

```
Note:  confidence interval is with respect to p=c/n.
Note:  c = #{|T| >= |T(obs)|}
```

◁

For an application of a permutation test to a problem in epidemiology, see Hayes and Moulton (2009, 190–193).

❑ Technical note

`permute` reports confidence intervals for p to emphasize that it is based on the binomial estimator for proportions. When the variability implied by the confidence interval makes conclusions difficult, you may increase the number of replications to determine more precisely the significance of the test statistic of interest. In other words, the value of p from `permute` will converge to the true permutation p-value as the number of replications gets arbitrarily large. ❑

Saved results

`permute` saves the following in `r()`:

Scalars

`r(N)`	sample size	`r(k_exp)`	number of standard expressions
`r(N_reps)`	number of requested replications	`r(k_eexp)`	number of `_b`/`_se` expressions
`r(level)`	confidence level		

Macros

`r(cmd)`	`permute`	`r(left)`	`left` or empty
`r(command)`	*command* following colon	`r(right)`	`right` or empty
`r(permvar)`	permutation variable	`r(seed)`	initial random-number seed
`r(title)`	title in output	`r(event)`	`T <= T(obs)`, `T >= T(obs)`, or `|T| <= |T(obs)|`
`r(exp#)`	#th expression		

Matrices

`r(b)`	observed statistics	`r(p)`	observed proportions
`r(c)`	count when `r(event)` is true	`r(se)`	standard errors of observed proportions
`r(reps)`	number of nonmissing results	`r(ci)`	confidence intervals of observed proportions

Methods and formulas

`permute` is implemented as an ado-file.

References

Ängquist, L. 2010. Stata tip 92: Manual implementation of permutations and bootstraps. *Stata Journal* 10: 686–688.

Good, P. I. 2006. *Resampling Methods: A Practical Guide to Data Analysis*. 3rd ed. Boston: Birkhäuser.

Hayes, R. J., and L. H. Moulton. 2009. *Cluster Randomised Trials*. Boca Raton, FL: Chapman & Hall/CRC.

Kaiser, J. 2007. An exact and a Monte Carlo proposal to the Fisher–Pitman permutation tests for paired replicates and for independent samples. *Stata Journal* 7: 402–412.

Kaiser, J., and M. G. Lacy. 2009. A general-purpose method for two-group randomization tests. *Stata Journal* 9: 70–85.

Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **jackknife** — Jackknife estimation

[R] **simulate** — Monte Carlo simulations

Title

pk — Pharmacokinetic (biopharmaceutical) data

Description

The term pk refers to pharmacokinetic data and the Stata commands, all of which begin with the letters pk, designed to do some of the analyses commonly performed in the pharmaceutical industry. The system is intended for the analysis of pharmacokinetic data, although some of the commands are for general use.

The pk commands are

`pkexamine`	[R] **pkexamine**	Calculate pharmacokinetic measures
`pksumm`	[R] **pksumm**	Summarize pharmacokinetic data
`pkshape`	[R] **pkshape**	Reshape (pharmacokinetic) Latin-square data
`pkcross`	[R] **pkcross**	Analyze crossover experiments
`pkequiv`	[R] **pkequiv**	Perform bioequivalence tests
`pkcollapse`	[R] **pkcollapse**	Generate pharmacokinetic measurement dataset

Remarks

Several types of clinical trials are commonly performed in the pharmaceutical industry. Examples include combination trials, multicenter trials, equivalence trials, and active control trials. For each type of trial, there is an optimal study design for estimating the effects of interest. Currently, the pk system can be used to analyze equivalence trials, which are usually conducted using a crossover design; however, it is possible to use a parallel design and still draw conclusions about equivalence.

Equivalence trials assess bioequivalence between two drugs. Although proving that two drugs behave the same is impossible, the United States Food and Drug Administration believes that if the absorption properties of two drugs are similar, the two drugs will produce similar effects and have similar safety profiles. Generally, the goal of an equivalence trial is to assess the equivalence of a generic drug to an existing drug. This goal is commonly accomplished by comparing a confidence interval about the difference between a pharmacokinetic measurement of two drugs with a confidence limit constructed from U.S. federal regulations. If the confidence interval is entirely within the confidence limit, the drugs are declared bioequivalent. Another approach to assessing bioequivalence is to use the method of interval hypotheses testing. `pkequiv` is used to conduct these tests of bioequivalence.

Several pharmacokinetic measures can be used to ascertain how available a drug is for cellular absorption. The most common measure is the area under the time-versus-concentration curve (AUC). Another common measure of drug availability is the maximum concentration ($C_{\max}$) achieved by the drug during the follow-up period. Stata reports these and other less common measures of drug availability, including the time at which the maximum drug concentration was observed and the duration of the period during which the subject was being measured. Stata also reports the elimination rate, that is, the rate at which the drug is metabolized, and the drug's half-life, that is, the time it takes for the drug concentration to fall to one-half of its maximum concentration.

`pkexamine` computes and reports all the pharmacokinetic measures that Stata produces, including four calculations of the area under the time-versus-concentration curve. The standard area under the curve from 0 to the maximum observed time ($\text{AUC}_{0,t_{\max}}$) is computed using cubic splines or the

trapezoidal rule. Additionally, pkexamine also computes the area under the curve from 0 to infinity by extending the standard time-versus-concentration curve from the maximum observed time by using three different methods. The first method simply extends the standard curve by using a least-squares linear fit through the last few data points. The second method extends the standard curve by fitting a decreasing exponential curve through the last few data points. Finally, the third method extends the curve by fitting a least-squares linear regression line on the log concentration. The mathematical details of these extensions are described in *Methods and formulas* of [R] **pkexamine**.

Data from an equivalence trial may also be analyzed using methods appropriate to the particular study design. When you have a crossover design, pkcross can be used to fit an appropriate ANOVA model. As an aside, a crossover design is simply a restricted Latin square; therefore, pkcross can also be used to analyze any Latin-square design.

There are some practical concerns when dealing with data from equivalence trials. Primarily, the data must be organized in a manner that Stata can use. The pk commands include pkcollapse and pkshape, which are designed to help transform data from a common format to one that is suitable for analysis with Stata.

In the following example, we illustrate several different data formats that are often encountered in pharmaceutical research and describe how these formats can be transformed to formats that can be analyzed with Stata.

▷ Example 1

Assume that we have one subject and are interested in determining the drug profile for that subject. A reasonable experiment would be to give the subject the drug and then measure the concentration of the drug in the subject's blood over a given period. For example, here is a part of a dataset from Chow and Liu (2009, 13):

```
. use http://www.stata-press.com/data/r12/auc
. list, abbrev(14)
```

	id	time	concentration
1.	1	0	0
2.	1	.5	0
3.	1	1	2.8
4.	1	1.5	4.4
5.	1	2	4.4
6.	1	3	4.7
7.	1	4	4.1
8.	1	6	4
9.	1	8	3.6
10.	1	12	3
11.	1	16	2.5
12.	1	24	2
13.	1	32	1.6

Examining these data, we notice that the concentration quickly increases, plateaus for a short period, and then slowly decreases over time. pkexamine is used to calculate the pharmacokinetic measures of interest. pkexamine is explained in detail in [R] **pkexamine**. The output is

```
. pkexamine time conc
                                    Maximum concentration =       4.7
                                  Time of maximum concentration =         3
                                Time of last observation (Tmax) =        32
                                           Elimination rate =    0.0279
                                                  Half life =   24.8503

Area under the curve
```

AUC [0, Tmax]	AUC [0, inf.) Linear of log conc.	AUC [0, inf.) Linear fit	AUC [0, inf.) Exponential fit
85.24	142.603	107.759	142.603

```
Fit based on last 3 points.
```

Clinical trials, however, require that data be collected on more than one subject. There are several ways to enter raw measured data collected on several subjects. It would be reasonable to enter for each subject the drug concentration value at specific points in time. Such data could be

```
id   conc1   conc2   conc3   conc4    conc5   conc6   conc7
 1       0       1       4       7        5       3       1
 2       0       2       6       5        4       3       2
 3       0       1       2       3        5       4       1
```

where `conc1` is the concentration at the first measured time, `conc2` is the concentration at the second measured time, etc. This format requires that each drug concentration measurement be made at the same time on each subject. Another more flexible way to enter the data is to have an observation with three variables for each time measurement on a subject. Each observation would have a subject ID, the time at which the measurement was made, and the corresponding drug concentration at that time. The data would be

```
. use http://www.stata-press.com/data/r12/pkdata
. list id concA time, sepby(id)
```

	id	concA	time
1.	1	0	0
2.	1	3.073403	.5
3.	1	5.188444	1
4.	1	5.898577	1.5
5.	1	5.096378	2
6.	1	6.094085	3
7.	1	5.158772	4
8.	1	5.7065	6
9.	1	5.272467	8
10.	1	4.4576	12
11.	1	5.146423	16
12.	1	4.947427	24
13.	1	1.920421	32
14.	2	0	0
15.	2	2.48462	.5
16.	2	4.883569	1
17.	2	7.253442	1.5
18.	2	5.849345	2
19.	2	6.761085	3
20.	2	4.33839	4
21.	2	5.04199	6
22.	2	4.25128	8
23.	2	6.205004	12
24.	2	5.566165	16
25.	2	3.689007	24
26.	2	3.644063	32
27.	3	0	0
	(output omitted)		
207.	20	4.673281	24
208.	20	3.487347	32

Stata expects the data to be organized in the second form. If your data are organized as described in the first dataset, you will need to use `reshape` to change the data to the second form; see [D] **reshape**. Because the data in the second (or long) format contain information for one drug on several subjects, `pksumm` can be used to produce summary statistics of the pharmacokinetic measurements. The output is

```
. pksumm id time concA
.................
 Summary statistics for the pharmacokinetic measures
                                                  Number of observations =    16
```

Measure	Mean	Median	Variance	Skewness	Kurtosis	p-value
auc	151.63	152.18	127.58	-0.34	2.07	0.55
aucline	397.09	219.83	178276.59	2.69	9.61	0.00
aucexp	668.60	302.96	720356.98	2.67	9.54	0.00
auclog	665.95	298.03	752573.34	2.71	9.70	0.00
half	90.68	29.12	17750.70	2.36	7.92	0.00
ke	0.02	0.02	0.00	0.88	3.87	0.08
cmax	7.37	7.42	0.40	-0.64	2.75	0.36
tomc	3.38	3.00	7.25	2.27	7.70	0.00
tmax	32.00	32.00	0.00	.	.	.

Until now, we have been concerned with the profile of only one drug. We have characterized the profile of that drug by individual subjects by using `pkexamine` and by a group of subjects by using `pksumm`. The goal of an equivalence trial, however, is to compare two drugs, which we will do in the rest of this example.

For equivalence trials, the study design most often used is the crossover design. For a complete discussion of crossover designs, see Ratkowsky, Evans, and Alldredge (1993).

In brief, crossover designs require that each subject be given both treatments at two different times. The order in which the treatments are applied changes between groups. For example, if we had 20 subjects numbered 1–20, the first 10 would receive treatment A during the first period of the study, and then they would be given treatment B. The second 10 subjects would be given treatment B during the first period of the study, and then they would be given treatment A. Each subject in the study will have four variables that describe the observation: a subject identifier, a sequence identifier that indicates the order of treatment, and two outcome variables, one for each treatment. The outcome variables for each subject are the pharmacokinetic measures. The data must be transformed from a series of measurements on individual subjects to data containing the pharmacokinetic measures for each subject. In Stata parlance, this is referred to as a collapse, which can be done with `pkcollapse`; see [R] **pkcollapse**.

Here is a part of our data:

```
. list, sepby(id)
```

	id	seq	time	concA	concB
1.	1	1	0	0	0
2.	1	1	.5	3.073403	3.712592
3.	1	1	1	5.188444	6.230602
4.	1	1	1.5	5.898577	7.885944
5.	1	1	2	5.096378	9.241735
6.	1	1	3	6.094085	13.10507
7.	1	1	4	5.158772	.169429
8.	1	1	6	5.7065	8.759894
9.	1	1	8	5.272467	7.985409
10.	1	1	12	4.4576	7.740126
11.	1	1	16	5.146423	7.607208
12.	1	1	24	4.947427	7.588428
13.	1	1	32	1.920421	2.791115
14.	2	1	0	0	0
15.	2	1	.5	2.48462	.9209593
16.	2	1	1	4.883569	5.925818
17.	2	1	1.5	7.253442	8.710549
18.	2	1	2	5.849345	10.90552
19.	2	1	3	6.761085	8.429898
20.	2	1	4	4.33839	5.573152
21.	2	1	6	5.04199	6.32341
22.	2	1	8	4.25128	.5251224
23.	2	1	12	6.205004	7.415988
24.	2	1	16	5.566165	6.323938
25.	2	1	24	3.689007	1.133553
26.	2	1	32	3.644063	5.759489
27.	3	1	0	0	0
			(*output omitted*)		
207.	20	2	24	4.673281	6.059818
208.	20	2	32	3.487347	5.213639

This format is similar to the second format described above, except that now we have measurements for two drugs at each time for each subject. We transform these data with `pkcollapse`:

```
. pkcollapse time concA concB, id(id) keep(seq) stat(auc)
.............................
. list, sep(8) abbrev(10)
```

	id	seq	auc_concA	auc_concB
1.	1	1	150.9643	218.5551
2.	2	1	146.7606	133.3201
3.	3	1	160.6548	126.0635
4.	4	1	157.8622	96.17461
5.	5	1	133.6957	188.9038
6.	7	1	160.639	223.6922
7.	8	1	131.2604	104.0139
8.	9	1	168.5186	237.8962
9.	10	2	137.0627	139.7382
10.	12	2	153.4038	202.3942
11.	13	2	163.4593	136.7848
12.	14	2	146.0462	104.5191
13.	15	2	158.1457	165.8654
14.	18	2	147.1977	139.235
15.	19	2	164.9988	166.2391
16.	20	2	145.3823	158.5146

For this example, we chose to use the AUC for two drugs as our pharmacokinetic measure. We could have used any of the measures computed by `pkexamine`. In addition to the AUCs, the dataset also contains a sequence variable for each subject indicating when each treatment was administered.

The data produced by `pkcollapse` are in what Stata calls wide format; that is, there is one observation per subject containing two or more outcomes. To use `pkcross` and `pkequiv`, we need to transform these data to long format. This goal can be accomplished using `pkshape`; see [R] **pkshape**.

Consider the first subject in the dataset. This subject is in sequence one, which means that treatment A was applied during the first period of the study and treatment B was applied in the second period of the study. We need to split the first observation into two observations so that the outcome measure is only in one variable. Also we need two new variables, one indicating the treatment the subject received and another recording the period of the study when the subject received that treatment. We might expect the expansion of the first subject to be

id	sequence	auc	treat	period
1	1	150.9643	A	1
1	1	218.5551	B	2

We see that subject number 1 was in sequence 1, had an AUC of 150.9643 when treatment A was applied in the first period of the study, and had an AUC of 218.5551 when treatment B was applied.

Similarly, the expansion of subject 10 (the first subject in sequence 2) would be

id	sequence	auc	treat	period
10	2	137.0627	B	1
10	2	139.7382	A	2

Here treatment B was applied to the subject during the first period of the study, and treatment A was applied to the subject during the second period of the study.

An additional complication is common in crossover study designs. The treatment applied in the first period of the study might still have some effect on the outcome in the second period. In this example,

each subject was given one treatment followed by another treatment. To get accurate estimates of treatment effects, it is necessary to account for the effect that the first treatment has in the second period of the study. This is called the carryover effect. We must, therefore, have a variable that indicates which treatment was applied in the first treatment period. `pkshape` creates a variable that indicates the carryover effect. For treatments applied during the first treatment period, there will never be a carryover effect. Thus the expanded data created by `pkshape` for subject 1 will be

id	sequence	outcome	treat	period	carry
1	1	150.9643	A	1	0
1	1	218.5551	B	2	A

and the data for subject 10 will be

id	sequence	outcome	treat	period	carry
10	2	137.0627	B	1	0
10	2	139.7382	A	2	B

We `pkshape` the data:

```
. pkshape id seq auc*, order(ab ba)
. sort id sequence period
. list, sep(16)
```

	id	sequence	outcome	treat	carry	period
1.	1	1	150.9643	1	0	1
2.	1	1	218.5551	2	1	2
3.	2	1	146.7606	1	0	1
4.	2	1	133.3201	2	1	2
5.	3	1	160.6548	1	0	1
6.	3	1	126.0635	2	1	2
7.	4	1	157.8622	1	0	1
8.	4	1	96.17461	2	1	2
9.	5	1	133.6957	1	0	1
10.	5	1	188.9038	2	1	2
11.	7	1	160.639	1	0	1
12.	7	1	223.6922	2	1	2
13.	8	1	131.2604	1	0	1
14.	8	1	104.0139	2	1	2
15.	9	1	168.5186	1	0	1
16.	9	1	237.8962	2	1	2
17.	10	2	137.0627	2	0	1
18.	10	2	139.7382	1	2	2
19.	12	2	153.4038	2	0	1
20.	12	2	202.3942	1	2	2
21.	13	2	163.4593	2	0	1
22.	13	2	136.7848	1	2	2
23.	14	2	146.0462	2	0	1
24.	14	2	104.5191	1	2	2
25.	15	2	158.1457	2	0	1
26.	15	2	165.8654	1	2	2
27.	18	2	147.1977	2	0	1
28.	18	2	139.235	1	2	2
29.	19	2	164.9988	2	0	1
30.	19	2	166.2391	1	2	2
31.	20	2	145.3823	2	0	1
32.	20	2	158.5146	1	2	2

As an aside, crossover designs do not require that each subject receive each treatment, but if they do, the crossover design is referred to as a complete crossover design.

The last dataset is organized in a manner that can be analyzed with Stata. To fit an ANOVA model to these data, we can use `anova` or `pkcross`. To conduct equivalence tests, we can use `pkequiv`. This example is further analyzed in [R] **pkcross** and [R] **pkequiv**.

◁

References

Chow, S.-C., and J.-P. Liu. 2009. *Design and Analysis of Bioavailability and Bioequivalence Studies*. 3rd ed. Boca Raton, FL: Chapman & Hall/CRC.

Ratkowsky, D. A., M. A. Evans, and J. R. Alldredge. 1993. *Cross-over Experiments: Design, Analysis, and Application*. New York: Dekker.

Title

pkcollapse — Generate pharmacokinetic measurement dataset

Syntax

`pkcollapse` *time concentration* [*if*] `,` `id(`*id_var*`)` [*options*]

options	Description
Main	
* `id(`*id_var*`)`	subject ID variable
`stat(`*measures*`)`	create specified *measures*; default is all
`trapezoid`	use trapezoidal rule; default is cubic splines
`fit(#)`	use # points to estimate $\text{AUC}_{0,\infty}$; default is `fit(3)`
`keep(`*varlist*`)`	keep variables in *varlist*
`force`	force collapse
`nodots`	suppress dots during calculation

*`id(`*id_var*`)` is required.

measures	Description
`auc`	area under the concentration-time curve ($\text{AUC}_{0,\infty}$)
`aucline`	area under the concentration-time curve from 0 to ∞ using a linear extension
`aucexp`	area under the concentration-time curve from 0 to ∞ using an exponential extension
`auclog`	area under the log-concentration-time curve extended with a linear fit
`half`	half-life of the drug
`ke`	elimination rate
`cmax`	maximum concentration
`tmax`	time at last concentration
`tomc`	time of maximum concentration

Menu

Statistics > Epidemiology and related > Other > Generate pharmacokinetic measurement dataset

Description

`pkcollapse` generates new variables with the pharmacokinetic summary measures of interest.

`pkcollapse` is one of the pk commands. Please read [R] **pk** before reading this entry.

Options

Main

`id(`*id_var*`)` is required and specifies the variable that contains the subject ID over which `pkcollapse` is to operate.

`stat(`*measures*`)` specifies the measures to be generated. The default is to generate all the measures.

`trapezoid` tells Stata to use the trapezoidal rule when calculating the AUC. The default is to use cubic splines, which give better results for most functions. When the curve is irregular, `trapezoid` may give better results.

`fit(#)` specifies the number of points to use in estimating the $\text{AUC}_{0,\infty}$. The default is `fit(3)`, the last three points. This number should be viewed as a minimum; the appropriate number of points will depend on your data.

`keep(`*varlist*`)` specifies the variables to be kept during the collapse. Variables not specified with the `keep()` option will be dropped. When `keep()` is specified, the keep variables are checked to ensure that all values of the variables are the same within *id_var*.

`force` forces the collapse, even when the values of the `keep()` variables are different within the *id_var*.

`nodots` suppresses the display of dots during calculation.

Remarks

`pkcollapse` generates all the summary pharmacokinetic measures.

▷ Example 1

We demonstrate the use of `pkcollapse` with the data described in [R] **pk**. We have drug concentration data on 15 subjects. Each subject is measured at 13 time points over a 32-hour period. Some of the records are

```
. use http://www.stata-press.com/data/r12/pkdata
. list, sep(0)
```

	id	seq	time	concA	concB
1.	1	1	0	0	0
2.	1	1	.5	3.073403	3.712592
3.	1	1	1	5.188444	6.230602
4.	1	1	1.5	5.898577	7.885944
5.	1	1	2	5.096378	9.241735
6.	1	1	3	6.094085	13.10507
			(*output omitted*)		
14.	2	1	0	0	0
15.	2	1	.5	2.48462	.9209593
16.	2	1	1	4.883569	5.925818
17.	2	1	1.5	7.253442	8.710549
18.	2	1	2	5.849345	10.90552
19.	2	1	3	6.761085	8.429898
			(*output omitted*)		
207.	20	2	24	4.673281	6.059818
208.	20	2	32	3.487347	5.213639

Although pksumm allows us to view all the pharmacokinetic measures, we can create a dataset with the measures by using pkcollapse.

```
. pkcollapse time concA concB, id(id) stat(auc) keep(seq)
.............................
. list, sep(8) abbrev(10)
```

	id	seq	auc_concA	auc_concB
1.	1	1	150.9643	218.5551
2.	2	1	146.7606	133.3201
3.	3	1	160.6548	126.0635
4.	4	1	157.8622	96.17461
5.	5	1	133.6957	188.9038
6.	7	1	160.639	223.6922
7.	8	1	131.2604	104.0139
8.	9	1	168.5186	237.8962
9.	10	2	137.0627	139.7382
10.	12	2	153.4038	202.3942
11.	13	2	163.4593	136.7848
12.	14	2	146.0462	104.5191
13.	15	2	158.1457	165.8654
14.	18	2	147.1977	139.235
15.	19	2	164.9988	166.2391
16.	20	2	145.3823	158.5146

The resulting dataset, which we will call pkdata2, contains 1 observation per subject. This dataset is in wide format. If we want to use pkcross or pkequiv, we must transform these data to long format, which we do in the last example of [R] **pkshape**.

◁

Methods and formulas

pkcollapse is implemented as an ado-file.

The statistics generated by pkcollapse are described in [R] **pkexamine**.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data

Title

pkcross — Analyze crossover experiments

Syntax

`pkcross` *outcome* [*if*] [*in*] [, *options*]

options	Description
Model	
`sequence(`*varname*`)`	sequence variable; default is `sequence(sequence)`
`treatment(`*varname*`)`	treatment variable; default is `treatment(treat)`
`period(`*varname*`)`	period variable; default is `period(period)`
`id(`*varname*`)`	ID variable
`carryover(`*varname*`)`	name of carryover variable; default is `carryover(carry)`
`carryover(none)`	omit carryover effects from model; default is `carryover(carry)`
`model(`*string*`)`	specify the model to fit
`sequential`	estimate sequential instead of partial sums of squares
Parameterization	
`param(3)`	estimate mean and the period, treatment, and sequence effects; assume no carryover effects exist; the default
`param(1)`	estimate mean and the period, treatment, and carryover effects; assume no sequence effects exist
`param(2)`	estimate mean, period and treatment effects, and period-by-treatment interaction; assume no sequence or carryover effects exist
`param(4)`	estimate mean, period and treatment effects, and period-by-treatment interaction; assume no period or crossover effects exist

Menu

Statistics > Epidemiology and related > Other > Analyze crossover experiments

Description

`pkcross` analyzes data from a crossover design experiment. When analyzing pharmaceutical trial data, if the treatment, carryover, and sequence variables are known, the omnibus test for separability of the treatment and carryover effects is calculated.

`pkcross` is one of the pk commands. Please read [R] **pk** before reading this entry.

Options

Model

`sequence(`*varname*`)` specifies the variable that contains the sequence in which the treatment was administered. If this option is not specified, `sequence(sequence)` is assumed.

`treatment(`*varname*`)` specifies the variable that contains the treatment information. If this option is not specified, `treatment(treat)` is assumed.

`period(`*varname*`)` specifies the variable that contains the period information. If this option is not specified, `period(period)` is assumed.

`id(`*varname*`)` specifies the variable that contains the subject identifiers. If this option is not specified, `id(id)` is assumed.

`carryover(`*varname*`|`**`none`**`)` specifies the variable that contains the carryover information. If `carry(none)` is specified, the carryover effects are omitted from the model. If this option is not specified, `carryover(carry)` is assumed.

`model(`*string*`)` specifies the model to be fit. For higher-order crossover designs, this option can be useful if you want to fit a model other than the default. However, `anova` (see [R] **anova**) can also be used to fit a crossover model. The default model for higher-order crossover designs is outcome predicted by sequence, period, treatment, and carryover effects. By default, the model statement is `model(sequence period treat carry)`.

`sequential` specifies that sequential sums of squares be estimated.

Parameterization

`param(#)` specifies which of the four parameterizations to use for the analysis of a 2×2 crossover experiment. This option is ignored with higher-order crossover designs. The default is `param(3)`. See the technical note for 2×2 crossover designs for more details.

`param(3)` estimates the overall mean, the period effects, the treatment effects, and the sequence effects, assuming that no carryover effects exist. This is the default parameterization.

`param(1)` estimates the overall mean, the period effects, the treatment effects, and the carryover effects, assuming that no sequence effects exist.

`param(2)` estimates the overall mean, the period effects, the treatment effects, and the period-by-treatment interaction, assuming that no sequence or carryover effects exist.

`param(4)` estimates the overall mean, the sequence effects, the treatment effects, and the sequence-by-treatment interaction, assuming that no period or crossover effects exist. When the sequence by treatment is equivalent to the period effect, this reduces to the third parameterization.

Remarks

`pkcross` is designed to analyze crossover experiments. Use `pkshape` first to reshape your data; see [R] **pkshape**. `pkcross` assumes that the data were reshaped by `pkshape` or are organized in the same manner as produced with `pkshape`. Washout periods are indicated by the number 0. See the technical note in this entry for more information on analyzing 2×2 crossover experiments.

❑ Technical note

The 2×2 crossover design cannot be used to estimate more than four parameters because there are only four pieces of information (the four cell means) collected. `pkcross` uses ANOVA models to analyze the data, so one of the four parameters must be the overall mean of the model, leaving just 3 degrees of freedom to estimate the remaining effects (period, sequence, treatment, and carryover). Thus the model is overparameterized. Estimation of treatment and carryover effects requires the assumption of either no period effects or no sequence effects. Some researchers maintain that it estimating carryover effects at the expense of other effects is a bad idea. This is a limitation of this

design. pkcross implements four parameterizations for this model. They are numbered sequentially from one to four and are described in *Options*.

❑

▷ Example 1

Consider the example data published in Chow and Liu (2009, 71) and described in [R] **pkshape**. We have entered and reshaped the data with pkshape and have variables that identify the subjects, periods, treatments, sequence, and carryover treatment. To compute the ANOVA table, use pkcross:

```
. use http://www.stata-press.com/data/r12/chowliu
. pkshape id seq period1 period2, order(ab ba)
. pkcross outcome
                                        sequence variable = sequence
                                          period variable = period
                                       treatment variable = treat
                                       carryover variable = carry
                                              id variable = id

          Analysis of variance (ANOVA) for a 2x2 crossover study
Source of Variation |      SS       df        MS          F     Prob > F
--------------------+---------------------------------------------------
Intersubjects       |
     Sequence effect |     276.00        1      276.00       0.37     0.5468
           Residuals |   16211.49       22      736.89       4.41     0.0005
--------------------+---------------------------------------------------
Intrasubjects       |
    Treatment effect |      62.79        1       62.79       0.38     0.5463
       Period effect |      35.97        1       35.97       0.22     0.6474
           Residuals |    3679.43       22      167.25
--------------------+---------------------------------------------------
               Total |   20265.68       47
Omnibus measure of separability of treatment and carryover =   29.2893%
```

There is evidence of intersubject variability, but there are no other significant effects. The omnibus test for separability is a measure reflecting the degree to which the study design allows the treatment effects to be estimated independently of the carryover effects. The measure of separability of the treatment and carryover effects indicates approximately 29% separability, which can be interpreted as the degree to which the treatment and carryover effects are orthogonal. This is a characteristic of the design of the study. For a complete discussion, see Ratkowsky, Evans, and Alldredge (1993). Compared to the output in Chow and Liu (2009), the sequence effect is mislabeled as a carryover effect. See Ratkowsky, Evans, and Alldredge (1993, sec. 3.2) for a complete discussion of the mislabeling.

By specifying `param(1)`, we obtain parameterization 1 for this model.

```
. pkcross outcome, param(1)
                                                sequence variable = sequence
                                                  period variable = period
                                               treatment variable = treat
                                               carryover variable = carry
                                                      id variable = id

          Analysis of variance (ANOVA) for a 2x2 crossover study
 Source of Variation | Partial SS   df        MS          F     Prob > F
---------------------+------------------------------------------------------
      Treatment effect |     301.04    1      301.04      0.67      0.4189
         Period effect |     255.62    1      255.62      0.57      0.4561
      Carryover effect |     276.00    1      276.00      0.61      0.4388
             Residuals |   19890.92   44      452.07
---------------------+------------------------------------------------------
                 Total |   20265.68   47
Omnibus measure of separability of treatment and carryover =   29.2893%
```

▷ Example 2

Consider the case of a two-treatment, four-sequence, two-period crossover design. This design is commonly referred to as Balaam's design (Balaam 1968). Ratkowsky, Evans, and Alldredge (1993, 140) published the following data from an amantadine trial, originally published by Taka and Armitage (1983):

```
. use http://www.stata-press.com/data/r12/balaam, clear
. list, sep(0)
```

	id	seq	period1	period2	period3
1.	1	-ab	9	8.75	8.75
2.	2	-ab	12	10.5	9.75
3.	3	-ab	17	15	18.5
4.	4	-ab	21	21	21.5
5.	1	-ba	23	22	18
6.	2	-ba	15	15	13
7.	3	-ba	13	14	13.75
8.	4	-ba	24	22.75	21.5
9.	5	-ba	18	17.75	16.75
10.	1	-aa	14	12.5	14
11.	2	-aa	27	24.25	22.5
12.	3	-aa	19	17.25	16.25
13.	4	-aa	30	28.25	29.75
14.	1	-bb	21	20	19.51
15.	2	-bb	11	10.5	10
16.	3	-bb	20	19.5	20.75
17.	4	-bb	25	22.5	23.5

The sequence identifier must be a string with zeros to indicate washout or baseline periods, or a number. If the sequence identifier is numeric, the `order` option must be specified with `pkshape`. If the sequence identifier is a string, `pkshape` will create sequence, period, and treatment identifiers without the `order` option. In this example, the dash is used to indicate a baseline period, which is an invalid code for this purpose. As a result, the data must be encoded; see [D] **encode**.

```
. encode seq, gen(num_seq)
. pkshape id num_seq period1 period2 period3, order(0aa 0ab 0ba 0bb)
. pkcross outcome, se
                                                sequence variable = sequence
                                                  period variable = period
                                               treatment variable = treat
                                               carryover variable = carry
                                                      id variable = id
```

Analysis of variance (ANOVA) for a crossover study

Source of Variation	SS	df	MS	F	Prob > F
Intersubjects					
Sequence effect	285.82	3	95.27	1.01	0.4180
Residuals	1221.49	13	93.96	59.96	0.0000
Intrasubjects					
Period effect	15.13	2	7.56	6.34	0.0048
Treatment effect	8.48	1	8.48	8.86	0.0056
Carryover effect	0.11	1	0.11	0.12	0.7366
Residuals	29.56	30	0.99		
Total	1560.59	50			

```
Omnibus measure of separability of treatment and carryover =   64.6447%
```

In this example, the sequence specifier used dashes instead of zeros to indicate a baseline period during which no treatment was given. For `pkcross` to work, we need to encode the string sequence variable and then use the `order` option with `pkshape`. A word of caution: `encode` does not necessarily choose the first sequence to be sequence 1, as in this example. Always double-check the sequence numbering when using `encode`.

◁

Example 3

Continuing with the example from [R] **pkshape**, we fit an ANOVA model.

```
. use http://www.stata-press.com/data/r12/pkdata3, clear
. list, sep(8)
```

	id	sequence	outcome	treat	carry	period
1.	1	1	150.9643	A	0	1
2.	2	1	146.7606	A	0	1
3.	3	1	160.6548	A	0	1
4.	4	1	157.8622	A	0	1
5.	5	1	133.6957	A	0	1
6.	7	1	160.639	A	0	1
7.	8	1	131.2604	A	0	1
8.	9	1	168.5186	A	0	1
9.	10	2	137.0627	B	0	1
10.	12	2	153.4038	B	0	1
11.	13	2	163.4593	B	0	1
12.	14	2	146.0462	B	0	1
13.	15	2	158.1457	B	0	1
14.	18	2	147.1977	B	0	1
15.	19	2	164.9988	B	0	1
16.	20	2	145.3823	B	0	1
17.	1	1	218.5551	B	A	2
18.	2	1	133.3201	B	A	2
19.	3	1	126.0635	B	A	2
20.	4	1	96.17461	B	A	2
21.	5	1	188.9038	B	A	2
22.	7	1	223.6922	B	A	2
23.	8	1	104.0139	B	A	2
24.	9	1	237.8962	B	A	2
25.	10	2	139.7382	A	B	2
26.	12	2	202.3942	A	B	2
27.	13	2	136.7848	A	B	2
28.	14	2	104.5191	A	B	2
29.	15	2	165.8654	A	B	2
30.	18	2	139.235	A	B	2
31.	19	2	166.2391	A	B	2
32.	20	2	158.5146	A	B	2

The ANOVA model is fit using pkcross:

```
. pkcross outcome
                                                sequence variable = sequence
                                                  period variable = period
                                               treatment variable = treat
                                               carryover variable = carry
                                                     id variable = id
```

Analysis of variance (ANOVA) for a 2x2 crossover study

Source of Variation	SS	df	MS	F	Prob > F
Intersubjects					
Sequence effect	378.04	1	378.04	0.29	0.5961
Residuals	17991.26	14	1285.09	1.40	0.2691
Intrasubjects					
Treatment effect	455.04	1	455.04	0.50	0.4931
Period effect	419.47	1	419.47	0.46	0.5102
Residuals	12860.78	14	918.63		
Total	32104.59	31			

Omnibus measure of separability of treatment and carryover = 29.2893%

◁

▷ Example 4

Consider the case of a six-treatment crossover trial in which the squares are not variance balanced. The following dataset is from a partially balanced crossover trial published by Patterson and Lucas (1962) and reproduced in Ratkowsky, Evans, and Alldredge (1993, 231):

```
. use http://www.stata-press.com/data/r12/nobalance
. list, sep(4)
```

	cow	seq	period1	period2	period3	period4	block
1.	1	adbe	38.7	37.4	34.3	31.3	1
2.	2	baed	48.9	46.9	42	39.6	1
3.	3	ebda	34.6	32.3	28.5	27.1	1
4.	4	deab	35.2	33.5	28.4	25.1	1
5.	1	dafc	32.9	33.1	27.5	25.1	2
6.	2	fdca	30.4	29.5	26.7	23.1	2
7.	3	cfad	30.8	29.3	26.4	23.2	2
8.	4	acdf	25.7	26.1	23.4	18.7	2
9.	1	efbc	25.4	26	23.9	19.9	3
10.	2	becf	21.8	23.9	21.7	17.6	3
11.	3	fceb	21.4	22	19.4	16.6	3
12.	4	cbfe	22.8	21	18.6	16.1	3

When there is no variance balance in the design, a square or blocking variable is needed to indicate in which treatment cell a sequence was observed, but the mechanical steps are the same.

```
. pkshape cow seq period1 period2 period3 period4
. pkcross outcome, model(block cow|block period|block treat carry) se
```

```
                    Number of obs =      48     R-squared     =  0.9965
                    Root MSE      = .740408     Adj R-squared =  0.9903
```

Source	Seq. SS	df	MS	F	Prob > F
Model	2650.1331	30	88.3377701	161.14	0.0000
block	1607.01128	2	803.505642	1465.71	0.0000
cow|block	628.706274	9	69.8562527	127.43	0.0000
period|block	408.031253	9	45.3368059	82.70	0.0000
treat	2.50000057	5	.500000114	0.91	0.4964
carry	3.88428906	5	.776857812	1.42	0.2680
Residual	9.31945887	17	.548203463		
Total	2659.45256	47	56.584097		

When the model statement is used and the omnibus measure of separability is desired, specify the variables in the `treatment()`, `carryover()`, and `sequence()` options to `pkcross`. ◁

Methods and formulas

`pkcross` is implemented as an ado-file.

`pkcross` uses ANOVA to fit models for crossover experiments; see [R] **anova**.

The omnibus measure of separability is

$$S = 100(1 - V)\%$$

where V is Cramér's V and is defined as

$$V = \left\{ \frac{\frac{\chi^2}{N}}{\min(r-1, c-1)} \right\}^{\frac{1}{2}}$$

The χ^2 is calculated as

$$\chi^2 = \sum_i \sum_j \left\{ \frac{(O_{ij} - E_{ij})^2}{E_{ij}} \right\}$$

where O and E are the observed and expected counts in a table of the number of times each treatment is followed by the other treatments.

References

Balaam, L. N. 1968. A two-period design with t^2 experimental units. *Biometrics* 24: 61–73.

Chow, S.-C., and J.-P. Liu. 2009. *Design and Analysis of Bioavailability and Bioequivalence Studies*. 3rd ed. Boca Raton, FL: Chapman & Hall/CRC.

Kutner, M. H., C. J. Nachtsheim, J. Neter, and W. Li. 2005. *Applied Linear Statistical Models*. 5th ed. New York: McGraw–Hill/Irwin.

Patterson, H. D., and H. L. Lucas. 1962. Change-over designs. Technical Bulletin 147, North Carolina Agricultural Experiment Station and the USDA.

Ratkowsky, D. A., M. A. Evans, and J. R. Alldredge. 1993. *Cross-over Experiments: Design, Analysis, and Application*. New York: Dekker.

Taka, M. T., and P. Armitage. 1983. Autoregressive models in clinical trials. *Communications in Statistics, Theory and Methods* 12: 865–876.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data

Title

pkequiv — Perform bioequivalence tests

Syntax

`pkequiv` *outcome treatment period sequence id* [*if*] [*in*] [`,` *options*]

options	Description
Options	
`compare(`*string*`)`	compare the two specified values of the treatment variable
`limit(#)`	equivalence limit (between 0.10 and 0.99); default is 0.2
`level(#)`	set confidence level; default is `level(90)`
`fieller`	calculate confidence interval by Fieller's theorem
`symmetric`	calculate symmetric equivalence interval
`anderson`	Anderson and Hauck hypothesis test for bioequivalence
`tost`	two one-sided hypothesis tests for bioequivalence
`noboot`	do not estimate probability that CI lies within confidence limits

Menu

Statistics > Epidemiology and related > Other > Bioequivalence tests

Description

`pkequiv` performs bioequivalence testing for two treatments. By default, `pkequiv` calculates a standard confidence interval symmetric about the difference between the two treatment means. `pkequiv` also calculates confidence intervals symmetric about zero and intervals based on Fieller's theorem. Also, `pkequiv` can perform interval hypothesis tests for bioequivalence.

`pkequiv` is one of the pk commands. Please read [R] **pk** before reading this entry.

Options

Options

`compare(`*string*`)` specifies the two treatments to be tested for equivalence. Sometimes there may be more than two treatments, but the equivalence can be determined only between any two treatments.

`limit(#)` specifies the equivalence limit. The default is 0.2. The equivalence limit can be changed only symmetrically; that is, it is not possible to have a 0.15 lower limit and a 0.2 upper limit in the same test.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(90)`. This setting is not controlled by the `set level` command.

`fieller` specifies that an equivalence interval based on Fieller's theorem be calculated.

`symmetric` specifies that a symmetric equivalence interval be calculated.

`anderson` specifies that the Anderson and Hauck (1983) hypothesis test for bioequivalence be computed. This option is ignored when calculating equivalence intervals based on Fieller's theorem or when calculating a confidence interval that is symmetric about zero.

`tost` specifies that the two one-sided hypothesis tests for bioequivalence be computed. This option is ignored when calculating equivalence intervals based on Fieller's theorem or when calculating a confidence interval that is symmetric about zero.

`noboot` prevents the estimation of the probability that the confidence interval lies within the confidence limits. If this option is not specified, this probability is estimated by resampling the data.

Remarks

`pkequiv` is designed to conduct tests for bioequivalence based on data from a crossover experiment. `pkequiv` requires that the user specify the *outcome*, *treatment*, *period*, *sequence*, and *id* variables. The data must be in the same format as that produced by `pkshape`; see [R] **pkshape**.

Example 1

Continuing with example 4 from [R] **pkshape**, we will conduct equivalence testing.

```
. use http://www.stata-press.com/data/r12/pkdata3
. list, sep(4)
```

	id	sequence	outcome	treat	carry	period
1.	1	1	150.9643	A	0	1
2.	2	1	146.7606	A	0	1
3.	3	1	160.6548	A	0	1
4.	4	1	157.8622	A	0	1
5.	5	1	133.6957	A	0	1
6.	7	1	160.639	A	0	1
7.	8	1	131.2604	A	0	1
8.	9	1	168.5186	A	0	1
9.	10	2	137.0627	B	0	1
10.	12	2	153.4038	B	0	1
11.	13	2	163.4593	B	0	1
12.	14	2	146.0462	B	0	1
13.	15	2	158.1457	B	0	1
14.	18	2	147.1977	B	0	1
15.	19	2	164.9988	B	0	1
16.	20	2	145.3823	B	0	1
17.	1	1	218.5551	B	A	2
18.	2	1	133.3201	B	A	2
19.	3	1	126.0635	B	A	2
20.	4	1	96.17461	B	A	2
21.	5	1	188.9038	B	A	2
22.	7	1	223.6922	B	A	2
23.	8	1	104.0139	B	A	2
24.	9	1	237.8962	B	A	2
25.	10	2	139.7382	A	B	2
26.	12	2	202.3942	A	B	2
27.	13	2	136.7848	A	B	2
28.	14	2	104.5191	A	B	2
29.	15	2	165.8654	A	B	2
30.	18	2	139.235	A	B	2
31.	19	2	166.2391	A	B	2
32.	20	2	158.5146	A	B	2

Now we can conduct a bioequivalence test between `treat` $= A$ and `treat` $= B$.

```
. set seed 1
. pkequiv outcome treat period seq id
      Classic confidence interval for bioequivalence
------------------------------------------------------------------------------
                    [equivalence limits]        [    test limits   ]
------------------------------------------------------------------------------
     difference:   -30.296        30.296        -11.332        26.416
          ratio:       80%          120%         92.519%      117.439%
------------------------------------------------------------------------------
probability test limits are within equivalence limits =    0.6410
note: reference treatment = 1
```

The default output for `pkequiv` shows a confidence interval for the difference of the means (test limits), the ratio of the means, and the federal equivalence limits. The classic confidence interval can be constructed around the difference between the average measure of effect for the two drugs or around the ratio of the average measure of effect for the two drugs. `pkequiv` reports both the difference measure and the ratio measure. For these data, U.S. federal government regulations state that the confidence interval for the difference must be entirely contained within the range $[-30.296, 30.296]$ and between 80% and 120% for the ratio. Here the test limits are within the equivalence limits. Although the test limits are inside the equivalence limits, there is only a 64% assurance that the observed confidence interval will be within the equivalence limits in the long run. This is an interesting case because, although this sample shows bioequivalence, the evaluation of the long-run performance indicates possible problems. These fictitious data were generated with high intersubject variability, which causes poor long-run performance.

If we conduct a bioequivalence test with the data published in Chow and Liu (2009, 71), which we introduced in [R] **pk** and fully described in [R] **pkshape**, we observe that the probability that the test limits are within the equivalence limits is high.

```
. use http://www.stata-press.com/data/r12/chowliu2
. set seed 1
. pkequiv outcome treat period seq id
      Classic confidence interval for bioequivalence
------------------------------------------------------------------------------
                    [equivalence limits]        [    test limits   ]
------------------------------------------------------------------------------
     difference:   -16.512        16.512         -8.698         4.123
          ratio:       80%          120%         89.464%      104.994%
------------------------------------------------------------------------------
probability test limits are within equivalence limits =    0.9980
note: reference treatment = 1
```

For these data, the test limits are well within the equivalence limits, and the probability that the test limits are within the equivalence limits is 99.8%.

◁

▷ Example 2

We compute a confidence interval that is symmetric about zero:

```
. pkequiv outcome treat period seq id, symmetric
      Westlake's symmetric confidence interval for bioequivalence
      ──────────────────────────────────────────────────────────────
                         [Equivalence limits]       [    Test mean   ]
      ──────────────────────────────────────────────────────────────
      Test formulation:     75.145    89.974               80.272
      ──────────────────────────────────────────────────────────────
      note: reference treatment = 1
```

The reported equivalence limit is constructed symmetrically about the reference mean, which is equivalent to constructing a confidence interval symmetric about zero for the difference in the two drugs. In the output above, we see that the test formulation mean of 80.272 is within the equivalence limits, indicating that the test drug is bioequivalent to the reference drug.

`pkequiv` displays interval hypothesis tests of bioequivalence if you specify the `tost` or the `anderson` option, or both. For example,

```
. set seed 1
. pkequiv outcome treat period seq id, tost anderson
      Classic confidence interval for bioequivalence
      ──────────────────────────────────────────────────────────────
                         [equivalence limits]        [    test limits   ]
      ──────────────────────────────────────────────────────────────
           difference:   -16.512       16.512         -8.698        4.123
                ratio:       80%         120%         89.464%     104.994%
      ──────────────────────────────────────────────────────────────
      probability test limits are within equivalence limits =    0.9980
      Schuirmann's two one-sided tests
      ──────────────────────────────────────────────────────────────
      upper test statistic =    -5.036                   p-value =     0.000
      lower test statistic =     3.810                   p-value =     0.001
      Anderson and Hauck's test
      ──────────────────────────────────────────────────────────────
      noncentrality parameter =     4.423
              test statistic =    -0.613      empirical p-value =    0.0005
      note: reference treatment = 1
```

Both of Schuirmann's one-sided tests are highly significant, suggesting that the two drugs are bioequivalent. A similar conclusion is drawn from the Anderson and Hauck test of bioequivalence. ◁

Saved results

`pkequiv` saves the following in `r()`:

Scalars

`r(stddev)`	pooled-sample standard deviation of period differences from both sequences
`r(uci)`	upper confidence interval for a classic interval
`r(lci)`	lower confidence interval for a classic interval
`r(delta)`	delta value used in calculating a symmetric confidence interval
`r(u3)`	upper confidence interval for Fieller's confidence interval
`r(l3)`	lower confidence interval for Fieller's confidence interval

Methods and formulas

pkequiv is implemented as an ado-file.

The lower confidence interval for the difference in the two treatments for the classic shortest confidence interval is

$$L_1 = \left(\overline{Y}_T - \overline{Y}_R\right) - t_{(\alpha,n_1+n_2-2)}\widehat{\sigma}_d\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}$$

The upper limit is

$$U_1 = \left(\overline{Y}_T - \overline{Y}_R\right) + t_{(\alpha,n_1+n_2-2)}\widehat{\sigma}_d\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}$$

The limits for the ratio measure are

$$L_2 = \left(\frac{L_1}{\overline{Y}_R}+1\right)100\%$$

and

$$U_2 = \left(\frac{U_1}{\overline{Y}_R}+1\right)100\%$$

where $\overline{Y}_T$ is the mean of the test formulation of the drug, $\overline{Y}_R$ is the mean of the reference formulation of the drug, and $t_{(\alpha,n_1+n_2-2)}$ is the t distribution with n_1+n_2-2 degrees of freedom. $\widehat{\sigma}_d$ is the pooled sample variance of the period differences from both sequences, defined as

$$\widehat{\sigma}_d = \frac{1}{n_1+n_2-2}\sum_{k=1}^{2}\sum_{i=1}^{n_k}\left(d_{ik}-\overline{d}_{.k}\right)^2$$

The upper and lower limits for the symmetric confidence interval are $\overline{Y}_R+\Delta$ and $\overline{Y}_R-\Delta$, where

$$\Delta = k_1\widehat{\sigma}_d\sqrt{\frac{1}{n_1}+\frac{1}{n_2}} - \left(\overline{Y}_T - \overline{Y}_R\right)$$

and (simultaneously)

$$\Delta = -k_2\widehat{\sigma}_d\sqrt{\frac{1}{n_1}+\frac{1}{n_2}} + 2\left(\overline{Y}_T - \overline{Y}_R\right)$$

and k_1 and k_2 are computed iteratively to satisfy the above equalities and the condition

$$\int_{k_1}^{k_2} f(t)dt = 1-2\alpha$$

where $f(t)$ is the probability density function of the t distribution with n_1+n_2-2 degrees of freedom.

See Chow and Liu (2009, 88–92) for details about calculating the confidence interval based on Fieller's theorem.

The two test statistics for the two one-sided tests of equivalence are

$$T_L = \frac{\left(\overline{Y}_T - \overline{Y}_R\right) - \theta_L}{\widehat{\sigma}_d\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

and

$$T_U = \frac{\left(\overline{Y}_T - \overline{Y}_R\right) - \theta_U}{\widehat{\sigma}_d\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

where $-\theta_L = \theta_U$ and are the regulated confidence limits.

The logic of the Anderson and Hauck test is tricky; see Chow and Liu (2009) for a complete explanation. However, the test statistic is

$$T_{AH} = \frac{\left(\overline{Y}_T - \overline{Y}_R\right) - \left(\frac{\theta_L + \theta_U}{2}\right)}{\widehat{\sigma}_d\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

and the noncentrality parameter is estimated by

$$\widehat{\delta} = \frac{\theta_U - \theta_L}{2\widehat{\sigma}_d\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

The empirical p-value is calculated as

$$p = F_t\left(|T_{AH}| - \widehat{\delta}\right) - F_t\left(-|T_{AH}| - \widehat{\delta}\right)$$

where F_t is the cumulative distribution function of the t distribution with $n_1 + n_2 - 2$ degrees of freedom.

References

Anderson, S., and W. W. Hauck. 1983. A new procedure for testing equivalence in comparative bioavailability and other clinical trials. *Communications in Statistics, Theory and Methods* 12: 2663–2692.

Chow, S.-C., and J.-P. Liu. 2009. *Design and Analysis of Bioavailability and Bioequivalence Studies*. 3rd ed. Boca Raton, FL: Chapman & Hall/CRC.

Fieller, E. C. 1954. Some problems in interval estimation. *Journal of the Royal Statistical Society, Series B* 16: 175–185.

Kutner, M. H., C. J. Nachtsheim, J. Neter, and W. Li. 2005. *Applied Linear Statistical Models*. 5th ed. New York: McGraw–Hill/Irwin.

Locke, C. S. 1984. An exact confidence interval from untransformed data for the ratio of two formulation means. *Journal of Pharmacokinetics and Biopharmaceutics* 12: 649–655.

Schuirmann, D. J. 1989. Confidence intervals for the ratio of two means from a cross-over study. In *Proceedings of the Biopharmaceutical Section*, 121–126. Washington, DC: American Statistical Association.

Westlake, W. J. 1976. Symmetrical confidence intervals for bioequivalence trials. *Biometrics* 32: 741–744.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data

Title

pkexamine — Calculate pharmacokinetic measures

Syntax

`pkexamine` *time concentration* [*if*] [*in*] [, *options*]

options	Description
Main	
`fit(#)`	use # points to estimate $AUC_{0,\infty}$; default is `fit(3)`
`trapezoid`	use trapezoidal rule; default is cubic splines
`graph`	graph the AUC
`line`	graph the linear extension
`log`	graph the log extension
`exp(#)`	plot the exponential fit for the $AUC_{0,\infty}$
AUC plot	
cline_options	affect rendition of plotted points connected by lines
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

`by` is allowed; see [D] **by**.

Menu

Statistics > Epidemiology and related > Other > Pharmacokinetic measures

Description

`pkexamine` calculates pharmacokinetic measures from time-and-concentration subject-level data. `pkexamine` computes and displays the maximum measured concentration, the time at the maximum measured concentration, the time of the last measurement, the elimination time, the half-life, and the area under the concentration-time curve (AUC). Three estimates of the area under the concentration-time curve from 0 to infinity ($AUC_{0,\infty}$) are also calculated.

`pkexamine` is one of the pk commands. Please read [R] **pk** before reading this entry.

Options

Main

`fit(#)` specifies the number of points, counting back from the last measurement, to use in fitting the extension to estimate the $\text{AUC}_{0,\infty}$. The default is `fit(3)`, or the last three points. This value should be viewed as a minimum; the appropriate number of points will depend on your data.

`trapezoid` specifies that the trapezoidal rule be used to calculate the AUC. The default is cubic splines, which give better results for most functions. When the curve is irregular, `trapezoid` may give better results.

`graph` tells `pkexamine` to graph the concentration-time curve.

`line` and `log` specify the estimates of the $\text{AUC}_{0,\infty}$ to display when graphing the $\text{AUC}_{0,\infty}$. These options are ignored, unless they are specified with the `graph` option.

`exp(#)` specifies that the exponential fit for the $\text{AUC}_{0,\infty}$ be plotted. You must specify the maximum time value to which you want to plot the curve, and this time value must be greater than the maximum time measurement in the data. If you specify 0, the curve will be plotted to the point at which the linear extension would cross the x axis. This option is not valid with the `line` or `log` option and is ignored, unless the `graph` option is also specified.

AUC plot

cline_options affect the rendition of the plotted points connected by lines; see [G-3] ***cline_options***.

marker_options specify the look of markers. This look includes the marker symbol, the marker size, and its color and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

`pkexamine` computes summary statistics for a given patient in a pharmacokinetic trial. If `by` *idvar*`:` is specified, statistics will be displayed for each subject in the data.

▷ Example 1

Chow and Liu (2009, 13) present data on a study examining primidone concentrations versus time for a subject over a 32-hour period after dosing.

```
. use http://www.stata-press.com/data/r12/auc
. list, abbrev(14)
```

	id	time	concentration
1.	1	0	0
2.	1	.5	0
3.	1	1	2.8
4.	1	1.5	4.4
5.	1	2	4.4
6.	1	3	4.7
7.	1	4	4.1
8.	1	6	4
9.	1	8	3.6
10.	1	12	3
11.	1	16	2.5
12.	1	24	2
13.	1	32	1.6

We use `pkexamine` to produce the summary statistics:

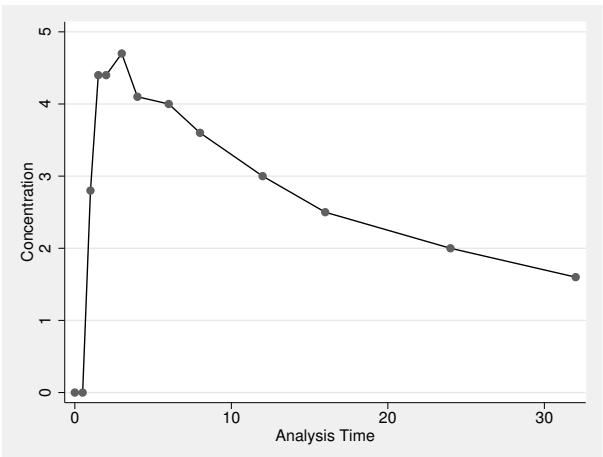
```
. pkexamine time conc, graph
```

```
                        Maximum concentration =       4.7
                  Time of maximum concentration =         3
Time of last observation (Tmax) =        32
                        Elimination rate =    0.0279
                               Half life =   24.8503
```

Area under the curve

AUC [0, Tmax]	AUC [0, inf.) Linear of log conc.	AUC [0, inf.) Linear fit	AUC [0, inf.) Exponential fit
85.24	142.603	107.759	142.603

Fit based on last 3 points.



The maximum concentration of 4.7 occurs at time 3, and the time of the last observation (Tmax) is 32. In addition to the AUC, which is calculated from 0 to the maximum value of `time`, `pkexamine` also reports the area under the curve, computed by extending the curve with each of three methods: a linear fit to the log of the concentration, a linear regression line, and a decreasing exponential regression line. See *Methods and formulas* for details on these three methods.

By default, all extensions to the AUC are based on the last three points. Looking at the graph for these data, it seems more appropriate to use the last seven points to estimate the $\text{AUC}_{0,\infty}$:

```
. pkexamine time conc, fit(7)
```

```
                                  Maximum concentration =       4.7
                              Time of maximum concentration =         3
                            Time of last observation (Tmax) =        32
                                        Elimination rate =    0.0349
                                               Half life =   19.8354

Area under the curve
```

AUC [0, Tmax]	AUC [0, inf.) Linear of log conc.	AUC [0, inf.) Linear fit	AUC [0, inf.) Exponential fit
85.24	131.027	96.805	129.181

```
Fit based on last 7 points.
```

This approach decreased the estimate of the $\text{AUC}_{0,\infty}$ for all extensions. To see a graph of the $\text{AUC}_{0,\infty}$ using a linear extension, specify the `graph` and `line` options.

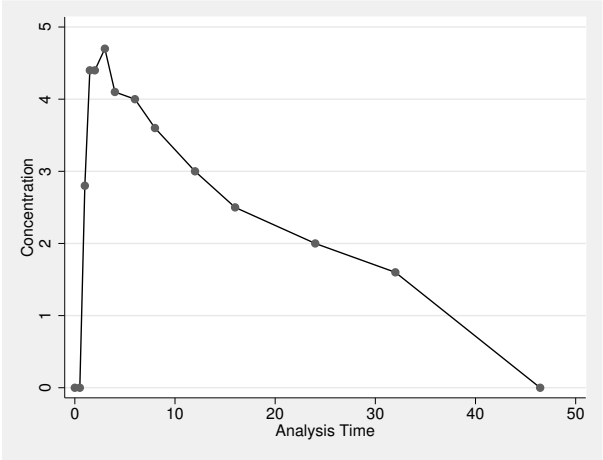
```
. pkexamine time conc, fit(7) graph line
```

```
                                  Maximum concentration =       4.7
                              Time of maximum concentration =         3
                            Time of last observation (Tmax) =        32
                                        Elimination rate =    0.0349
                                               Half life =   19.8354

Area under the curve
```

AUC [0, Tmax]	AUC [0, inf.) Linear of log conc.	AUC [0, inf.) Linear fit	AUC [0, inf.) Exponential fit
85.24	131.027	96.805	129.181

```
Fit based on last 7 points.
```



Saved results

`pkexamine` saves the following in `r()`:

Scalars

`r(auc)`	area under the concentration curve
`r(half)`	half-life of the drug
`r(ke)`	elimination rate
`r(tmax)`	time at last concentration measurement
`r(cmax)`	maximum concentration
`r(tomc)`	time of maximum concentration
`r(auc_line)`	$\text{AUC}_{0,\infty}$ estimated with a linear fit
`r(auc_exp)`	$\text{AUC}_{0,\infty}$ estimated with an exponential fit
`r(auc_ln)`	$\text{AUC}_{0,\infty}$ estimated with a linear fit of the natural log

Methods and formulas

`pkexamine` is implemented as an ado-file.

Let i index the observations sorted by time, let k be the number of observations, and let f be the number of points specified in the `fit(#)` option.

The $\text{AUC}_{0,t_{\max}}$ is defined as

$$\text{AUC}_{0,t_{\max}} = \int_0^{t_{\max}} C_t dt$$

where C_t is the concentration at time t. By default, the integral is calculated numerically using cubic splines. However, if the trapezoidal rule is used, the $\text{AUC}_{0,t_{\max}}$ is given as

$$\text{AUC}_{0,t_{\max}} = \sum_{i=2}^{k} \frac{C_{i-1} + C_i}{2} (t_i - t_{i-1})$$

The $\text{AUC}_{0,\infty}$ is the $\text{AUC}_{0,t_{\max}}$ + $\text{AUC}_{t_{\max},\infty}$, or

$$\text{AUC}_{0,\infty} = \int_0^{t_{\max}} C_t dt + \int_{t_{\max}}^{\infty} C_t dt$$

When using the linear extension to the $\text{AUC}_{0,t_{\max}}$, the integration is cut off when the line crosses the x axis. The log extension is a linear extension on the log concentration scale. The area for the exponential extension is

$$\text{AUC}_{0,\infty} = \int_{t_{\max}}^{\infty} e^{-(\beta_0 + t\beta_1)} dt = -\frac{e^{-(\beta_0 + t_{\max}\beta_1)}}{\beta_1}$$

The elimination rate K_{eq} is the negative of the slope from a linear regression of log concentration on time fit to the number of points specified in the `fit(#)` option:

$$K_{\text{eq}} = -\frac{\sum_{i=k-f+1}^{k} \left(t_i - \bar{t}\right)\left(\ln C_i - \overline{\ln C}\right)}{\sum_{i=k-f+1}^{k} \left(t_i - \bar{t}\right)^2}$$

The half-life is

$$t_{\text{half}} = \frac{\ln 2}{K_{\text{eq}}}$$

Reference

Chow, S.-C., and J.-P. Liu. 2009. *Design and Analysis of Bioavailability and Bioequivalence Studies.* 3rd ed. Boca Raton, FL: Chapman & Hall/CRC.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data

Title

pkshape — Reshape (pharmacokinetic) Latin-square data

Syntax

`pkshape` *id sequence period1 period2* [*period list*] [`,` *options*]

options	Description
`order(`*string*`)`	apply treatments in specified order
`outcome(`*newvar*`)`	name for outcome variable; default is `outcome(outcome)`
`treatment(`*newvar*`)`	name for treatment variable; default is `treatment(treat)`
`carryover(`*newvar*`)`	name for carryover variable; default is `carryover(carry)`
`sequence(`*newvar*`)`	name for sequence variable; default is `sequence(sequence)`
`period(`*newvar*`)`	name for period variable; default is `period(period)`

Menu

Statistics > Epidemiology and related > Other > Reshape pharmacokinetic latin-square data

Description

`pkshape` reshapes the data for use with `anova`, `pkcross`, and `pkequiv`; see [R] **anova**, [R] **pkcross**, and [R] **pkequiv**. Latin-square and crossover data are often organized in a manner that cannot be analyzed easily with Stata. `pkshape` reorganizes the data in memory for use in Stata.

`pkshape` is one of the pk commands. Please read [R] **pk** before reading this entry.

Options

`order(`*string*`)` specifies the order in which treatments were applied. If the `sequence()` specifier is a string variable that specifies the order, this option is not necessary. Otherwise, `order()` specifies how to generate the treatment and carryover variables. Any string variable can be used to specify the order. For crossover designs, any washout periods can be indicated with the number 0.

`outcome(`*newvar*`)` specifies the name for the outcome variable in the reorganized data. By default, `outcome(outcome)` is used.

`treatment(`*newvar*`)` specifies the name for the treatment variable in the reorganized data. By default, `treatment(treat)` is used.

`carryover(`*newvar*`)` specifies the name for the carryover variable in the reorganized data. By default, `carryover(carry)` is used.

`sequence(`*newvar*`)` specifies the name for the sequence variable in the reorganized data. By default, `sequence(sequence)` is used.

`period(`*newvar*`)` specifies the name for the period variable in the reorganized data. By default, `period(period)` is used.

Remarks

Often data from a Latin-square experiment are naturally organized in a manner that Stata cannot manage easily. `pkshape` reorganizes Latin-square data so that they can be used with `anova` (see [R] **anova**) or any pk command. This includes the classic 2×2 crossover design commonly used in pharmaceutical research, as well as many other Latin-square designs.

▷ Example 1

Consider the example data published in Chow and Liu (2009, 71). There are 24 patients, 12 in each sequence. Sequence 1 consists of the reference formulation followed by the test formulation; sequence 2 is the test formulation followed by the reference formulation. The measurements reported are the $\text{AUC}_{0-t_{\max}}$ for each patient and for each period.

```
. use http://www.stata-press.com/data/r12/chowliu
. list, sep(4)
```

	id	seq	period1	period2
1.	1	1	74.675	73.675
2.	4	1	96.4	93.25
3.	5	1	101.95	102.125
4.	6	1	79.05	69.45
5.	11	1	79.05	69.025
6.	12	1	85.95	68.7
7.	15	1	69.725	59.425
8.	16	1	86.275	76.125
9.	19	1	112.675	114.875
10.	20	1	99.525	116.25
11.	23	1	89.425	64.175
12.	24	1	55.175	74.575
13.	2	2	74.825	37.35
14.	3	2	86.875	51.925
15.	7	2	81.675	72.175
16.	8	2	92.7	77.5
17.	9	2	50.45	71.875
18.	10	2	66.125	94.025
19.	13	2	122.45	124.975
20.	14	2	99.075	85.225
21.	17	2	86.35	95.925
22.	18	2	49.925	67.1
23.	21	2	42.7	59.425
24.	22	2	91.725	114.05

Because the outcome for one person is in two different variables, the treatment that was applied to an individual is a function of the period and the sequence. To analyze this treatment using `anova`, all the outcomes must be in one variable, and each covariate must be in its own variable. To reorganize these data, use `pkshape`:

```
. pkshape id seq period1 period2, order(ab ba)
. sort seq id treat
```

```
. list, sep(8)
```

	id	sequence	outcome	treat	carry	period
1.	1	1	74.675	1	0	1
2.	1	1	73.675	2	1	2
3.	4	1	96.4	1	0	1
4.	4	1	93.25	2	1	2
5.	5	1	101.95	1	0	1
6.	5	1	102.125	2	1	2
7.	6	1	79.05	1	0	1
8.	6	1	69.45	2	1	2
9.	11	1	79.05	1	0	1
10.	11	1	69.025	2	1	2
11.	12	1	85.95	1	0	1
12.	12	1	68.7	2	1	2
13.	15	1	69.725	1	0	1
14.	15	1	59.425	2	1	2
15.	16	1	86.275	1	0	1
16.	16	1	76.125	2	1	2
17.	19	1	112.675	1	0	1
18.	19	1	114.875	2	1	2
19.	20	1	99.525	1	0	1
20.	20	1	116.25	2	1	2
21.	23	1	89.425	1	0	1
22.	23	1	64.175	2	1	2
23.	24	1	55.175	1	0	1
24.	24	1	74.575	2	1	2
25.	2	2	37.35	1	2	2
26.	2	2	74.825	2	0	1
27.	3	2	51.925	1	2	2
28.	3	2	86.875	2	0	1
29.	7	2	72.175	1	2	2
30.	7	2	81.675	2	0	1
31.	8	2	77.5	1	2	2
32.	8	2	92.7	2	0	1
33.	9	2	71.875	1	2	2
34.	9	2	50.45	2	0	1
35.	10	2	94.025	1	2	2
36.	10	2	66.125	2	0	1
37.	13	2	124.975	1	2	2
38.	13	2	122.45	2	0	1
39.	14	2	85.225	1	2	2
40.	14	2	99.075	2	0	1
41.	17	2	95.925	1	2	2
42.	17	2	86.35	2	0	1
43.	18	2	67.1	1	2	2
44.	18	2	49.925	2	0	1
45.	21	2	59.425	1	2	2
46.	21	2	42.7	2	0	1
47.	22	2	114.05	1	2	2
48.	22	2	91.725	2	0	1

Now the data are organized into separate variables that indicate each factor level for each of the covariates, so the data may be used with `anova` or `pkcross`; see [R] **anova** and [R] **pkcross**.

◁

Example 2

Consider the study of background music on bank teller productivity published in Kutner et al. (2005). The data are

Week	Monday	Tuesday	Wednesday	Thursday	Friday
1	18(D)	17(C)	14(A)	21(B)	17(E)
2	13(C)	34(B)	21(E)	16(A)	15(D)
3	7(A)	29(D)	32(B)	27(E)	13(C)
4	17(E)	13(A)	24(C)	31(D)	25(B)
5	21(B)	26(E)	26(D)	31(C)	7(A)

The numbers are the productivity scores, and the letters represent the treatment. We entered the data into Stata:

```
. use http://www.stata-press.com/data/r12/music, clear
. list
```

	id	seq	day1	day2	day3	day4	day5
1.	1	dcabe	18	17	14	21	17
2.	2	cbead	13	34	21	16	15
3.	3	adbec	7	29	32	27	13
4.	4	eacdb	17	13	24	31	25
5.	5	bedca	21	26	26	31	7

We reshape these data with `pkshape`:

```
. pkshape id seq day1 day2 day3 day4 day5
. list, sep(0)
```

	id	sequence	outcome	treat	carry	period
1.	3	1	7	1	0	1
2.	5	2	21	3	0	1
3.	2	3	13	5	0	1
4.	1	4	18	2	0	1
5.	4	5	17	4	0	1
6.	3	1	29	2	1	2
7.	5	2	26	4	3	2
8.	2	3	34	3	5	2
9.	1	4	17	5	2	2
10.	4	5	13	1	4	2
11.	3	1	32	3	2	3
12.	5	2	26	2	4	3
13.	2	3	21	4	3	3
14.	1	4	14	1	5	3
15.	4	5	24	5	1	3
16.	3	1	27	4	3	4
17.	5	2	31	5	2	4
18.	2	3	16	1	4	4
19.	1	4	21	3	1	4
20.	4	5	31	2	5	4
21.	3	1	13	5	4	5
22.	5	2	7	1	5	5
23.	2	3	15	2	1	5
24.	1	4	17	4	3	5
25.	4	5	25	3	2	5

Here the `sequence` variable is a string variable that specifies how the treatments were applied, so the `order` option is not used. When the sequence variable is a string and the `order` is specified, the arguments from the `order` option are used. We could now produce an ANOVA table:

```
. anova outcome seq period treat
```

```
                  Number of obs =      25     R-squared     =  0.8666
                  Root MSE      = 3.96232     Adj R-squared =  0.7331

          Source | Partial SS    df       MS           F     Prob > F
-----------------+----------------------------------------------------
           Model |      1223.6    12  101.966667       6.49     0.0014
                 |
        sequence |           82     4        20.5       1.31     0.3226
          period |        477.2     4       119.3       7.60     0.0027
           treat |        664.4     4       166.1      10.58     0.0007
                 |
        Residual |        188.4    12        15.7
-----------------+----------------------------------------------------
           Total |         1412    24  58.8333333
```

Example 3

Consider the Latin-square crossover example published in Kutner et al. (2005). The example is about apple sales given different methods for displaying apples.

Pattern	Store	Week 1	Week 2	Week 3
1	1	9(B)	12(C)	15(A)
	2	4(B)	12(C)	9(A)
2	1	12(A)	14(B)	3(C)
	2	13(A)	14(B)	3(C)
3	1	7(C)	18(A)	6(B)
	2	5(C)	20(A)	4(B)

We entered the data into Stata:

```
. use http://www.stata-press.com/data/r12/applesales, clear
. list, sep(2)
```

```
     +-------------------------------------------+
     | id   seq   p1   p2   p3   square          |
     |-------------------------------------------|
  1. |  1     1    9   12   15        1          |
  2. |  2     1    4   12    9        2          |
     |-------------------------------------------|
  3. |  3     2   12   14    3        1          |
  4. |  4     2   13   14    3        2          |
     |-------------------------------------------|
  5. |  5     3    7   18    6        1          |
  6. |  6     3    5   20    4        2          |
     +-------------------------------------------+
```

Now the data can be reorganized using descriptive names for the outcome variables.

```
. pkshape id seq p1 p2 p3, order(bca abc cab) seq(pattern) period(order)
> treat(displays)
```

```
. anova outcome pattern order display id|pattern
                          Number of obs =      18     R-squared     =  0.9562
                          Root MSE      = 1.59426     Adj R-squared =  0.9069
```

Source	Partial SS	df	MS	F	Prob > F
Model	443.666667	9	49.2962963	19.40	0.0002
pattern	.333333333	2	.166666667	0.07	0.9370
order	233.333333	2	116.666667	45.90	0.0000
displays	189	2	94.5	37.18	0.0001
id|pattern	21	3	7	2.75	0.1120
Residual	20.3333333	8	2.54166667		
Total	464	17	27.2941176		

These are the same results reported by Kutner et al. (2005).

◁

▷ Example 4

We continue with example 1 from [R] **pkcollapse**; the data are

```
. use http://www.stata-press.com/data/r12/pkdata2, clear
. list, sep(4) abbrev(10)
```

	id	seq	auc_concA	auc_concB
1.	1	1	150.9643	218.5551
2.	2	1	146.7606	133.3201
3.	3	1	160.6548	126.0635
4.	4	1	157.8622	96.17461
5.	5	1	133.6957	188.9038
6.	7	1	160.639	223.6922
7.	8	1	131.2604	104.0139
8.	9	1	168.5186	237.8962
9.	10	2	137.0627	139.7382
10.	12	2	153.4038	202.3942
11.	13	2	163.4593	136.7848
12.	14	2	146.0462	104.5191
13.	15	2	158.1457	165.8654
14.	18	2	147.1977	139.235
15.	19	2	164.9988	166.2391
16.	20	2	145.3823	158.5146

```
. pkshape id seq auc_concA auc_concB, order(ab ba)
. sort period id
```

```
. list, sep(4)
```

	id	sequence	outcome	treat	carry	period
1.	1	1	150.9643	1	0	1
2.	2	1	146.7606	1	0	1
3.	3	1	160.6548	1	0	1
4.	4	1	157.8622	1	0	1
5.	5	1	133.6957	1	0	1
6.	7	1	160.639	1	0	1
7.	8	1	131.2604	1	0	1
8.	9	1	168.5186	1	0	1
9.	10	2	137.0627	2	0	1
10.	12	2	153.4038	2	0	1
11.	13	2	163.4593	2	0	1
12.	14	2	146.0462	2	0	1
13.	15	2	158.1457	2	0	1
14.	18	2	147.1977	2	0	1
15.	19	2	164.9988	2	0	1
16.	20	2	145.3823	2	0	1
17.	1	1	218.5551	2	1	2
18.	2	1	133.3201	2	1	2
19.	3	1	126.0635	2	1	2
20.	4	1	96.17461	2	1	2
21.	5	1	188.9038	2	1	2
22.	7	1	223.6922	2	1	2
23.	8	1	104.0139	2	1	2
24.	9	1	237.8962	2	1	2
25.	10	2	139.7382	1	2	2
26.	12	2	202.3942	1	2	2
27.	13	2	136.7848	1	2	2
28.	14	2	104.5191	1	2	2
29.	15	2	165.8654	1	2	2
30.	18	2	139.235	1	2	2
31.	19	2	166.2391	1	2	2
32.	20	2	158.5146	1	2	2

◁

We call the resulting dataset `pkdata3`. We conduct equivalence testing on the data in [R] **pkequiv**, and we fit an ANOVA model to these data in the third example of [R] **pkcross**.

Methods and formulas

`pkshape` is implemented as an ado-file.

References

Chow, S.-C., and J.-P. Liu. 2009. *Design and Analysis of Bioavailability and Bioequivalence Studies*. 3rd ed. Boca Raton, FL: Chapman & Hall/CRC.

Kutner, M. H., C. J. Nachtsheim, J. Neter, and W. Li. 2005. *Applied Linear Statistical Models*. 5th ed. New York: McGraw–Hill/Irwin.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data

Title

pksumm — Summarize pharmacokinetic data

Syntax

`pksumm` *id time concentration* [*if*] [*in*] [, *options*]

options	Description
Main	
`trapezoid`	use trapezoidal rule to calculate AUC; default is cubic splines
`fit(#)`	use # points to estimate AUC; default is `fit(3)`
`notimechk`	do not check whether follow-up time for all subjects is the same
`nodots`	suppress the dots during calculation
`graph`	graph the distribution of *statistic*
`stat(`*statistic*`)`	graph the specified statistic; default is `stat(auc)`
Histogram, Density plots, Y axis, X axis, Titles, Legend, Overall	
histogram_options	any option other than `by()` documented in [R] **histogram**

statistic	Description
`auc`	area under the concentration-time curve ($AUC_{0,\infty}$); the default
`aucline`	area under the concentration-time curve from 0 to ∞ using a linear extension
`aucexp`	area under the concentration-time curve from 0 to ∞ using an exponential extension
`auclog`	area under the log-concentration-time curve extended with a linear fit
`half`	half-life of the drug
`ke`	elimination rate
`cmax`	maximum concentration
`tmax`	time at last concentration
`tomc`	time of maximum concentration

Menu

Statistics > Epidemiology and related > Other > Summarize pharmacokinetic data

Description

`pksumm` obtains summary measures based on the first four moments from the empirical distribution of each pharmacokinetic measurement and tests the null hypothesis that the distribution of that measurement is normally distributed.

`pksumm` is one of the pk commands. Please read [R] **pk** before reading this entry.

Options

Main

`trapezoid` specifies that the trapezoidal rule be used to calculate the AUC. The default is cubic splines, which give better results for most situations. When the curve is irregular, the trapezoidal rule may give better results.

`fit(#)` specifies the number of points, counting back from the last time measurement, to use in fitting the extension to estimate the $AUC_{0,\infty}$. The default is `fit(3)`, the last three points. This default should be viewed as a minimum; the appropriate number of points will depend on the data.

`notimechk` suppresses the check that the follow-up time for all subjects is the same. By default, `pksumm` expects the maximum follow-up time to be equal for all subjects.

`nodots` suppresses the progress dots during calculation. By default, a period is displayed for every call to calculate the pharmacokinetic measures.

`graph` requests a graph of the distribution of the statistic specified with `stat()`.

`stat(`*statistic*`)` specifies the statistic that `pksumm` should graph. The default is `stat(auc)`. If the `graph` option is not specified, this option is ignored.

Histogram, Density plots, Y axis, X axis, Titles, Legend, Overall

histogram_options are any of the options documented in [R] **histogram**, excluding `by()`. For `pksumm`, `fraction` is the default, not `density`.

Remarks

`pksumm` produces summary statistics for the distribution of nine common pharmacokinetic measurements. If there are more than eight subjects, `pksumm` also computes a test for normality on each measurement. The nine measurements summarized by `pksumm` are listed above and are described in *Methods and formulas* of [R] **pkexamine**.

▷ Example 1

We demonstrate the use of `pksumm` on a variation of the data described in [R] **pk**. We have drug concentration data on 15 subjects, each measured at 13 time points over a 32-hour period. A few of the records are

```
. use http://www.stata-press.com/data/r12/pksumm
. list, sep(0)
```

	id	time	conc
1.	1	0	0
2.	1	.5	3.073403
3.	1	1	5.188444
4.	1	1.5	5.898577
5.	1	2	5.096378
6.	1	3	6.094085
	(*output omitted*)		
183.	15	0	0
184.	15	.5	3.86493
185.	15	1	6.432444
186.	15	1.5	6.969195
187.	15	2	6.307024
188.	15	3	6.509584
189.	15	4	6.555091
190.	15	6	7.318319
191.	15	8	5.329813
192.	15	12	5.411624
193.	15	16	3.891397
194.	15	24	5.167516
195.	15	32	2.649686

We can use `pksumm` to view the summary statistics for all the pharmacokinetic parameters.

```
. pksumm id time conc
.............
 Summary statistics for the pharmacokinetic measures
                                                Number of observations =    15
```

Measure	Mean	Median	Variance	Skewness	Kurtosis	p-value
auc	150.74	150.96	123.07	-0.26	2.10	0.69
aucline	408.30	214.17	188856.87	2.57	8.93	0.00
aucexp	691.68	297.08	762679.94	2.56	8.87	0.00
auclog	688.98	297.67	797237.24	2.59	9.02	0.00
half	94.84	29.39	18722.13	2.26	7.37	0.00
ke	0.02	0.02	0.00	0.89	3.70	0.09
cmax	7.36	7.42	0.42	-0.60	2.56	0.44
tomc	3.47	3.00	7.62	2.17	7.18	0.00
tmax	32.00	32.00	0.00	.	.	.

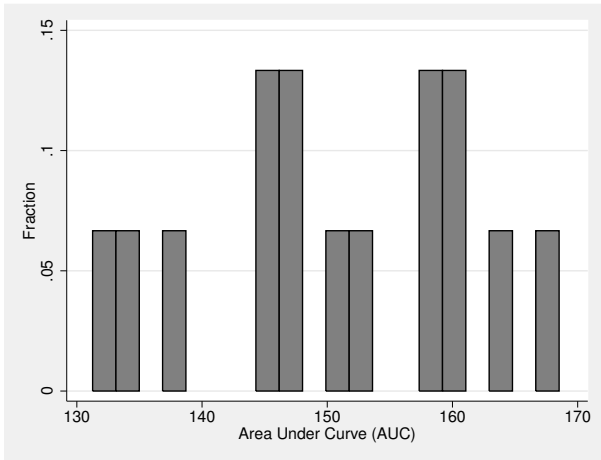
For the 15 subjects, the mean $\text{AUC}_{0,t_{\max}}$ is 150.74, and $\sigma^2 = 123.07$. The skewness of -0.26 indicates that the distribution is slightly skewed left. The p-value of 0.69 for the χ^2 test of normality indicates that we cannot reject the null hypothesis that the distribution is normal.

If we were to consider any of the three variants of the $\text{AUC}_{0,\infty}$, we would see that there is huge variability and that the distribution is heavily skewed. A skewness different from 0 and a kurtosis different from 3 are expected because the distribution of the $\text{AUC}_{0,\infty}$ is not normal.

We now graph the distribution of $\text{AUC}_{0,t_{\max}}$ by specifying the `graph` option.

```
. pksumm id time conc, graph bin(20)
.............
 Summary statistics for the pharmacokinetic measures
                                                  Number of observations =    15
```

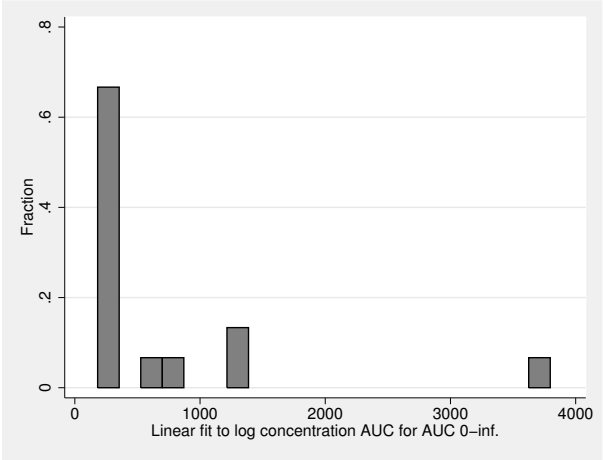
Measure	Mean	Median	Variance	Skewness	Kurtosis	p-value
auc	150.74	150.96	123.07	-0.26	2.10	0.69
aucline	408.30	214.17	188856.87	2.57	8.93	0.00
aucexp	691.68	297.08	762679.94	2.56	8.87	0.00
auclog	688.98	297.67	797237.24	2.59	9.02	0.00
half	94.84	29.39	18722.13	2.26	7.37	0.00
ke	0.02	0.02	0.00	0.89	3.70	0.09
cmax	7.36	7.42	0.42	-0.60	2.56	0.44
tomc	3.47	3.00	7.62	2.17	7.18	0.00
tmax	32.00	32.00	0.00	.	.	.



`graph`, by default, plots $\text{AUC}_{0,t_{\max}}$. To plot a graph of one of the other pharmacokinetic measurements, we need to specify the `stat()` option. For example, we can ask Stata to produce a plot of the $\text{AUC}_{0,\infty}$ using the log extension:

```
. pksumm id time conc, stat(auclog) graph bin(20)
.............
 Summary statistics for the pharmacokinetic measures
                                                  Number of observations =    15
```

Measure	Mean	Median	Variance	Skewness	Kurtosis	p-value
auc	150.74	150.96	123.07	-0.26	2.10	0.69
aucline	408.30	214.17	188856.87	2.57	8.93	0.00
aucexp	691.68	297.08	762679.94	2.56	8.87	0.00
auclog	688.98	297.67	797237.24	2.59	9.02	0.00
half	94.84	29.39	18722.13	2.26	7.37	0.00
ke	0.02	0.02	0.00	0.89	3.70	0.09
cmax	7.36	7.42	0.42	-0.60	2.56	0.44
tomc	3.47	3.00	7.62	2.17	7.18	0.00
tmax	32.00	32.00	0.00	.	.	.



Methods and formulas

`pksumm` is implemented as an ado-file.

The χ^2 test for normality is conducted with `sktest`; see [R] **sktest** for more information on the test of normality.

The statistics reported by `pksumm` are identical to those reported by `summarize` and `sktest`; see [R] **summarize** and [R] **sktest**.

Also see

[R] **pk** — Pharmacokinetic (biopharmaceutical) data

Title

poisson — Poisson regression

Syntax

```
poisson depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
exposure(*varname*$_e$)	include ln(*varname*$_e$) in model with coefficient constrained to 1
offset(*varname*$_o$)	include *varname*$_o$ in model with coefficient constrained to 1
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, opg, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
irr	report incidence-rate ratios
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
coeflegend	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar, *indepvars*, *varname*$_e$, and *varname*$_o$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, fracpoly, jackknife, mfp, mi estimate, nestreg, rolling, statsby, stepwise, and svy are allowed; see [U] **11.1.10 Prefix commands**.

vce(bootstrap) and vce(jackknife) are not allowed with the mi estimate prefix; see [MI] **mi estimate**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

vce() and weights are not allowed with the svy prefix; see [SVY] **svy**.

fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

coeflegend does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Count outcomes > Poisson regression

Description

poisson fits a Poisson regression of *depvar* on *indepvars*, where *depvar* is a nonnegative count variable.

If you have panel data, see [XT] **xtpoisson**.

Options

Model

noconstant, exposure(*varname*$_e$), offset(*varname*$_o$), constraints(*constraints*), collinear; see [R] **estimation options**.

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

level(#); see [R] **estimation options**.

irr reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. irr may be specified at estimation or when replaying previously estimated results.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with poisson but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

The basic idea of Poisson regression was outlined by Coleman (1964, 378–379). See Cameron and Trivedi (1998; 2010, chap. 17) and Johnson, Kemp, and Kotz (2005, chap. 4) for information about the Poisson distribution. See Cameron and Trivedi (1998), Long (1997, chap. 8), Long and Freese (2006, chap. 8), McNeil (1996, chap. 6), and Selvin (2004, chap. 9) for an introduction to Poisson regression. Also see Selvin (2004, chap. 5) for a discussion of the analysis of spatial distributions, which includes a discussion of the Poisson distribution. An early example of Poisson regression was Cochran (1940).

Poisson regression fits models of the number of occurrences (counts) of an event. The Poisson distribution has been applied to diverse events, such as the number of soldiers kicked to death by horses in the Prussian army (von Bortkiewicz 1898); the pattern of hits by buzz bombs launched against London during World War II (Clarke 1946); telephone connections to a wrong number (Thorndike 1926); and disease incidence, typically with respect to time, but occasionally with respect to space. The basic assumptions are as follows:

1. There is a quantity called the *incidence rate* that is the rate at which events occur. Examples are 5 per second, 20 per 1,000 person-years, 17 per square meter, and 38 per cubic centimeter.
2. The incidence rate can be multiplied by *exposure* to obtain the expected number of observed events. For example, a rate of 5 per second multiplied by 30 seconds means that 150 events are expected; a rate of 20 per 1,000 person-years multiplied by 2,000 person-years means that 40 events are expected; and so on.
3. Over very small exposures ϵ, the probability of finding more than one event is small compared with ϵ.
4. Nonoverlapping exposures are mutually independent.

With these assumptions, to find the probability of k events in an exposure of size E, you divide E into n subintervals E_1, E_2, ..., E_n, and approximate the answer as the binomial probability of observing k successes in n trials. If you let $n \to \infty$, you obtain the Poisson distribution.

In the Poisson regression model, the incidence rate for the jth observation is assumed to be given by

$$r_j = e^{\beta_0+\beta_1 x_{1,j}+\cdots+\beta_k x_{k,j}}$$

If E_j is the exposure, the expected number of events, C_j, will be

$$\begin{aligned} C_j &= E_j e^{\beta_0+\beta_1 x_{1,j}+\cdots+\beta_k x_{k,j}} \\ &= e^{\ln(E_j)+\beta_0+\beta_1 x_{1,j}+\cdots+\beta_k x_{k,j}} \end{aligned}$$

This model is fit by `poisson`. Without the `exposure()` or `offset()` options, E_j is assumed to be 1 (equivalent to assuming that exposure is unknown), and controlling for exposure, if necessary, is your responsibility.

Comparing rates is most easily done by calculating *incidence-rate ratios* (IRRs). For instance, what is the relative incidence rate of chromosome interchanges in cells as the intensity of radiation increases; the relative incidence rate of telephone connections to a wrong number as load increases; or the relative incidence rate of deaths due to cancer for females relative to males? That is, you want to hold all the x's in the model constant except one, say, the ith. The IRR for a one-unit change in x_i is

$$\frac{e^{\ln(E)+\beta_1 x_1+\cdots+\beta_i(x_i+1)+\cdots+\beta_k x_k}}{e^{\ln(E)+\beta_1 x_1+\cdots+\beta_i x_i+\cdots+\beta_k x_k}} = e^{\beta_i}$$

More generally, the IRR for a Δx_i change in x_i is $e^{\beta_i \Delta x_i}$. The `lincom` command can be used after `poisson` to display incidence-rate ratios for any group relative to another; see [R] **lincom**.

▷ Example 1

Chatterjee and Hadi (2006, 162) give the number of injury incidents and the proportion of flights for each airline out of the total number of flights from New York for nine major U.S. airlines in one year:

```
. use http://www.stata-press.com/data/r12/airline
. list
```

	airline	injuries	n	XYZowned
1.	1	11	0.0950	1
2.	2	7	0.1920	0
3.	3	7	0.0750	0
4.	4	19	0.2078	0
5.	5	9	0.1382	0
6.	6	4	0.0540	1
7.	7	3	0.1292	0
8.	8	1	0.0503	0
9.	9	3	0.0629	1

To their data, we have added a fictional variable, `XYZowned`. We will imagine that an accusation is made that the airlines owned by XYZ Company have a higher injury rate.

```
. poisson injuries XYZowned, exposure(n) irr
Iteration 0:   log likelihood = -23.027197
Iteration 1:   log likelihood = -23.027177
Iteration 2:   log likelihood = -23.027177
Poisson regression                                Number of obs   =          9
                                                  LR chi2(1)      =       1.77
                                                  Prob > chi2     =     0.1836
Log likelihood = -23.027177                       Pseudo R2       =     0.0370
```

injuries	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
XYZowned	1.463467	.406872	1.37	0.171	.8486578	2.523675
_cons	58.04416	8.558145	27.54	0.000	43.47662	77.49281
ln(n)	1	(exposure)				

We specified `irr` to see the IRRs rather than the underlying coefficients. We estimate that XYZ Airlines' injury rate is 1.46 times larger than that for other airlines, but the 95% confidence interval is 0.85 to 2.52; we cannot even reject the hypothesis that XYZ Airlines has a lower injury rate.

◁

❑ Technical note

In example 1, we assumed that each airline's exposure was proportional to its fraction of flights out of New York. What if "large" airlines, however, also used larger planes, and so had even more passengers than would be expected, given this measure of exposure? A better measure would be each airline's fraction of passengers on flights out of New York, a number that we do not have. Even so, we suppose that `n` represents this number to some extent, so a better estimate of the effect might be

```
. gen lnN=ln(n)
. poisson injuries XYZowned lnN
Iteration 0:   log likelihood = -22.333875
Iteration 1:   log likelihood = -22.332276
Iteration 2:   log likelihood = -22.332276
Poisson regression                              Number of obs   =          9
                                                LR chi2(2)      =      19.15
                                                Prob > chi2     =     0.0001
Log likelihood = -22.332276                     Pseudo R2       =     0.3001

------------------------------------------------------------------------------
    injuries |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
    XYZowned |   .6840667   .3895877     1.76   0.079    -.0795111    1.447645
         lnN |   1.424169   .3725155     3.82   0.000     .6940517    2.154285
       _cons |   4.863891   .7090501     6.86   0.000     3.474178    6.253603
------------------------------------------------------------------------------
```

Here rather than specifying the `exposure()` option, we explicitly included the variable that would normalize for exposure in the model. We did not specify the `irr` option, so we see coefficients rather than IRRs. We started with the model

$$\text{rate} = e^{\beta_0+\beta_1 \text{XYZowned}}$$

The observed counts are therefore

$$\text{count} = ne^{\beta_0+\beta_1 \text{XYZowned}} = e^{\ln(n)+\beta_0+\beta_1 \text{XYZowned}}$$

which amounts to constraining the coefficient on $\ln(\texttt{n})$ to 1. This is what was estimated when we specified the `exposure(n)` option. In the above model, we included the normalizing exposure ourselves and, rather than constraining the coefficient to be 1, estimated the coefficient.

The estimated coefficient is 1.42, a respectable distance away from 1, and is consistent with our speculation that larger airlines also use larger airplanes. With this small amount of data, however, we also have a wide confidence interval that includes 1.

Our estimated *coefficient* on `XYZowned` is now 0.684, and the implied IRR is $e^{0.684} \approx 1.98$ (which we could also see by typing `poisson, irr`). The 95% confidence interval for the coefficient still includes 0 (the interval for the IRR includes 1), so although the point estimate is now larger, we still cannot be certain of our results.

Our expert opinion would be that, although there is not enough evidence to support the charge, there is enough evidence to justify collecting more data.

❑

▷ Example 2

In a famous age-specific study of coronary disease deaths among male British doctors, Doll and Hill (1966) reported the following data (reprinted in Rothman, Greenland, and Lash [2008, 264]):

	Smokers		Nonsmokers	
Age	Deaths	Person-years	Deaths	Person-years
35–44	32	52,407	2	18,790
45–54	104	43,248	12	10,673
55–64	206	28,612	28	5,710
65–74	186	12,663	28	2,585
75–84	102	5,317	31	1,462

The first step is to enter these data into Stata, which we have done:

```
. use http://www.stata-press.com/data/r12/dollhill3, clear
. list
```

	agecat	smokes	deaths	pyears
1.	1	1	32	52,407
2.	2	1	104	43,248
3.	3	1	206	28,612
4.	4	1	186	12,663
5.	5	1	102	5,317
6.	1	0	2	18,790
7.	2	0	12	10,673
8.	3	0	28	5,710
9.	4	0	28	2,585
10.	5	0	31	1,462

`agecat` 1 corresponds to 35–44, `agecat` 2 to 45–54, and so on. The most "natural" analysis of these data would begin by introducing indicator variables for each age category and one indicator for smoking:

```
. poisson deaths smokes i.agecat, exposure(pyears) irr
Iteration 0:   log likelihood = -33.823284
Iteration 1:   log likelihood = -33.600471
Iteration 2:   log likelihood = -33.600153
Iteration 3:   log likelihood = -33.600153
Poisson regression                              Number of obs   =         10
                                                LR chi2(5)      =     922.93
                                                Prob > chi2     =     0.0000
Log likelihood = -33.600153                     Pseudo R2       =     0.9321
```

deaths	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
smokes	1.425519	.1530638	3.30	0.001	1.154984	1.759421
agecat						
2	4.410584	.8605197	7.61	0.000	3.009011	6.464997
3	13.8392	2.542638	14.30	0.000	9.654328	19.83809
4	28.51678	5.269878	18.13	0.000	19.85177	40.96395
5	40.45121	7.775511	19.25	0.000	27.75326	58.95885
_cons	.0003636	.0000697	-41.30	0.000	.0002497	.0005296
ln(pyears)	1	(exposure)				

In the above, we specified `irr` to obtain IRRs. We estimate that smokers have 1.43 times the mortality rate of nonsmokers. See, however, example 1 in [R] **poisson postestimation**.

◁

Saved results

poisson saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(chi2)	χ^2
e(p)	significance
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	poisson
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Siméon-Denis Poisson (1781–1840) was a French mathematician and physicist who contributed to several fields: his name is perpetuated in Poisson brackets, Poisson's constant, Poisson's differential equation, Poisson's integral, and Poisson's ratio. Among many other results, he produced a version of the law of large numbers. His rather misleadingly titled *Recherches sur la probabilité des jugements* embraces a complete treatise on probability, as the subtitle indicates, including what is now known as the Poisson distribution. That, however, was discovered earlier by the Huguenot–British mathematician Abraham de Moivre (1667–1754).

Methods and formulas

`poisson` is implemented as an ado-file.

The log likelihood (with weights w_j and offsets) is given by

$$\Pr(Y=y) = \frac{e^{-\lambda}\lambda^{y}}{y!}$$

$$\xi_j = \mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$$

$$f(y_j) = \frac{e^{-\exp(\xi_j)}e^{\xi_j y_j}}{y_j!}$$

$$\ln L = \sum_{j=1}^{n} w_j \left\{-e^{\xi_j} + \xi_j y_j - \ln(y_j!)\right\}$$

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`poisson` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **poisson postestimation** — Postestimation tools for poisson

[R] **glm** — Generalized linear models

[R] **nbreg** — Negative binomial regression

[R] **tpoisson** — Truncated Poisson regression

[R] **zip** — Zero-inflated Poisson regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtpoisson** — Fixed-effects, random-effects, and population-averaged Poisson models

[U] **20 Estimation and postestimation commands**

Title

poisson postestimation — Postestimation tools for poisson

Description

The following postestimation command is of special interest after `poisson`:

Command	Description
`estat gof`	goodness-of-fit test

`estat gof` is not appropriate after the `svy` prefix. For information about `estat gof`, see below.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Special-interest postestimation command

`estat gof` performs a goodness-of-fit test of the model. Both the deviance statistic and the Pearson statistic are reported. If the tests are significant, the Poisson regression model is inappropriate. Then you could try a negative binomial model; see [R] **nbreg**.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]
```

statistic	Description
Main	
`n`	number of events; the default
`ir`	incidence rate
`pr(`*n*`)`	probability $\Pr(y_j = n)$
`pr(`*a*`,`*b*`)`	probability $\Pr(a \leq y_j \leq b)$
`xb`	linear prediction
`stdp`	standard error of the linear prediction
`score`	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`n`, the default, calculates the predicted number of events, which is $\exp(\mathbf{x}_j\boldsymbol{\beta})$ if neither `offset()` nor `exposure()` was specified when the model was fit; $\exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$ if `offset()` was specified; or $\exp(\mathbf{x}_j\boldsymbol{\beta}) \times \text{exposure}_j$ if `exposure()` was specified.

`ir` calculates the incidence rate $\exp(\mathbf{x}_j\boldsymbol{\beta})$, which is the predicted number of events when exposure is 1. Specifying `ir` is equivalent to specifying `n` when neither `offset()` nor `exposure()` was specified when the model was fit.

`pr(`*n*`)` calculates the probability $\Pr(y_j = n)$, where *n* is a nonnegative integer that may be specified as a number or a variable.

`pr(`*a*`,`*b*`)` calculates the probability $\Pr(a \leq y_j \leq b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b \geq .$) means $+\infty$;
`pr(20,.)` calculates $\Pr(y_j \geq 20)$;
`pr(20,`*b*`)` calculates $\Pr(y_j \geq 20)$ in observations for which $b \geq .$ and calculates $\Pr(20 \leq y_j \leq b)$ elsewhere.

`pr(.,`*b*`)` produces a syntax error. A missing value in an observation of the variable *a* causes a missing value in that observation for `pr(`*a*`,`*b*`)`.

`xb` calculates the linear prediction, which is $\mathbf{x}_j\boldsymbol{\beta}$ if neither `offset()` nor `exposure()` was specified; $\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$ if `offset()` was specified; or $\mathbf{x}_j\boldsymbol{\beta} + \ln(\text{exposure}_j)$ if `exposure()` was specified; see `nooffset` below.

`stdp` calculates the standard error of the linear prediction.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

`nooffset` is relevant only if you specified `offset()` or `exposure()` when you fit the model. It modifies the calculations made by `predict` so that they ignore the offset or exposure variable; the linear prediction is treated as $\mathbf{x}_j\boldsymbol{\beta}$ rather than as $\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j$ or $\mathbf{x}_j\boldsymbol{\beta}+\ln(\text{exposure}_j)$. Specifying `predict ..., nooffset` is equivalent to specifying `predict ..., ir`.

Syntax for estat gof

```
estat gof
```

Menu

Statistics > Postestimation > Reports and statistics

Remarks

▷ Example 1

Continuing with example 2 of [R] **poisson**, we use `estat gof` to determine whether the model fits the data well.

```
. use http://www.stata-press.com/data/r12/dollhill3
. poisson deaths smokes i.agecat, exp(pyears) irr
  (output omitted)
. estat gof
        Deviance goodness-of-fit =  12.13244
        Prob > chi2(4)           =    0.0164
        Pearson goodness-of-fit  =  11.15533
        Prob > chi2(4)           =    0.0249
```

The deviance goodness-of-fit test tells us that, given the model, we can reject the hypothesis that these data are Poisson distributed at the 1.64% significance level. The Pearson goodness-of-fit test tells us that we can reject the hypothesis at the 2.49% significance level.

So let us now back up and be more careful. We can most easily obtain the incidence-rate ratios within age categories by using `ir`; see [ST] **epitab**:

```
. ir deaths smokes pyears, by(agecat) nohet
```

agecat	IRR	[95% Conf.	Interval]	M-H Weight	
1	5.736638	1.463557	49.40468	1.472169	(exact)
2	2.138812	1.173714	4.272545	9.624747	(exact)
3	1.46824	.9863624	2.264107	23.34176	(exact)
4	1.35606	.9081925	2.096412	23.25315	(exact)
5	.9047304	.6000757	1.399687	24.31435	(exact)
Crude	1.719823	1.391992	2.14353		(exact)
M-H combined	1.424682	1.154703	1.757784		

We find that the mortality incidence ratios are greatly different within age category, being highest for the youngest categories and actually dropping below 1 for the oldest. (In the last case, we might argue that those who smoke and who have not died by age 75 are self-selected to be particularly robust.)

Seeing this, we will now parameterize the smoking effects separately for each age category, although we will begin by constraining the smoking effects on age categories 3 and 4 to be equivalent:

```
. constraint 1 smokes#3.agecat = smokes#4.agecat
. poisson deaths c.smokes#agecat i.agecat, exposure(pyears) irr constraints(1)
Iteration 0:   log likelihood =  -31.95424
Iteration 1:   log likelihood = -27.796801
Iteration 2:   log likelihood = -27.574177
Iteration 3:   log likelihood = -27.572645
Iteration 4:   log likelihood = -27.572645
Poisson regression                                Number of obs   =         10
                                                  Wald chi2(8)    =     632.14
Log likelihood = -27.572645                       Prob > chi2     =     0.0000
 ( 1)  [deaths]3.agecat#c.smokes - [deaths]4.agecat#c.smokes = 0
```

deaths	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
agecat#c.smokes						
1	5.736637	4.181256	2.40	0.017	1.374811	23.93711
2	2.138812	.6520701	2.49	0.013	1.176691	3.887609
3	1.412229	.2017485	2.42	0.016	1.067343	1.868557
4	1.412229	.2017485	2.42	0.016	1.067343	1.868557
5	.9047304	.1855513	-0.49	0.625	.6052658	1.35236
agecat						
2	10.5631	8.067701	3.09	0.002	2.364153	47.19623
3	47.671	34.37409	5.36	0.000	11.60056	195.8978
4	98.22765	70.85012	6.36	0.000	23.89324	403.8244
5	199.2099	145.3356	7.26	0.000	47.67693	832.3648
_cons	.0001064	.0000753	-12.94	0.000	.0000266	.0004256
ln(pyears)	1	(exposure)				

```
. estat gof
        Deviance goodness-of-fit =  .0774185
        Prob > chi2(1)           =    0.7808
        Pearson goodness-of-fit  =  .0773882
        Prob > chi2(1)           =    0.7809
```

The goodness-of-fit is now small; we are no longer running roughshod over the data. Let us now consider simplifying the model. The point estimate of the incidence-rate ratio for smoking in age category 1 is much larger than that for smoking in age category 2, but the confidence interval for `smokes#1.agecat` is similarly wide. Is the difference real?

```
. test smokes#1.agecat = smokes#2.agecat
 ( 1)  [deaths]1b.agecat#c.smokes - [deaths]2.agecat#c.smokes = 0
           chi2(  1) =    1.56
         Prob > chi2 =    0.2117
```

The point estimates may be far apart, but there is insufficient data, and we may be observing random differences. With that success, might we also combine the smokers in age categories 3 and 4 with those in 1 and 2?

```
. test smokes#2.agecat = smokes#3.agecat, accum
 ( 1)  [deaths]1b.agecat#c.smokes - [deaths]2.agecat#c.smokes = 0
 ( 2)  [deaths]2.agecat#c.smokes - [deaths]3.agecat#c.smokes = 0
           chi2(  2) =    4.73
         Prob > chi2 =    0.0938
```

Combining age categories 1–4 may be overdoing it—the 9.38% significance level is enough to stop us, although others may disagree.

Thus we now fit our final model:

```
. constraint 2 smokes#1.agecat = smokes#2.agecat
. poisson deaths c.smokes#agecat i.agecat, exposure(pyears) irr constraints(1/2)
Iteration 0:   log likelihood = -31.550722
Iteration 1:   log likelihood = -28.525057
Iteration 2:   log likelihood = -28.514535
Iteration 3:   log likelihood = -28.514535
Poisson regression                              Number of obs   =         10
                                                Wald chi2(7)    =     642.25
Log likelihood = -28.514535                     Prob > chi2     =     0.0000
 ( 1)  [deaths]3.agecat#c.smokes - [deaths]4.agecat#c.smokes = 0
 ( 2)  [deaths]1b.agecat#c.smokes - [deaths]2.agecat#c.smokes = 0
```

deaths	IRR	Std. Err.	z	P>|z|	[95% Conf.	Interval]
agecat#c.smokes						
1	2.636259	.7408403	3.45	0.001	1.519791	4.572907
2	2.636259	.7408403	3.45	0.001	1.519791	4.572907
3	1.412229	.2017485	2.42	0.016	1.067343	1.868557
4	1.412229	.2017485	2.42	0.016	1.067343	1.868557
5	.9047304	.1855513	-0.49	0.625	.6052658	1.35236
agecat						
2	4.294559	.8385329	7.46	0.000	2.928987	6.296797
3	23.42263	7.787716	9.49	0.000	12.20738	44.94164
4	48.26309	16.06939	11.64	0.000	25.13068	92.68856
5	97.87965	34.30881	13.08	0.000	49.24123	194.561
_cons	.0002166	.0000652	-28.03	0.000	.0001201	.0003908
ln(pyears)	1	(exposure)				

The above strikes us as a fair representation of the data. The probabilities of observing the deaths seen in these data are estimated using the following `predict` command:

```
. predict p, pr(0, deaths)
. list deaths p
```

	deaths	p
1.	32	.6891766
2.	104	.4456625
3.	206	.5455328
4.	186	.4910622
5.	102	.5263011
6.	2	.227953
7.	12	.7981917
8.	28	.4772961
9.	28	.6227565
10.	31	.5475718

The probability $\Pr(y \leq \texttt{deaths})$ ranges from 0.23 to 0.80.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

In the following, we use the same notation as in [R] **poisson**.

The equation-level scores are given by

$$\text{score}(\mathbf{x}\boldsymbol{\beta})_j = y_j - e^{\xi_j}$$

The deviance (D) and Pearson (P) goodness-of-fit statistics are given by

$$\ln L_{\max} = \sum_{j=1}^{n} w_j \left[-y_j\{\ln(y_j) - 1\} - \ln(y_j!)\right]$$

$$\chi^2_D = -2\{\ln L - \ln L_{\max}\}$$

$$\chi^2_P = \sum_{j=1}^{n} \frac{w_j(y_j - e^{\xi_j})^2}{e^{\xi_j}}$$

Also see

[R] **poisson** — Poisson regression

[U] **20 Estimation and postestimation commands**

Title

predict — Obtain predictions, residuals, etc., after estimation

Syntax

After single-equation (SE) *models*

```
predict [type] newvar [if] [in] [, single_options]
```

After multiple-equation (ME) *models*

```
predict [type] newvar [if] [in] [, multiple_options]
predict [type] { stub* | newvar1 ... newvarq } [if] [in], scores
```

single_options	Description
Main	
`xb`	calculate linear prediction
`stdp`	calculate standard error of the prediction
`score`	calculate first derivative of the log likelihood with respect to $\mathbf{x}_j\beta$
Options	
`nooffset`	ignore any `offset()` or `exposure()` variable
other_options	command-specific options

multiple_options	Description
Main	
`equation(`*eqno*`[ , `*eqno*`])`	specify equations
`xb`	calculate linear prediction
`stdp`	calculate standard error of the prediction
`stddp`	calculate the difference in linear predictions
Options	
`nooffset`	ignore any `offset()` or `exposure()` variable
other_options	command-specific options

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Description

`predict` calculates predictions, residuals, influence statistics, and the like after estimation. Exactly what `predict` can do is determined by the previous estimation command; command-specific options are documented with each estimation command. Regardless of command-specific options, the actions of `predict` share certain similarities across estimation commands:

1. `predict` *newvar* creates *newvar* containing "predicted values"—numbers related to the $E(y_j|\mathbf{x}_j)$. For instance, after linear regression, `predict` *newvar* creates $\mathbf{x}_j\mathbf{b}$ and, after probit, creates the probability $\Phi(\mathbf{x}_j\mathbf{b})$.
2. `predict` *newvar*`, xb` creates *newvar* containing $\mathbf{x}_j\mathbf{b}$. This may be the same result as option 1 (for example, linear regression) or different (for example, probit), but regardless, option `xb` is allowed.
3. `predict` *newvar*`, stdp` creates *newvar* containing the standard error of the linear prediction $\mathbf{x}_j\mathbf{b}$.
4. `predict` *newvar*`,` *other_options* may create *newvar* containing other useful quantities; see `help` or the reference manual entry for the particular estimation command to find out about other available options.
5. `nooffset` added to any of the above commands requests that the calculation ignore any offset or exposure variable specified by including the `offset(`*varname*$_o$`)` or `exposure(`*varname*$_e$`)` option when you fit the model.

`predict` can be used to make in-sample or out-of-sample predictions:

6. `predict` calculates the requested statistic for all possible observations, whether they were used in fitting the model or not. `predict` does this for standard options 1–3 and generally does this for estimator-specific options 4.
7. `predict` *newvar* `if e(sample), ...` restricts the prediction to the estimation subsample.
8. Some statistics make sense only with respect to the estimation subsample. In such cases, the calculation is automatically restricted to the estimation subsample, and the documentation for the specific option states this. Even so, you can still specify `if e(sample)` if you are uncertain.
9. `predict` can make out-of-sample predictions even using other datasets. In particular, you can

```
. use ds1
. (fit a model)
. use two                       /* another dataset         */
. predict yhat, ...             /* fill in the predictions */
```

Options

Main

`xb` calculates the linear prediction from the fitted model. That is, all models can be thought of as estimating a set of parameters b_1, b_2, ..., b_k, and the linear prediction is $\widehat{y}_j = b_1x_{1j} + b_2x_{2j} + \cdots + b_kx_{kj}$, often written in matrix notation as $\widehat{\mathbf{y}}_j = \mathbf{x}_j\mathbf{b}$. For linear regression, the values $\widehat{y}_j$ are called the predicted values or, for out-of-sample predictions, the forecast. For logit and probit, for example, $\widehat{y}_j$ is called the logit or probit index.

$x_{1j}, x_{2j}, \ldots, x_{kj}$ are obtained from the data currently in memory and do not necessarily correspond to the data on the independent variables used to fit the model (obtaining b_1, b_2, ..., b_k).

`stdp` calculates the standard error of the linear prediction. Here the prediction means the same thing as the "index", namely, $\mathbf{x}_j\mathbf{b}$. The statistic produced by `stdp` can be thought of as the standard error of the predicted expected value, or mean index, for the observation's covariate pattern. The standard error of the prediction is also commonly referred to as the standard error of the fitted value. The calculation can be made in or out of sample.

`stddp` is allowed only after you have previously fit a multiple-equation model. The standard error of the difference in linear predictions ($\mathbf{x}_{1j}\mathbf{b} - \mathbf{x}_{2j}\mathbf{b}$) between equations 1 and 2 is calculated. This option requires that `equation(`*eqno*$_1$`,`*eqno*$_2$`)` be specified.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$. Here $\ln L$ refers to the log-likelihood function.

`scores` is the ME model equivalent of the `score` option, resulting in multiple equation-level score variables. An equation-level score variable is created for each equation in the model; ancillary parameters—such as $\ln\sigma$ and $\operatorname{atanh}\rho$—make up separate equations.

`equation(`*eqno*`[ ,`*eqno*`])`—synonym `outcome()`—is relevant only when you have previously fit a multiple-equation model. It specifies the equation to which you are referring.

`equation()` is typically filled in with one *eqno*—it would be filled in that way with options `xb` and `stdp`, for instance. `equation(#1)` would mean the calculation is to be made for the first equation, `equation(#2)` would mean the second, and so on. You could also refer to the equations by their names. `equation(income)` would refer to the equation named income and `equation(hours)` to the equation named hours.

If you do not specify `equation()`, results are the same as if you specified `equation(#1)`.

Other statistics, such as `stddp`, refer to between-equation concepts. In those cases, you might specify `equation(#1,#2)` or `equation(income,hours)`. When two equations must be specified, `equation()` is required.

Options

`nooffset` may be combined with most statistics and specifies that the calculation should be made, ignoring any offset or exposure variable specified when the model was fit.

This option is available, even if it is not documented for `predict` after a specific command. If neither the `offset(`*varname*$_o$`)` option nor the `exposure(`*varname*$_e$`)` option was specified when the model was fit, specifying `nooffset` does nothing.

other_options refers to command-specific options that are documented with each command.

Remarks

Remarks are presented under the following headings:

Estimation-sample predictions
Out-of-sample predictions
Residuals
Single-equation (SE) models
SE model scores
Multiple-equation (ME) models
ME model scores

Most of the examples are presented using linear regression, but the general syntax is applicable to all estimators.

You can think of any estimation command as estimating a set of coefficients b_1, b_2, …, b_k corresponding to the variables x_1, x_2, …, x_k, along with a (possibly empty) set of ancillary statistics γ_1, γ_2, …, γ_m. All estimation commands save the b_is and γ_is. `predict` accesses that saved information and combines it with the data currently in memory to make various calculations. For instance, `predict` can calculate the linear prediction, $\widehat{y}_j = b_1x_{1j} + b_2x_{2j} + \cdots + b_kx_{kj}$. The data on which `predict` makes the calculation can be the same data used to fit the model or a different dataset—it does not matter. `predict` uses the saved parameter estimates from the model, obtains

the corresponding values of x for each observation in the data, and then combines them to produce the desired result.

Estimation-sample predictions

▷ Example 1

We have a 74-observation dataset on automobiles, including the mileage rating (`mpg`), the car's weight (`weight`), and whether the car is foreign (`foreign`). We fit the model

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight if foreign
```

Source	SS	df	MS	Number of obs =	22
				F(1, 20) =	17.47
Model	427.990298	1	427.990298	Prob > F =	0.0005
Residual	489.873338	20	24.4936669	R-squared =	0.4663
				Adj R-squared =	0.4396
Total	917.863636	21	43.7077922	Root MSE =	4.9491

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.010426	.0024942	-4.18	0.000	-.0156287	-.0052232
_cons	48.9183	5.871851	8.33	0.000	36.66983	61.16676

If we were to type `predict pmpg` now, we would obtain the linear predictions for all 74 observations. To obtain the predictions just for the sample on which we fit the model, we could type

```
. predict pmpg if e(sample)
(option xb assumed; fitted values)
(52 missing values generated)
```

Here `e(sample)` is true only for foreign cars because we typed `if foreign` when we fit the model and because there are no missing values among the relevant variables. If there had been missing values, `e(sample)` would also account for those.

By the way, the `if e(sample)` restriction can be used with any Stata command, so we could obtain summary statistics on the estimation sample by typing

```
. summarize if e(sample)
```
(*output omitted*)

◁

Out-of-sample predictions

By out-of-sample predictions, we mean predictions extending beyond the estimation sample. In the example above, typing `predict pmpg` would generate linear predictions using all 74 observations.

`predict` will work on other datasets, too. You can use a new dataset and type `predict` to obtain results for that sample.

▷ Example 2

Using the same auto dataset, assume that we wish to fit the model

$$\texttt{mpg} = \beta_1\texttt{weight} + \beta_2\ln(\texttt{weight}) + \beta_3\texttt{foreign} + \beta_4$$

We first create the ln(weight) variable, and then type the `regress` command:

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. generate lnweight = ln(weight)
. regress mpg weight lnweight foreign
```

Source	SS	df	MS	Number of obs =	74
				F(3, 70) =	52.36
Model	1690.27997	3	563.426657	Prob > F =	0.0000
Residual	753.179489	70	10.759707	R-squared =	0.6918
				Adj R-squared =	0.6785
Total	2443.45946	73	33.4720474	Root MSE =	3.2802

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	.003304	.0038995	0.85	0.400	-.0044734	.0110813
lnweight	-29.59133	11.52018	-2.57	0.012	-52.5676	-6.615061
foreign	-2.125299	1.052324	-2.02	0.047	-4.224093	-.0265044
_cons	248.0548	80.37079	3.09	0.003	87.76035	408.3493

If we typed `predict pmpg` now, we would obtain predictions for all 74 cars in the current data. Instead, we are going to use a new dataset.

The dataset `newautos.dta` contains the make, weight, and place of manufacture of two cars, the Pontiac Sunbird and the Volvo 260. Let's use the dataset and create the predictions:

```
. use http://www.stata-press.com/data/r12/newautos, clear
(New Automobile Models)
. list
```

	make	weight	foreign
1.	Pont. Sunbird	2690	Domestic
2.	Volvo 260	3170	Foreign

```
. predict mpg
(option xb assumed; fitted values)
variable lnweight not found
r(111);
```

Things did not work. We typed `predict mpg`, and Stata responded with the message "variable lnweight not found". `predict` can calculate predicted values on a different dataset only if that dataset contains the variables that went into the model. Here our dataset does not contain a variable called `lnweight`. `lnweight` is just the log of weight, so we can create it and try again:

```
. generate lnweight = ln(weight)
. predict mpg
(option xb assumed; fitted values)
```

```
. list
```

	make	weight	foreign	lnweight	mpg
1.	Pont. Sunbird	2690	Domestic	7.897296	23.25097
2.	Volvo 260	3170	Foreign	8.061487	17.85295

We obtained our predicted values. The Pontiac Sunbird has a predicted mileage rating of 23.3 mpg, whereas the Volvo 260 has a predicted rating of 17.9 mpg.

◁

Residuals

▷ Example 3

With many estimators, `predict` can calculate more than predicted values. With most regression-type estimators, we can, for instance, obtain residuals. Using our regression example, we return to our original data and obtain residuals by typing

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. generate lnweight = ln(weight)
. regress mpg weight lnweight foreign
  (output omitted)
. predict double resid, residuals
. summarize resid
```

Variable	Obs	Mean	Std. Dev.	Min	Max
resid	74	-1.51e-15	3.212091	-5.453078	13.83719

We could do this without refitting the model. Stata always remembers the last set of estimates, even as we use new datasets.

It was not necessary to type the `double` in `predict double resid, residuals`, but we wanted to remind you that you can specify the type of a variable in front of the variable's name; see [U] **11.4.2 Lists of new variables**. We made the new variable `resid` a `double` rather than the default `float`.

If you want your residuals to have a mean as close to zero as possible, remember to request the extra precision of `double`. If we had not specified `double`, the mean of `resid` would have been roughly 10^{-9} rather than 10^{-14}. Although 10^{-14} sounds more precise than 10^{-9}, the difference really does not matter.

◁

For linear regression, `predict` can also calculate standardized residuals and Studentized residuals with the options `rstandard` and `rstudent`; for examples, see [R] **regress postestimation**.

Single-equation (SE) models

If you have not read the discussion above on using `predict` after linear regression, please do so. And `predict`'s default calculation almost always produces a statistic in the same metric as the dependent variable of the fitted model—for example, predicted counts for Poisson regression. In any case, `xb` can always be specified to obtain the linear prediction.

`predict` can calculate the standard error of the prediction, which is obtained by using the covariance matrix of the estimators.

▷ Example 4

After most binary outcome models (for example, `logistic`, `logit`, `probit`, `cloglog`, `scobit`), `predict` calculates the probability of a positive outcome if we do not tell it otherwise. We can specify the `xb` option if we want the linear prediction (also known as the logit or probit index). The odd abbreviation `xb` is meant to suggest $\mathbf{x}\boldsymbol{\beta}$. In logit and probit models, for example, the predicted probability is $p = F(\mathbf{x}\boldsymbol{\beta})$, where $F()$ is the logistic or normal cumulative distribution function, respectively.

```
. logistic foreign mpg weight
  (output omitted)
. predict phat
(option pr assumed; Pr(foreign))
. predict idxhat, xb
. summarize foreign phat idxhat
```

Variable	Obs	Mean	Std. Dev.	Min	Max
foreign	74	.2972973	.4601885	0	1
phat	74	.2972973	.3052979	.000729	.8980594
idxhat	74	-1.678202	2.321509	-7.223107	2.175845

Because this is a logit model, we could obtain the predicted probabilities ourselves from the predicted index

```
. generate phat2 = exp(idxhat)/(1+exp(idxhat))
```

but using `predict` without options is easier.

◁

▷ Example 5

For all models, `predict` attempts to produce a predicted value in the same metric as the dependent variable of the model. We have seen that for dichotomous outcome models, the default statistic produced by `predict` is the probability of a success. Similarly, for Poisson regression, the default statistic produced by `predict` is the predicted count for the dependent variable. You can always specify the `xb` option to obtain the linear combination of the coefficients with an observation's x values (the inner product of the coefficients and x values). For `poisson` (without an explicit exposure), this is the natural log of the count.

```
. use http://www.stata-press.com/data/r12/airline, clear
. poisson injuries XYZowned
  (output omitted)
. predict injhat
(option n assumed; predicted number of events)
```

```
. predict idx, xb
. generate exp_idx = exp(idx)
. summarize injuries injhat exp_idx idx
```

Variable	Obs	Mean	Std. Dev.	Min	Max
injuries	9	7.111111	5.487359	1	19
injhat	9	7.111111	.8333333	6	7.666667
exp_idx	9	7.111111	.8333333	6	7.666667
idx	9	1.955174	.1225612	1.791759	2.036882

We note that our "hand-computed" prediction of the count (`exp_idx`) matches what was produced by the default operation of `predict`.

If our model has an exposure-time variable, we can use `predict` to obtain the linear prediction with or without the exposure. Let's verify what we are getting by obtaining the linear prediction with and without exposure, transforming these predictions to count predictions and comparing them with the default count prediction from `predict`. We must remember to multiply by the exposure time when using `predict ..., nooffset`.

```
. use http://www.stata-press.com/data/r12/airline, clear
. poisson injuries XYZowned, exposure(n)
  (output omitted)
. predict double injhat
(option n assumed; predicted number of events)
. predict double idx, xb
. generate double exp_idx = exp(idx)
. predict double idxn, xb nooffset
. generate double exp_idxn = exp(idxn)*n
. summarize injuries injhat exp_idx exp_idxn idx idxn
```

Variable	Obs	Mean	Std. Dev.	Min	Max
injuries	9	7.111111	5.487359	1	19
injhat	9	7.111111	3.10936	2.919621	12.06158
exp_idx	9	7.111111	3.10936	2.919621	12.06158
exp_idxn	9	7.111111	3.10936	2.919621	12.06158
idx	9	1.869722	.4671044	1.071454	2.490025
idxn	9	4.18814	.1904042	4.061204	4.442013

Looking at the identical means and standard deviations for `injhat`, `exp_idx`, and `exp_idxn`, we see that we can reproduce the default computations of `predict` for `poisson` estimations. We have also demonstrated the relationship between the count predictions and the linear predictions with and without exposure.

◁

SE model scores

▷ Example 6

With most maximum likelihood estimators, `predict` can calculate equation-level scores. The first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$ is the equation-level score.

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. logistic foreign mpg weight
  (output omitted)
```

```
. predict double sc, score
. summarize sc
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
          sc |         74   -1.37e-12    .3533133  -.8760856   .8821309
```

See [P] **_robust** and [SVY] **variance estimation** for details regarding the role equation-level scores play in linearization-based variance estimators. ◁

❑ Technical note

`predict` after some estimation commands, such as `regress` and `cnsreg`, allows the `score` option as a synonym for the `residuals` option. ❑

Multiple-equation (ME) models

If you have not read the above discussion on using `predict` after SE models, please do so. With the exception of the ability to select specific equations to predict from, the use of `predict` after ME models follows almost the same form that it does for SE models.

▷ Example 7

The details of prediction statistics that are specific to particular ME models are documented with the estimation command. If you are using ME commands that do not have separate discussions on obtaining predictions, read *Obtaining predicted values* in [R] **mlogit postestimation**, even if your interest is not in multinomial logistic regression. As a general introduction to the ME models, we will demonstrate `predict` after `sureg`:

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. sureg (price foreign displ) (weight foreign length)
Seemingly unrelated regression
------------------------------------------------------------------------------
Equation              Obs  Parms        RMSE    "R-sq"       chi2         P
------------------------------------------------------------------------------
price                  74      2    2202.447    0.4348      45.21    0.0000
weight                 74      2    245.5238    0.8988     658.85    0.0000
------------------------------------------------------------------------------

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
price        |
     foreign |   3137.894   697.3805     4.50   0.000     1771.054    4504.735
displacement |   23.06938   3.443212     6.70   0.000     16.32081    29.81795
       _cons |   680.8438   859.8142     0.79   0.428    -1004.361    2366.049
-------------+----------------------------------------------------------------
weight       |
     foreign |  -154.883    75.3204    -2.06   0.040    -302.5082   -7.257674
      length |   30.67594   1.531981    20.02   0.000     27.67331    33.67856
       _cons |  -2699.498   302.3912    -8.93   0.000    -3292.173   -2106.822
------------------------------------------------------------------------------
```

sureg estimated two equations, one called price and the other weight; see [R] **sureg**.

```
. predict pred_p, equation(price)
(option xb assumed; fitted values)
. predict pred_w, equation(weight)
(option xb assumed; fitted values)
. summarize price pred_p weight pred_w
```

Variable	Obs	Mean	Std. Dev.	Min	Max
price	74	6165.257	2949.496	3291	15906
pred_p	74	6165.257	1678.805	2664.81	10485.33
weight	74	3019.459	777.1936	1760	4840
pred_w	74	3019.459	726.0468	1501.602	4447.996

You may specify the equation by name, as we did above, or by number: equation(#1) means the same thing as equation(price) in this case.

◁

ME model scores

▷ Example 8

For ME models, predict allows you to specify a stub when generating equation-level score variables. predict generates new variables using this stub by appending an equation index. Depending upon the command, the index will start with 0 or 1. Here is an example where predict starts indexing the score variables with 0.

```
. ologit rep78 mpg weight
  (output omitted)
. predict double sc*, scores
. summarize sc*
```

Variable	Obs	Mean	Std. Dev.	Min	Max
sc0	69	-1.33e-11	.5337363	-.9854088	.921433
sc1	69	-7.69e-13	.186919	-.2738537	.9854088
sc2	69	-2.87e-11	.4061637	-.5188487	1.130178
sc3	69	-1.04e-10	.5315368	-1.067351	.8194842
sc4	69	1.47e-10	.360525	-.921433	.6140182

Although it involves much more typing, we could also specify the new variable names individually.

```
. predict double (sc_xb sc_1 sc_2 sc_3 sc_4), scores
. summarize sc_*
```

Variable	Obs	Mean	Std. Dev.	Min	Max
sc_xb	69	-1.33e-11	.5337363	-.9854088	.921433
sc_1	69	-7.69e-13	.186919	-.2738537	.9854088
sc_2	69	-2.87e-11	.4061637	-.5188487	1.130178
sc_3	69	-1.04e-10	.5315368	-1.067351	.8194842
sc_4	69	1.47e-10	.360525	-.921433	.6140182

◁

Methods and formulas

`predict` is implemented as an ado-file.

Denote the previously estimated coefficient vector as $\mathbf{b}$ and its estimated variance matrix as $\mathbf{V}$. `predict` works by recalling various aspects of the model, such as $\mathbf{b}$, and combining that information with the data currently in memory. Let's write $\mathbf{x}_j$ for the jth observation currently in memory.

The *predicted value* (`xb` option) is defined as $\widehat{y}_j = \mathbf{x}_j\mathbf{b} + \text{offset}_j$

The *standard error of the prediction* (the `stdp` option) is defined as $s_{p_j} = \sqrt{\mathbf{x}_j\mathbf{V}\mathbf{x}_j'}$

The *standard error of the difference in linear predictions* between equations 1 and 2 is defined as

$$s_{dp_j} = \{(\mathbf{x}_{1j}, -\mathbf{x}_{2j}, \mathbf{0}, \ldots, \mathbf{0})\,\mathbf{V}\,(\mathbf{x}_{1j}, -\mathbf{x}_{2j}, \mathbf{0}, \ldots, \mathbf{0})'\}^{\frac{1}{2}}$$

See the individual estimation commands for information about calculating command-specific `predict` statistics.

Also see

[R] **predictnl** — Obtain nonlinear predictions, standard errors, etc., after estimation

[P] **_predict** — Obtain predictions, residuals, etc., after estimation programming command

[U] **20 Estimation and postestimation commands**

Title

predictnl — Obtain nonlinear predictions, standard errors, etc., after estimation

Syntax

`predictnl` [*type*] *newvar* = *pnl_exp* [*if*] [*in*] [, *options*]

options	Description
Main	
`se(`*newvar*`)`	create *newvar* containing standard errors
`variance(`*newvar*`)`	create *newvar* containing variances
`wald(`*newvar*`)`	create *newvar* containing the Wald test statistic
`p(`*newvar*`)`	create *newvar* containing the significance level (p-value) of the Wald test
`ci(`*newvars*`)`	create *newvars* containing lower and upper confidence intervals
`level(`#`)`	set confidence level; default is `level(95)`
`g(`*stub*`)`	create *stub*`1`, *stub*`2`, ..., *stub*`k` variables containing observation-specific derivatives
Advanced	
`iterate(`#`)`	maximum iterations for finding optimal step size; default is 100
`force`	calculate standard errors, etc., even when possibly inappropriate

Menu

Statistics > Postestimation > Nonlinear predictions

Description

`predictnl` calculates (possibly) nonlinear predictions after any Stata estimation command and optionally calculates the variances, standard errors, Wald test statistics, significance levels, and confidence limits for these predictions. Unlike its companion nonlinear postestimation commands `testnl` and `nlcom`, `predictnl` generates functions of the data (that is, predictions), not scalars. The quantities generated by `predictnl` are thus vectorized over the observations in the data.

Consider some general prediction, $g(\boldsymbol{\theta}, \mathbf{x}_i)$, for $i = 1, \ldots, n$, where $\boldsymbol{\theta}$ are the model parameters and $\mathbf{x}_i$ are some data for the ith observation; $\mathbf{x}_i$ is assumed fixed. Typically, $g(\boldsymbol{\theta}, \mathbf{x}_i)$ is estimated by $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$, where $\widehat{\boldsymbol{\theta}}$ are the estimated model parameters, which are stored in `e(b)` following any Stata estimation command.

In its most common use, `predictnl` generates two variables: one containing the estimated prediction, $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$, the other containing the estimated standard error of $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$. The calculation of standard errors (and other obtainable quantities that are based on the standard errors, such as test statistics) is based on the delta method, an approximation appropriate in large samples; see *Methods and formulas*.

`predictnl` can be used with `svy` estimation results (assuming that `predict` is also allowed), see [SVY] **svy postestimation**.

The specification of $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$ is handled by specifying *pnl_exp*, and the values of $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$ are stored in the new variable *newvar* of storage type *type*. *pnl_exp* is any valid Stata expression and may also contain calls to two special functions unique to `predictnl`:

1. `predict(`[*predict_options*]`)`: When you are evaluating *pnl_exp*, `predict()` is a convenience function that replicates the calculation performed by the command

   ```
   predict ..., predict_options
   ```

   As such, the `predict()` function may be used either as a shorthand for the formula used to make this prediction or when the formula is not readily available. When used without arguments, `predict()` replicates the default prediction for that particular estimation command.

2. `xb(`[*eqno*]`)`: The `xb()` function replicates the calculation of the linear predictor $\mathbf{x}_i\mathbf{b}$ for equation *eqno*. If `xb()` is specified without *eqno*, the linear predictor for the first equation (or the only equation in single-equation estimation) is obtained.

   For example, `xb(#1)` (or equivalently, `xb()` with no arguments) translates to the linear predictor for the first equation, `xb(#2)` for the second, and so on. You could also refer to the equations by their names, such as `xb(income)`.

   When specifying *pnl_exp*, both of these functions may be used repeatedly, in combination, and in combination with other Stata functions and expressions. See *Remarks* for examples that use both of these functions.

Options

Main

`se(`*newvar*`)` adds *newvar* of storage type *type*, where for each `i` in the prediction sample, *newvar*`[i]` contains the estimated standard error of $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$.

`variance(`*newvar*`)` adds *newvar* of storage type *type*, where for each `i` in the prediction sample, *newvar*`[i]` contains the estimated variance of $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$.

`wald(`*newvar*`)` adds *newvar* of storage type *type*, where for each `i` in the prediction sample, *newvar*`[i]` contains the Wald test statistic for the test of the hypothesis $H_0\colon g(\boldsymbol{\theta}, \mathbf{x}_i) = 0$.

`p(`*newvar*`)` adds *newvar* of storage type *type*, where *newvar*`[i]` contains the significance level (p-value) of the Wald test of $H_0\colon g(\boldsymbol{\theta}, \mathbf{x}_i) = 0$ versus the two-sided alternative.

`ci(`*newvars*`)` requires the specification of two *newvars*, such that the ith observation of each will contain the left and right endpoints (respectively) of a confidence interval for $g(\boldsymbol{\theta}, \mathbf{x}_i)$. The level of the confidence intervals is determined by `level(#)`.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`g(`*stub*`)` specifies that new variables, *stub*`1`, *stub*`2`, ..., *stub*`k` be created, where `k` is the dimension of $\boldsymbol{\theta}$. *stub*`1` will contain the observation-specific derivatives of $g(\boldsymbol{\theta}, \mathbf{x}_i)$ with respect to the first element, θ_1, of $\boldsymbol{\theta}$; *stub*`2` will contain the derivatives of $g(\boldsymbol{\theta}, \mathbf{x}_i)$ with respect to θ_2, etc.; If the derivative of $g(\boldsymbol{\theta}, \mathbf{x}_i)$ with respect to a particular coefficient in $\boldsymbol{\theta}$ equals zero for all observations in the prediction sample, the *stub* variable for that coefficient is not created. The ordering of the parameters in $\boldsymbol{\theta}$ is precisely that of the stored vector of parameter estimates `e(b)`.

Advanced

`iterate(#)` specifies the maximum number of iterations used to find the optimal step size in the calculation of numerical derivatives of $g(\boldsymbol{\theta}, \mathbf{x}_i)$ with respect to $\boldsymbol{\theta}$. By default, the maximum number of iterations is 100, but convergence is usually achieved after only a few iterations. You should rarely have to use this option.

`force` forces the calculation of standard errors and other inference-related quantities in situations where `predictnl` would otherwise refuse to do so. The calculation of standard errors takes place by evaluating (at $\widehat{\boldsymbol{\theta}}$) the numerical derivative of $g(\boldsymbol{\theta}, \mathbf{x}_i)$ with respect to $\boldsymbol{\theta}$. If `predictnl` detects that $g()$ is possibly a function of random quantities other than $\widehat{\boldsymbol{\theta}}$, it will refuse to calculate standard errors or any other quantity derived from them. The `force` option forces the calculation to take place anyway. If you use the `force` option, there is no guarantee that any inference quantities (for example, standard errors) will be correct or that the values obtained can be interpreted.

Remarks

Remarks are presented under the following headings:

Introduction
Nonlinear transformations and standard errors
Using xb() and predict()
Multiple-equation (ME) estimators
Test statistics and significance levels
Manipulability
Confidence intervals

Introduction

`predictnl` and `nlcom` both use the delta method. They take a nonlinear transformation of the estimated parameter vector from some fitted model and apply the delta method to calculate the variance, standard error, Wald test statistic, etc., of this transformation. `nlcom` is designed for scalar functions of the parameters, and `predictnl` is designed for functions of the parameters and of the data, that is, for predictions.

Nonlinear transformations and standard errors

We begin by fitting a probit model to the low-birthweight data of Hosmer and Lemeshow (2000, 25). The data are described in detail in example 1 of [R] **logistic**.

```
. use http://www.stata-press.com/data/r12/lbw
(Hosmer & Lemeshow data)
. probit low lwt smoke ptl ht
Iteration 0:   log likelihood =   -117.336
Iteration 1:   log likelihood = -106.75886
Iteration 2:   log likelihood = -106.67852
Iteration 3:   log likelihood = -106.67851
Probit regression                                 Number of obs   =        189
                                                  LR chi2(4)      =      21.31
                                                  Prob > chi2     =     0.0003
Log likelihood = -106.67851                       Pseudo R2       =     0.0908
------------------------------------------------------------------------------
         low |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         lwt |  -.0095164   .0036875    -2.58   0.010    -.0167438   -.0022891
       smoke |   .3487004   .2041772     1.71   0.088    -.0514794    .7488803
         ptl |    .365667   .1921201     1.90   0.057    -.0108815    .7422154
          ht |   1.082355    .410673     2.64   0.008     .2774503    1.887259
       _cons |   .4238985   .4823224     0.88   0.379    -.5214361    1.369233
------------------------------------------------------------------------------
```

After we fit such a model, we first would want to generate the predicted probabilities of a low birthweight, given the covariate values in the estimation sample. This is easily done using `predict` after `probit`, but it doesn't answer the question, "What are the standard errors of those predictions?"

For the time being, we will consider ourselves ignorant of any automated way to obtain the predicted probabilities after `probit`. The formula for the prediction is

$$\Pr(y \neq 0|\mathbf{x}_i) = \Phi(\mathbf{x}_i\boldsymbol{\beta})$$

where Φ is the standard cumulative normal. Thus for this example, $g(\boldsymbol{\theta}, \mathbf{x}_i) = \Phi(\mathbf{x}_i\boldsymbol{\beta})$. Armed with the formula, we can use `predictnl` to generate the predictions and their standard errors:

```
. predictnl phat = normal(_b[_cons] + _b[ht]*ht + _b[ptl]*ptl +
> _b[smoke]*smoke + _b[lwt]*lwt), se(phat_se)
. list phat phat_se lwt smoke ptl ht in -10/l
```

	phat	phat_se	lwt	smoke	ptl	ht
180.	.2363556	.042707	120	0	0	0
181.	.6577712	.1580714	154	0	1	1
182.	.2793261	.0519958	106	0	0	0
183.	.1502118	.0676338	190	1	0	0
184.	.5702871	.0819911	101	1	1	0
185.	.4477045	.079889	95	1	0	0
186.	.2988379	.0576306	100	0	0	0
187.	.4514706	.080815	94	1	0	0
188.	.5615571	.1551051	142	0	0	1
189.	.7316517	.1361469	130	1	0	1

Thus subject 180 in our data has an estimated probability of low birthweight of 23.6% with standard error 4.3%.

Used without options, `predictnl` is not much different from `generate`. By specifying the `se(phat_se)` option, we were able to obtain a variable containing the standard errors of the predictions; therein lies the utility of `predictnl`.

Using xb() and predict()

As was the case above, a prediction is often not a function of a few isolated parameters and their corresponding variables but instead is some (possibly elaborate) function of the entire linear predictor. For models with many predictors, the brute-force expression for the linear predictor can be cumbersome to type. An alternative is to use the inline function `xb()`. `xb()` is a shortcut for having to type `_b[_cons] + _b[ht]*ht + _b[ptl]*ptl + ...`,

```
. drop phat phat_se
. predictnl phat = normal(xb()), se(phat_se)
. list phat phat_se lwt smoke ptl ht in -10/l
```

	phat	phat_se	lwt	smoke	ptl	ht
180.	.2363556	.042707	120	0	0	0
181.	.6577712	.1580714	154	0	1	1
182.	.2793261	.0519958	106	0	0	0
183.	.1502118	.0676338	190	1	0	0
184.	.5702871	.0819911	101	1	1	0
185.	.4477045	.079889	95	1	0	0
186.	.2988379	.0576306	100	0	0	0
187.	.4514706	.080815	94	1	0	0
188.	.5615571	.1551051	142	0	0	1
189.	.7316517	.1361469	130	1	0	1

which yields the same results. This approach is easier, produces more readable code, and is less prone to error, such as forgetting to include a term in the sum.

Here we used `xb()` without arguments because we have only one equation in our model. In multiple-equation (ME) settings, `xb()` (or equivalently `xb(#1)`) yields the linear predictor from the first equation, `xb(#2)` from the second, etc. You can also refer to equations by their names, for example, `xb(income)`.

❑ Technical note

Most estimation commands in Stata allow the postestimation calculation of linear predictors and their standard errors via `predict`. For example, to obtain these for the first (or only) equation in the model, you could type

```
predict xbvar, xb
predict stdpvar, stdp
```

Equivalently, you could type

```
predictnl xbvar = xb(), se(stdpvar)
```

but we recommend the first method, as it is faster. As we demonstrated above, however, `predictnl` is more general.

❑

Returning to our probit example, we can further simplify the calculation by using the inline function `predict()`. `predict(`*pred_options*`)` works by substituting, within our `predictnl` expression, the calculation performed by

```
predict ..., pred_options
```

In our example, we are interested in the predicted probabilities after a probit regression, normally obtained via

```
predict ..., p
```

We can obtain these predictions (and standard errors) by using

```
. drop phat phat_se
. predictnl phat = predict(p), se(phat_se)
. list phat phat_se lwt smoke ptl ht in -10/l
```

	phat	phat_se	lwt	smoke	ptl	ht
180.	.2363556	.042707	120	0	0	0
181.	.6577712	.1580714	154	0	1	1
182.	.2793261	.0519958	106	0	0	0
183.	.1502118	.0676338	190	1	0	0
184.	.5702871	.0819911	101	1	1	0
185.	.4477045	.079889	95	1	0	0
186.	.2988379	.0576306	100	0	0	0
187.	.4514706	.080815	94	1	0	0
188.	.5615571	.1551051	142	0	0	1
189.	.7316517	.1361469	130	1	0	1

which again replicates what we have already done by other means. However, this version did not require knowledge of the formula for the predicted probabilities after a probit regression—`predict(p)` took care of that for us.

Because the predicted probability is the default prediction after `probit`, we could have just used `predict()` without arguments, namely,

```
. predictnl phat = predict(), se(phat_se)
```

Also, the expression *pnl_exp* can be inordinately complicated, with multiple calls to `predict()` and `xb()`. For example,

```
. predictnl phat = normal(invnormal(predict()) + predict(xb)/xb() - 1),
> se(phat_se)
```

is perfectly valid and will give the same result as before, albeit a bit inefficiently.

❑ Technical note

When using `predict()` and `xb()`, the *formula* for the calculation is substituted within *pnl_exp*, not the values that result from the application of that formula. To see this, note the subtle difference between

```
. predict xbeta, xb
. predictnl phat = normal(xbeta), se(phat_se)
```

and

```
. predictnl phat = normal(xb()), se(phat_se)
```

Both sequences will yield the same `phat`, yet for the first sequence, `phat_se` will equal zero for all observations. The reason is that, once evaluated, `xbeta` will contain the values of the linear predictor, yet these values are treated as fixed and nonstochastic as far as `predictnl` is concerned. By contrast, because `xb()` is shorthand for the formula used to calculate the linear predictor, it contains not values, but references to the estimated regression coefficients and corresponding variables. Thus the second method produces the desired result. ❑

Multiple-equation (ME) estimators

In [R] **mlogit**, data on insurance choice (Tarlov et al. 1989; Wells et al. 1989) were examined, and a multinomial logit was used to assess the effects of age, gender, race, and site of study (one of three sites) on the type of insurance:

```
. use http://www.stata-press.com/data/r12/sysdsn1, clear
(Health insurance data)
. mlogit insure age male nonwhite i.site, nolog
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(10)     =      42.99
                                                Prob > chi2     =     0.0000
Log likelihood = -534.36165                     Pseudo R2       =     0.0387
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.011745	.0061946	-1.90	0.058	-.0238862	.0003962
male	.5616934	.2027465	2.77	0.006	.1643175	.9590693
nonwhite	.9747768	.2363213	4.12	0.000	.5115955	1.437958
site						
2	.1130359	.2101903	0.54	0.591	-.2989296	.5250013
3	-.5879879	.2279351	-2.58	0.010	-1.034733	-.1412433
_cons	.2697127	.3284422	0.82	0.412	-.3740222	.9134476
Uninsure						
age	-.0077961	.0114418	-0.68	0.496	-.0302217	.0146294
male	.4518496	.3674867	1.23	0.219	-.268411	1.17211
nonwhite	.2170589	.4256361	0.51	0.610	-.6171725	1.05129
site						
2	-1.211563	.4705127	-2.57	0.010	-2.133751	-.2893747
3	-.2078123	.3662926	-0.57	0.570	-.9257327	.510108
_cons	-1.286943	.5923219	-2.17	0.030	-2.447872	-.1260134

Of particular interest is the estimation of the relative risk, which, for a given selection, is the ratio of the probability of making that selection to the probability of selecting the base category (`Indemnity` here), given a set of covariate values. In a multinomial logit model, the relative risk (when comparing to the base category) simplifies to the exponentiated linear predictor for that selection.

Using this example, we can estimate the observation-specific relative risks of selecting a prepaid plan over the base category (with standard errors) by either referring to the `Prepaid` equation by name or number,

```
. predictnl RRppaid = exp(xb(Prepaid)), se(SERRppaid)
```

or

```
. predictnl RRppaid = exp(xb(#1)), se(SERRppaid)
```

because `Prepaid` is the first equation in the model.

Those of us for whom the simplified formula for the relative risk does not immediately come to mind may prefer to calculate the relative risk directly from its definition, that is, as a ratio of two predicted probabilities. After `mlogit`, the predicted probability for a category may be obtained using `predict`, but we must specify the category as the outcome:

```
. predictnl RRppaid = predict(outcome(Prepaid))/predict(outcome(Indemnity)),
> se(SERRppaid)
(1 missing value generated)
. list RRppaid SERRppaid age male nonwhite site in 1/10
```

	RRppaid	SERRpp~d	age	male	nonwhite	site
1.	.6168578	.1503759	73.722107	0	0	2
2.	1.056658	.1790703	27.89595	0	0	2
3.	.8426442	.1511281	37.541397	0	0	1
4.	1.460581	.3671465	23.641327	0	1	3
5.	.9115747	.1324168	40.470901	0	0	2
6.	1.034701	.1696923	29.683777	0	0	2
7.	.9223664	.1344981	39.468857	0	0	2
8.	1.678312	.4216626	26.702255	1	0	1
9.	.9188519	.2256017	63.101974	0	1	3
10.	.5766296	.1334877	69.839828	0	0	1

The "(1 missing value generated)" message is not an error; further examination of the data would reveal that `age` is missing in one observation and that the offending observation (among others) is not in the estimation sample. Just as with `predict`, `predictnl` can generate predictions in or out of the estimation sample.

Thus we estimate (among other things) that a white, female, 73-year-old from site 2 is less likely to choose a prepaid plan over an indemnity plan—her relative risk is about 62% with standard error 15%.

Test statistics and significance levels

Often a standard error calculation is just a means to an end, and what is really desired is a test of the hypothesis,

$$H_0 : g(\boldsymbol{\theta}, \mathbf{x}_i) = 0$$

versus the two-sided alternative.

We can use `predictnl` to obtain the Wald test statistics or significance levels (or both) for the above tests, whether or not we want standard errors. To obtain the Wald test statistics, we use the `wald()` option; for significance levels, we use `p()`.

Returning to our `mlogit` example, suppose that we wanted for each observation a test of whether the relative risk of choosing a prepaid plan over an indemnity plan is different from one. One way to do this would be to define $g()$ to be the relative risk minus one and then test whether $g()$ is different from zero.

```
. predictnl RRm1 = exp(xb(Prepaid)) - 1, wald(W_RRm1) p(sig_RRm1)
(1 missing value generated)
note: significance levels are with respect to the chi-squared(1) distribution.
. list RRm1 W_RRm1 sig_RRm1 age male nonwhite in 1/10
```

	RRm1	W_RRm1	sig_RRm1	age	male	nonwhite
1.	-.3831422	6.491778	.0108375	73.722107	0	0
2.	.0566578	.100109	.7516989	27.89595	0	0
3.	-.1573559	1.084116	.2977787	37.541397	0	0
4.	.4605812	1.573743	.2096643	23.641327	0	1
5.	-.0884253	.4459299	.5042742	40.470901	0	0
6.	.0347015	.0418188	.8379655	29.683777	0	0
7.	-.0776336	.3331707	.563798	39.468857	0	0
8.	.6783119	2.587788	.1076906	26.702255	1	0
9.	-.0811482	.1293816	.719074	63.101974	0	1
10.	-.4233705	10.05909	.001516	69.839828	0	0

The newly created variable `W_RRm1` contains the Wald test statistic for each observation, and `sig_RRm1` contains the level of significance. Thus our 73-year-old white female represented by the first observation would have a relative risk of choosing prepaid over indemnity that is significantly different from 1, at least at the 5% level. For this test, it was not necessary to generate a variable containing the standard error of the relative risk minus 1, but we could have done so had we wanted. We could have also omitted specifying `wald(W_RRm1)` if all we cared about were, say, the significance levels of the tests.

In this regard, `predictnl` acts as an observation-specific version of `testnl`, with the test results vectorized over the observations in the data. The significance levels are pointwise—they are not adjusted to reflect any simultaneous testing over the observations in the data.

Manipulability

There are many ways to specify $g(\boldsymbol{\theta}, \mathbf{x}_i)$ to yield tests such that, for multiple specifications of $g()$, the theoretical conditions for which

$$H_0 : g(\boldsymbol{\theta}, \mathbf{x}_i) = 0$$

is true will be equivalent. However, this does not mean that the tests themselves will be equivalent. This is known as the manipulability of the Wald test for nonlinear hypotheses; also see [R] **boxcox**.

As an example, consider the previous section where we defined $g()$ to be the relative risk between choosing a prepaid plan over an indemnity plan, minus 1. We could also have defined $g()$ to be the risk difference—the probability of choosing a prepaid plan minus the probability of choosing an indemnity plan. Either specification of $g()$ yields a mathematically equivalent specification of $H_0 : g() = 0$; that is, the risk difference will equal zero when the relative risk equals one. However, the tests themselves do not give the same results:

```
. predictnl RD = predict(outcome(Prepaid)) - predict(outcome(Indemnity)),
> wald(W_RD) p(sig_RD)
(1 missing value generated)
note: significance levels are with respect to the chi-squared(1) distribution.
. list RD W_RD sig_RD RRm1 W_RRm1 sig_RRm1 in 1/10
```

	RD	W_RD	sig_RD	RRm1	W_RRm1	sig_RRm1
1.	-.2303744	4.230243	.0397097	-.3831422	6.491778	.0108375
2.	.0266902	.1058542	.7449144	.0566578	.100109	.7516989
3.	-.0768078	.9187646	.3377995	-.1573559	1.084116	.2977787
4.	.1710702	2.366535	.1239619	.4605812	1.573743	.2096643
5.	-.0448509	.4072922	.5233471	-.0884253	.4459299	.5042742
6.	.0165251	.0432816	.835196	.0347015	.0418188	.8379655
7.	-.0391535	.3077611	.5790573	-.0776336	.3331707	.563798
8.	.22382	4.539085	.0331293	.6783119	2.587788	.1076906
9.	-.0388409	.1190183	.7301016	-.0811482	.1293816	.719074
10.	-.2437626	6.151558	.0131296	-.4233705	10.05909	.001516

In certain cases (such as subject 8), the difference can be severe enough to potentially change the conclusion. The reason for this inconsistency is that the nonlinear Wald test is actually a standard Wald test of a first-order Taylor approximation of $g()$, and this approximation can differ according to how $g()$ is specified.

As such, keep in mind the manipulability of nonlinear Wald tests when drawing scientific conclusions.

Confidence intervals

We can also use `predictnl` to obtain confidence intervals for the observation-specific $g(\boldsymbol{\theta}, \mathbf{x}_i)$ by using the `ci()` option to specify two new variables to contain the left and right endpoints of the confidence interval, respectively. For example, we could generate confidence intervals for the risk differences calculated previously:

```
. drop RD
. predictnl RD = predict(outcome(Prepaid)) - predict(outcome(Indemnity)),
> ci(RD_lcl RD_rcl)
(1 missing value generated)
note: Confidence intervals calculated using Z critical values.
. list RD RD_lcl RD_rcl age male nonwhite in 1/10
```

	RD	RD_lcl	RD_rcl	age	male	nonwhite
1.	-.2303744	-.4499073	-.0108415	73.722107	0	0
2.	.0266902	-.1340948	.1874752	27.89595	0	0
3.	-.0768078	-.2338625	.080247	37.541397	0	0
4.	.1710702	-.0468844	.3890248	23.641327	0	1
5.	-.0448509	-.1825929	.092891	40.470901	0	0
6.	.0165251	-.1391577	.1722078	29.683777	0	0
7.	-.0391535	-.177482	.099175	39.468857	0	0
8.	.22382	.0179169	.4297231	26.702255	1	0
9.	-.0388409	-.2595044	.1818226	63.101974	0	1
10.	-.2437626	-.4363919	-.0511332	69.839828	0	0

The confidence level, here, 95%, is either set using the `level()` option or obtained from the current default level, `c(level)`; see [U] **20.7 Specifying the width of confidence intervals**.

From the above output, we can see that, for subjects 1, 8, and 10, a 95% confidence interval for the risk difference does not contain zero, meaning that, for these subjects, there is some evidence of a significant difference in risks.

The confidence intervals calculated by `predictnl` are pointwise; there is no adjustment (such as a Bonferroni correction) made so that these confidence intervals may be considered jointly at the specified level.

Methods and formulas

`predictnl` is implemented as an ado-file.

For the ith observation, consider the transformation $g(\boldsymbol{\theta}, \mathbf{x}_i)$, estimated by $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$, for the $1 \times k$ parameter vector $\boldsymbol{\theta}$ and data $\mathbf{x}_i$ ($\mathbf{x}_i$ is assumed fixed). The variance of $g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)$ is estimated by

$$\widehat{\text{Var}}\left\{g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)\right\} = \mathbf{GVG}'$$

where $\mathbf{G}$ is the vector of derivatives

$$\mathbf{G} = \left\{ \left. \frac{\partial g(\boldsymbol{\theta}, \mathbf{x}_i)}{\partial \boldsymbol{\theta}} \right|_{\boldsymbol{\theta}=\widehat{\boldsymbol{\theta}}} \right\}_{(1\times k)}$$

and $\mathbf{V}$ is the estimated variance–covariance matrix of $\widehat{\boldsymbol{\theta}}$. Standard errors, $\widehat{\text{se}}\{g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)\}$, are obtained as the square roots of the variances.

The Wald test statistic for testing

$$H_0 \colon g(\boldsymbol{\theta}, \mathbf{x}_i) = 0$$

versus the two-sided alternative is given by

$$W_i = \frac{\left\{g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)\right\}^2}{\widehat{\text{Var}}\left\{g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)\right\}}$$

When the variance–covariance matrix of $\widehat{\boldsymbol{\theta}}$ is an asymptotic covariance matrix, W_i is approximately distributed as χ^2 with 1 degree of freedom. For linear regression, W_i is taken to be approximately distributed as $F_{1,r}$, where r is the residual degrees of freedom from the original model fit. The levels of significance of the observation-by-observation tests of H_0 versus the two-sided alternative are given by

$$p_i = \Pr(T > W_i)$$

where T is either a χ^2- or F-distributed random variable, as described above.

A $(1-\alpha) \times 100\%$ confidence interval for $g(\boldsymbol{\theta}, \mathbf{x}_i)$ is given by

$$g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i) \pm z_{\alpha/2} \left[\widehat{\text{se}}\left\{g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)\right\}\right]$$

when W_i is χ^2-distributed, and

$$g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i) \pm t_{\alpha/2,r} \left[\widehat{\text{se}}\left\{g(\widehat{\boldsymbol{\theta}}, \mathbf{x}_i)\right\}\right]$$

when W_i is F-distributed. z_p is the $1-p$ quantile of the standard normal distribution, and $t_{p,r}$ is the $1-p$ quantile of the t distribution with r degrees of freedom.

References

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Also see

[R] **lincom** — Linear combinations of estimators

[R] **nlcom** — Nonlinear combinations of estimators

[R] **predict** — Obtain predictions, residuals, etc., after estimation

[R] **test** — Test linear hypotheses after estimation

[R] **testnl** — Test nonlinear hypotheses after estimation

[U] **20 Estimation and postestimation commands**

Title

probit — Probit regression

Syntax

```
probit depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
offset(*varname*)	include *varname* in model with coefficient constrained to 1
asis	retain perfect predictor variables
constraints(*constraints*)	apply specified linear constraints
collinear	keep collinear variables
SE/Robust	
vce(*vcetype*)	*vcetype* may be oim, robust, cluster *clustvar*, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
nocoef	do not display the coefficient table; seldom used
coeflegend	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, fracpoly, jackknife, mfp, mi estimate, nestreg, rolling, statsby, stepwise, and svy are allowed; see [U] **11.1.10 Prefix commands**.

vce(bootstrap) and vce(jackknife) are not allowed with the mi estimate prefix; see [MI] **mi estimate**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

vce(), nocoef, and weights are not allowed with the svy prefix; see [SVY] **svy**.

fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

nocoef and coeflegend do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Binary outcomes > Probit regression

Description

probit fits a maximum-likelihood probit model.

If estimating on grouped data, see the bprobit command described in [R] **glogit**.

Several auxiliary commands may be run after probit, logit, or logistic; see [R] **logistic postestimation** for a description of these commands.

See [R] **logistic** for a list of related estimation commands.

Options

Model

noconstant, offset(*varname*), constraints(*constraints*), collinear; see [R] **estimation options**.

asis specifies that all specified variables and observations be retained in the maximization process. This option is typically not specified and may introduce numerical instability. Normally probit drops variables that perfectly predict success or failure in the dependent variable along with their associated observations. In those cases, the effective coefficient on the dropped variables is infinity (negative infinity) for variables that completely determine a success (failure). Dropping the variable and perfectly predicted observations has no effect on the likelihood or estimates of the remaining coefficients and increases the numerical stability of the optimization process. Specifying this option forces retention of perfect predictor variables and their associated observations.

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

level(#); see [R] **estimation options**.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

The following options are available with probit but are not shown in the dialog box:

nocoef specifies that the coefficient table not be displayed. This option is sometimes used by programmers but is of no use interactively.

coeflegend; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Robust standard errors
Model identification

`probit` fits maximum likelihood models with dichotomous dependent (left-hand-side) variables coded as 0/1 (more precisely, coded as 0 and not 0).

▷ Example 1

We have data on the make, weight, and mileage rating of 22 foreign and 52 domestic automobiles. We wish to fit a probit model explaining whether a car is foreign based on its weight and mileage. Here is an overview of our data:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. keep make mpg weight foreign
. describe
Contains data from http://www.stata-press.com/data/r12/auto.dta
  obs:            74                          1978 Automobile Data
 vars:             4                          13 Apr 2011 17:45
 size:         1,702                           (_dta has notes)
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
make            str18  %-18s                  Make and Model
mpg             int    %8.0g                  Mileage (mpg)
weight          int    %8.0gc                 Weight (lbs.)
foreign         byte   %8.0g       origin     Car type
-------------------------------------------------------------------------------
Sorted by:  foreign
     Note:  dataset has changed since last saved
. inspect foreign
foreign:  Car type                              Number of Observations
------------------                                        ------------------------------
                                                Total   Integers   Nonintegers
|   #                       Negative              -          -          -
|   #                       Zero                 52         52          -
|   #                       Positive             22         22          -
|   #                                           ----       ----       ----
|   #   #                   Total                74         74          -
|   #   #                   Missing               -
+-----------------------                       ----
0                       1                     74
   (2 unique values)
      foreign is labeled and all values are documented in the label.
```

The `foreign` variable takes on two unique values, 0 and 1. The value 0 denotes a domestic car, and 1 denotes a foreign car.

The model that we wish to fit is

$$\Pr(\texttt{foreign} = 1) = \Phi(\beta_0 + \beta_1\texttt{weight} + \beta_2\texttt{mpg})$$

where Φ is the cumulative normal distribution.

To fit this model, we type

```
. probit foreign weight mpg
Iteration 0:   log likelihood =  -45.03321
Iteration 1:   log likelihood = -27.914626
  (output omitted)
Iteration 5:   log likelihood = -26.844189
Probit regression                                 Number of obs   =         74
                                                  LR chi2(2)      =      36.38
                                                  Prob > chi2     =     0.0000
Log likelihood = -26.844189                       Pseudo R2       =     0.4039

------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0023355   .0005661    -4.13   0.000    -.003445   -.0012261
         mpg |  -.1039503   .0515689    -2.02   0.044    -.2050235   -.0028772
       _cons |   8.275464   2.554142     3.24   0.001     3.269437    13.28149
------------------------------------------------------------------------------
```

We find that heavier cars are less likely to be foreign and that cars yielding better gas mileage are also less likely to be foreign, at least holding the weight of the car constant.

See [R] **maximize** for an explanation of the output.

◁

❑ Technical note

Stata interprets a value of 0 as a negative outcome (failure) and treats all other values (except missing) as positive outcomes (successes). Thus if your dependent variable takes on the values 0 and 1, then 0 is interpreted as failure and 1 as success. If your dependent variable takes on the values 0, 1, and 2, then 0 is still interpreted as failure, but both 1 and 2 are treated as successes.

If you prefer a more formal mathematical statement, when you type `probit` y x, Stata fits the model

$$\Pr(y_j \neq 0 \mid \mathbf{x}_j) = \Phi(\mathbf{x}_j\boldsymbol{\beta})$$

where Φ is the standard cumulative normal.

❑

Robust standard errors

If you specify the `vce(robust)` option, `probit` reports robust standard errors; see [U] **20.20 Obtaining robust variance estimates**.

▷ Example 2

For the model from example 1, the robust calculation increases the standard error of the coefficient on `mpg` by almost 15%:

```
. probit foreign weight mpg, vce(robust) nolog
Probit regression                                 Number of obs   =         74
                                                  Wald chi2(2)    =      30.26
                                                  Prob > chi2     =     0.0000
Log pseudolikelihood = -26.844189                 Pseudo R2       =     0.4039

------------------------------------------------------------------------------
             |               Robust
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0023355   .0004934    -4.73   0.000    -.0033025   -.0013686
         mpg |  -.1039503   .0593548    -1.75   0.080    -.2202836    .0123829
       _cons |   8.275464   2.539177     3.26   0.001     3.298769    13.25216
------------------------------------------------------------------------------
```

Without vce(robust), the standard error for the coefficient on mpg was reported to be 0.052 with a resulting confidence interval of $[-0.21, -0.00]$.

◁

▷ Example 3

The vce(cluster *clustvar*) option can relax the independence assumption required by the probit estimator to independence between clusters. To demonstrate, we will switch to a different dataset.

We are studying unionization of women in the United States and have a dataset with 26,200 observations on 4,434 women between 1970 and 1988. We will use the variables age (the women were 14–26 in 1968, and our data span the age range of 16–46), grade (years of schooling completed, ranging from 0 to 18), not_smsa (28% of the person-time was spent living outside an SMSA—standard metropolitan statistical area), south (41% of the person-time was in the South), and year. Each of these variables is included in the regression as a covariate along with the interaction between south and year. This interaction, along with the south and year variables, is specified in the probit command using factor-variables notation, south##c.year. We also have variable union, indicating union membership. Overall, 22% of the person-time is marked as time under union membership, and 44% of these women have belonged to a union.

We fit the following model, ignoring that the women are observed an average of 5.9 times each in these data:

```
. use http://www.stata-press.com/data/r12/union, clear
(NLS Women 14-24 in 1968)
. probit union age grade not_smsa south##c.year
Iteration 0:   log likelihood =  -13864.23
Iteration 1:   log likelihood = -13545.541
Iteration 2:   log likelihood = -13544.385
Iteration 3:   log likelihood = -13544.385
Probit regression                                 Number of obs   =      26200
                                                  LR chi2(6)      =     639.69
                                                  Prob > chi2     =     0.0000
Log likelihood = -13544.385                       Pseudo R2       =     0.0231
------------------------------------------------------------------------------
       union |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0118481   .0029072     4.08   0.000     .0061502     .017546
       grade |   .0267365   .0036689     7.29   0.000     .0195457    .0339273
    not_smsa |  -.1293525   .0202595    -6.38   0.000    -.1690604   -.0896445
    1.south |  -.8281077   .2472219    -3.35   0.001    -1.312654   -.3435618
        year |  -.0080931   .0033469    -2.42   0.016    -.0146529   -.0015333
             |
south#c.year |
          1  |   .0057369   .0030917     1.86   0.064    -.0003226    .0117965
             |
       _cons |  -.6542487   .2007777    -3.26   0.001    -1.047766   -.2607316
------------------------------------------------------------------------------
```

The reported standard errors in this model are probably meaningless. Women are observed repeatedly, and so the observations are not independent. Looking at the coefficients, we find a large southern effect against unionization and a time trend for the south that is almost significantly different from the overall downward trend. The vce(cluster *clustvar*) option provides a way to fit this model and obtains correct standard errors:

```
. probit union age grade not_smsa south##c.year, vce(cluster id)
Iteration 0:   log pseudolikelihood =  -13864.23
Iteration 1:   log pseudolikelihood = -13545.541
Iteration 2:   log pseudolikelihood = -13544.385
Iteration 3:   log pseudolikelihood = -13544.385
Probit regression                                 Number of obs   =      26200
                                                  Wald chi2(6)    =     166.53
                                                  Prob > chi2     =     0.0000
Log pseudolikelihood = -13544.385                 Pseudo R2       =     0.0231
                              (Std. Err. adjusted for 4434 clusters in idcode)
------------------------------------------------------------------------------
             |               Robust
       union |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0118481   .0056625     2.09   0.036     .0007499    .0229463
       grade |   .0267365   .0078124     3.42   0.001     .0114244    .0420486
    not_smsa |  -.1293525   .0403885    -3.20   0.001    -.2085125   -.0501925
     1.south |  -.8281077   .3201584    -2.59   0.010    -1.455607   -.2006089
        year |  -.0080931   .0060829    -1.33   0.183    -.0200153    .0038292
             |
south#c.year |
          1  |   .0057369   .0040133     1.43   0.153     -.002129    .0136029
             |
       _cons |  -.6542487   .3485976    -1.88   0.061    -1.337487      .02899
------------------------------------------------------------------------------
```

These standard errors are larger than those reported by the inappropriate conventional calculation. By comparison, another model we could fit is an equal-correlation population-averaged probit model:

```
. xtprobit union age grade not_smsa south##c.year, pa
Iteration 1: tolerance = .12544249
Iteration 2: tolerance = .0034686
Iteration 3: tolerance = .00017448
Iteration 4: tolerance = 8.382e-06
Iteration 5: tolerance = 3.997e-07
GEE population-averaged model                 Number of obs      =     26200
Group variable:                     idcode    Number of groups   =      4434
Link:                               probit    Obs per group: min =         1
Family:                           binomial                   avg =       5.9
Correlation:                  exchangeable                   max =        12
                                                Wald chi2(6)       =    242.57
Scale parameter:                         1      Prob > chi2        =    0.0000
------------------------------------------------------------------------------
       union |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0089699   .0053208     1.69   0.092    -.0014586    .0193985
       grade |   .0333174   .0062352     5.34   0.000     .0210966    .0455382
    not_smsa |  -.0715717    .027543    -2.60   0.009    -.1255551   -.0175884
     1.south |  -1.017368    .207931    -4.89   0.000    -1.424905   -.6098308
        year |  -.0062708   .0055314    -1.13   0.257    -.0171122    .0045706
             |
south#c.year |
          1  |   .0086294     .00258     3.34   0.001     .0035727     .013686
             |
       _cons |  -.8670997    .294771    -2.94   0.003     -1.44484   -.2893592
------------------------------------------------------------------------------
```

The coefficient estimates are similar, but these standard errors are smaller than those produced by `probit, vce(cluster` *clustvar*`)`, as we would expect. If the equal-correlation assumption is valid, the population-averaged probit estimator above should be more efficient.

Is the assumption valid? That is a difficult question to answer. The default population-averaged estimates correspond to an assumption of exchangeable correlation within person. It would not be unreasonable to assume an AR(1) correlation within person or to assume that the observations are correlated but that we do not wish to impose any structure. See [XT] **xtprobit** and [XT] **xtgee** for full details.

◁

`probit, vce(cluster` *clustvar*`)` is robust to assumptions about within-cluster correlation. That is, it inefficiently sums within cluster for the standard error calculation rather than attempting to exploit what might be assumed about the within-cluster correlation.

Model identification

The `probit` command has one more feature that is probably the most useful. It will automatically check the model for identification and, if the model is underidentified, drop whatever variables and observations are necessary for estimation to proceed.

▷ Example 4

Have you ever fit a probit model where one or more of your independent variables perfectly predicted one or the other outcome?

For instance, consider the following data:

Outcome y	Independent variable x
0	1
0	1
0	0
1	0

Say that we wish to predict the outcome on the basis of the independent variable. The outcome is always zero when the independent variable is one. In our data, $\Pr(y = 0 \mid x = 1) = 1$, which means that the probit coefficient on x must be minus infinity with a corresponding infinite standard error. At this point, you may suspect that we have a problem.

Unfortunately, not all such problems are so easily detected, especially if you have many independent variables in your model. If you have ever had such difficulties, then you have experienced one of the more unpleasant aspects of computer optimization. The computer has no idea that it is trying to solve for an infinite coefficient as it begins its iterative process. All it knows is that, at each step, making the coefficient a little bigger, or a little smaller, works wonders. It continues on its merry way until either 1) the whole thing comes crashing to the ground when a numerical overflow error occurs or 2) it reaches some predetermined cutoff that stops the process. Meanwhile, you have been waiting. And the estimates that you finally receive, if any, may be nothing more than numerical roundoff.

Stata watches for these sorts of problems, alerts you, fixes them, and then properly fits the model.

Let's return to our automobile data. Among the variables we have in the data is one called `repair` that takes on three values. A value of 1 indicates that the car has a poor repair record, 2 indicates an average record, and 3 indicates a better-than-average record. Here is a tabulation of our data:

```
. use http://www.stata-press.com/data/r12/repair
(1978 Automobile Data)
. tabulate foreign repair
```

Car type	repair 1	2	3	Total
Domestic	10	27	9	46
Foreign	0	3	9	12
Total	10	30	18	58

All the cars with poor repair records (`repair` = 1) are domestic. If we were to attempt to predict `foreign` on the basis of the repair records, the predicted probability for the `repair` = 1 category would have to be zero. This in turn means that the probit coefficient must be minus infinity, and that would set most computer programs buzzing.

Let's try using Stata on this problem.

```
. probit foreign b3.repair
note: 1.repair != 0 predicts failure perfectly
      1.repair dropped and 10 obs not used
Iteration 0:   log likelihood = -26.992087
Iteration 1:   log likelihood = -22.276479
Iteration 2:   log likelihood = -22.229184
Iteration 3:   log likelihood = -22.229138
Iteration 4:   log likelihood = -22.229138
Probit regression                                 Number of obs   =         48
                                                  LR chi2(1)      =       9.53
                                                  Prob > chi2     =     0.0020
Log likelihood = -22.229138                       Pseudo R2       =     0.1765
```

foreign	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
repair						
1	0	(empty)				
2	-1.281552	.4297326	-2.98	0.003	-2.123812	-.4392911
_cons	9.89e-17	.295409	0.00	1.000	-.578991	.578991

Remember that all the cars with poor repair records (`repair` = 1) are domestic, so the model cannot be fit, or at least it cannot be fit if we restrict ourselves to finite coefficients. Stata noted that fact "note: 1.repair != 0 predicts failure perfectly". This is Stata's mathematically precise way of saying what we said in English. When `repair` is 1, the car is domestic.

Stata then went on to say, "1.repair dropped and 10 obs not used". This is Stata eliminating the problem. First, `1.repair` had to be removed from the model because it would have an infinite coefficient. Then the 10 observations that led to the problem had to be eliminated, as well, so as not to bias the remaining coefficients in the model. The 10 observations that are not used are the 10 domestic cars that have poor repair records.

Stata then fit what was left of the model, using the remaining observations. Because no observations remained for cars with poor repair records, Stata reports "(empty)" in the row for `repair` = 1.

◁

❑ Technical note

Stata is pretty smart about catching these problems. It will catch "one-way causation by a dummy variable", as we demonstrated above.

Stata also watches for "two-way causation", that is, a variable that perfectly determines the outcome, both successes and failures. Here Stata says that the variable "predicts outcome perfectly" and stops. Statistics dictate that no model can be fit.

Stata also checks your data for collinear variables; it will say "so-and-so omitted because of collinearity". No observations need to be eliminated here and model fitting will proceed without the offending variable.

It will also catch a subtle problem that can arise with continuous data. For instance, if we were estimating the chances of surviving the first year after an operation, and if we included in our model `age`, and if all the persons over 65 died within the year, Stata will say, "age $>$ 65 predicts failure perfectly". It will then inform us about how it resolves the issue and fit what can be fit of our model.

`probit` (and `logit`, `logistic`, and `ivprobit`) will also occasionally fail to converge and then display messages such as

```
Note: 4 failures and 0 successes completely determined.
```

The cause of this message and what to do if you see it are described in [R] **logit**.

❑

Saved results

`probit` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_cds)`	number of completely determined successes
`e(N_cdf)`	number of completely determined failures
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(r2_p)`	pseudo-R-squared
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance of model test
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	probit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(mns)	vector of means of the independent variables
e(rules)	information about perfect predictors
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

probit is implemented as an ado-file.

Probit analysis originated in connection with bioassay, and the word probit, a contraction of "probability unit", was suggested by Bliss (1934a, 1934b). For an introduction to probit and logit, see, for example, Aldrich and Nelson (1984), Cameron and Trivedi (2010), Greene (2012), Long (1997), Pampel (2000), or Powers and Xie (2008). Long and Freese (2006, chap. 4) and Jones (2007, chap. 3) provide introductions to probit and logit, along with Stata examples.

The log-likelihood function for probit is

$$\ln L = \sum_{j \in S} w_j \ln \Phi(\mathbf{x}_j \boldsymbol{\beta}) + \sum_{j \notin S} w_j \ln\Big\{1 - \Phi(\mathbf{x}_j \boldsymbol{\beta})\Big\}$$

where Φ is the cumulative normal and w_j denotes the optional weights. $\ln L$ is maximized, as described in [R] **maximize**.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. The scores are calculated as $\mathbf{u}_j = \{\phi(\mathbf{x}_j\mathbf{b})/\Phi(\mathbf{x}_j\mathbf{b})\}\mathbf{x}_j$ for the positive outcomes and $-[\phi(\mathbf{x}_j\mathbf{b})/\{1-\Phi(\mathbf{x}_j\mathbf{b})\}]\mathbf{x}_j$ for the negative outcomes, where ϕ is the normal density.

`probit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

Chester Ittner Bliss (1899–1979) was born in Ohio. He was educated as an entomologist, earning degrees from Ohio State and Columbia, and was employed by the United States Department of Agriculture until 1933. When he lost his job because of the Depression, Bliss then worked with R. A. Fisher in London and at the Institute of Plant Protection in Leningrad before returning to a post at the Connecticut Agricultural Experiment Station in 1938. He was also a lecturer at Yale for 25 years. Among many contributions to biostatistics, his development and application of probit methods to biological problems are outstanding.

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Also see

[R] **probit postestimation** — Postestimation tools for probit

[R] **asmprobit** — Alternative-specific multinomial probit regression

[R] **biprobit** — Bivariate probit regression

[R] **brier** — Brier score decomposition

[R] **glm** — Generalized linear models

[R] **hetprob** — Heteroskedastic probit model

[R] **ivprobit** — Probit model with continuous endogenous regressors

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **logit** — Logistic regression, reporting coefficients

[R] **mprobit** — Multinomial probit regression

[R] **roc** — Receiver operating characteristic (ROC) analysis

[R] **scobit** — Skewed logistic regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtprobit** — Random-effects and population-averaged probit models

[U] **20 Estimation and postestimation commands**

Title

probit postestimation — Postestimation tools for probit

Description

The following postestimation commands are of special interest after `probit`:

Command	Description
`estat classification`	report various summary statistics, including the classification table
`estat gof`	Pearson or Hosmer–Lemeshow goodness-of-fit test
`lroc`	compute area under ROC curve and graph the curve
`lsens`	graph sensitivity and specificity versus probability cutoff

These commands are not appropriate after the `svy` prefix.

For information about these commands, see [R] **logistic postestimation**.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset rules asif]
```

statistic	Description
Main	
pr	probability of a positive outcome; the default
xb	linear prediction
stdp	standard error of the linear prediction
* deviance	deviance residual
score	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of a positive outcome.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`deviance` calculates the deviance residual.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `probit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`rules` requests that Stata use any rules that were used to identify the model when making the prediction. By default, Stata calculates missing for excluded observations.

`asif` requests that Stata ignore the rules and exclusion criteria and calculate predictions for all observations possible using the estimated parameter from the model.

Remarks

Remarks are presented under the following headings:

Obtaining predicted values
Performing hypothesis tests

Obtaining predicted values

Once you have fit a probit model, you can obtain the predicted probabilities by using the `predict` command for both the estimation sample and other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**. Here we will make only a few additional comments.

`predict` without arguments calculates the predicted probability of a positive outcome. With the `xb` option, `predict` calculates the linear combination $\mathbf{x}_j\mathbf{b}$, where $\mathbf{x}_j$ are the independent variables in the jth observation and $\mathbf{b}$ is the estimated parameter vector. This is known as the index function because the cumulative density indexed at this value is the probability of a positive outcome.

In both cases, Stata remembers any rules used to identify the model and calculates missing for excluded observations unless `rules` or `asif` is specified. This is covered in the following example.

With the `stdp` option, `predict` calculates the standard error of the prediction, which is *not* adjusted for replicated covariate patterns in the data.

You can calculate the unadjusted-for-replicated-covariate-patterns diagonal elements of the hat matrix, or leverage, by typing

```
. predict pred
. predict stdp, stdp
. generate hat = stdp^2*pred*(1-pred)
```

▷ Example 1

In example 4 of [R] **probit**, we fit the probit model `probit foreign b3.repair`. To obtain predicted probabilities, we type

```
. predict p
(option pr assumed; Pr(foreign))
(10 missing values generated)
. summarize foreign p
```

Variable	Obs	Mean	Std. Dev.	Min	Max
foreign	58	.2068966	.4086186	0	1
p	48	.25	.1956984	.1	.5

Stata remembers any rules used to identify the model and sets predictions to missing for any excluded observations. In the previous example, `probit` dropped the variable `1.repair` from our model and excluded 10 observations. When we typed `predict p`, those same 10 observations were again excluded and their predictions set to missing.

`predict`'s `rules` option uses the rules in the prediction. During estimation, we were told, "1.repair != 0 predicts failure perfectly", so the rule is that when `1.repair` is not zero, we should predict 0 probability of success or a positive outcome:

```
. predict p2, rules
. summarize foreign p p2
```

Variable	Obs	Mean	Std. Dev.	Min	Max
foreign	58	.2068966	.4086186	0	1
p	48	.25	.1956984	.1	.5
p2	58	.2068966	.2016268	0	.5

`predict`'s `asif` option ignores the rules and the exclusion criteria and calculates predictions for all observations possible using the estimated parameters from the model:

```
. predict p3, asif
. summarize for p p2 p3
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
     foreign |         58    .2068966    .4086186         0          1
           p |         48         .25    .1956984        .1         .5
          p2 |         58    .2068966    .2016268         0         .5
          p3 |         58    .2931034    .2016268        .1         .5
```

Which is right? By default, `predict` uses the most conservative approach. If many observations had been excluded due to a simple rule, we could be reasonably certain that the `rules` prediction is correct. The `asif` prediction is correct only if the exclusion is a fluke and we would be willing to exclude the variable from the analysis, anyway. Then, however, we should refit the model to include the excluded observations. ◁

Performing hypothesis tests

After estimation with `probit`, you can perform hypothesis tests by using the `test` or `testnl` command; see [U] **20 Estimation and postestimation commands**.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

predict after probit

Let index j be used to index observations, not covariate patterns. Define M_j for each observation as the total number of observations sharing j's covariate pattern. Define Y_j as the total number of positive responses among observations sharing j's covariate pattern. Define p_j as the predicted probability of a positive outcome for observation j.

For $M_j > 1$, the deviance residual d_j is defined as

$$d_j = \pm\left(2\left[Y_j \ln\left(\frac{Y_j}{M_j p_j}\right) + (M_j - Y_j)\ln\left\{\frac{M_j - Y_j}{M_j(1-p_j)}\right\}\right]\right)^{1/2}$$

where the sign is the same as the sign of $(Y_j - M_j p_j)$. In the limiting cases, the deviance residual is given by

$$d_j = \begin{cases} -\sqrt{2M_j|\ln(1-p_j)|} & \text{if } Y_j = 0 \\ \sqrt{2M_j|\ln p_j|} & \text{if } Y_j = M_j \end{cases}$$

Also see

[R] **probit** — Probit regression

[R] **logistic postestimation** — Postestimation tools for logistic

[U] **20 Estimation and postestimation commands**

Title

proportion — Estimate proportions

Syntax

```
proportion varlist [if] [in] [weight] [, options]
```

options	Description
Model	
`stdize(`*varname*`)`	variable identifying strata for standardization
`stdweight(`*varname*`)`	weight variable for standardization
`nostdrescale`	do not rescale the standard weight variable
`nolabel`	suppress value labels from *varlist*
`missing`	treat missing values like other values
if/in/over	
`over(`*varlist*`[ , nolabel ])`	group over subpopulations defined by *varlist*; optionally, suppress group labels
SE/Cluster	
`vce(`*vcetype*`)`	*vcetype* may be `analytic`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noheader`	suppress table header
`nolegend`	suppress table legend
display_options	control column formats and line width
`coeflegend`	display legend instead of statistics

`bootstrap`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Proportions

Description

`proportion` produces estimates of proportions, along with standard errors, for the categories identified by the values in each variable of *varlist*.

Options

Model

`stdize(`*varname*`)` specifies that the point estimates be adjusted by direct standardization across the strata identified by *varname*. This option requires the `stdweight()` option.

`stdweight(`*varname*`)` specifies the weight variable associated with the standard strata identified in the `stdize()` option. The standardization weights must be constant within the standard strata.

`nostdrescale` prevents the standardization weights from being rescaled within the `over()` groups. This option requires `stdize()` but is ignored if the `over()` option is not specified.

`nolabel` specifies that value labels attached to the variables in *varlist* be ignored.

`missing` specifies that missing values in *varlist* be treated as valid categories, rather than omitted from the analysis (the default).

if/in/over

`over(`*varlist* [`, nolabel`]`)` specifies that estimates be computed for multiple subpopulations, which are identified by the different values of the variables in *varlist*.

When this option is supplied with one variable name, such as `over(`*varname*`)`, the value labels of *varname* are used to identify the subpopulations. If *varname* does not have labeled values (or there are unlabeled values), the values themselves are used, provided that they are nonnegative integers. Noninteger values, negative values, and labels that are not valid Stata names are substituted with a default identifier.

When `over()` is supplied with multiple variable names, each subpopulation is assigned a unique default identifier.

`nolabel` requests that value labels attached to the variables identifying the subpopulations be ignored.

SE/Cluster

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(analytic)`, the default, uses the analytically derived variance estimator associated with the sample proportion.

Reporting

`level(#)`; see [R] **estimation options**.

`noheader` prevents the table header from being displayed. This option implies `nolegend`.

`nolegend` prevents the table legend identifying the subpopulations from being displayed.

display_options: `cformat(%`*fmt*`)` and `nolstretch`; see [R] **estimation options**.

The following option is available with `proportion` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

▷ Example 1

We can estimate the proportion of each repair rating in the auto data:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. proportion rep78
Proportion estimation                 Number of obs    =        69
```

	Proportion	Std. Err.	[95% Conf.	Interval]
rep78				
1	.0289855	.0203446	-.0116115	.0695825
2	.115942	.0388245	.0384689	.1934152
3	.4347826	.0601159	.3148232	.554742
4	.2608696	.0532498	.1546113	.3671278
5	.1594203	.0443922	.070837	.2480036

Here we use the `missing` option to include missing values as a category of `rep78`:

```
. proportion rep78, missing
Proportion estimation                 Number of obs    =        74
      _prop_6: rep78 = .
```

	Proportion	Std. Err.	[95% Conf.	Interval]
rep78				
1	.027027	.0189796	-.0107994	.0648534
2	.1081081	.0363433	.0356761	.1805401
3	.4054054	.0574637	.2908804	.5199305
4	.2432432	.0502154	.1431641	.3433224
5	.1486486	.0416364	.0656674	.2316299
_prop_6	.0675676	.0293776	.0090181	.1261171

◁

▷ Example 2

We can also estimate proportions over groups:

```
. proportion rep78, over(foreign)
Proportion estimation                Number of obs    =      69

       _prop_1: rep78 = 1
       _prop_2: rep78 = 2
       _prop_3: rep78 = 3
       _prop_4: rep78 = 4
       _prop_5: rep78 = 5
      Domestic: foreign = Domestic
       Foreign: foreign = Foreign
```

Over	Proportion	Std. Err.	[95% Conf.	Interval]
_prop_1				
Domestic	.0416667	.0291477	-.0164966	.0998299
Foreign	.	(no observations)		
_prop_2				
Domestic	.1666667	.0543607	.0581916	.2751417
Foreign	.	(no observations)		
_prop_3				
Domestic	.5625	.0723605	.4181069	.7068931
Foreign	.1428571	.0782461	-.0132805	.2989948
_prop_4				
Domestic	.1875	.0569329	.0738921	.3011079
Foreign	.4285714	.1106567	.2077595	.6493834
_prop_5				
Domestic	.0416667	.0291477	-.0164966	.0998299
Foreign	.4285714	.1106567	.2077595	.6493834

◁

Saved results

`proportion` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_over)`	number of subpopulations
`e(N_stdize)`	number of standard strata
`e(N_clust)`	number of clusters
`e(k_eq)`	number of equations in `e(b)`
`e(df_r)`	sample degrees of freedom
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`proportion`
`e(cmdline)`	command as typed
`e(varlist)`	*varlist*
`e(stdize)`	*varname* from `stdize()`
`e(stdweight)`	*varname* from `stdweight()`
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(cluster)`	name of cluster variable

e(over)	*varlist* from over()
e(over_labels)	labels from over() variables
e(over_namelist)	names from e(over_labels)
e(namelist)	proportion identifiers
e(label#)	labels from #th variable in *varlist*
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(marginsnotok)	predictions disallowed by margins
Matrices	
e(b)	vector of proportion estimates
e(V)	(co)variance estimates
e(_N)	vector of numbers of nonmissing observations
e(_N_stdsum)	number of nonmissing observations within the standard strata
e(_p_stdize)	standardizing proportions
e(error)	error code corresponding to e(b)
Functions	
e(sample)	marks estimation sample

Methods and formulas

proportion is implemented as an ado-file.

Proportions are means of indicator variables; see [R] **mean**.

References

Cochran, W. G. 1977. *Sampling Techniques*. 3rd ed. New York: Wiley.

Stuart, A., and J. K. Ord. 1994. *Kendall's Advanced Theory of Statistics: Distribution Theory, Vol I*. 6th ed. London: Arnold.

Also see

[R] **proportion postestimation** — Postestimation tools for proportion

[R] **mean** — Estimate means

[R] **ratio** — Estimate ratios

[R] **total** — Estimate totals

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **poststratification** — Poststratification for survey data

[SVY] **subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **variance estimation** — Variance estimation for survey data

[U] **20 Estimation and postestimation commands**

Title

proportion postestimation — Postestimation tools for proportion

Description

The following postestimation commands are available after `proportion`:

Command	Description
`estat`	VCE
`estat` (svy)	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **proportion** — Estimate proportions

[SVY] **svy postestimation** — Postestimation tools for svy

[U] **20 Estimation and postestimation commands**

Title

prtest — One- and two-sample tests of proportions

Syntax

One-sample test of proportion

```
prtest varname == #p [if] [in] [, level(#)]
```

Two-sample test of proportions

```
prtest varname1 == varname2 [if] [in] [, level(#)]
```

Two-group test of proportions

```
prtest varname [if] [in], by(groupvar) [level(#)]
```

Immediate form of one-sample test of proportion

```
prtesti #obs1 #p1 #p2 [, level(#) count]
```

Immediate form of two-sample test of proportions

```
prtesti #obs1 #p1 #obs2 #p2 [, level(#) count]
```

`by` is allowed with `prtest`; see [D] **by**.

Menu

one-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > One-sample proportion test

two-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-sample proportion test

two-group

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-group proportion test

immediate command: one-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > One-sample proportion calculator

immediate command: two-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-sample proportion calculator

Description

`prtest` performs tests on the equality of proportions using large-sample statistics.

In the first form, `prtest` tests that *varname* has a proportion of $\#_p$. In the second form, `prtest` tests that $varname_1$ and $varname_2$ have the same proportion. In the third form, `prtest` tests that *varname* has the same proportion within the two groups defined by *groupvar*.

`prtesti` is the immediate form of `prtest`; see [U] **19 Immediate commands**.

The `bitest` command is a better version of the first form of `prtest` in that it gives exact p-values. Researchers should use `bitest` when possible, especially for small samples; see [R] **bitest**.

Options

Main

`by(`*groupvar*`)` specifies a numeric variable that contains the group information for a given observation. This variable must have only two values. Do not confuse the `by()` option with the `by` prefix; both may be specified.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`count` specifies that integer counts instead of proportions be used in the immediate forms of `prtest`. In the first syntax, `prtesti` expects that $\#_{\text{obs1}}$ and $\#_{p1}$ are counts—$\#_{p1} \leq \#_{\text{obs1}}$—and $\#_{p2}$ is a proportion. In the second syntax, `prtesti` expects that all four numbers are integer counts, that $\#_{\text{obs1}} \geq \#_{p1}$, and that $\#_{\text{obs2}} \geq \#_{p2}$.

Remarks

The `prtest` output follows the output of `ttest` in providing a lot of information. Each proportion is presented along with a confidence interval. The appropriate one- or two-sample test is performed, and the two-sided and both one-sided results are included at the bottom of the output. For a two-sample test, the calculated difference is also presented with its confidence interval. This command may be used for both large-sample testing and large-sample interval estimation.

▷ Example 1: One-sample test of proportion

In the first form, `prtest` tests whether the mean of the sample is equal to a known constant. Assume that we have a sample of 74 automobiles. We wish to test whether the proportion of automobiles that are foreign is different from 40%.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. prtest foreign == .4
One-sample test of proportion                 foreign: Number of obs =       74
------------------------------------------------------------------------------
    Variable |       Mean   Std. Err.                     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     foreign |   .2972973   .0531331                      .1931583    .4014363
------------------------------------------------------------------------------
    p = proportion(foreign)                                       z =  -1.8034
Ho: p = 0.4

     Ha: p < 0.4                 Ha: p != 0.4                 Ha: p > 0.4
 Pr(Z < z) = 0.0357         Pr(|Z| > |z|) = 0.0713          Pr(Z > z) = 0.9643
```

The test indicates that we cannot reject the hypothesis that the proportion of foreign automobiles is 0.40 at the 5% significance level.

◁

▷ Example 2: Two-sample test of proportions

We have two headache remedies that we give to patients. Each remedy's effect is recorded as 0 for failing to relieve the headache and 1 for relieving the headache. We wish to test the equality of the proportion of people relieved by the two treatments.

```
. use http://www.stata-press.com/data/r12/cure
. prtest cure1 == cure2
Two-sample test of proportions                  cure1: Number of obs =       50
                                                cure2: Number of obs =       59
------------------------------------------------------------------------------
    Variable |       Mean   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       cure1 |         .52   .0706541                      .3815205    .6584795
       cure2 |   .7118644   .0589618                      .5963013    .8274275
-------------+----------------------------------------------------------------
        diff |  -.1918644   .0920245                     -.372229   -.0114998
             |  under Ho:   .0931155    -2.06   0.039
------------------------------------------------------------------------------
       diff = prop(cure1) - prop(cure2)                          z =  -2.0605
   Ho: diff = 0

   Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(Z < z) = 0.0197         Pr(|Z| < |z|) = 0.0394          Pr(Z > z) = 0.9803
```

We find that the proportions are statistically different from each other at any level greater than 3.9%.

◁

▷ Example 3: Immediate form of one-sample test of proportion

`prtesti` is like `prtest`, except that you specify summary statistics rather than variables as arguments. For instance, we are reading an article that reports the proportion of registered voters among 50 randomly selected eligible voters as 0.52. We wish to test whether the proportion is 0.7:

```
. prtesti 50 .52 .70
One-sample test of proportion                       x: Number of obs =       50
------------------------------------------------------------------------------
    Variable |       Mean   Std. Err.                      [95% Conf. Interval]
-------------+----------------------------------------------------------------
           x |         .52   .0706541                      .3815205    .6584795
------------------------------------------------------------------------------
       p = proportion(x)                                         z =  -2.7775
Ho: p = 0.7

    Ha: p < 0.7                  Ha: p != 0.7                  Ha: p > 0.7
 Pr(Z < z) = 0.0027         Pr(|Z| > |z|) = 0.0055          Pr(Z > z) = 0.9973
```

◁

▷ Example 4: Immediate form of two-sample test of proportions

To judge teacher effectiveness, we wish to test whether the same proportion of people from two classes will answer an advanced question correctly. In the first classroom of 30 students, 40% answered the question correctly, whereas in the second classroom of 45 students, 67% answered the question correctly.

```
. prtesti 30 .4 45 .67
Two-sample test of proportions                     x: Number of obs =       30
                                                   y: Number of obs =       45
------------------------------------------------------------------------------
    Variable |       Mean   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
           x |         .4   .0894427                      .2246955    .5753045
           y |        .67   .0700952                       .532616     .807384
-------------+----------------------------------------------------------------
        diff |       -.27   .1136368                     -.4927241   -.0472759
             |  under Ho:   .1169416    -2.31   0.021
------------------------------------------------------------------------------
        diff = prop(x) - prop(y)                                  z =  -2.3088
    Ho: diff = 0

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(Z < z) = 0.0105         Pr(|Z| < |z|) = 0.0210          Pr(Z > z) = 0.9895
```

◁

Saved results

`prtest` and `prtesti` save the following in `r()`:

Scalars

`r(z)`	z statistic	`r(N_#)`	number of observations for variable #
`r(P_#)`	proportion for variable #		

Methods and formulas

`prtest` and `prtesti` are implemented as ado-files.

See Acock (2010, 149–155) for additional examples of tests of proportions using Stata.

A large-sample $100(1-\alpha)\%$ confidence interval for a proportion p is

$$\widehat{p} \pm z_{1-\alpha/2}\sqrt{\frac{\widehat{p}\,\widehat{q}}{n}}$$

and a $100(1-\alpha)\%$ confidence interval for the difference of two proportions is given by

$$(\widehat{p}_1 - \widehat{p}_2) \pm z_{1-\alpha/2}\sqrt{\frac{\widehat{p}_1\widehat{q}_1}{n_1} + \frac{\widehat{p}_2\widehat{q}_2}{n_2}}$$

where $\widehat{q} = 1 - \widehat{p}$ and z is calculated from the inverse cumulative standard normal distribution.

The one-tailed and two-tailed tests of a population proportion use a normally distributed test statistic calculated as

$$z = \frac{\widehat{p} - p_0}{\sqrt{p_0 q_0 / n}}$$

where p_0 is the hypothesized proportion. A test of the difference of two proportions also uses a normally distributed test statistic calculated as

$$z = \frac{\widehat{p}_1 - \widehat{p}_2}{\sqrt{\widehat{p}_p \widehat{q}_p (1/n_1 + 1/n_2)}}$$

where

$$\widehat{p}_p = \frac{x_1 + x_2}{n_1 + n_2}$$

and x_1 and x_2 are the total number of successes in the two populations.

References

Acock, A. C. 2010. *A Gentle Introduction to Stata*. 3rd ed. College Station, TX: Stata Press.

Wang, D. 2000. sg154: Confidence intervals for the ratio of two binomial proportions by Koopman's method. *Stata Technical Bulletin* 58: 16–19. Reprinted in *Stata Technical Bulletin Reprints*, vol. 10, pp. 244–247. College Station, TX: Stata Press.

Also see

[R] **bitest** — Binomial probability test

[R] **proportion** — Estimate proportions

[R] **ttest** — Mean-comparison tests

[MV] **hotelling** — Hotelling's T-squared generalized means test

Title

pwcompare — Pairwise comparisons

Syntax

`pwcompare` *marginlist* [`,` *options*]

where *marginlist* is a list of factor variables or interactions that appear in the current estimation results or `_eqns` to reference equations. The variables may be typed with or without the `i.` prefix, and you may use any factor-variable syntax:

```
. pwcompare i.sex i.group i.sex#i.group
. pwcompare sex group sex#group
. pwcompare sex##group
```

options	Description
Main	
`mcompare(`*method*`)`	adjust for multiple comparisons; default is `mcompare(noadjust)`
`asobserved`	treat all factor variables as observed
Equations	
`equation(`*eqspec*`)`	perform comparisons within equation *eqspec*
`atequations`	perform comparisons within each equation
Advanced	
`emptycells(`*empspec*`)`	treatment of empty cells for balanced factors
`noestimcheck`	suppress estimability checks
Reporting	
`level(#)`	confidence level; default is `level(95)`
`cieffects`	show effects table with confidence intervals; the default
`pveffects`	show effects table with p-values
`effects`	show effects table with confidence intervals and p-values
`cimargins`	show table of margins and confidence intervals
`groups`	show table of margins and group codes
`sort`	sort the margins or contrasts within each term
`post`	post margins and their VCEs as estimation results
display_options	control column formats, line width, and suppress blank lines between terms
eform_option	report exponentiated contrasts

method	Description
noadjust	do not adjust for multiple comparisons; the default
bonferroni [adjustall]	Bonferroni's method; adjust across all terms
sidak [adjustall]	Šidák's method; adjust across all terms
scheffe	Scheffé's method
* tukey	Tukey's method
* snk	Student–Newman–Keuls' method
* duncan	Duncan's method
* dunnett	Dunnett's method

* tukey, snk, duncan, and dunnett are only allowed with results from anova, manova, regress, and mvreg. tukey, snk, duncan, and dunnett are not allowed with results from svy.

Time-series operators are allowed if they were used in the estimation.

Menu

Statistics > Postestimation > Pairwise comparisons

Description

pwcompare performs pairwise comparisons across the levels of factor variables from the most recently fit model. pwcompare can compare estimated cell means, marginal means, intercepts, marginal intercepts, slopes, or marginal slopes—collectively called margins. pwcompare reports the comparisons as contrasts (differences) of margins along with significance tests or confidence intervals for the contrasts. The tests and confidence intervals can be adjusted for multiple comparisons.

pwcompare can be used with svy estimation results; see [SVY] **svy postestimation**.

See [R] **margins, pwcompare** for performing pairwise comparisons of margins of linear and nonlinear predictions.

Options

Main

mcompare(*method*) specifies the method for computing p-values and confidence intervals that account for multiple comparisons within a factor-variable term.

Most methods adjust the comparisonwise error rate, α_c, to achieve a prespecified experimentwise error rate, α_e.

mcompare(noadjust) is the default; it specifies no adjustment.

$$\alpha_c = \alpha_e$$

mcompare(bonferroni) adjusts the comparisonwise error rate based on the upper limit of the Bonferroni inequality:

$$\alpha_e \leq m\alpha_c$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = \alpha_e/m$$

`mcompare(sidak)` adjusts the comparisonwise error rate based on the upper limit of the probability inequality

$$\alpha_e \leq 1 - (1 - \alpha_c)^m$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = 1 - (1 - \alpha_e)^{1/m}$$

This adjustment is exact when the m comparisons are independent.

`mcompare(scheffe)` controls the experimentwise error rate using the F (or χ^2) distribution with degrees of freedom equal to the rank of the term.

For results from `anova`, `regress`, `manova`, and `mvreg` (see [R] **anova**, [R] **regress**, [MV] **manova**, and [R] **mvreg**), `pwcompare` allows the following additional methods. These methods are not allowed with results that used `vce(robust)` or `vce(cluster` *clustvar*`)`.

`mcompare(tukey)` uses what is commonly referred to as Tukey's honestly significant difference. This method uses the Studentized range distribution instead of the t distribution.

`mcompare(snk)` is a variation on `mcompare(tukey)` that counts only the number of margins in the range for a given comparison instead of the full number of margins.

`mcompare(duncan)` is a variation on `mcompare(snk)` with additional adjustment to the significance probabilities.

`mcompare(dunnett)` uses Dunnett's method for making comparisons with a reference category.

`mcompare(`*method* `adjustall)` specifies that the multiple-comparison adjustments count all comparisons across all terms rather than performing multiple comparisons term by term. This leads to more conservative adjustments when multiple variables or terms are specified in *marginlist*. This option is compatible only with the `bonferroni` and `sidak` methods.

`asobserved` specifies that factor covariates be evaluated using the cell frequencies observed when the model was fit. The default is to treat all factor covariates as though there were an equal number of observations at each level.

Equations

`equation(`*eqspec*`)` specifies the equation from which margins are to be computed. The default is to compute margins from the first equation.

`atequations` specifies that the margins be computed within each equation.

Advanced

`emptycells(`*empspec*`)` specifies how empty cells are handled in interactions involving factor variables that are being treated as balanced.

`emptycells(strict)` is the default; it specifies that margins involving empty cells be treated as not estimable.

`emptycells(reweight)` specifies that the effects of the observed cells be increased to accommodate any missing cells. This makes the margins estimable but changes their interpretation.

`noestimcheck` specifies that `pwcompare` not check for estimability. By default, the requested margins are checked and those found not estimable are reported as such. Nonestimability is usually caused by empty cells. If `noestimcheck` is specified, estimates are computed in the usual way and reported even though the resulting estimates are manipulable, which is to say they can differ across equivalent models having different parameterizations.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**. The significance level used by the `groups` option is $100 - \#$, expressed as a percentage.

`cieffects` specifies that a table of the pairwise comparisons with their standard errors and confidence intervals be reported. This is the default.

`pveffects` specifies that a table of the pairwise comparisons with their standard errors, test statistics, and p-values be reported.

`effects` specifies that a table of the pairwise comparisons with their standard errors, test statistics, p-values, and confidence intervals be reported.

`cimargins` specifies that a table of the margins with their standard errors and confidence intervals be reported.

`groups` specifies that a table of the margins with their standard errors and group codes be reported. Margins with the same letter in the group code are not significantly different at the specified significance level.

`sort` specifies that the reported tables be sorted on the margins or differences in each term.

`post` causes `pwcompare` to behave like a Stata estimation (e-class) command. `pwcompare` posts the vector of estimated margins along with the estimated variance–covariance matrix to `e()`, so you can treat the estimated margins just as you would results from any other estimation command. For example, you could use `test` to perform simultaneous tests of hypotheses on the margins, or you could use `lincom` to create linear combinations.

display_options: `vsquish`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`.

`vsquish` specifies that the blank space separating factor-variable terms or time-series–operated variables from other variables in the model be suppressed.

`cformat(%`*fmt*`)` specifies how to format contrasts or margins, standard errors, and confidence limits in the table of pairwise comparisons.

`pformat(%`*fmt*`)` specifies how to format p-values in the table of pairwise comparisons.

`sformat(%`*fmt*`)` specifies how to format test statistics in the table of pairwise comparisons.

`nolstretch` specifies that the width of the table of pairwise comparisons not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the table of pairwise comparisons up to the width of the Results window. To change the default, use `set lstretch off`. `nolstretch` is not shown in the dialog box.

eform_option specifies that the contrasts table be displayed in exponentiated form. e^{contrast} is displayed rather than contrast. Standard errors and confidence intervals are also transformed. See [R] ***eform_option*** for the list of available options.

Remarks

`pwcompare` performs pairwise comparisons of margins across the levels of factor variables from the most recently fit model. The margins can be estimated cell means, marginal means, intercepts, marginal intercepts, slopes, or marginal slopes. With the exception of slopes, we can also consider these margins to be marginal linear predictions.

The margins are calculated as linear combinations of the coefficients. Let k be the number of levels for a factor term in our model; then there are k margins for that term, and

$$m = \binom{k}{2} = \frac{k(k-1)}{2}$$

unique pairwise comparisons of those margins.

The confidence intervals and p-values for these pairwise comparisons can be adjusted to account for multiple comparisons. Bonferroni's, Šidák's, and Scheffé's adjustments can be made for multiple comparisons after fitting any type of model. In addition, Tukey's, Student–Newman–Keuls', Duncan's, and Dunnett's adjustments are available when fitting ANOVA, linear regression, MANOVA, or multivariate regression models.

Remarks are presented under the following headings:

Pairwise comparisons of means
  Marginal means
  All pairwise comparisons
Overview of multiple-comparison methods
  Fisher's protected least-significant difference (LSD)
  Bonferroni's adjustment
  Šidák's adjustment
  Scheffé's adjustment
  Tukey's HSD adjustment
  Student–Newman–Keuls' adjustment
  Duncan's adjustment
  Dunnett's adjustment
Example adjustments using one-way models
  Fisher's protected LSD
  Tukey's HSD
  Dunnett's method for comparisons to a control
Two-way models
Pairwise comparisons of slopes
Nonlinear models
Multiple-equation models
Unbalanced data
Empty cells

Pairwise comparisons of means

Suppose we are interested in the effects of five different fertilizers on wheat yield. We could estimate the following linear regression model to determine the effect of each type of fertilizer on the yield.

```
. use http://www.stata-press.com/data/r12/yield
(Artificial wheat yield dataset)
. regress yield i.fertilizer
```

Source	SS	df	MS	Number of obs =	200
				F(4, 195) =	5.33
Model	1078.84207	4	269.710517	Prob > F =	0.0004
Residual	9859.55334	195	50.561812	R-squared =	0.0986
				Adj R-squared =	0.0801
Total	10938.3954	199	54.9668111	Root MSE =	7.1107

yield	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
fertilizer						
2	3.62272	1.589997	2.28	0.024	.4869212	6.758518
3	.4906299	1.589997	0.31	0.758	-2.645169	3.626428
4	4.922803	1.589997	3.10	0.002	1.787005	8.058602
5	-1.238328	1.589997	-0.78	0.437	-4.374127	1.89747
_cons	41.36243	1.124298	36.79	0.000	39.14509	43.57977

In this simple case, the coefficients for fertilizers 2 through 5 indicate the difference in the mean yield for that fertilizer versus the mean yield for fertilizer 1. That the standard errors of all four coefficients are identical results from having perfectly balanced data.

Marginal means

We can use `pwcompare` with the `cimargins` option to compute the mean yield for each of the fertilizers.

```
. pwcompare fertilizer, cimargins
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Margin	Std. Err.	Unadjusted [95% Conf.	Interval]
fertilizer				
1	41.36243	1.124298	39.14509	43.57977
2	44.98515	1.124298	42.7678	47.20249
3	41.85306	1.124298	39.63571	44.0704
4	46.28523	1.124298	44.06789	48.50258
5	40.1241	1.124298	37.90676	42.34145

Looking at the confidence intervals for fertilizers 1 and 2 in the table above, we might be tempted to conclude that these means are not significantly different because the intervals overlap. However, as discussed in *Interaction plots* of [R] **marginsplot**, we cannot draw conclusions about the differences in means by looking at confidence intervals for the means themselves. Instead, we would need to look at confidence intervals for the difference in means.

All pairwise comparisons

By default, `pwcompare` calculates all pairwise differences of the margins, in this case pairwise differences of the mean yields.

```
. pwcompare fertilizer
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	Unadjusted [95% Conf.	Interval]
fertilizer				
2 vs 1	3.62272	1.589997	.4869212	6.758518
3 vs 1	.4906299	1.589997	-2.645169	3.626428
4 vs 1	4.922803	1.589997	1.787005	8.058602
5 vs 1	-1.238328	1.589997	-4.374127	1.89747
3 vs 2	-3.13209	1.589997	-6.267889	.0037086
4 vs 2	1.300083	1.589997	-1.835715	4.435882
5 vs 2	-4.861048	1.589997	-7.996847	-1.725249
4 vs 3	4.432173	1.589997	1.296375	7.567972
5 vs 3	-1.728958	1.589997	-4.864757	1.406841
5 vs 4	-6.161132	1.589997	-9.29693	-3.025333

If a confidence interval does not include zero, the means for the compared fertilizers are significantly different. Therefore, at the 5% significance level, we would reject the hypothesis that the means for fertilizers 1 and 2 are equivalent—as we would do for `4 vs 1`, `5 vs 2`, `4 vs 3`, and `5 vs 4`.

We may prefer to see the p-values instead of looking at confidence intervals to determine whether the pairwise differences are significantly different from zero. We could use the `pveffects` option to see the differences with standard errors and p-values, or we could use the `effects` option to see both p-values and confidence intervals in the same table. Here we specify `effects` as well as the `sort` option so that the differences are sorted from smallest to largest.

```
. pwcompare fertilizer, effects sort
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	Unadjusted t	Unadjusted P>|t|	Unadjusted [95% Conf.	Interval]
fertilizer						
5 vs 4	-6.161132	1.589997	-3.87	0.000	-9.29693	-3.025333
5 vs 2	-4.861048	1.589997	-3.06	0.003	-7.996847	-1.725249
3 vs 2	-3.13209	1.589997	-1.97	0.050	-6.267889	.0037086
5 vs 3	-1.728958	1.589997	-1.09	0.278	-4.864757	1.406841
5 vs 1	-1.238328	1.589997	-0.78	0.437	-4.374127	1.89747
3 vs 1	.4906299	1.589997	0.31	0.758	-2.645169	3.626428
4 vs 2	1.300083	1.589997	0.82	0.415	-1.835715	4.435882
2 vs 1	3.62272	1.589997	2.28	0.024	.4869212	6.758518
4 vs 3	4.432173	1.589997	2.79	0.006	1.296375	7.567972
4 vs 1	4.922803	1.589997	3.10	0.002	1.787005	8.058602

We find that 5 of the 10 pairs of means are significantly different at the 5% significance level.

We can use the `groups` option to obtain a table that identifies groups whose means are not significantly different by assigning them the same letter.

```
. pwcompare fertilizer, groups sort
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Margin	Std. Err.	Unadjusted Groups
fertilizer			
5	40.1241	1.124298	A
1	41.36243	1.124298	A
3	41.85306	1.124298	AB
2	44.98515	1.124298	BC
4	46.28523	1.124298	C

```
Note: Margins sharing a letter in the group label
      are not significantly different at the 5%
      level.
```

The letter A that is assigned to fertilizers 5, 1, and 3 designates that the mean yields for these fertilizers are not different at the 5% level.

Overview of multiple-comparison methods

For a single test, if we choose a 5% significance level, we would have a 5% chance of concluding that two margins are different when the population values are actually equal. This is known as making a type I error. When we perform $m = k(k-1)/2$ pairwise comparisons of the k margins, we have m opportunities to make a type I error.

pwcompare with the mcompare() option allows us to adjust the confidence intervals and p-values for each comparison to account for the increased probability of making a type I error when making multiple comparisons. Bonferroni's adjustment, Šidák's adjustment, and Scheffé's adjustment can be used when making pairwise comparisons of the margins after any estimation command. Tukey's honestly significant difference, Student–Newman–Keuls' method, Duncan's method, and Dunnett's method are only available when fitting linear models after anova, manova, regress, or mvreg.

Fisher's protected least-significant difference (LSD)

pwcompare does not offer an mcompare() option specifically for Fisher's protected least-significant difference (LSD). In this methodology, no adjustment is made to the confidence intervals or p-values. However, it is protected in the sense that no pairwise comparisons are tested unless the joint test for the corresponding term in the model is significant. Therefore, the default mcompare(noadjust) corresponds to Fisher's protected LSD assuming that the corresponding joint test was performed before using pwcompare.

Milliken and Johnson (2009) recommend using this methodology for planned comparisons, assuming the corresponding joint test is significant.

Bonferroni's adjustment

mcompare(bonferroni) adjusts significance levels based on the Bonferroni inequality, which, in the case of multiple testing, tells us that the maximum error rate for all comparisons is the sum of the error rates for the individual comparisons. Assuming that we are using the same significance level for all tests, the experimentwise error rate is the error rate for a single test multiplied by the

number of comparisons. Therefore, a p-value for each comparison can be computed by multiplying the unadjusted p-value by the total number of comparisons. If the adjusted p-value is greater than 1, then `pwcompare` will report a p-value of 1.

Bonferroni's adjustment is popular because it is easy to compute manually and because it can be applied to any set of tests, not only the pairwise comparisons available in `pwcompare`. In addition, this method does not require equal sample sizes.

Because Bonferroni's adjustment is so general, it is more conservative than many of the other adjustments. It is especially conservative when a large number of tests is being performed.

Šidák's adjustment

`mcompare(sidak)` performs an adjustment using Šidák's method. This adjustment, like Bonferroni's adjustment, is derived from an inequality. However, in this case, the inequality is based on the probability of not making a type I error. For a single test, the probability that we do not make a type I error is $1 - \alpha$. For two independent tests, both using α as a significance level, the probability is $(1 - \alpha)(1 - \alpha)$. Likewise, for m independent tests, the probability of not making a type I error is $(1 - \alpha)^m$. Therefore, the probability of making one or more type I errors is $1 - (1 - \alpha)^m$. When tests are not independent, the probability of making at least one error is less than $1 - (1 - \alpha)^m$. Therefore, we can compute an adjusted p-value as $1 - (1 - {}_up)^m$, where ${}_up$ is the unadjusted p-value for a single comparison.

Šidák's method is also conservative although slightly less so than Bonferroni's method. Like Bonferroni's method, this method does not require equal sample sizes.

Scheffé's adjustment

Scheffé's adjustment is used when `mcompare(scheffe)` is specified. This adjustment is derived from the joint F test and its correspondence to the maximum normalized comparison. To adjust for multiple comparisons, the absolute value of the t statistic for a particular comparison can be compared with a critical value of $\sqrt{(k-1)F_{k-1,\nu}}$, where ν is the residual degrees of freedom. $F_{k-1,\nu}$ is the distribution of the joint F test for the corresponding term in a one-way ANOVA model. Winer, Brown, and Michels (1991, 191–195) discuss this in detail. For estimation commands that report z statistics instead of t statistics for the tests on coefficients, a χ^2 distribution is used instead of an F distribution.

Scheffé's method allows for making all possible comparisons of the k margins, not just the pairwise comparisons. Unlike the methods described above, it does not take into account the number of comparisons that are currently being made. Therefore, this method is even more conservative than the others. Because this method adjusts for all possible comparisons of the levels of the term, Milliken and Johnson (2009) recommend using this procedure when making unplanned contrasts that are suggested by the data. As Winer, Brown, and Michels (1991, 191) put it, this method is often used to adjust for "unfettered data snooping". When using this adjustment, a contrast will never be significant if the joint F or χ^2 test for the term is not also significant.

This is another method that does not require equal sample sizes.

Tukey's HSD adjustment

Tukey's adjustment is also referred to as Tukey's honestly significant difference (HSD) and is used when `mcompare(tukey)` is specified. It is often applied to all pairwise comparisons of means. Tukey's HSD is commonly used as a post hoc test although this is not a requirement.

To adjust for multiple comparisons, Tukey's method compares the absolute value of the t statistic from the individual comparison with a critical value based on a Studentized range distribution with parameter equal to the number of levels in the term. When applied to pairwise comparisons of means,

$$q = \frac{\text{mean}_{\max} - \text{mean}_{\min}}{s}$$

follows a Studentized range distribution with parameter k and ν degrees of freedom. Here $\text{mean}_{\max}$ and $\text{mean}_{\min}$ are the largest and smallest marginal means, and s is an estimate of the standard error of the means.

Now for the comparison of the smallest and largest means, we can say that the probability of not making a type I error is

$$\Pr\left(\frac{\text{mean}_{\max} - \text{mean}_{\min}}{s} \leq q_{k,\nu}\right) = 1 - \alpha$$

Then the following inquality holds for all pairs of means simultaneously:

$$\Pr\left(\frac{|\text{mean}_i - \text{mean}_j|}{s} \leq q_{k,\nu}\right) \geq 1 - \alpha$$

Based on this procedure, Tukey's HSD computes the p-value for each of the individual comparisons using the Studentized range distribution. However, because the equality holds only for the difference in the largest and smallest means, this procedure produces conservative tests for the remaining comparisons. Winer, Brown, and Michels (1991, 172–182) discuss this in further detail.

Tukey's HSD requires equal sample sizes.

Student–Newman–Keuls' adjustment

The Student–Newman–Keuls (SNK) method is used when `mcompare(snk)` is specified. It is a modification to Tukey's method and is less conservative. In this procedure, we first order the means. We then test the difference in the smallest and largest means using a critical value from the Studentized range distribution with parameter k, where k is the number of levels in the term. This step uses the same methodology as in Tukey's procedure. However, in the next step, we will then test for differences in the two sets of means that are the endpoints of the two ranges including $k - 1$ means. Specifically, we test the difference in the smallest mean and the second-largest mean using a critical value from the Studentized range distribution with parameter $k - 1$. We would also test the difference in the second-smallest mean and the largest mean using this critical value. Likewise, the means that are the endpoints of ranges including $k - 2$ means when ordered are tested using the Studentized range distribution with parameter $k - 2$, and so on.

As with Tukey's method, equal sample sizes are required.

Duncan's adjustment

When `mcompare(duncan)` is specified, tests are adjusted for multiple comparisons using Duncan's method, which is sometimes referred to as Duncan's new multiple range method. This adjustment produces tests that are less conservative than both Tukey's HSD and SNK. This procedure is performed in the same manner as SNK except that the p-values for the individual comparisons are adjusted as $1-(1-{}_{\text{snk}}p_i)^{1/(r+1)}$, where ${}_{\text{snk}}p$ is the p-value computed using the SNK method and r represents the number of means that, when ordered, fall between the two that are being compared.

Again equal sample sizes are required for this adjustment.

Dunnett's adjustment

Dunnett's adjustment is obtained by specifying `mcompare(dunnett)`. It is used when one of the levels of a factor can be considered a control or reference level with which each of the other levels is being compared. When Dunnett's adjustment is requested, $k-1$ instead of $k(k-1)/2$ pairwise comparisons are made. Dunnett (1955, 1964) developed tables of critical values for what Miller (1981, 76) refers to as the "many-one t statistic". The t statistics for individual comparisons are compared with these critical values when making many comparisons to a single reference level.

This method also requires equal sample sizes.

Example adjustments using one-way models

Fisher's protected LSD

Fisher's protected LSD requires that we first verify that the joint test for a term in our model is significant before proceeding with pairwise comparisons. Using our previous example, we could have first used the `contrast` command to obtain a joint test for the effects of fertilizer.

```
. contrast fertilizer
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	df	F	P>F
fertilizer	4	5.33	0.0004
Residual	195		

This test for the effects of fertilizer is highly significant. Now we can say we are using Fisher's protected LSD when looking at the unadjusted p-values that were obtained from our previous command,

```
. pwcompare fertilizer, effects sort
```

Tukey's HSD

Because we fit a linear regression model and are interested in all pairwise comparisons of the marginal means, we may instead choose to use Tukey's HSD.

```
. pwcompare fertilizer, effects sort mcompare(tukey)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer	10

	Contrast	Std. Err.	Tukey t	Tukey P>|t|	Tukey [95% Conf.	Interval]
fertilizer						
5 vs 4	-6.161132	1.589997	-3.87	0.001	-10.53914	-1.78312
5 vs 2	-4.861048	1.589997	-3.06	0.021	-9.239059	-.4830368
3 vs 2	-3.13209	1.589997	-1.97	0.285	-7.510101	1.245921
5 vs 3	-1.728958	1.589997	-1.09	0.813	-6.106969	2.649053
5 vs 1	-1.238328	1.589997	-0.78	0.936	-5.616339	3.139683
3 vs 1	.4906299	1.589997	0.31	0.998	-3.887381	4.868641
4 vs 2	1.300083	1.589997	0.82	0.925	-3.077928	5.678095
2 vs 1	3.62272	1.589997	2.28	0.156	-.7552913	8.000731
4 vs 3	4.432173	1.589997	2.79	0.046	.0541623	8.810185
4 vs 1	4.922803	1.589997	3.10	0.019	.5447922	9.300815

This time, our p-values have been modified, and we find that only four of the pairwise differences are considered significantly different from zero at the 5% level.

If we only are interested in performing pairwise comparisons of a subset of our means, we can use factor-variable operators to select the levels of the factor that we want to compare. Here we exclude all comparisons involving fertilizer 1.

```
. pwcompare i(2/5).fertilizer, effects sort mcompare(tukey)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer	6

	Contrast	Std. Err.	Tukey t	Tukey P>|t|	Tukey [95% Conf.	Interval]
fertilizer						
5 vs 4	-6.161132	1.589997	-3.87	0.001	-10.28133	-2.040937
5 vs 2	-4.861048	1.589997	-3.06	0.013	-8.981242	-.7408538
3 vs 2	-3.13209	1.589997	-1.97	0.203	-7.252284	.9881042
5 vs 3	-1.728958	1.589997	-1.09	0.698	-5.849152	2.391236
4 vs 2	1.300083	1.589997	0.82	0.846	-2.820111	5.420278
4 vs 3	4.432173	1.589997	2.79	0.030	.3119792	8.552368

The adjusted p-values and confidence intervals differ from those in the previous output because Tukey's adjustment takes into account the total number of comparisons being made when determining the appropriate degrees of freedom to use for the Studentized range distribution.

Dunnett's method for comparisons to a control

If one of our five fertilizer groups represents fields where no fertilizer was applied, we may want to use Dunnett's method to compare each of the four fertilizers with the control group. In this case, we make only $k - 1$ comparisons for k groups.

```
. pwcompare fertilizer, effects mcompare(dunnett)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer	4

	Contrast	Std. Err.	Dunnett t	Dunnett P>|t|	Dunnett [95% Conf.	Interval]
fertilizer						
2 vs 1	3.62272	1.589997	2.28	0.079	-.2918331	7.537273
3 vs 1	.4906299	1.589997	0.31	0.994	-3.423923	4.405183
4 vs 1	4.922803	1.589997	3.10	0.008	1.00825	8.837356
5 vs 1	-1.238328	1.589997	-0.78	0.852	-5.152881	2.676225

In our previous `regress` command, fertilizer 1 was treated as the base. Therefore, by default, it was treated as the control when using Dunnett's adjustment, and the pairwise comparisons are equivalent to the coefficients reported by `regress`. Based on our `regress` output, we would conclude that fertilizers 2 and 4 are different from fertilizer 1 at the 5% level. However, using Dunnett's adjustment, we find only fertilizer 4 to be different from fertilizer 1 at this same significance level.

If the model is fit without a base level for a factor variable, then `pwcompare` will choose the first level as the reference level. If we want to make comparisons with a different level than the one `mcompare(dunnett)` chooses by default, we can use the `b.` operator to override the default. Here we use fertilizer 5 as the reference level.

```
. pwcompare b5.fertilizer, effects sort mcompare(dunnett)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer	4

	Contrast	Std. Err.	Dunnett t	Dunnett P>|t|	Dunnett [95% Conf.	Interval]
fertilizer						
1 vs 5	1.238328	1.589997	0.78	0.852	-2.676225	5.152881
3 vs 5	1.728958	1.589997	1.09	0.649	-2.185595	5.643511
2 vs 5	4.861048	1.589997	3.06	0.009	.9464951	8.775601
4 vs 5	6.161132	1.589997	3.87	0.001	2.246579	10.07568

Two-way models

In the previous examples, we have performed pairwise comparisons after fitting a model with a single factor. Now we include two factors and their interaction in our model.

```
. regress yield fertilizer##irrigation
```

Source	SS	df	MS		
Model	6200.81605	9	688.979561	Number of obs	= 200
Residual	4737.57936	190	24.9346282	F(9, 190)	= 27.63
				Prob > F	= 0.0000
Total	10938.3954	199	54.9668111	R-squared	= 0.5669
				Adj R-squared	= 0.5464
				Root MSE	= 4.9935

yield	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
fertilizer						
2	1.882256	1.57907	1.19	0.235	-1.232505	4.997016
3	-.5687418	1.57907	-0.36	0.719	-3.683502	2.546019
4	4.904999	1.57907	3.11	0.002	1.790239	8.01976
5	-1.217496	1.57907	-0.77	0.442	-4.332257	1.897264
1.irrigation	8.899721	1.57907	5.64	0.000	5.784961	12.01448
fertilizer# irrigation						
2 1	3.480928	2.233143	1.56	0.121	-.9240084	7.885865
3 1	2.118743	2.233143	0.95	0.344	-2.286193	6.52368
4 1	.0356082	2.233143	0.02	0.987	-4.369328	4.440545
5 1	-.0416636	2.233143	-0.02	0.985	-4.4466	4.363273
_cons	36.91257	1.116571	33.06	0.000	34.7101	39.11504

We can perform pairwise comparisons of the cell means defined by the fertilizer and irrigation interaction.

```
. pwcompare fertilizer#irrigation, sort groups mcompare(tukey)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer#irrigation	45

	Margin	Std. Err.	Tukey Groups
fertilizer#irrigation			
5 0	35.69507	1.116571	A
3 0	36.34383	1.116571	A
1 0	36.91257	1.116571	AB
2 0	38.79482	1.116571	AB
4 0	41.81757	1.116571	BC
5 1	44.55313	1.116571	CD
1 1	45.81229	1.116571	CDE
3 1	47.36229	1.116571	DEF
4 1	50.7529	1.116571	EF
2 1	51.17547	1.116571	F

```
Note: Margins sharing a letter in the group label are
      not significantly different at the 5% level.
```

Based on Tukey's HSD and a 5% significance level, we would conclude that the mean yield for fertilizer 5 without irrigation is not significantly different from the mean yields for fertilizers 1, 2, and 3 when used without irrigation but is significantly different from the remaining means.

Up to this point, most of the pairwise comparisons that we have performed could have also been obtained with `pwmean` (see [R] **pwmean**) if we had not been interested in examining the results from the estimation command before making pairwise comparisons of the means. For instance, we could reproduce the results from the above `pwcompare` command by typing

```
. pwmean yield, over(fertilizer irrigation) sort group mcompare(tukey)
```

However, `pwcompare` extends the capabilities of `pwmean` in many ways. For instance, `pwmean` only allows for pairwise comparisons of the cell means determined by the highest level interaction of the variables specified in the `over()` option. However, `pwcompare` allows us to fit a single model, such as the two-way model that we fit above,

```
. regress yield fertilizer##irrigation
```

and compute pairwise comparisons of the marginal means for only one of the variables in the model:

```
. pwcompare fertilizer, sort effects mcompare(tukey)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer	10

	Contrast	Std. Err.	Tukey t	Tukey P>|t|	Tukey [95% Conf.	Interval]
fertilizer						
5 vs 4	-6.161132	1.116571	-5.52	0.000	-9.236338	-3.085925
5 vs 2	-4.861048	1.116571	-4.35	0.000	-7.936255	-1.785841
3 vs 2	-3.13209	1.116571	-2.81	0.044	-6.207297	-.0568832
5 vs 3	-1.728958	1.116571	-1.55	0.532	-4.804165	1.346249
5 vs 1	-1.238328	1.116571	-1.11	0.802	-4.313535	1.836879
3 vs 1	.4906299	1.116571	0.44	0.992	-2.584577	3.565837
4 vs 2	1.300083	1.116571	1.16	0.772	-1.775123	4.37529
2 vs 1	3.62272	1.116571	3.24	0.012	.5475131	6.697927
4 vs 3	4.432173	1.116571	3.97	0.001	1.356967	7.50738
4 vs 1	4.922803	1.116571	4.41	0.000	1.847597	7.99801

Here the standard errors for the differences in marginal means and the residual degrees of freedom are based on the full model. Therefore, the results will differ from those obtained from `pwcompare` after fitting the one-way model with only `fertilizer` (or equivalently using `pwmean`).

Pairwise comparisons of slopes

If we fit a model with a factor variable that is interacted with a continuous variable, `pwcompare` will even allow us to make pairwise comparisons of the slopes of the continuous variable for the levels of the factor variable.

In this case, we have a continuous variable, `NO3_N`, indicating the amount of nitrate nitrogen already existing in the soil, based on a sample taken from each field.

```
. regress yield fertilizer##c.NO3_N
```

Source	SS	df	MS		
Model	7005.69932	9	778.411035	Number of obs =	200
Residual	3932.69609	190	20.6984005	F(9, 190) =	37.61
				Prob > F =	0.0000
				R-squared =	0.6405
				Adj R-squared =	0.6234
Total	10938.3954	199	54.9668111	Root MSE =	4.5495

yield	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
fertilizer						
2	18.65019	8.452061	2.21	0.029	1.97826	35.32212
3	-13.34076	10.07595	-1.32	0.187	-33.21585	6.534327
4	24.35061	9.911463	2.46	0.015	4.799973	43.90125
5	17.58529	8.446736	2.08	0.039	.9238646	34.24671
NO3_N	4.915653	.7983509	6.16	0.000	3.340884	6.490423
fertilizer# c.NO3_N						
2	-1.282039	.8953419	-1.43	0.154	-3.048126	.4840487
3	-1.00571	.9025862	-1.11	0.267	-2.786087	.7746662
4	-2.97627	.9136338	-3.26	0.001	-4.778438	-1.174102
5	-3.275947	.8247385	-3.97	0.000	-4.902767	-1.649127
_cons	-5.459168	7.638241	-0.71	0.476	-20.52581	9.607477

These are the pairwise differences of the slopes of NO3_N for each pair of fertilizers:

```
. pwcompare fertilizer#c.NO3_N, pveffects sort mcompare(scheffe)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
fertilizer#c.NO3_N	10

	Contrast	Std. Err.	Scheffe t	Scheffe P>|t|
fertilizer#c.NO3_N				
5 vs 1	-3.275947	.8247385	-3.97	0.004
4 vs 1	-2.97627	.9136338	-3.26	0.034
5 vs 3	-2.270237	.4691771	-4.84	0.000
5 vs 2	-1.993909	.4550851	-4.38	0.001
4 vs 3	-1.97056	.612095	-3.22	0.038
4 vs 2	-1.694232	.6013615	-2.82	0.099
2 vs 1	-1.282039	.8953419	-1.43	0.727
3 vs 1	-1.00571	.9025862	-1.11	0.871
5 vs 4	-.2996772	.4900939	-0.61	0.984
3 vs 2	.276328	.5844405	0.47	0.994

Using Scheffé's adjustment, we find that five of the pairs have significantly different slopes at the 5% level.

Nonlinear models

pwcompare can also perform pairwise comparisons of the marginal linear predictions after fitting a nonlinear model. For instance, we can use the dataset from *Beyond linear models* in [R] **contrast** and fit the following logistic regression model of patient satisfaction on hospital:

```
. use http://www.stata-press.com/data/r12/hospital
(Artificial hospital satisfaction data)
. logit satisfied i.hospital
Iteration 0:   log likelihood = -393.72216
Iteration 1:   log likelihood = -387.55736
Iteration 2:   log likelihood =  -387.4768
Iteration 3:   log likelihood = -387.47679
Logistic regression                             Number of obs   =        802
                                                LR chi2(2)      =      12.49
                                                Prob > chi2     =     0.0019
Log likelihood = -387.47679                     Pseudo R2       =     0.0159
```

satisfied	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
hospital						
2	.5348129	.2136021	2.50	0.012	.1161604	.9534654
3	.7354519	.2221929	3.31	0.001	.2999618	1.170942
_cons	1.034708	.1391469	7.44	0.000	.7619855	1.307431

For this model, the marginal linear predictions are the predicted log odds for each hospital and can be obtained with the cimargins option:

```
. pwcompare hospital, cimargins
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Margin	Std. Err.	Unadjusted [95% Conf.	Interval]
hospital				
1	1.034708	.1391469	.7619855	1.307431
2	1.569521	.1620618	1.251886	1.887157
3	1.77016	.1732277	1.43064	2.10968

The pairwise comparisons are, therefore, differences in the log odds. We can specify mcompare(bonferroni) and effects to request Bonferroni-adjusted p-values and confidence intervals.

```
. pwcompare hospital, effects mcompare(bonferroni)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
satisfied	
hospital	3

	Contrast	Std. Err.	Bonferroni z	Bonferroni P>|z|	Bonferroni [95% Conf.	Interval]
satisfied						
hospital						
2 vs 1	.5348129	.2136021	2.50	0.037	.0234537	1.046172
3 vs 1	.7354519	.2221929	3.31	0.003	.2035265	1.267377
3 vs 2	.200639	.2372169	0.85	1.000	-.3672535	.7685314

For nonlinear models, only Bonferroni's adjustment, Šidák's adjustment, and Scheffé's adjustment are available.

If we want pairwise comparisons reported as odds ratios, we can specify the `or` option.

```
. pwcompare hospital, effects mcompare(bonferroni) or
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
satisfied	
hospital	3

	Odds Ratio	Std. Err.	Bonferroni z	Bonferroni P>|z|	Bonferroni [95% Conf.	Interval]
satisfied						
hospital						
2 vs 1	1.707129	.3646464	2.50	0.037	1.023731	2.846733
3 vs 1	2.086425	.4635888	3.31	0.003	1.225718	3.551525
3 vs 2	1.222183	.2899226	0.85	1.000	.6926341	2.156597

Notice that these tests are still performed on the marginal linear predictions. The odds ratios reported here are the exponentiated versions of the pairwise differences of log odds in the previous output. For further discussion, see [R] **contrast**.

Multiple-equation models

`pwcompare` works with models containing multiple equations. Commands such as `intreg` and `gnbreg` allow their ancillary parameters to be modeled as a function of independent variables, and `pwcompare` can compare the margins within these equations. The `equation()` option can be used to specify the equation for which pairwise comparisons of the margins should be made. The `atequations` option specifies that pairwise comparisons be computed for each equation. In addition, `pwcompare` allows a special pseudofactor for equation—called `_eqns`—when working with results from `manova`, `mvreg`, `mlogit`, and `mprobit`.

Here we use the jaw fracture dataset described in example 4 of [MV] **manova**. We fit a multivariate regression model including one independent factor variable, `fracture`.

```
. use http://www.stata-press.com/data/r12/jaw
(Table 4.6 Two-Way Unbalanced Data for Fractures of the Jaw -- Rencher (1998))
. mvreg y1 y2 y3 = i.fracture
```

Equation	Obs	Parms	RMSE	"R-sq"	F	P
y1	27	3	10.42366	0.2966	5.060804	0.0147
y2	27	3	6.325398	0.1341	1.858342	0.1777
y3	27	3	5.976973	0.1024	1.368879	0.2735

	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
y1						
fracture						
2	-8.833333	4.957441	-1.78	0.087	-19.06499	1.398322
3	6	5.394759	1.11	0.277	-5.134235	17.13423
_cons	37	3.939775	9.39	0.000	28.8687	45.1313
y2						
fracture						
2	-5.761905	3.008327	-1.92	0.067	-11.97079	.446977
3	-3.053571	3.273705	-0.93	0.360	-9.810166	3.703023
_cons	38.42857	2.390776	16.07	0.000	33.49425	43.36289
y3						
fracture						
2	4.261905	2.842618	1.50	0.147	-1.60497	10.12878
3	.9285714	3.093377	0.30	0.767	-5.455846	7.312989
_cons	58.57143	2.259083	25.93	0.000	53.90891	63.23395

`pwcompare` performs pairwise comparisons of the margins using the coefficients from the first equation by default:

```
. pwcompare fracture, mcompare(bonferroni)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
y1	
fracture	3

	Contrast	Std. Err.	Bonferroni [95% Conf.	Interval]
y1				
fracture				
2 vs 1	-8.833333	4.957441	-21.59201	3.925341
3 vs 1	6	5.394759	-7.884173	19.88417
3 vs 2	14.83333	4.75773	2.588644	27.07802

We can use the equation() option to get pwcompare to perform comparisons in the y2 equation:

```
. pwcompare fracture, equation(y2) mcompare(bonferroni)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
y2	
fracture	3

	Contrast	Std. Err.	Bonferroni [95% Conf.	Interval]
y2				
fracture				
2 vs 1	-5.761905	3.008327	-13.50426	1.980449
3 vs 1	-3.053571	3.273705	-11.47891	5.371769
3 vs 2	2.708333	2.887136	-4.722119	10.13879

Because we are working with mvreg results, we can use the _eqns pseudofactor to compare the margins between the three dependent variables. The levels of _eqns index the equations: 1 for the first equation, 2 for the second, and 3 for the third.

```
. pwcompare _eqns, mcompare(bonferroni)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Number of Comparisons
_eqns	3

	Contrast	Std. Err.	Bonferroni [95% Conf.	Interval]
_eqns				
2 vs 1	-.5654762	2.545923	-7.117768	5.986815
3 vs 1	24.24603	2.320677	18.27344	30.21862
3 vs 2	24.81151	2.368188	18.71664	30.90637

For the previous command, the only methods available are mcompare(bonferroni), mcompare(sidak), or mcompare(scheffe). Methods that use the Studentized range are not appropriate for making comparisons across equations.

Unbalanced data

pwcompare treats all factors as balanced when it computes the marginal means. By "balanced", we mean that the number of observations in each combination of factor levels (in each cell mean) is equal. We can alternatively specify the asobserved option when we have unbalanced data to obtain marginal means that are based on the observed cell frequencies from the model fit. For more details on the difference in these two types of marginal means and a discussion of when each may be appropriate, see [R] **margins** and [R] **contrast**.

In addition, when our data are not balanced, some of the multiple-comparison adjustments are no longer appropriate. Tukey's method, Student–Newman–Keuls' method, Duncan's method, and Dunnett's method assume equal numbers of observations per group.

Here we use an unbalanced dataset and fit a two-way ANOVA model for cholesterol levels on race and age group. Then we perform pairwise comparisons of the mean cholesterol levels for each race, requesting Šidák's adjustment as well as marginal means that are computed using the observed cell frequencies.

```
. use http://www.stata-press.com/data/r12/cholesterol3
(Artificial cholesterol data, unbalanced)
. anova chol race##agegrp
                          Number of obs =      67     R-squared     =  0.8179
                          Root MSE      = 8.37496     Adj R-squared =  0.7689
                 Source | Partial SS    df       MS           F     Prob > F
------------------------+----------------------------------------------------
                  Model |  16379.9926    14  1169.99947       16.68     0.0000
                        |
                   race |  230.754396     2  115.377198        1.64     0.2029
                 agegrp |  13857.9877     4  3464.49693       49.39     0.0000
          race#agegrp |  857.815209     8  107.226901        1.53     0.1701
                        |
               Residual |   3647.2774    52    70.13995
------------------------+----------------------------------------------------
                  Total |    20027.27    66  303.443485
. pwcompare race, asobserved mcompare(sidak)
Pairwise comparisons of marginal linear predictions
Margins      : asobserved
------------------------------
             |  Number of
             | Comparisons
-------------+----------------
        race |           3
------------------------------

------------------------------------------------------------------------------
             |                                                    Sidak
             |   Contrast   Std. Err.      [95% Conf. Interval]
-------------+----------------------------------------------------------------
        race |
   2 vs 1    |  -7.232433   2.686089     -13.85924   -.6056277
   3 vs 1    |  -5.231198   2.651203     -11.77194    1.309541
   3 vs 2    |   2.001235   2.414964     -3.956682    7.959152
------------------------------------------------------------------------------
```

Empty cells

An empty cell is a combination of the levels of factor variables that is not observed in the estimation sample. When we have empty cells in our data, the marginal means involving those empty cells are not estimable as described in [R] **margins**. In addition, all pairwise comparisons involving a marginal mean that is not estimable are themselves not estimable. Here we use a dataset where we do not have any observations for white individuals in the 20–29 age group. We can use the `emptycells(reweight)` option to reweight the nonempty cells so that we can estimate the marginal mean for whites and compute pairwise comparisons involving that marginal mean.

```
. use http://www.stata-press.com/data/r12/cholesterol2
(Artificial cholesterol data, empty cells)
. tabulate race agegrp
```

race	agegrp					Total
	10-19	20-29	30-39	40-59	60-79	
black	5	5	5	5	5	25
white	5	0	5	5	5	20
other	5	5	5	5	5	25
Total	15	10	15	15	15	70

```
. anova chol race##agegrp
```

```
                          Number of obs =      70     R-squared     =  0.7582
                          Root MSE      = 9.47055     Adj R-squared =  0.7021
```

Source	Partial SS	df	MS	F	Prob > F
Model	15751.6113	13	1211.66241	13.51	0.0000
race	305.49046	2	152.74523	1.70	0.1914
agegrp	14387.8559	4	3596.96397	40.10	0.0000
race#agegrp	795.807574	7	113.686796	1.27	0.2831
Residual	5022.71559	56	89.6913498		
Total	20774.3269	69	301.077201		

```
. pwcompare race, emptycells(reweight)
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
Empty cells  : reweight
```

	Contrast	Std. Err.	Unadjusted [95% Conf.	Interval]
race				
2 vs 1	2.922769	2.841166	-2.768769	8.614308
3 vs 1	-4.12621	2.678677	-9.492244	1.239824
3 vs 2	-7.048979	2.841166	-12.74052	-1.35744

For further details on the `emptycells(reweight)` option, see [R] **margins** and [R] **contrast**.

Saved results

pwcompare saves the following in r():

Scalars

r(df_r)	variance degrees of freedom, from e(df_r)
r(k_terms)	number of terms in *marginlist*
r(level)	confidence level of confidence intervals
r(balanced)	1 if fully balanced data; 0 otherwise

Macros

r(cmd)	pwcompare
r(cmdline)	command as typed
r(est_cmd)	e(cmd) from original estimation results
r(est_cmdline)	e(cmdline) from original estimation results
r(title)	title in output
r(emptycells)	*empspec* from emptycells()
r(groups#)	group codes for the #th margin in r(b)
r(mcmethod_vs)	*method* from mcompare()
r(mctitle_vs)	title for *method* from mcompare()
r(mcadjustall_vs)	adjustall or empty
r(margin_method)	asbalanced or asobserved
r(vce)	*vcetype* specified in vce() in original estimation command

Matrices

r(b)	margin estimates
r(V)	variance–covariance matrix of the margin estimates
r(error)	margin estimability codes; 0 means estimable, 8 means not estimable
r(table)	matrix containing the margins with their standard errors, test statistics, p-values, and confidence intervals
r(M)	matrix that produces the margins from the model coefficients
r(b_vs)	margin difference estimates
r(V_vs)	variance–covariance matrix of the margin difference estimates
r(error_vs)	margin difference estimability codes; 0 means estimable, 8 means not estimable
r(table_vs)	matrix containing the margin differences with their standard errors, test statistics, p-values, and confidence intervals
r(L)	matrix that produces the margin differences from the model coefficients
r(k_groups)	number of significance groups for each term

pwcompare with the post option also saves the following in e():

Scalars

e(df_r)	variance degrees of freedom, from e(df_r)
e(k_terms)	number of terms in *marginlist*
e(balanced)	1 if fully balanced data; 0 otherwise

Macros

e(cmd)	pwcompare
e(cmdline)	command as typed
e(est_cmd)	e(cmd) from original estimation results
e(est_cmdline)	e(cmdline) from original estimation results
e(title)	title in output
e(emptycells)	*empspec* from emptycells()
e(margin_method)	asbalanced or asobserved
e(vce)	*vcetype* specified in vce() in original estimation command
e(properties)	b V

Matrices

e(b)	margin estimates
e(V)	variance–covariance matrix of the margin estimates
e(error)	margin estimability codes; 0 means estimable, 8 means not estimable
e(M)	matrix that produces the margins from the model coefficients
e(b_vs)	margin difference estimates
e(V_vs)	variance–covariance matrix of the margin difference estimates
e(error_vs)	margin difference estimability codes; 0 means estimable, 8 means not estimable
e(L)	matrix that produces the margin differences from the model coefficients
e(k_groups)	number of significance groups for each term

Methods and formulas

pwcompare is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Notation
Unadjusted comparisons
Bonferroni's method
Šidák's method
Scheffé's method
Tukey's method
Student–Newman–Keuls' method
Duncan's method
Dunnett's method

Notation

pwcompare performs comparisons of margins; see *Methods and formulas* in [R] **contrast**.

If there are k margins for a given factor term, then there are

$$m = \binom{k}{2} = \frac{k(k-1)}{2}$$

unique pairwise comparisons. Let the ith pairwise comparison be denoted by

$$\widehat{\delta}_i = l_i'\mathbf{b}$$

where $\mathbf{b}$ is a column vector of coefficients from the fitted model and l_i is a column vector that forms the corresponding linear combination. If $\widehat{\mathbf{V}}$ denotes the estimated variance matrix for $\mathbf{b}$, then the standard error for $\widehat{\delta}_i$ is given by

$$\widehat{\mathrm{se}}(\widehat{\delta}_i) = \sqrt{l_i'\widehat{\mathbf{V}}l_i}$$

The corresponding test statistic is then

$$t_i = \frac{\widehat{\delta}_i}{\widehat{\mathrm{se}}(\widehat{\delta}_i)}$$

and the limits for a $100(1-\alpha)\%$ confidence interval for the expected value of $\widehat{\delta}_i$ are

$$\widehat{\delta}_i \pm c_i(\alpha)\,\widehat{\mathrm{se}}(\widehat{\delta}_i)$$

where $c_i(\alpha)$ is the critical value corresponding to the chosen multiple-comparison method.

Unadjusted comparisons

`pwcompare` computes unadjusted p-values and confidence intervals by default. `pwcompare` uses the t distribution with $\nu =$ `e(df_r)` degrees of freedom when `e(df_r)` is posted by the estimation command. The unadjusted two-sided p-value is

$${}_up_i = 2\Pr(t_\nu > |t_i|)$$

and the unadjusted critical value ${}_uc_i(\alpha)$ satisfies the following probability statement:

$$\alpha = 2\Pr\{t_\nu > {}_uc_i(\alpha)\}$$

`pwcompare` uses the standard normal distribution when `e(df_r)` is not posted.

Bonferroni's method

For `mcompare(bonferroni)`, the adjusted p-value is

$${}_bp_i = \min(1, m\,{}_up_i)$$

and the adjusted critical value is

$${}_bc_i(\alpha) = {}_uc_i(\alpha/m)$$

Šidák's method

For `mcompare(sidak)`, the adjusted p-value is

$$_{\text{si}}p_i = 1 - (1 - {}_u p_i)^m$$

and the adjusted critical value is

$$_{\text{si}}c_i(\alpha) = {}_u c_i\left\{1 - (1-\alpha)^{1/m}\right\}$$

Scheffé's method

For `mcompare(scheffe)`, the adjusted p-value is

$$_{\text{sc}}p_i = \Pr\left(F_{d,\nu} > t_i^2/d\right)$$

where $F_{d,\nu}$ is distributed as an F with d numerator and ν denominator degrees of freedom and d is the rank of the VCE for the term. The adjusted critical value satisfies the following probability statement:

$$\alpha = \Pr\left[F_{d,\nu} > \{{}_{\text{sc}}c_i(\alpha)\}^2/d\right]$$

`pwcompare` uses the χ^2 distribution when `e(df_r)` is not posted.

Tukey's method

For `mcompare(tukey)`, the adjusted p-value is

$$_t p_i = \Pr\left(q_{k,\nu} > |t_i|\sqrt{2}\right)$$

where $q_{k,\nu}$ is distributed as the Studentized range statistic for k means and ν residual degrees of freedom (Miller 1981). The adjusted critical value satisfies the following probability statement:

$$\alpha = \Pr\left\{q_{k,\nu} > {}_t c_i(\alpha)\sqrt{2}\right\}$$

Student–Newman–Keuls' method

For `mcompare(snk)`, suppose t_i is comparing two margins that have r other margins between them. Then the adjusted p-value is

$$_{\text{snk}}p_i = \Pr\left(q_{r+2,\nu} > |t_i|\sqrt{2}\right)$$

where r ranges from 0 to $k-2$. The adjusted critical value $_{\text{snk}}c_i(\alpha)$ satisfies the following probability statement:

$$\alpha = \Pr\left\{q_{r+2,\nu} > {}_{\text{snk}}c_i(\alpha)\sqrt{2}\right\}$$

Duncan's method

For `mcompare(duncan)`, the adjusted p-value is

$$_{\text{dunc}}p_i = 1 - (1 - {}_{\text{snk}}p_i)^{1/(r+1)}$$

and the adjusted critical value is

$$_{\text{dunc}}c_i(\alpha) = {}_{\text{snk}}c_i\left\{1 - (1-\alpha)^{r+1}\right\}$$

Dunnett's method

For `mcompare(dunnett)`, the margins are compared with a reference category, resulting in only $k-1$ pairwise comparisons. The adjusted p-value is

$$_{\text{dunn}}p_i = \Pr(d_{k-1,\nu} > |t_i|)$$

where $d_{k-1,\nu}$ is distributed as the many-one t statistic (Miller 1981, 76). The adjusted critical value $_{\text{dunn}}c_i(\alpha)$ satisfies the following probability statement:

$$\alpha = \Pr\left\{d_{k-1,\nu} > {}_{\text{dunn}}c_i(\alpha)\right\}$$

The multiple-comparison methods for `mcompare(tukey)`, `mcompare(snk)`, `mcompare(duncan)`, and `mcompare(dunnett)` assume the normal distribution with equal variance and sample size for each marginal mean; thus these methods are allowed only with results from `anova`, `regress`, `manova`, and `mvreg`. These options will cause `pwcompare` to report a footnote if unbalanced factors are detected.

References

Dunnett, C. W. 1955. A multiple comparison for comparing several treatments with a control. *Journal of the American Statistical Association* 50: 1096–1121.

——. 1964. New tables for multiple comparisons with a control. *Biometrics* 20: 482–491.

Miller, R. G., Jr. 1981. *Simultaneous Statistical Inference*. 2nd ed. New York: Springer.

Milliken, G. A., and D. E. Johnson. 2009. *Analysis of Messy Data, Volume 1: Designed Experiments*. 2nd ed. Boca Raton, FL: CRC Press.

Searle, S. R. 1997. *Linear Models for Unbalanced Data*. New York: Wiley.

Winer, B. J., D. R. Brown, and K. M. Michels. 1991. *Statistical Principles in Experimental Design*. 3rd ed. New York: McGraw–Hill.

Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **pwcompare postestimation** — Postestimation tools for pwcompare

[R] **lincom** — Linear combinations of estimators

[R] **margins** — Marginal means, predictive margins, and marginal effects

[R] **margins, pwcompare** — Pairwise comparisons of margins

[R] **test** — Test linear hypotheses after estimation

Title

pwcompare postestimation — Postestimation tools for pwcompare

Description

The following postestimation commands are available after `pwcompare, post`:

Command	Description
`estat`	VCE; `estat vce` only
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Remarks

When we use the `post` option with `pwcompare`, the marginal linear predictions are posted as estimation results, and we can use postestimation commands to perform further analysis on them.

In *Pairwise comparisons of means* of [R] **pwcompare**, we fit a regression of wheat yield on types of fertilizers.

```
. use http://www.stata-press.com/data/r12/yield
(Artificial wheat yield dataset)
. regress yield i.fertilizer
  (output omitted)
```

We also used `pwcompare` with the `cimargins` option to obtain the marginal mean yield for each fertilizer. We can add the `post` option to this command to post these marginal means and their VCEs as estimation results.

```
. pwcompare fertilizer, cimargins post
Pairwise comparisons of marginal linear predictions
Margins      : asbalanced
```

	Margin	Std. Err.	Unadjusted [95% Conf.	Interval]
fertilizer				
1	41.36243	1.124298	39.14509	43.57977
2	44.98515	1.124298	42.7678	47.20249
3	41.85306	1.124298	39.63571	44.0704
4	46.28523	1.124298	44.06789	48.50258
5	40.1241	1.124298	37.90676	42.34145

Now we can use `nlcom` to compute a percentage improvement in the mean yield for fertilizer 2 when compared with fertilizer 1.

```
. nlcom (pct_chg: 100*(_b[2.fertilizer] - _b[1.fertilizer])/_b[1.fertilizer])
     pct_chg:  100*(_b[2.fertilizer] - _b[1.fertilizer])/_b[1.fertilizer]
```

	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
pct_chg	8.758479	4.015932	2.18	0.030	.838243	16.67872

The mean yield for fertilizer 2 is about 9% higher than that of fertilizer 1, with a standard error of 4%.

Also see

[R] **pwcompare** — Pairwise comparisons

Title

pwmean — Pairwise comparisons of means

Syntax

`pwmean` *varname*`, over(`*varlist*`)` [*options*]

options	Description
Main	
* `over(`*varlist*`)`	compare means across each combination of the levels in *varlist*
`mcompare(`*method*`)`	adjust for multiple comparisons; default is `mcompare(noadjust)`
Reporting	
`level(#)`	confidence level; default is `level(95)`
`cieffects`	display a table of mean differences and confidence intervals; the default
`pveffects`	display a table of mean differences and p-values
`effects`	display a table of mean differences with p-values and confidence intervals
`cimeans`	display a table of means and confidence intervals
`groups`	display a table of means with codes that group them with other means that are not significantly different
`sort`	sort results tables by displayed mean or difference
display_options	control column formats and line width

* `over(`*varlist*`)` is required.

method	Description
`noadjust`	do not adjust for multiple comparisons; the default
`bonferroni`	Bonferroni's method
`sidak`	Šidák's method
`scheffe`	Scheffé's method
`tukey`	Tukey's method
`snk`	Student–Newman–Keuls' method
`duncan`	Duncan's method
`dunnett`	Dunnett's method

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Pairwise comparisons of means

Description

pwmean performs pairwise comparisons of means. It computes all pairwise differences of the means of *varname* over the combination of the levels of the variables in *varlist*. The tests and confidence intervals for the pairwise comparisons assume equal variances across groups. pwmean also allows for adjusting the confidence intervals and p-values to account for multiple comparisons using Bonferroni's method, Scheffé's method, Tukey's method, Dunnett's method, and others.

See [R] **pwcompare** for performing pairwise comparisons of means, estimated marginal means, and other types of marginal linear predictions after anova, regress, and most other estimation commands.

See [R] **margins, pwcompare** for performing pairwise comparisons of marginal probabilities and other linear and nonlinear predictions after estimation commands.

Options

Main

over(*varlist*) is required and specifies that means are computed for each combination of the levels of the variables in *varlist*.

mcompare(*method*) specifies the method for computing p-values and confidence intervals that account for multiple comparisons.

Most methods adjust the comparisonwise error rate, α_c, to achieve a prespecified experimentwise error rate, α_e.

mcompare(noadjust) is the default; it specifies no adjustment.

$$\alpha_c = \alpha_e$$

mcompare(bonferroni) adjusts the comparisonwise error rate based on the upper limit of the Bonferroni inequality:

$$\alpha_e \leq m\alpha_c$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = \alpha_e/m$$

mcompare(sidak) adjusts the comparisonwise error rate based on the upper limit of the probability inequality

$$\alpha_e \leq 1 - (1 - \alpha_c)^m$$

where m is the number of comparisons within the term.

The adjusted comparisonwise error rate is

$$\alpha_c = 1 - (1 - \alpha_e)^{1/m}$$

This adjustment is exact when the m comparisons are independent.

mcompare(scheffe) controls the experimentwise error rate using the F (or χ^2) distribution with degrees of freedom equal to $k - 1$ where k is the number of means being compared.

mcompare(tukey) uses what is commonly referred to as Tukey's honestly significant difference. This method uses the Studentized range distribution instead of the t distribution.

`mcompare(snk)` is a variation on `mcompare(tukey)` that counts only the number of means participating in the range for a given comparison instead of the full number of means.

`mcompare(duncan)` is a variation on `mcompare(snk)` with additional adjustment to the significance probabilities.

`mcompare(dunnett)` uses Dunnett's method for making comparisons with a reference category.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**. The significance level used by the `groups` option is $100 - \#$, expressed as a percentage.

`cieffects` specifies that a table of the pairwise comparisons of means with their standard errors and confidence intervals be reported. This is the default.

`pveffects` specifies that a table of the pairwise comparisons of means with their standard errors, test statistics, and p-values be reported.

`effects` specifies that a table of the pairwise comparisons of means with their standard errors, test statistics, p-values, and confidence intervals be reported.

`cimeans` specifies that a table of the means with their standard errors and confidence intervals be reported.

`groups` specifies that a table of the means with their standard errors and group codes be reported. Means with the same letter in the group code are not significantly different at the specified significance level.

`sort` specifies that the reported tables be sorted by the mean or difference that is displayed in the table.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`.

`cformat(%`*fmt*`)` specifies how to format means, standard errors, and confidence limits in the table of pairwise comparison of means.

`pformat(%`*fmt*`)` specifies how to format p-values in the table of pairwise comparison of means.

`sformat(%`*fmt*`)` specifies how to format test statistics in the table of pairwise comparison of means.

`nolstretch` specifies that the width of the table of estimated comparisons not be automatically widened to accommodate longer variable names. The default, `lstretch`, is to automatically widen the table of estimated comparisons up to the width of the Results window. To change the default, use `set lstretch off`. `nolstretch` is not shown in the dialog box.

Remarks

`pwmean` performs pairwise comparisons (differences) of means, assuming a common variance among groups. It can easily adjust the p-values and confidence intervals for the differences to account for the elevated type I error rate due to multiple comparisons. Adjustments for multiple comparisons can be made using Bonferroni's method, Scheffé's method, Tukey's method, Dunnett's method, and others.

Remarks are presented under the following headings:

Group means
Pairwise differences of means
Group output
Adjusting for multiple comparisons
Tukey's method
Dunnett's method
Multiple over() variables
Equal variance assumption

Group means

Suppose we have data on the wheat yield of fields that were each randomly assigned an application of one of five types of fertilizers. Let's first look at the mean yield for each type of fertilizer.

```
. use http://www.stata-press.com/data/r12/yield
(Artificial wheat yield dataset)
. pwmean yield, over(fertilizer) cimeans
Pairwise comparisons of means with equal variances
over         : fertilizer
```

			Unadjusted	
yield	Mean	Std. Err.	[95% Conf.	Interval]
fertilizer				
1	41.36243	1.124298	39.14509	43.57977
2	44.98515	1.124298	42.7678	47.20249
3	41.85306	1.124298	39.63571	44.0704
4	46.28523	1.124298	44.06789	48.50258
5	40.1241	1.124298	37.90676	42.34145

Pairwise differences of means

We can compute all pairwise differences in mean wheat yields for the types of fertilizers.

```
. pwmean yield, over(fertilizer) effects
Pairwise comparisons of means with equal variances
over         : fertilizer
```

			Unadjusted		Unadjusted	
yield	Contrast	Std. Err.	t	P>|t|	[95% Conf.	Interval]
fertilizer						
2 vs 1	3.62272	1.589997	2.28	0.024	.4869212	6.758518
3 vs 1	.4906299	1.589997	0.31	0.758	-2.645169	3.626428
4 vs 1	4.922803	1.589997	3.10	0.002	1.787005	8.058602
5 vs 1	-1.238328	1.589997	-0.78	0.437	-4.374127	1.89747
3 vs 2	-3.13209	1.589997	-1.97	0.050	-6.267889	.0037086
4 vs 2	1.300083	1.589997	0.82	0.415	-1.835715	4.435882
5 vs 2	-4.861048	1.589997	-3.06	0.003	-7.996847	-1.725249
4 vs 3	4.432173	1.589997	2.79	0.006	1.296375	7.567972
5 vs 3	-1.728958	1.589997	-1.09	0.278	-4.864757	1.406841
5 vs 4	-6.161132	1.589997	-3.87	0.000	-9.29693	-3.025333

The contrast in the row labeled (2 vs 1) is the difference in the mean wheat yield for fertilizer 2 and fertilizer 1. At a 5% significance level, we conclude that there is a difference in the means for these two fertilizers. Likewise, the rows labeled (4 vs 1), (5 vs 2), (4 vs 3) and (5 vs 4) show differences in these pairs of means. In all, we find that 5 of the 10 mean differences are significantly different from zero at a 5% significance level.

We can specify the sort option to order the differences from smallest to largest in the table.

```
. pwmean yield, over(fertilizer) effects sort
Pairwise comparisons of means with equal variances
over          : fertilizer
```

			Unadjusted		Unadjusted	
yield	Contrast	Std. Err.	t	P>|t|	[95% Conf.	Interval]
fertilizer						
5 vs 4	-6.161132	1.589997	-3.87	0.000	-9.29693	-3.025333
5 vs 2	-4.861048	1.589997	-3.06	0.003	-7.996847	-1.725249
3 vs 2	-3.13209	1.589997	-1.97	0.050	-6.267889	.0037086
5 vs 3	-1.728958	1.589997	-1.09	0.278	-4.864757	1.406841
5 vs 1	-1.238328	1.589997	-0.78	0.437	-4.374127	1.89747
3 vs 1	.4906299	1.589997	0.31	0.758	-2.645169	3.626428
4 vs 2	1.300083	1.589997	0.82	0.415	-1.835715	4.435882
2 vs 1	3.62272	1.589997	2.28	0.024	.4869212	6.758518
4 vs 3	4.432173	1.589997	2.79	0.006	1.296375	7.567972
4 vs 1	4.922803	1.589997	3.10	0.002	1.787005	8.058602

Ordering the pairwise differences is particularly convenient when we are comparing means for a large number of groups.

Group output

We can use the group option to see the mean of each group and a visual representation of the tests for differences.

```
. pwmean yield, over(fertilizer) group sort
Pairwise comparisons of means with equal variances
over          : fertilizer
```

			Unadjusted
yield	Mean	Std. Err.	Groups
fertilizer			
5	40.1241	1.124298	A
1	41.36243	1.124298	A
3	41.85306	1.124298	AB
2	44.98515	1.124298	BC
4	46.28523	1.124298	C

```
Note: Means sharing a letter in the group label
      are not significantly different at the 5%
      level.
```

Fertilizers 5, 1, and 3 are all in group A. This means that at our 5% level of significance, we have insufficient information to distinguish their means. Likewise, fertilizers 3 and 2 are in group B and cannot be distinguished at the 5% level. The same is true for fertilizers 2 and 4 in group C.

Fertilizer 5 and fertilizer 2 have no letters in common, indicating that the mean yields of these two groups are significantly different at the 5% level. We can conclude that any other fertilizers without a letter in common have significantly different means as well.

Adjusting for multiple comparisons

The statistics in the examples above take no account that we are performing 10 comparisons. With our 5% significance level and assuming the comparisons are independent, we expect 1 in 20 tests of comparisons to be significant, even if all the population means are truly the same. If we are performing many comparisons, then we should account for the fact that some tests will be found significant by chance alone. More formally, the test for each pairwise comparison is made without adjusting for the elevated type I experimentwise error rate that is introduced when performing multiple tests. We can use the `mcompare()` option to adjust the confidence intervals and p-values for multiple comparisons.

Tukey's method

Of the available adjustments for multiple comparisons, Tukey's honestly significant difference, Student–Newman–Keuls' method, and Duncan's method are most often used when performing all pairwise comparisons of means. Of these, Tukey's method is the most conservative and Duncan's method is the least conservative. For further discussion of each of the multiple-comparison adjustments, see [R] **pwcompare**.

Here we use Tukey's adjustment to compute p-values and confidence intervals for the pairwise differences.

```
. pwmean yield, over(fertilizer) effects sort mcompare(tukey)
Pairwise comparisons of means with equal variances
over          : fertilizer
```

	Number of Comparisons
fertilizer	10

yield	Contrast	Std. Err.	Tukey t	Tukey P>|t|	Tukey [95% Conf.	Interval]
fertilizer						
5 vs 4	-6.161132	1.589997	-3.87	0.001	-10.53914	-1.78312
5 vs 2	-4.861048	1.589997	-3.06	0.021	-9.239059	-.4830368
3 vs 2	-3.13209	1.589997	-1.97	0.285	-7.510101	1.245921
5 vs 3	-1.728958	1.589997	-1.09	0.813	-6.106969	2.649053
5 vs 1	-1.238328	1.589997	-0.78	0.936	-5.616339	3.139683
3 vs 1	.4906299	1.589997	0.31	0.998	-3.887381	4.868641
4 vs 2	1.300083	1.589997	0.82	0.925	-3.077928	5.678095
2 vs 1	3.62272	1.589997	2.28	0.156	-.7552913	8.000731
4 vs 3	4.432173	1.589997	2.79	0.046	.0541623	8.810185
4 vs 1	4.922803	1.589997	3.10	0.019	.5447922	9.300815

When using a 5% significance level, Tukey's adjustment indicates that four pairs of means are different. With the adjustment, we no longer conclude that the difference in the mean yields for fertilizers 2 and 1 is significantly different from zero.

Dunnett's method

Now let's suppose that fertilizer 1 actually represents fields on which no fertilizer was applied. In this case, we can use Dunnett's method for comparing each of the fertilizers to the control.

```
. pwmean yield, over(fertilizer) effects mcompare(dunnett)
Pairwise comparisons of means with equal variances
over         : fertilizer
```

	Number of Comparisons
fertilizer	4

yield	Contrast	Std. Err.	Dunnett t	Dunnett P>|t|	Dunnett [95% Conf.	Interval]
fertilizer						
2 vs 1	3.62272	1.589997	2.28	0.079	-.2918331	7.537273
3 vs 1	.4906299	1.589997	0.31	0.994	-3.423923	4.405183
4 vs 1	4.922803	1.589997	3.10	0.008	1.00825	8.837356
5 vs 1	-1.238328	1.589997	-0.78	0.852	-5.152881	2.676225

Using Dunnett's adjustment, we conclude that only fertilizer 4 produces a mean yield that is significantly different from the mean yield of the field with no fertilizer applied.

By default, `pwmean` treats the lowest level of the group variable as the control. If, for instance, fertilizer 3 was our control group, we could type

```
. pwmean yield, over(b3.fertilizer) effects mcompare(dunnett)
```

using the `b3.` factor-variable operator to specify this level as the reference level.

Multiple over() variables

When we specify more than one variable in the `over()` option, pairwise comparisons are performed for the means defined by each combination of levels of these variables.

```
. pwmean yield, over(fertilizer irrigation) group
Pairwise comparisons of means with equal variances
over         : fertilizer irrigation
```

yield	Mean	Std. Err.	Unadjusted Groups
fertilizer#irrigation			
1 0	36.91257	1.116571	A
1 1	45.81229	1.116571	B
2 0	38.79482	1.116571	A C
2 1	51.17547	1.116571	E
3 0	36.34383	1.116571	A
3 1	47.36229	1.116571	B
4 0	41.81757	1.116571	CD
4 1	50.7529	1.116571	E
5 0	35.69507	1.116571	A
5 1	44.55313	1.116571	B D

```
Note: Means sharing a letter in the group label are not
      significantly different at the 5% level.
```

Here the row labeled `1 0` is the mean for the fields treated with fertilizer 1 and without irrigation. This mean is significantly different from the mean of all fertilizer/irrigation pairings that do not have an A in the "Unadjusted Groups" column. These include all pairings where the fields were irrigated as well as the fields treated with fertilizer 4 but without irrigation.

Equal variance assumption

`pwmean` performs multiple comparisons assuming that there is a common variance for all groups. In the case of two groups, this is equivalent to performing the familiar two-sample t test when equal variances are assumed.

```
. ttest yield, by(irrigation)
Two-sample t test with equal variances
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
0	100	37.91277	.5300607	5.300607	36.86102	38.96453
1	100	47.93122	.5630353	5.630353	46.81403	49.0484
combined	200	42.92199	.5242462	7.413961	41.8882	43.95579
diff		-10.01844	.7732872		-11.54338	-8.493509

```
    diff = mean(0) - mean(1)                                      t = -12.9557
Ho: diff = 0                     degrees of freedom =      198

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0000         Pr(|T| > |t|) = 0.0000          Pr(T > t) = 1.0000
```

```
. pwmean yield, over(irrigation) effects
Pairwise comparisons of means with equal variances
over          : irrigation
```

yield	Contrast	Std. Err.	Unadjusted t	Unadjusted P>|t|	Unadjusted [95% Conf.	Interval]
irrigation						
1 vs 0	10.01844	.7732872	12.96	0.000	8.493509	11.54338

The signs for the difference, the test statistic, and the confidence intervals are reversed because the difference is taken in the opposite direction. The p-value from `pwmean` is equivalent to the one for the two-sided test in the `ttest` output.

`pwmean` extends the capabilities of `ttest` to allow for simultaneously comparing all pairs of means and to allow for using one common variance estimate for all the tests instead of computing a separate pooled variance for each pair of means when using multiple `ttest` commands. In addition, `pwmean` allows adjustments for multiple comparisons, many of which rely on an assumption of equal variances among groups.

Saved results

`pwmean` saves the following in `e()`:

Scalars

`e(df_r)`	variance degrees of freedom
`e(balanced)`	`1` if fully balanced data; `0` otherwise

Macros

`e(cmd)`	`pwmean`
`e(cmdline)`	command as typed
`e(title)`	title in output
`e(depvar)`	name of variable from which the means are computed
`e(over)`	*varlist* from `over()`
`e(properties)`	`b V`

Matrices

`e(b)`	mean estimates
`e(V)`	variance–covariance matrix of the mean estimates
`e(error)`	mean estimability codes; `0` means estimable, `8` means not estimable
`e(b_vs)`	mean difference estimates
`e(V_vs)`	variance–covariance matrix of the mean difference estimates
`e(error_vs)`	mean difference estimability codes; `0` means estimable, `8` means not estimable
`e(k_groups)`	number of significance groups for each term

Methods and formulas

`pwmean` is implemented as an ado-file.

`pwmean` is a convenience command that uses `pwcompare` after fitting a fully factorial linear model. See *Methods and formulas* described in [R] **pwcompare**.

Reference

Searle, S. R. 1997. *Linear Models for Unbalanced Data*. New York: Wiley.

Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **pwcompare** — Pairwise comparisons

[R] **margins** — Marginal means, predictive margins, and marginal effects

[R] **margins, pwcompare** — Pairwise comparisons of margins

[R] **ttest** — Mean-comparison tests

Title

pwmean postestimation — Postestimation tools for pwmean

Description

The following postestimation commands are available after `pwmean`:

Command	Description
`estat`	VCE; `estat vce` only
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

Remarks

In *Pairwise differences of means* of [R] **pwmean**, we computed all pairwise differences in mean wheat yields for five fertilizers.

```
. use http://www.stata-press.com/data/r12/yield
(Artificial wheat yield dataset)
. pwmean yield, over(fertilizer)
Pairwise comparisons of means with equal variances
over         : fertilizer
```

yield	Contrast	Std. Err.	Unadjusted [95% Conf.	Interval]
fertilizer				
2 vs 1	3.62272	1.589997	.4869212	6.758518
3 vs 1	.4906299	1.589997	-2.645169	3.626428
4 vs 1	4.922803	1.589997	1.787005	8.058602
5 vs 1	-1.238328	1.589997	-4.374127	1.89747
3 vs 2	-3.13209	1.589997	-6.267889	.0037086
4 vs 2	1.300083	1.589997	-1.835715	4.435882
5 vs 2	-4.861048	1.589997	-7.996847	-1.725249
4 vs 3	4.432173	1.589997	1.296375	7.567972
5 vs 3	-1.728958	1.589997	-4.864757	1.406841
5 vs 4	-6.161132	1.589997	-9.29693	-3.025333

After `pwmean`, we can use `testnl` to test whether the improvement in mean wheat yield when using fertilizer 4 instead of fertilizer 5 is significantly different from 10%.

```
. testnl (_b[4.fertilizer] - _b[5.fertilizer])/_b[5.fertilizer] = 0.1
  (1)  (_b[4.fertilizer] - _b[5.fertilizer])/_b[5.fertilizer] = 0.1
             F(1, 195) =        1.57
              Prob > F =        0.2121
```

The improvement is not significantly different from 10%.

Also see

[R] **pwmean** — Pairwise comparisons of means

Title

qc — Quality control charts

Syntax

Draw a c chart

`cchart` *defect_var unit_var* [, *cchart_options*]

Draw a p (fraction-defective) chart

`pchart` *reject_var unit_var ssize_var* [, *pchart_options*]

Draw an R (range or dispersion) chart

`rchart` *varlist* [*if*] [*in*] [, *rchart_options*]

Draw an $\overline{\text{X}}$ *(control line) chart*

`xchart` *varlist* [*if*] [*in*] [, *xchart_options*]

Draw vertically aligned $\overline{\text{X}}$ *and R charts*

`shewhart` *varlist* [*if*] [*in*] [, *shewhart_options*]

cchart_options	Description
Main	
`nograph`	suppress graph
Plot	
connect_options	affect rendition of the plotted points
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Control limits	
`clopts(`*cline_options*`)`	affect rendition of the control limits
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

pchart_options	Description
Main	
`stabilized`	stabilize the p chart when sample sizes are unequal
`nograph`	suppress graph
`generate(`*newvar*$_f$ *newvar*$_{\rm lcl}$ *newvar*$_{\rm ucl}$`)`	store the fractions of defective elements and the lower and upper control limits
Plot	
connect_options	affect rendition of the plotted points
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Control limits	
`clopts(`*cline_options*`)`	affect rendition of the control limits
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

rchart_options	Description
Main	
`std(#)`	user-specified standard deviation
`nograph`	suppress graph
Plot	
connect_options	affect rendition of the plotted points
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Control limits	
`clopts(`*cline_options*`)`	affect rendition of the control limits
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

xchart_options	Description
Main	
`std(#)`	user-specified standard deviation
`mean(#)`	user-specified mean
`lower(#) upper(#)`	lower and upper limits of the X-bar limits
`nograph`	suppress graph
Plot	
connect_options	affect rendition of the plotted points
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Control limits	
`clopts(`*cline_options*`)`	affect rendition of the control limits
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

shewhart_options	Description
Main	
`std(#)`	user-specified standard deviation
`mean(#)`	user-specified mean
`nograph`	suppress graph
Plot	
connect_options	affect rendition of the plotted points
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Control limits	
`clopts(`*cline_options*`)`	affect rendition of the control limits
Y axis, X axis, Titles, Legend, Overall	
combine_options	any options documented in [G-2] **graph combine**

Menu

cchart

Statistics > Other > Quality control > C chart

pchart

Statistics > Other > Quality control > P chart

rchart

Statistics > Other > Quality control > R chart

xchart

Statistics > Other > Quality control > X-bar chart

shewhart

Statistics > Other > Quality control > Vertically aligned X-bar and R chart

Description

These commands provide standard quality-control charts. `cchart` draws a c chart; `pchart`, a p (fraction-defective) chart; `rchart`, an R (range or dispersion) chart; `xchart`, an $\overline{X}$ (control line) chart; and `shewhart`, vertically aligned $\overline{X}$ and R charts.

Options

Main

`stabilized` stabilizes the p chart when sample sizes are unequal.

`std(#)` specifies the standard deviation of the process. The R chart is calculated (based on the range) if this option is not specified.

`mean(#)` specifies the grand mean, which is calculated if not specified.

`lower(#)` and `upper(#)` must be specified together or not at all. They specify the lower and upper limits of the $\overline{X}$ chart. Calculations based on the mean and standard deviation (whether specified by option or calculated) are used otherwise.

`nograph` suppresses the graph.

`generate(`*newvar*$_f$ *newvar*$_{\rm lcl}$ *newvar*$_{\rm ucl}$`)` stores the plotted values in the p chart. *newvar*$_f$ will contain the fractions of defective elements; *newvar*$_{\rm lcl}$ and *newvar*$_{\rm ucl}$ will contain the lower and upper control limits, respectively.

Plot

connect_options affect whether lines connect the plotted points and the rendition of those lines; see [G-3] ***connect_options***.

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Control limits

`clopts(`*cline_options*`)` affects the rendition of the control limits; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

combine_options (`shewhart` only) are any of the options documented in [G-2] **graph combine**. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Control charts may be used to define the goal of a repetitive process, to control that process, and to determine if the goal has been achieved. Walter A. Shewhart of Bell Telephone Laboratories devised the first control chart in 1924. In 1931, Shewhart published *Economic Control of Quality of Manufactured Product*. According to Burr, "Few fields of knowledge have ever been so completely explored and charted in the first exposition" (1976, 29). Shewhart states that "a phenomenon will be said to be controlled when, through the use of past experience, we can predict, at least within limits, how the phenomenon may be expected to vary in the future. Here it is understood that prediction within limits means that we can state, at least approximately, the probability that the observed phenomenon will fall within given limits" (1931, 6).

For more information on quality-control charts, see Burr (1976), Duncan (1986), Harris (1999), or Ryan (2000).

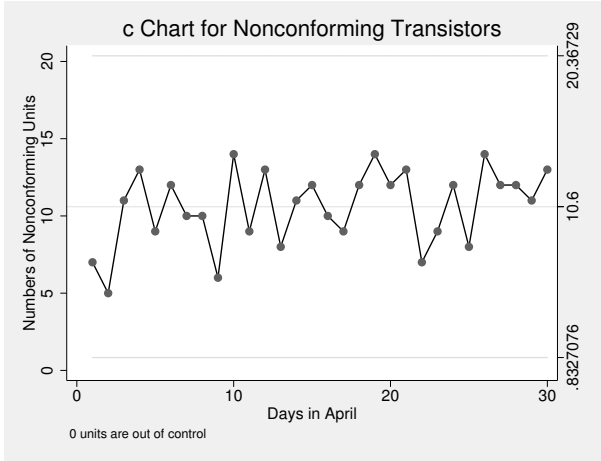
▷ Example 1: cchart

`cchart` graphs a c chart showing the number of nonconformities in a unit, where *defect_var* records the number of defects in each inspection unit and *unit_var* records the unit number. The unit numbers need not be in order. For instance, consider the following example dataset from Ryan (2000, 156):

```
. use http://www.stata-press.com/data/r12/ncu
. describe
Contains data from http://www.stata-press.com/data/r12/ncu.dta
  obs:            30
 vars:             2                          31 Mar 2011 03:56
 size:           240
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
day             float  %9.0g                  Days in April
defects         float  %9.0g                  Numbers of Nonconforming Units
-------------------------------------------------------------------------------
Sorted by:
. list in 1/5
```

	day	defects
1.	1	7
2.	2	5
3.	3	11
4.	4	13
5.	5	9

```
. cchart defects day, title(c Chart for Nonconforming Transistors)
```



The expected number of defects is 10.6, with lower and upper control limits of 0.8327 and 20.37, respectively. No units are out of control.

◁

▷ Example 2: pchart

`pchart` graphs a p chart, which shows the fraction of nonconforming items in a subgroup, where *reject_var* records the number rejected in each inspection unit, *unit_var* records the inspection unit number, and *ssize_var* records the number inspected in each unit.

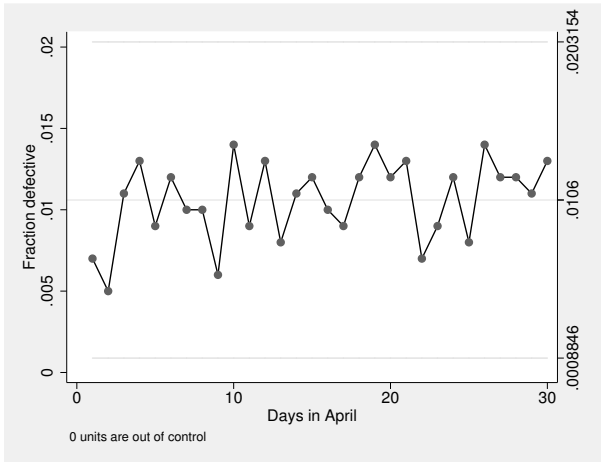
Consider the example dataset from Ryan (2000, 156) of the number of nonconforming transistors out of 1,000 inspected each day during the month of April:

```
. use http://www.stata-press.com/data/r12/ncu2
. describe
Contains data from http://www.stata-press.com/data/r12/ncu2.dta
  obs:            30
 vars:             3                          31 Mar 2011 14:13
 size:           360
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
day             float  %9.0g                  Days in April
rejects         float  %9.0g                  Numbers of Nonconforming Units
ssize           float  %9.0g                  Sample size
-------------------------------------------------------------------------------
Sorted by:
```

```
. list in 1/5
```

	day	rejects	ssize
1.	1	7	1000
2.	2	5	1000
3.	3	11	1000
4.	4	13	1000
5.	5	9	1000

```
. pchart rejects day ssize
```



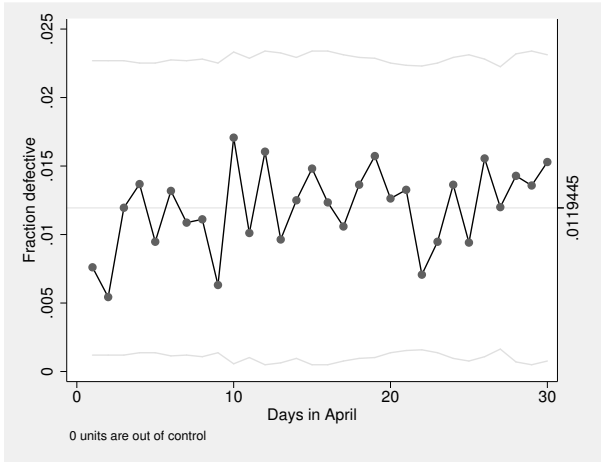
All the points are within the control limits, which are 0.0009 for the lower limit and 0.0203 for the upper limit.

Here the sample sizes are fixed at 1,000, so the `ssize` variable contains 1,000 for each observation. Sample sizes need not be fixed, however. Say that our data were slightly different:

```
. use http://www.stata-press.com/data/r12/ncu3
. list in 1/5
```

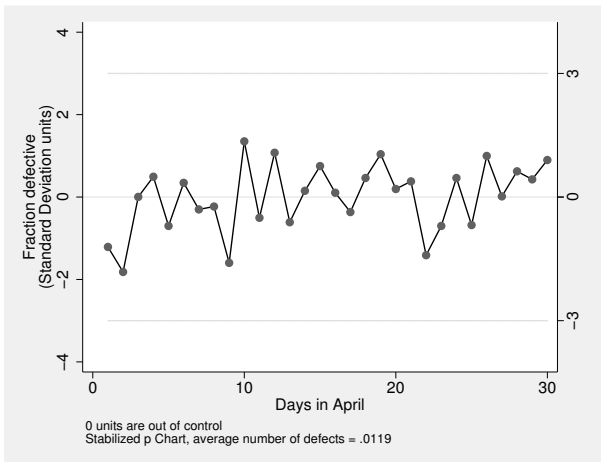
	day	rejects	ssize
1.	1	7	920
2.	2	5	920
3.	3	11	920
4.	4	13	950
5.	5	9	950

```
. pchart rejects day ssize
```



Here the control limits are, like the sample size, no longer constant. The `stabilize` option will stabilize the control chart:

```
. pchart rejects day ssize, stabilize
```



Example 3: rchart

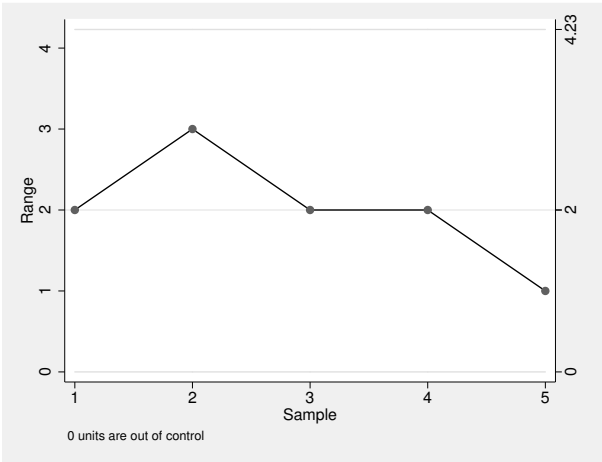
`rchart` displays an R chart showing the range for repeated measurements at various times. Variables within observations record measurements. Observations represent different samples.

For instance, say that we take five samples of 5 observations each. In our first sample, our measurements are 10, 11, 10, 11, and 12. The data are

```
. list
```

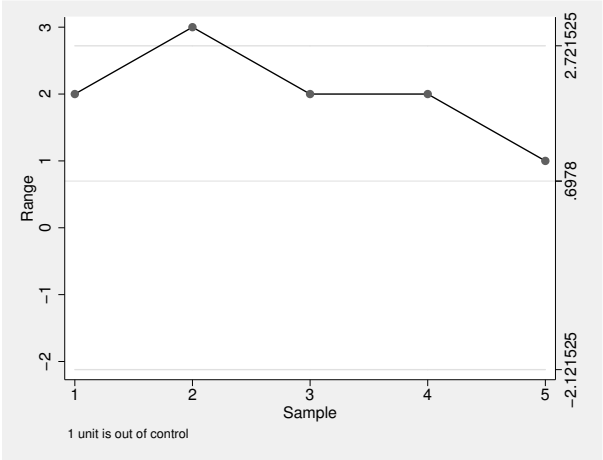
	m1	m2	m3	m4	m5
1.	10	11	10	11	12
2.	12	10	9	10	9
3.	10	11	10	12	10
4.	9	9	9	10	11
5.	12	12	12	12	13

```
. rchart m1-m5, connect(l)
```



The expected range in each sample is 2 with lower and upper control limits of 0 and 4.23, respectively. If we know that the process standard deviation is 0.3, we could specify

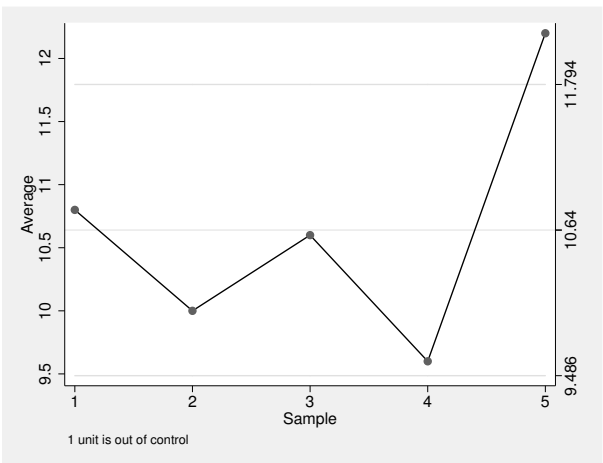
```
. rchart m1-m5, connect(l) std(.3)
```



Example 4: xchart

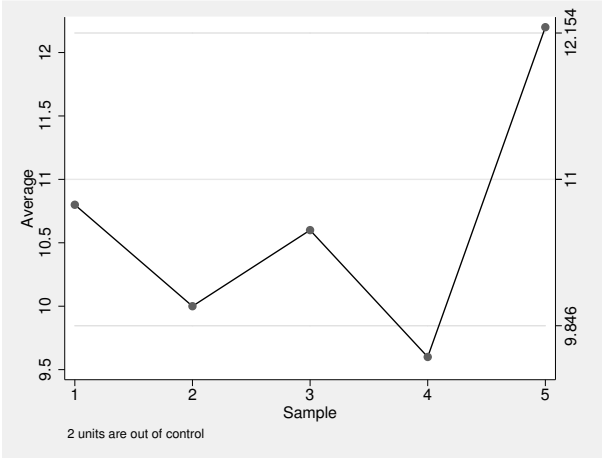
`xchart` graphs an $\overline{X}$ chart for repeated measurements at various times. Variables within observations record measurements, and observations represent different samples. Using the same data as in the previous example, we type

```
. xchart m1-m5, connect(l)
```



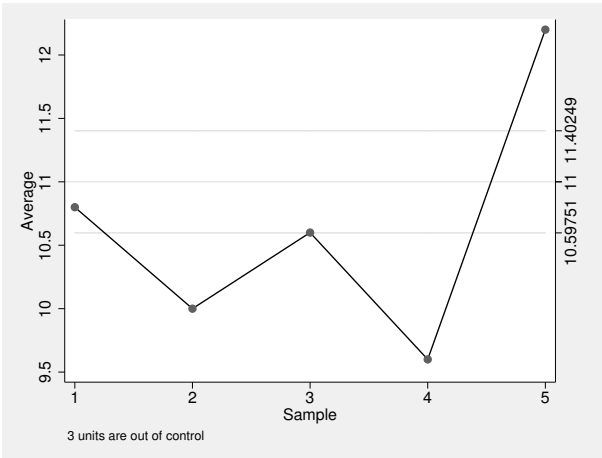
The average measurement in the sample is 10.64, and the lower and upper control limits are 9.486 and 11.794, respectively. Suppose that we knew from prior information that the mean of the process is 11. Then we would type

```
. xchart m1-m5, connect(l) mean(11)
```



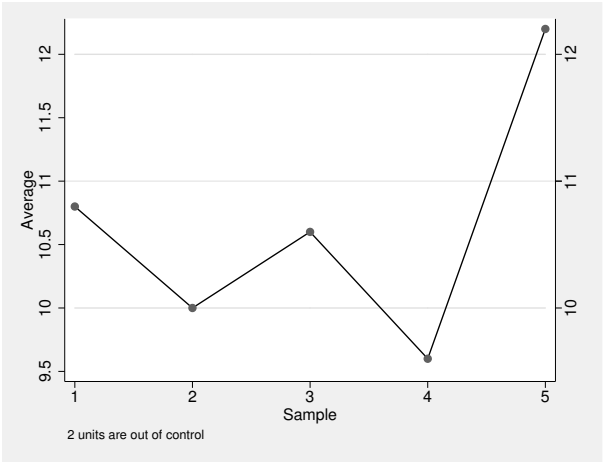
If we also know that the standard deviation of the process is 0.3, we could type

```
. xchart m1-m5, connect(l) mean(11) std(.3)
```



Finally, `xchart` allows us to specify our own control limits:

```
. xchart m1-m5, connect(l) mean(11) lower(10) upper(12)
```



◁

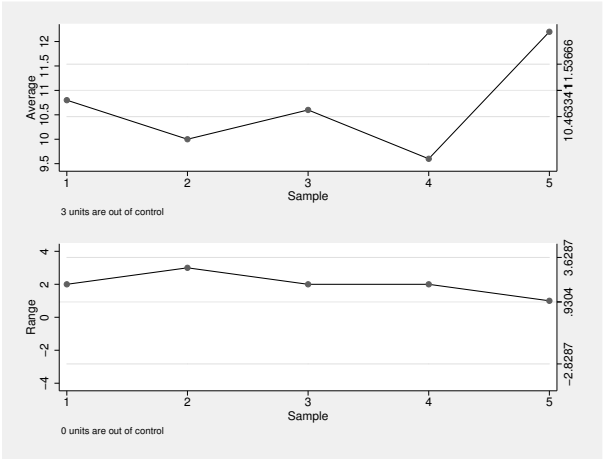
Walter Andrew Shewhart (1891–1967) was born in Illinois and educated as a physicist, with degrees from the Universities of Illinois and California. After a brief period teaching physics, he worked for the Western Electric Company and (from 1925) the Bell Telephone Laboratories. His name is most associated with control charts used in quality controls, but his many other interests ranged generally from quality assurance to the philosophy of science.

▷ Example 5: shewhart

`shewhart` displays a vertically aligned $\overline{X}$ and R chart in the same image. To produce the best-looking combined image possible, you will want to use the `xchart` and `rchart` commands separately and then combine the graphs. `shewhart`, however, is more convenient.

Using the same data as previously, but realizing that the standard deviation should have been 0.4, we type

```
. shewhart m1-m5, connect(l) mean(11) std(.4)
```



Saved results

`cchart` saves the following in `r()`:

Scalars

`r(cbar)`	expected number of nonconformities
`r(lcl_c)`	lower control limit
`r(ucl_c)`	upper control limit
`r(N)`	number of observations
`r(out_c)`	number of units out of control
`r(below_c)`	number of units below the lower limit
`r(above_c)`	number of units above the upper limit

`pchart` saves the following in `r()`:

Scalars

`r(pbar)`	average fraction of nonconformities
`r(lcl_p)`	lower control limit
`r(ucl_p)`	upper control limit
`r(N)`	number of observations
`r(out_p)`	number of units out of control
`r(below_p)`	number of units below the lower limit
`r(above_p)`	number of units above the upper limit

`rchart` saves the following in `r()`:

Scalars

`r(central_line)`	ordinate of the central line
`r(lcl_r)`	lower control limit
`r(ucl_r)`	upper control limit
`r(N)`	number of observations
`r(out_r)`	number of units out of control
`r(below_r)`	number of units below the lower limit
`r(above_r)`	number of units above the upper limit

`xchart` saves the following in `r()`:

Scalars

`r(xbar)`	grand mean
`r(lcl_x)`	lower control limit
`r(ucl_x)`	upper control limit
`r(N)`	number of observations
`r(out_x)`	number of units out of control
`r(below_x)`	number of units below the lower limit

`shewhart` saves in `r()` the combination of saved results from `xchart` and `rchart`.

Methods and formulas

`cchart`, `pchart`, `rchart`, `xchart`, and `shewhart` are implemented as ado-files.

For the c chart, the number of defects per unit, C, is taken to be a value of a random variable having a Poisson distribution. If k is the number of units available for estimating λ, the parameter of the Poisson distribution, and if C_i is the number of defects in the ith unit, then λ is estimated by $\overline{C} = \sum_i C_i/k$. Then

$$\begin{aligned}\text{central line} &= \overline{C}\\ \text{UCL} &= \overline{C} + 3\sqrt{\overline{C}}\\ \text{LCL} &= \overline{C} - 3\sqrt{\overline{C}}\end{aligned}$$

Control limits for the p chart are based on the sampling theory for proportions, using the normal approximation to the binomial. If k samples are taken, the estimator of p is given by $\overline{p} = \sum_i \widehat{p}_i/k$, where $\widehat{p}_i = x_i/n_i$, and x_i is the number of defects in the ith sample of size n_i. The central line and the control limits are given by

$$\begin{aligned}\text{central line} &= \overline{p}\\ \text{UCL} &= \overline{p} + 3\sqrt{\overline{p}(1-\overline{p})/n_i}\\ \text{LCL} &= \overline{p} - 3\sqrt{\overline{p}(1-\overline{p})/n_i}\end{aligned}$$

Control limits for the R chart are based on the distribution of the range of samples of size n from a normal population. If the standard deviation of the process, σ, is known,

$$\begin{aligned}\text{central line} &= d_2\sigma\\ \text{UCL} &= D_2\sigma\\ \text{LCL} &= D_1\sigma\end{aligned}$$

where d_2, D_1, and D_2 are functions of the number of observations in the sample and are obtained from the table published in Beyer (1976).

When σ is unknown,

$$\begin{aligned}\text{central line} &= \overline{R}\\ \text{UCL} &= (D_2/d_2)\overline{R}\\ \text{LCL} &= (D_1/d_2)\overline{R}\end{aligned}$$

where $\overline{R} = \sum_i R_i/k$ is the range of the k sample ranges R_i.

Control limits for the $\overline{\mathrm{X}}$ chart are given by

$$\begin{aligned}\text{central line} &= \overline{x}\\ \text{UCL} &= \overline{x} + (3/\sqrt{n})\sigma\\ \text{LCL} &= \overline{x} - (3/\sqrt{n})\sigma\end{aligned}$$

if σ is known. If σ is unknown,

$$\begin{aligned}\text{central line} &= \overline{x}\\ \text{UCL} &= \overline{x} + A_2\overline{R}\\ \text{LCL} &= \overline{x} - A_2\overline{R}\end{aligned}$$

where $\overline{R}$ is the average range as defined above and A_2 is a function (op. cit.) of the number of observations in the sample.

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Also see

[R] **serrbar** — Graph standard error bar chart

Title

qreg — Quantile regression

The documentation for [R] **qreg** has been updated. To see the latest PDF of [R] **qreg**, click here.

Syntax

Quantile regression

`qreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *qreg_options*]

Interquantile range regression

`iqreg` *depvar* [*indepvars*] [*if*] [*in*] [, *iqreg_options*]

Simultaneous-quantile regression

`sqreg` *depvar* [*indepvars*] [*if*] [*in*] [, *sqreg_options*]

Bootstrapped quantile regression

`bsqreg` *depvar* [*indepvars*] [*if*] [*in*] [, *bsqreg_options*]

Internal estimation command for quantile regression

`_qreg` [*depvar* [*indepvars*] [*if*] [*in*] [*weight*]] [, *_qreg_options*]

qreg_options	Description
Model	
`quantile(#)`	estimate # quantile; default is `quantile(.5)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats and line width
Optimization	
optimization_options	control the optimization process; seldom used
`wlsiter(#)`	attempt # weighted least-squares iterations before doing linear programming iterations

iqreg_options	Description
Model	
`quantiles(# #)`	interquantile range; default is `quantiles(.25 .75)`
`reps(#)`	perform # bootstrap replications; default is `reps(20)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nodots`	suppress display of the replication dots
display_options	control column formats and line width

sqreg_options	Description
Model	
`quantiles(#` [`#` [`# ...`]]`)`	estimate # quantiles; default is `quantiles(.5)`
`reps(#)`	perform # bootstrap replications; default is `reps(20)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nodots`	suppress display of the replication dots
display_options	control column formats and line width

bsqreg_options	Description
Model	
`quantile(#)`	estimate # quantile; default is `quantile(.5)`
`reps(#)`	perform # bootstrap replications; default is `reps(20)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats and line width

_qreg_options	Description
`quantile(#)`	estimate # quantile; default is `quantile(.5)`
`level(#)`	set confidence level; default is `level(95)`
`accuracy(#)`	relative accuracy required for linear programming algorithm; should not be specified
optimization_options	control the optimization process; seldom used

`by`, `mi estimate`, `rolling`, `statsby`, and `xi` are allowed by `qreg`, `iqreg`, `sqreg`, and `bsqreg`; `fracpoly`, `mfp`, `nestreg`, and `stepwise` are allowed only with `qreg`; see [U] **11.1.10 Prefix commands**.
`qreg` and `_qreg` allow `aweights` and `fweights`; see [U] **11.1.6 weight**.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

qreg

Statistics > Nonparametric analysis > Quantile regression

iqreg

Statistics > Nonparametric analysis > Interquantile regression

sqreg

Statistics > Nonparametric analysis > Simultaneous-quantile regression

bsqreg

Statistics > Nonparametric analysis > Bootstrapped quantile regression

Description

qreg fits quantile (including median) regression models, also known as least–absolute-value models (LAV or MAD) and minimum L1-norm models.

iqreg estimates interquantile range regressions, regressions of the difference in quantiles. The estimated variance–covariance matrix of the estimators (VCE) is obtained via bootstrapping.

sqreg estimates simultaneous-quantile regression. It produces the same coefficients as qreg for each quantile. Reported standard errors will be similar, but sqreg obtains an estimate of the VCE via bootstrapping, and the VCE includes between-quantile blocks. Thus you can test and construct confidence intervals comparing coefficients describing different quantiles.

bsqreg is equivalent to sqreg with one quantile.

_qreg is the internal estimation command for quantile regression. _qreg is not intended to be used directly; see *Methods and formulas* below.

Options for qreg

Model

quantile(#) specifies the quantile to be estimated and should be a number between 0 and 1, exclusive. Numbers larger than 1 are interpreted as percentages. The default value of 0.5 corresponds to the median.

Reporting

level(#); see [R] **estimation options**.

display_options: cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Optimization

optimization_options: iterate(#), [no]log, trace. iterate() specifies the maximum number of iterations; log/nolog specifies whether to show the iteration log; and trace specifies that the iteration log should include the current parameter vector. These options are seldom used.

wlsiter(#) specifies the number of weighted least-squares iterations that will be attempted before the linear programming iterations are started. The default value is 1. If there are convergence problems, increasing this number should help.

Options for iqreg

Model

quantiles(# #) specifies the quantiles to be compared. The first number must be less than the second, and both should be between 0 and 1, exclusive. Numbers larger than 1 are interpreted as percentages. Not specifying this option is equivalent to specifying quantiles(.25 .75), meaning the interquartile range.

reps(#) specifies the number of bootstrap replications to be used to obtain an estimate of the variance–covariance matrix of the estimators (standard errors). reps(20) is the default and is arguably too small. reps(100) would perform 100 bootstrap replications. reps(1000) would perform 1,000 replications.

Reporting

`level(#)`; see [R] **estimation options**.

`nodots` suppresses display of the replication dots.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Options for sqreg

Model

`quantiles(# [# [# ...]])` specifies the quantiles to be estimated and should contain numbers between 0 and 1, exclusive. Numbers larger than 1 are interpreted as percentages. The default value of 0.5 corresponds to the median.

`reps(#)` specifies the number of bootstrap replications to be used to obtain an estimate of the variance–covariance matrix of the estimators (standard errors). `reps(20)` is the default and is arguably too small. `reps(100)` would perform 100 bootstrap replications. `reps(1000)` would perform 1,000 replications.

Reporting

`level(#)`; see [R] **estimation options**.

`nodots` suppresses display of the replication dots.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Options for bsqreg

Model

`quantile(#)` specifies the quantile to be estimated and should be a number between 0 and 1, exclusive. Numbers larger than 1 are interpreted as percentages. The default value of 0.5 corresponds to the median.

`reps(#)` specifies the number of bootstrap replications to be used to obtain an estimate of the variance–covariance matrix of the estimators (standard errors). `reps(20)` is the default and is arguably too small. `reps(100)` would perform 100 bootstrap replications. `reps(1000)` would perform 1,000 replications.

Reporting

`level(#)`; see [R] **estimation options**.

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Options for _qreg

`quantile(#)` specifies the quantile to be estimated and should be a number between 0 and 1, exclusive. The default value of 0.5 corresponds to the median.

`level(#)`; see [R] **estimation options**.

`accuracy(#)` should not be specified; it specifies the relative accuracy required for the linear programming algorithm. If the potential for improving the sum of weighted deviations by deleting an observation from the basis is less than this on a percentage basis, the algorithm will be said to have converged. The default value is 10^{-10}.

optimization_options: `iterate(#)`, [`no`]`log`, `trace`. `iterate()` specifies the maximum number of iterations; `log`/`nolog` specifies whether to show the iteration log; and `trace` specifies that the iteration log should include the current parameter vector. These options are seldom used.

Remarks

Remarks are presented under the following headings:

Median regression
Generalized quantile regression
Estimated standard errors
Interquantile and simultaneous-quantile regression

Median regression

`qreg` without options fits quantile regression models. The most common form is median regression, where the object is to estimate the median of the dependent variable, conditional on the values of the independent variables. This method is similar to ordinary regression, where the objective is to estimate the mean of the dependent variable. Simply put, median regression finds a line through the data that minimizes the sum of the *absolute* residuals rather than the sum of the *squares* of the residuals, as in ordinary regression. Cameron and Trivedi (2010, chap. 7) provide a nice introduction to quantile regression using Stata.

▷ Example 1

Consider a two-group experimental design with 5 observations per group:

```
. use http://www.stata-press.com/data/r12/twogrp
. list
```

	x	y
1.	0	0
2.	0	1
3.	0	3
4.	0	4
5.	0	95
6.	1	14
7.	1	19
8.	1	20
9.	1	22
10.	1	23

```
. qreg y x
Iteration  1:  WLS sum of weighted deviations =  121.88268
Iteration  1: sum of abs. weighted deviations =       111
Iteration  2: sum of abs. weighted deviations =       110
Median regression                               Number of obs =        10
  Raw sum of deviations      157 (about 14)
  Min sum of deviations      110                Pseudo R2     =    0.2994
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
x	17	3.924233	4.33	0.003	7.950702	26.0493
_cons	3	2.774852	1.08	0.311	-3.39882	9.39882

We have estimated the equation

$$\mathrm{y}_{\mathrm{median}} = 3 + 17\,\mathrm{x}$$

We look back at our data. x takes on the values 0 and 1, so the median for the $\mathrm{x} = 0$ group is 3, whereas for $\mathrm{x} = 1$ it is $3 + 17 = 20$. The output reports that the raw sum of absolute deviations about 14 is 157; that is, the sum of $|\mathrm{y} - 14|$ is 157. Fourteen is the unconditional median of y, although in these data, any value between 14 and 19 could also be considered an unconditional median (we have an even number of observations, so the median is bracketed by those two values). In any case, the raw sum of deviations of y about the median would be the same no matter what number we choose between 14 and 19. (With a "median" of 14, the raw sum of deviations is 157. Now think of choosing a slightly larger number for the median and recalculating the sum. Half the observations will have larger negative residuals, but the other half will have smaller positive residuals, resulting in no net change.)

We turn now to the actual estimated equation. The sum of the absolute deviations about the solution $\mathrm{y}_{\mathrm{median}} = 3 + 17\mathrm{x}$ is 110. The pseudo-R^2 is calculated as $1 - 110/157 \approx 0.2994$. This result is based on the idea that the median regression is the maximum likelihood estimate for the double-exponential distribution.

◁

❑ Technical note

qreg is an alternative to regular regression or robust regression—see [R] **regress** and [R] **rreg**. Let's compare the results:

```
. regress y x
      Source |       SS       df       MS              Number of obs =      10
-------------+------------------------------           F(  1,     8) =    0.00
       Model |         2.5     1         2.5           Prob > F      =  0.9586
    Residual |      6978.4     8       872.3           R-squared     =  0.0004
-------------+------------------------------           Adj R-squared = -0.1246
       Total |      6980.9     9  775.655556           Root MSE      =  29.535
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
x	-1	18.6794	-0.05	0.959	-44.07477	42.07477
_cons	20.6	13.20833	1.56	0.157	-9.858465	51.05847

Unlike qreg, regress fits ordinary linear regression and is concerned with predicting the mean rather than the median, so both results are, in a technical sense, correct. Putting aside those technicalities, however, we tend to use either regression to describe the central tendency of the data, of which the mean is one measure and the median another. Thus we can ask, "which method better describes the central tendency of these data?"

Means—and therefore ordinary linear regression—are sensitive to outliers, and our data were purposely designed to contain two such outliers: 95 for `x` = 0 and 14 for `x` = 1. These two outliers dominated the ordinary regression and produced results that do not reflect the central tendency well—you are invited to enter the data and graph `y` against `x`.

Robust regression attempts to correct the outlier-sensitivity deficiency in ordinary regression:

```
. rreg y x, genwt(wt)
   Huber iteration 1:  maximum difference in weights = .7311828
   Huber iteration 2:  maximum difference in weights = .17695779
   Huber iteration 3:  maximum difference in weights = .03149585
Biweight iteration 4:  maximum difference in weights = .1979335
Biweight iteration 5:  maximum difference in weights = .23332905
Biweight iteration 6:  maximum difference in weights = .09960067
Biweight iteration 7:  maximum difference in weights = .02691458
Biweight iteration 8:  maximum difference in weights = .0009113
Robust regression                                     Number of obs =      10
                                                      F(  1,     8) =   80.63
                                                      Prob > F      =  0.0000
------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
           x |   18.16597   2.023114     8.98   0.000     13.50066    22.83128
       _cons |   2.000003   1.430558     1.40   0.200    -1.298869    5.298875
------------------------------------------------------------------------------
```

Here `rreg` discarded the first outlier completely. (We know this because we included the `genwt()` option on `rreg` and, after fitting the robust regression, examined the weights.) For the other "outlier", `rreg` produced a weight of 0.47.

In any case, the answers produced by `qreg` and `rreg` to describe the central tendency are similar, but the standard errors are different. In general, robust regression will have smaller standard errors because it is not as sensitive to the exact placement of observations near the median. Also, some authors (Rousseeuw and Leroy 1987, 11) have noted that quantile regression, unlike the median, may be sensitive to even one outlier, if its leverage is high enough. ❑

▷ Example 2

Let's now consider a less artificial example using the automobile data described in [U] **1.2.2 Example datasets**. Using median regression, we will regress each car's price on its weight and length and whether it is of foreign manufacture:

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. qreg price weight length foreign
Iteration  1:  WLS sum of weighted deviations =  112795.66
Iteration  1: sum of abs. weighted deviations =     111901
Iteration  2: sum of abs. weighted deviations =  110529.43
  (output omitted)
Iteration  8: sum of abs. weighted deviations =  108822.59
Median regression                               Number of obs =        74
  Raw sum of deviations   142205 (about 4934)
  Min sum of deviations 108822.6                Pseudo R2     =    0.2347
```

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	3.933588	.8602183	4.57	0.000	2.217937	5.649239
length	-41.25191	28.8693	-1.43	0.157	-98.82991	16.32609
foreign	3377.771	577.3391	5.85	0.000	2226.305	4529.237
_cons	344.6494	3260.244	0.11	0.916	-6157.702	6847.001

The estimated equation is

$$\texttt{price}_{\text{median}} = 3.93\,\texttt{weight} - 41.25\,\texttt{length} + 3377.8\,\texttt{foreign} + 344.65$$

The output may be interpreted in the same way as linear regression output; see [R] **regress**. The variables `weight` and `foreign` are significant, but `length` is not significant. The median price of the cars in these data is \$4,934. This value is a median (one of the two center observations), not *the* median, which would typically be defined as the midpoint of the two center observations.

◁

Generalized quantile regression

Generalized quantile regression is similar to median regression in that it estimates an equation describing a quantile other than the 0.5 (median) quantile. For example, specifying `quant(.25)` estimates the 25th percentile or the first quartile.

▷ Example 3

Again we will begin with the 10-observation artificial dataset we used at the beginning of *Median regression* above. We will estimate the 0.6667 quantile:

```
. use http://www.stata-press.com/data/r12/twogrp
. qreg y x, quant(0.6667)
Iteration  1:  WLS sum of weighted deviations =  152.32472
Iteration  1: sum of abs. weighted deviations =   138.0054
Iteration  2: sum of abs. weighted deviations =   136.6714
.6667 Quantile regression                       Number of obs =        10
  Raw sum of deviations 159.3334 (about 20)
  Min sum of deviations 136.6714                Pseudo R2     =    0.1422
```

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
x	18	54.21918	0.33	0.748	-107.0297	143.0297
_cons	4	38.33875	0.10	0.919	-84.40932	92.40932

The 0.6667 quantile in the data is 20. The estimated values are 4 for $x = 0$ and 22 for $x = 1$. These values are appropriate because the usual convention is to "count in" $(n + 1) \times$ quantile observations. ◁

▷ Example 4

Returning to real data, the equation for the 25th percentile of `price` based on `weight`, `length`, and `foreign` in our automobile data is

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)

. qreg price weight length foreign, quant(.25)
Iteration  1:  WLS sum of weighted deviations =  98938.466

Iteration  1: sum of abs. weighted deviations =  99457.766
Iteration  2: sum of abs. weighted deviations =  91339.779
  (output omitted)
Iteration 10: sum of abs. weighted deviations =  69603.554

.25 Quantile regression                             Number of obs =        74
  Raw sum of deviations  83825.5 (about 4187)
  Min sum of deviations 69603.55                    Pseudo R2     =    0.1697
```

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	1.831789	.668093	2.74	0.008	.4993194	3.164258
length	2.845558	24.78057	0.11	0.909	-46.57773	52.26885
foreign	2209.925	434.631	5.08	0.000	1343.081	3076.769
_cons	-1879.775	2808.067	-0.67	0.505	-7480.287	3720.737

Compared with our previous median regression, the coefficient on `length` now has a positive sign, and the coefficients on `foreign` and `weight` are reduced. The actual lower quantile is $4,187, substantially less than the median $4,934. It appears that the factors are weaker in this part of the distribution.

We can also estimate the upper quartile as a function of the same three variables:

```
. qreg price weight length foreign, quant(.75)
Iteration  1:  WLS sum of weighted deviations =  110931.48

Iteration  1: sum of abs. weighted deviations =  111305.91
Iteration  2: sum of abs. weighted deviations =  105989.57
  (output omitted)
Iteration  7: sum of abs. weighted deviations =  98395.935

.75 Quantile regression                             Number of obs =        74
  Raw sum of deviations 159721.5 (about 6342)
  Min sum of deviations 98395.94                    Pseudo R2     =    0.3840
```

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	9.22291	2.653579	3.48	0.001	3.930515	14.51531
length	-220.7833	80.13907	-2.76	0.007	-380.6156	-60.95096
foreign	3595.133	1727.704	2.08	0.041	149.3355	7040.931
_cons	20242.9	8534.529	2.37	0.020	3221.323	37264.49

This result tells a different story: `weight` is much more important, and `length` is now significant—with a negative coefficient! The prices of high-priced cars seem to be determined by factors different from those affecting the prices of low-priced cars.

◁

❑ Technical note

One explanation for having substantially different regression functions for different quantiles is that the data are heteroskedastic, as we will demonstrate below. The following statements create a sharply heteroskedastic set of data:

```
. drop _all
. set obs 10000
obs was 0, now 10000
. set seed 50550
. gen x = .1 + .9 * runiform()
. gen y = x * runiform()^2
```

Let's now fit the regressions for the 5th and 95th quantiles:

```
. qreg y x, quant(.05)
Iteration  1:  WLS sum of weighted deviations =  1080.7273

Iteration  1: sum of abs. weighted deviations =  1078.3192
Iteration  2: sum of abs. weighted deviations =  282.73545
  (output omitted)
Iteration  9: sum of abs. weighted deviations =  182.25244

.05 Quantile regression                              Number of obs =     10000
  Raw sum of deviations  182.357 (about .0009234)
  Min sum of deviations 182.2524                     Pseudo R2     =    0.0006

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
           x |    .002601   .0002737     9.50   0.000     .0020646    .0031374
       _cons |  -.0001393   .0001666    -0.84   0.403     -.000466    .0001874
------------------------------------------------------------------------------

. qreg y x, quant(.95)
Iteration  1:  WLS sum of weighted deviations =  1237.5569

Iteration  1: sum of abs. weighted deviations =  1238.0014
Iteration  2: sum of abs. weighted deviations =  456.65044
  (output omitted)
Iteration  5: sum of abs. weighted deviations =   338.4389

.95 Quantile regression                              Number of obs =     10000
  Raw sum of deviations 554.6889 (about .61326343)
  Min sum of deviations 338.4389                     Pseudo R2     =    0.3899

------------------------------------------------------------------------------
           y |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
           x |   .8898259   .0060398   147.33   0.000     .8779867     .901665
       _cons |   .0021514   .0036623     0.59   0.557    -.0050275    .0093302
------------------------------------------------------------------------------
```

The coefficient on `x`, in particular, differs markedly between the two estimates. For the mathematically inclined, it is not too difficult to show that the theoretical lines are $y = 0.0025\,x$ for the 5th percentile and $y = 0.9025\,x$ for the 95th, numbers in close agreement with our numerical results.

❑

Estimated standard errors

qreg estimates the variance–covariance matrix of the coefficients by using a method of Koenker and Bassett (1982) and Rogers (1993). This approach is described in *Methods and formulas* below. Rogers (1992) reports that, although this method seems adequate for homoskedastic errors, it appears to understate the standard errors for heteroskedastic errors. The irony is that exploring heteroskedastic errors is one of the major benefits of quantile regression. Gould (1992, 1997b) introduced generalized versions of qreg that obtain estimates of the standard errors by using bootstrap resampling (see Efron and Tibshirani [1993] or Wu [1986] for an introduction to bootstrap standard errors). The iqreg, sqreg, and bsqreg commands provide a bootstrapped estimate of the entire variance–covariance matrix of the estimators.

▷ Example 5

The first example of qreg on real data above was a median regression of price on weight, length, and foreign using the automobile data. Here is the result of repeating the estimation using bootstrap standard errors:

```
. set seed 1001
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. bsqreg price weight length foreign
(fitting base model)
(bootstrapping .....................)
Median regression, bootstrap(20) SEs                Number of obs =        74
  Raw sum of deviations   142205 (about 4934)
  Min sum of deviations 108822.6                    Pseudo R2     =    0.2347
```

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	3.933588	3.12446	1.26	0.212	-2.297951	10.16513
length	-41.25191	83.71266	-0.49	0.624	-208.2116	125.7077
foreign	3377.771	1057.281	3.19	0.002	1269.09	5486.452
_cons	344.6494	7053.301	0.05	0.961	-13722.72	14412.01

The coefficient estimates are the same—indeed, they are obtained using the same technique. Only the standard errors differ. Therefore, the t statistics, significance levels, and confidence intervals also differ.

Because bsqreg (as well as sqreg and iqreg) obtains standard errors by randomly resampling the data, the standard errors it produces will not be the same from run to run, unless we first set the random-number seed to the same number; see [R] **set seed**.

By default, bsqreg, sqreg, and iqreg use 20 replications. We can control the number of replications by specifying the reps() option:

```
. bsqreg price weight length foreign, reps(1000)
(fitting base model)
(bootstrapping ..................(output omitted)...)
Median regression, bootstrap(1000) SEs                Number of obs =        74
  Raw sum of deviations   142205 (about 4934)
  Min sum of deviations 108822.6                      Pseudo R2     =    0.2347
```

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	3.933588	2.659381	1.48	0.144	-1.370379	9.237555
length	-41.25191	69.29771	-0.60	0.554	-179.4618	96.95802
foreign	3377.771	1094.947	3.08	0.003	1193.967	5561.575
_cons	344.6494	5916.906	0.06	0.954	-11456.25	12145.55

A comparison of the standard errors is informative:

Variable	qreg	bsqreg reps(20)	bsqreg reps(1000)
weight	.8602	3.124	2.670
length	28.87	83.71	69.65
foreign	577.3	1057.	1094.
_cons	3260.	7053.	5945.

The results shown above are typical for models with heteroskedastic errors. (Our dependent variable is price; if our model had been in terms of ln(price), the standard errors estimated by qreg and bsqreg would have been nearly identical.) Also, even for heteroskedastic errors, 20 replications is generally sufficient for hypothesis tests against 0. ◁

Interquantile and simultaneous-quantile regression

Consider a quantile-regression model where the qth quantile is given by

$$Q_q(y) = a_q + b_{q,1}x_1 + b_{q,2}x_2$$

For instance, the 75th and 25th quantiles are given by

$$Q_{0.75}(y) = a_{0.75} + b_{0.75,1}x_1 + b_{0.75,2}x_2$$
$$Q_{0.25}(y) = a_{0.25} + b_{0.25,1}x_1 + b_{0.25,2}x_2$$

The difference in the quantiles is then

$$Q_{0.75}(y) - Q_{0.25}(y) = (a_{0.75} - a_{0.25}) + (b_{0.75,1} - b_{0.25,1})x_1 + (b_{0.75,2} - b_{0.25,2})x_2$$

qreg fits models such as $Q_{0.75}(y)$ and $Q_{0.25}(y)$. iqreg fits interquantile models, such as $Q_{0.75}(y) - Q_{0.25}(y)$. The relationships of the coefficients estimated by qreg and iqreg are exactly as shown: iqreg reports coefficients that are the difference in coefficients of two qreg models, and, of course, iqreg reports the appropriate standard errors, which it obtains by bootstrapping.

sqreg is like qreg in that it estimates the equations for the quantiles

$$Q_{0.75}(y) = a_{0.75} + b_{0.75,1}x_1 + b_{0.75,2}x_2$$
$$Q_{0.25}(y) = a_{0.25} + b_{0.25,1}x_1 + b_{0.25,2}x_2$$

The coefficients it obtains are the same that would be obtained by estimating each equation separately using qreg. sqreg differs from qreg in that it estimates the equations simultaneously and obtains an estimate of the entire variance–covariance matrix of the estimators by bootstrapping. Thus you can perform hypothesis tests concerning coefficients both within and across equations.

For example, to fit the above model, you could type

```
. qreg y x1 x2, quantile(.25)
. qreg y x1 x2, quantile(.75)
```

Doing this, you would obtain estimates of the parameters, but you could not test whether $b_{0.25,1} = b_{0.75,1}$ or, equivalently, $b_{0.75,1} - b_{0.25,1} = 0$. If your interest really is in the difference of coefficients, you could type

```
. iqreg y x1 x2, quantiles(.25 .75)
```

The "coefficients" reported would be the difference in quantile coefficients. You could also estimate both quantiles simultaneously and then test the equality of the coefficients:

```
. sqreg y x1 x2, quantiles(.25 .75)
. test [q25]x1 = [q75]x1
```

Whether you use iqreg or sqreg makes no difference for this test. sqreg, however, because it estimates the quantiles simultaneously, allows you to test other hypotheses. iqreg, by focusing on quantile differences, presents results in a way that is easier to read.

Finally, sqreg can estimate quantiles singly,

```
. sqreg y x1 x2, quantiles(.5)
```

and can thereby be used as a substitute for the slower bsqreg. (Gould [1997b] presents timings demonstrating that sqreg is faster than bsqreg.) sqreg can also estimate more than two quantiles simultaneously:

```
. sqreg y x1 x2, quantiles(.25 .5 .75)
```

▷ Example 6

In demonstrating qreg, we performed quantile regressions using the automobile data. We discovered that the regression of price on weight, length, and foreign produced vastly different coefficients for the 0.25, 0.5, and 0.75 quantile regressions. Here are the coefficients that we obtained:

Variable	25th percentile	50th percentile	75th percentile
weight	1.83	3.93	9.22
length	2.85	−41.25	−220.8
foreign	2209.9	3377.8	3595.1
_cons	−1879.8	344.6	20242.9

All we can say, having estimated these equations separately, is that price seems to depend differently on the weight, length, and foreign variables depending on the portion of the price distribution we examine. We cannot be more precise because the estimates have been made separately. With sqreg, however, we can estimate all the effects simultaneously:

```
. sqreg price weight length foreign, q(.25 .5 .75) reps(100)
(fitting base model)
(bootstrapping .................  (output omitted) .....)
Simultaneous quantile regression                    Number of obs =        74
  bootstrap(100) SEs                                .25 Pseudo R2 =    0.1697
                                                    .50 Pseudo R2 =    0.2347
                                                    .75 Pseudo R2 =    0.3840
```

price	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
q25						
weight	1.831789	1.244947	1.47	0.146	-.6511803	4.314758
length	2.845558	27.91648	0.10	0.919	-52.8321	58.52322
foreign	2209.925	911.6566	2.42	0.018	391.6836	4028.167
_cons	-1879.775	2756.871	-0.68	0.498	-7378.18	3618.63
q50						
weight	3.933588	2.732408	1.44	0.154	-1.516029	9.383205
length	-41.25191	75.8087	-0.54	0.588	-192.4476	109.9438
foreign	3377.771	921.578	3.67	0.000	1539.742	5215.8
_cons	344.6494	6810.32	0.05	0.960	-13238.1	13927.4
q75						
weight	9.22291	2.732795	3.37	0.001	3.772523	14.6733
length	-220.7833	87.38042	-2.53	0.014	-395.058	-46.50854
foreign	3595.133	1153.239	3.12	0.003	1295.07	5895.196
_cons	20242.9	9000.697	2.25	0.028	2291.579	38194.23

The coefficient estimates above are the same as those previously estimated, although the standard error estimates are a little different. `sqreg` obtains estimates of variance by bootstrapping. Rogers (1992) provides evidence that, for quantile regression, the bootstrap standard errors are better than those calculated analytically by Stata.

The important thing here, however, is that the full covariance matrix of the estimators has been estimated and stored, and thus it is now possible to perform hypothesis tests. Are the effects of `weight` the same at the 25th and 75th percentiles?

```
. test [q25]weight = [q75]weight
 ( 1)  [q25]weight - [q75]weight = 0
       F(  1,    70) =    8.29
            Prob > F =    0.0053
```

It appears that they are not. We can obtain a confidence interval for the difference by using `lincom`:

```
. lincom [q75]weight-[q25]weight
 ( 1)  - [q25]weight + [q75]weight = 0
```

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
(1)	7.391121	2.567684	2.88	0.005	2.270036	12.51221

Indeed, we could test whether the `weight` and `length` sets of coefficients are equal at the three quantiles estimated:

```
. quietly test [q25]weight = [q50]weight
. quietly test [q25]weight = [q75]weight, accum
```

```
. quietly test [q25]length = [q50]length, accum
. test [q25]length = [q75]length, accum
 ( 1)  [q25]weight - [q50]weight = 0
 ( 2)  [q25]weight - [q75]weight = 0
 ( 3)  [q25]length - [q50]length = 0
 ( 4)  [q25]length - [q75]length = 0
       F(  4,    70) =    2.21
            Prob > F =    0.0767
```

`iqreg` focuses on one quantile comparison but presents results that are more easily interpreted:

```
. set seed 1001
. iqreg price weight length foreign, q(.25 .75) reps(100) nodots
.75-.25 Interquantile regression                  Number of obs =        74
  bootstrap(100) SEs                              .75 Pseudo R2 =    0.3840
                                                  .25 Pseudo R2 =    0.1697
```

price	Coef.	Bootstrap Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	7.391121	2.467548	3.00	0.004	2.469752	12.31249
length	-223.6288	83.09868	-2.69	0.009	-389.3639	-57.89376
foreign	1385.208	1193.557	1.16	0.250	-995.2672	3765.683
_cons	22122.68	9009.159	2.46	0.017	4154.478	40090.88

Looking only at the 0.25 and 0.75 quantiles (the interquartile range), the `iqreg` command output is easily interpreted. Increases in `weight` correspond significantly to increases in `price` dispersion. Increases in `length` correspond to decreases in `price` dispersion. The `foreign` variable does not significantly change `price` dispersion.

Do not make too much of these results; the purpose of this example is simply to illustrate the `sqreg` and `iqreg` commands and to do so in a context that suggests why analyzing dispersion might be of interest.

`lincom` after `sqreg` produced the same t statistic for the interquartile range of `weight`, as did the `iqreg` command above. In general, they will not agree exactly because of the randomness of bootstrapping, unless the random-number seed is set to the same value before estimation (as was done here).

◁

Gould (1997a) presents simulation results showing that the coverage—the actual percentage of confidence intervals containing the true value—for `iqreg` is appropriate.

Saved results

qreg saves the following in e():

Scalars

e(N)	number of observations
e(df_m)	model degrees of freedom
e(df_r)	residual degrees of freedom
e(q)	quantile requested
e(q_v)	value of the quantile
e(sum_adev)	sum of absolute deviations
e(sum_rdev)	sum of raw deviations
e(f_r)	residual density estimate
e(rank)	rank of e(V)
e(convcode)	0 if converged; otherwise, return code for why nonconvergence

Macros

e(cmd)	qreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

iqreg saves the following in e():

Scalars

e(N)	number of observations
e(df_r)	residual degrees of freedom
e(q0)	lower quantile requested
e(q1)	upper quantile requested
e(reps)	number of replications
e(sumrdev0)	lower quantile sum of raw deviations
e(sumrdev1)	upper quantile sum of raw deviations
e(sumadev0)	lower quantile sum of absolute deviations
e(sumadev1)	upper quantile sum of absolute deviations
e(rank)	rank of e(V)
e(convcode)	0 if converged; otherwise, return code for why nonconvergence

Macros

e(cmd)	iqreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

sqreg saves the following in e():

Scalars

e(N)	number of observations
e(df_r)	residual degrees of freedom
e(n_q)	number of quantiles requested
e(q#)	the quantiles requested
e(reps)	number of replications
e(sumrdv#)	sum of raw deviations for q#
e(sumadv#)	sum of absolute deviations for q#
e(rank)	rank of e(V)
e(convcode)	0 if converged; otherwise, return code for why nonconvergence

Macros

e(cmd)	sqreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(eqnames)	names of equations
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

bsqreg saves the following in e():

Scalars

e(N)	number of observations
e(df_r)	residual degrees of freedom
e(q)	quantile requested
e(q_v)	value of the quantile
e(reps)	number of replications
e(sum_adev)	sum of absolute deviations
e(sum_rdev)	sum of raw deviations
e(rank)	rank of e(V)
e(convcode)	0 if converged; otherwise, return code for why nonconvergence

Macros

e(cmd)	bsqreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

_qreg saves the following in r():

Scalars

r(N)	number of observations
r(df_m)	model degrees of freedom
r(q)	quantile requested
r(q_v)	value of the quantile
r(sum_w)	sum of the weights
r(sum_adev)	sum of absolute deviations
r(sum_rdev)	sum of raw deviations
r(f_r)	residual density estimate
r(ic)	number of iterations
r(convcode)	1 if converged, 0 otherwise

Methods and formulas

qreg, iqreg, sqreg, and bsqreg are implemented as ado-files.

According to Stuart and Ord (1991, 1084), the method of minimum absolute deviations was first proposed by Boscovich in 1757 and was later developed by Laplace; Stigler (1986, 39–55) and Hald (1998, 97–103, 112–116) provide historical details. According to Bloomfield and Steiger (1980), Harris (1950) later observed that the problem of minimum absolute deviations could be turned into the linear programming problem that was first implemented by Wagner (1959). Interest has grown in this method because of interest in robust methods. Statistical and computational properties of minimum absolute deviation estimators are surveyed by Narula and Wellington (1982). Hao and Naiman (2007) provide an excellent introduction to quantile-regression methods.

Define q as the quantile to be estimated; the median is $q = 0.5$. For each observation i, let r_i be the residual

$$r_i = y_i - \sum_j \beta_j x_{ij}$$

Define the multiplier h_i

$$h_i = \begin{cases} 2q & \text{if } r_i > 0 \\ 2(1-q) & \text{otherwise} \end{cases}$$

The quantity being minimized with respect to β_j is $\sum_i |r_i| h_i$, so quantiles other than the median are estimated by weighting the residuals. For example, if we want to estimate the 75th percentile, we weight the negative residuals by 0.50 and the positive residuals by 1.50. It can be shown that the criterion is minimized when 75% of the residuals are negative.

This is set up as a linear programming problem and is solved via linear programming techniques, as suggested by Armstrong, Frome, and Kung (1979) and used by courtesy of Marcel Dekker, Inc. The definition of convergence is exact in the sense that no amount of added iterations could improve the solution. Each step is described by a set of observations through which the regression plane passes, called the *basis*. A step is taken by replacing a point in the basis if the sum of weighted absolute deviations can be improved. If this occurs, a line is printed in the iteration log. The linear programming method is started by doing a weighted least-squares (WLS) regression to identify a good set of observations to use as a starting basis. The WLS algorithm for $q = 0.5$ is taken from Schlossmacher (1973) with a generalization for $0 < q < 1$ implied from Hunter and Lange (2000).

The variances are estimated using a method suggested by Koenker and Bassett (1982). This method can be put into a form recommended by Huber (1967) for M estimates, where

$$\text{cov}(\boldsymbol{\beta}) = \mathbf{R}_2^{-1}\mathbf{R}_1\mathbf{R}_2^{-1}$$

$\mathbf{R}_1 = \mathbf{X}'\mathbf{W}\mathbf{W}'\mathbf{X}$ (in the Huber formulation), $\mathbf{W}$ is a diagonal matrix with elements

$$W_{ii} = \begin{cases} q/f_{\text{residuals}}(0) & \text{if } r > 0 \\ (1-q)/f_{\text{residuals}}(0) & \text{if } r < 0 \\ 0 & \text{otherwise} \end{cases}$$

and $\mathbf{R}_2$ is the design matrix $\mathbf{X}'\mathbf{X}$. This is derived from formula 3.11 in Koenker and Bassett, although their notation is much different. $f_{\text{residuals}}()$ refers to the density of the true residuals. Koenker and Bassett leave much unspecified, including how to obtain a density estimate for the errors in real data. At this point, we offer our contribution (Rogers 1993).

We first sort the residuals and locate the observation in the residuals corresponding to the quantile in question, taking into account weights if they are applied. We then calculate w_n, the square root of the sum of the weights. Unweighted data are equivalent to weighted data in which each observation has weight 1, resulting in $w_n = \sqrt{n}$. For analytically weighted data, the weights are rescaled so that the sum of the weights is the number of observations, resulting in $\sqrt{n}$ again. For frequency-weighted data, w_n literally is the square root of the sum of the weights.

We locate the closest observation in each direction, such that the sum of weights for all closer observations is w_n. If we run off the end of the dataset, we stop. We calculate w_s, the sum of weights for all observations in this middle space. Typically, w_s is slightly greater than w_n.

If there are k parameters, then exactly k of the residuals must be zero. Thus we calculate an adjusted weight $w_a = w_s - k$. The density estimate is the distance spanned by these observations divided by w_a. Because the distance spanned by this mechanism converges toward zero, this estimate of density converges in probability to the true density.

The pseudo-R^2 is calculated as

$$1 - \frac{\text{sum of weighted deviations about estimated quantile}}{\text{sum of weighted deviations about raw quantile}}$$

This is based on the likelihood for a double-exponential distribution $e^{h_i|r_i|}$.

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Also see

[R] **qreg postestimation** — Postestimation tools for qreg, iqreg, sqreg, and bsqreg

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **regress** — Linear regression

[R] **rreg** — Robust regression

[MI] **estimation** — Estimation commands for use with mi estimate

[U] **20 Estimation and postestimation commands**

Title

qreg postestimation — Postestimation tools for qreg, iqreg, sqreg, and bsqreg

Description

The following postestimation commands are available after `qreg`, `iqreg`, `bsqreg`, and `sqreg`:

Command	Description
`estat`	VCE and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

For qreg, iqreg, and bsqreg

```
predict [type] newvar [if] [in] [, [xb|stdp|residuals]]
```

For sqreg

```
predict [type] newvar [if] [in] [, equation(eqno[,eqno]) statistic]
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`stddp`	standard error of the difference in linear predictions
`residuals`	residuals

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`stddp` is allowed only after you have fit a model using `sqreg`. The standard error of the difference in linear predictions ($\mathbf{x}_{1j}\mathbf{b} - \mathbf{x}_{2j}\mathbf{b}$) between equations 1 and 2 is calculated.

`residuals` calculates the residuals, that is, $y_j - \mathbf{x}_j\mathbf{b}$.

`equation(`*eqno*`[ ,`*eqno*`])` specifies the equation to which you are making the calculation.

`equation()` is filled in with one *eqno* for the `xb`, `stdp`, and `residuals` options. `equation(#1)` would mean that the calculation is to be made for the first equation, `equation(#2)` would mean the second, and so on. You could also refer to the equations by their names. `equation(income)` would refer to the equation named income and `equation(hours)` to the equation named hours.

If you do not specify `equation()`, results are the same as if you had specified `equation(#1)`.

To use `stddp`, you must specify two equations. You might specify `equation(#1, #2)` or `equation(q80, q20)` to indicate the 80th and 20th quantiles.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **qreg** — Quantile regression

[U] **20 Estimation and postestimation commands**

Title

query — Display system parameters

Syntax

```
query [ memory | output | interface | graphics | efficiency | network |
  update | trace | mata | other ]
```

Description

query displays the settings of various Stata parameters.

Remarks

query provides more system information than you will ever want to know. You do not need to understand every line of output that query produces if all you need is one piece of information. Here is what happens when you type query:

```
. query
------------------------------------------------------------------------------
    Memory settings
        set maxvar          5000        2048-32767; max. vars allowed
        set matsize         400         10-11000; max. # vars in models
        set niceness        5           0-10
        set min_memory      0           0-1600gc
        set max_memory      .           32mc-1600gc or .
        set segmentsize     32mc        1mc-32gc
------------------------------------------------------------------------------
    Output settings
        set more            on
        set rmsg            off
        set dp              period      may be period or comma
        set linesize        80          characters
        set pagesize        27          lines
        ----------------------------------------------------------------------
        set level           95          percent confidence intervals
        ----------------------------------------------------------------------
        set showbaselevels              may be empty, off, on, or all
        set showemptycells              may be empty, off, or on
        set showomitted                 may be empty, off, or on
        set lstretch                    may be empty, off, or on
        ----------------------------------------------------------------------
        set cformat                     may be empty or a numerical format
        set pformat                     may be empty or a numerical format
        set sformat                     may be empty or a numerical format
        ----------------------------------------------------------------------
        set logtype         smcl        may be smcl or text
------------------------------------------------------------------------------
```

```
Interface settings
    set dockable        on
    set dockingguides   on
    set floatresults    off
    set floatwindows    off
    set locksplitters   off
    set pinnable        on
    set doublebuffer    on
    ------------------------------------------------------------------------------
    set linegap         1           pixels
    set scrollbufsize   204800      characters
    set fastscroll      on
    set reventries      5000        lines
    ------------------------------------------------------------------------------
    set maxdb           50          dialog boxes
------------------------------------------------------------------------------
Graphics settings
    set graphics        on
    set autotabgraphs   off
    set scheme          s2color
    set printcolor      automatic   may be automatic, asis, gs1, gs2, gs3
    set copycolor       automatic   may be automatic, asis, gs1, gs2, gs3
------------------------------------------------------------------------------
Efficiency settings
    set adosize         1000        kilobytes
------------------------------------------------------------------------------
Network settings
    set checksum        off
    set timeout1         30         seconds
    set timeout2        180         seconds
    ------------------------------------------------------------------------------
    set httpproxy       off
    set httpproxyhost
    set httpproxyport   80
    ------------------------------------------------------------------------------
    set httpproxyauth   off
    set httpproxyuser
    set httpproxypw
------------------------------------------------------------------------------
Update settings
    set update_query    on
    set update_interval 7
    set update_prompt   on
------------------------------------------------------------------------------
Trace (programming debugging) settings
    set trace           off
    set tracedepth      32000
    set traceexpand     on
    set tracesep        on
    set traceindent     on
    set tracenumber     off
    set tracehilite
------------------------------------------------------------------------------
```

```
    Mata settings
        set matastrict      off
        set matalnum        off
        set mataoptimize    on
        set matafavor       space       may be space or speed
        set matacache       400         kilobytes
        set matalibs        lmatabase;lmataado;lmataopt
        set matamofirst     off
-------------------------------------------------------------------------------
    Other settings
        set type            float       may be float or double
        set maxiter         16000       max iterations for estimation commands
        set searchdefault   local       may be local, net, or all
        set seed            X075bcd151f123bb5159a55e50022865746ad
        set varabbrev       on
        set emptycells      keep        may be keep or drop
        set processors      1
-------------------------------------------------------------------------------
```

The output is broken into several divisions: memory, output, interface, graphics, efficiency, network, update, trace, mata, and other settings. We will discuss each one in turn.

We generated the output above using Stata/SE for Windows. Here is what happens when we type `query` and we are running Stata/IC for Mac:

```
. query
-------------------------------------------------------------------------------
    Memory settings
        set maxvar          2048        (not settable in this version of Stata)
        set matsize         400         10-800; max. # vars in model
        set niceness        5           0-10
        set min_memory      0           0-1600g
        set max_memory      .           32m-1600g or .
        set segmentsize     32m         1m-32g
-------------------------------------------------------------------------------
    Output settings
        set more            on
        set rmsg            off
        set dp              period      may be period or comma
        set linesize        80          characters
        set pagesize        25          lines
        ---------------------------------------------------------------------
        set level           95          percent confidence intervals
        ---------------------------------------------------------------------
        set showbaselevels              may be empty, off, on, or all
        set showemptycells              may be empty, off, or on
        set showomitted                 may be empty, off, or on
        set lstretch                    may be empty, off, or on
        ---------------------------------------------------------------------
        set cformat                     may be empty or a numerical format
        set pformat                     may be empty or a numerical format
        set sformat                     may be empty or a numerical format
        ---------------------------------------------------------------------
        set logtype         smcl        may be smcl or text
        ---------------------------------------------------------------------
        set eolchar         unix        may be max or unix
        set notifyuser      on
        set playsnd         off
        set include_bitmap  on
-------------------------------------------------------------------------------
```

```
Interface settings
    set revkeyboard     on
    set varkeyboard     on
    set smoothfonts     on
    ------------------------------------------------------------------------
    set linegap         1           pixels
    set scrollbufsize   204800      characters
    set reventries      5000        lines
    ------------------------------------------------------------------------
    set maxdb           50          dialog boxes
-------------------------------------------------------------------------------
Graphics settings
    set graphics        on
    set scheme          s2color
    set printcolor      automatic   may be automatic, asis, gs1, gs2, gs3
    set copycolor       automatic   may be automatic, asis, gs1, gs2, gs3
-------------------------------------------------------------------------------
Efficiency settings
    set adosize         1000        kilobytes
-------------------------------------------------------------------------------
Network settings
    set checksum        off
    set timeout1        30          seconds
    set timeout2        180         seconds
    ------------------------------------------------------------------------
    set httpproxy       off
    set httpproxyhost
    set httpproxyport   80
    ------------------------------------------------------------------------
    set httpproxyauth   off
    set httpproxyuser
    set httpproxypw
-------------------------------------------------------------------------------
Update settings
    set update_query    on
    set update_interval 7
    set update_prompt   on
-------------------------------------------------------------------------------
Trace (programming debugging) settings
    set trace           off
    set tracedepth      32000
    set traceexpand     on
    set tracesep        on
    set traceindent     on
    set tracenumber     off
    set tracehilite
-------------------------------------------------------------------------------
Mata settings
    set matastrict      off
    set matalnum        off
    set mataoptimize    on
    set matafavor       space       may be space or speed
    set matacache       400         kilobytes
    set matalibs        lmatabase;lmataado;lmataopt
    set matamofirst     off
-------------------------------------------------------------------------------
```

```
Other settings
    set type            float      may be float or double
    set maxiter         16000      max iterations for estimation commands
    set searchdefault   local      may be local, net, or all
    set seed            X075bcd151f123bb5159a55e50022865746ad
    set varabbrev       on
    set emptycells      keep       may be keep or drop
    set processors      1
```

Memory settings

Memory settings indicate how memory is allocated, the maximum number of variables, and the maximum size of a matrix.

For more information, see

maxvar	[D]	**memory**
matsize	[R]	**matsize**
niceness	[D]	**memory**
min_memory	[D]	**memory**
max_memory	[D]	**memory**
segmentsize	[D]	**memory**

Output settings

Output settings show how Stata displays output on the screen and in log files.

For more information, see

more	[R]	**more**
rmsg	[P]	**rmsg**
dp	[D]	**format**
linesize	[R]	**log**
pagesize	[R]	**more**
level	[R]	**level**
showbaselevels	[R]	**set showbaselevels**
showemptycells	[R]	**set showbaselevels**
showomitted	[R]	**set showbaselevels**
cformat	[R]	**set cformat**
pformat	[R]	**set cformat**
sformat	[R]	**set cformat**
lstretch	[R]	**set**
logtype	[R]	**log**
eolchar	[R]	**set**
notifyuser	[R]	**set**
playsnd	[R]	**set**
include_bitmap	[R]	**set**

Interface settings

Interface settings control how Stata's interface works.

For more information, see

dockable	[R] **set**
dockingguides	[R] **set**
floatresults	[R] **set**
floatwindows	[R] **set**
locksplitters	[R] **set**
pinnable	[R] **set**
doublebuffer	[R] **set**
revkeyboard	[R] **set**
varkeyboard	[R] **set**
smoothfonts	[R] **set**
linegap	[R] **set**
scrollbufsize	[R] **set**
fastscroll	[R] **set**
reventries	[R] **set**
maxdb	[R] **db**

Graphics settings

Graphics settings indicate how Stata's graphics are displayed.

For more information, see

graphics	[G-2] **set graphics**
autotabgraphs	[R] **set**
scheme	[G-2] **set scheme**
printcolor	[G-2] **set printcolor**
copycolor	[G-2] **set printcolor**

Efficiency settings

The efficiency settings set the maximum amount of memory allocated to automatically loaded do-files, the maximum number of remembered-contents dialog boxes, and the use of virtual memory.

For more information, see

adosize	[P] **sysdir**

Network settings

Network settings determine how Stata interacts with the Internet.

For more information, see [R] **netio**.

Update settings

Update settings determine how Stata performs updates.

For more information, see [R] **update**.

Trace settings

Trace settings adjust Stata's behavior and are particularly useful in debugging code.

For more information, see [P] **trace**.

Mata settings

Mata settings affect Mata's system parameters.

For more information, see [M-3] **mata set**.

Other settings

The other settings are a miscellaneous collection.

For more information, see

`type`	[D] **generate**
`maxiter`	[R] **maximize**
`searchdefault`	[R] **search**
`seed`	[R] **set seed**
`varabbrev`	[R] **set**
`emptycells`	[R] **set**
`processors`	[R] **set**
`odbcmgr`	[D] **odbc**

In general, the parameters displayed by `query` can be changed by `set`; see [R] **set**.

Also see

[R] **set** — Overview of system parameters

[P] **creturn** — Return c-class values

[M-3] **mata set** — Set and display Mata system parameters

Title

ranksum — Equality tests on unmatched data

Syntax

Wilcoxon rank-sum test

`ranksum` *varname* [*if*] [*in*] , `by(`*groupvar*`)` [`porder`]

Nonparametric equality-of-medians test

`median` *varname* [*if*] [*in*] [*weight*] , `by(`*groupvar*`)` [*median_options*]

ranksum_options	Description
Main	
* `by(`*groupvar*`)`	grouping variable
`porder`	probability that variable for first group is larger than variable for second group

median_options	Description
Main	
* `by(`*groupvar*`)`	grouping variable
`exact`	perform Fisher's exact test
`medianties(below)`	assign values equal to the median to below group
`medianties(above)`	assign values equal to the median to above group
`medianties(drop)`	drop values equal to the median from the analysis
`medianties(split)`	split values equal to the median equally between the two groups

*`by(`*groupvar*`)` is required.
`by` is allowed with `ranksum` and `median`; see [D] **by**.
`fweights` are allowed with `median`; see [U] **11.1.6 weight**.

Menu

ranksum

Statistics > Nonparametric analysis > Tests of hypotheses > Wilcoxon rank-sum test

median

Statistics > Nonparametric analysis > Tests of hypotheses > K-sample equality-of-medians test

Description

`ranksum` tests the hypothesis that two independent samples (that is, *unmatched* data) are from populations with the same distribution by using the Wilcoxon rank-sum test, which is also known as the Mann–Whitney two-sample statistic (Wilcoxon 1945; Mann and Whitney 1947).

`median` performs a nonparametric *k*-sample test on the equality of medians. It tests the null hypothesis that the *k* samples were drawn from populations with the same median. For two samples, the chi-squared test statistic is computed both with and without a continuity correction.

`ranksum` and `median` are for use with *unmatched* data. For equality tests on matched data, see [R] **signrank**.

Options for ranksum

Main

`by(`*groupvar*`)` is required. It specifies the name of the grouping variable.

`porder` displays an estimate of the probability that a random draw from the first population is larger than a random draw from the second population.

Options for median

Main

`by(`*groupvar*`)` is required. It specifies the name of the grouping variable.

`exact` displays the significance calculated by Fisher's exact test. For two samples, both one- and two-sided probabilities are displayed.

`medianties(below | above | drop | split)` specifies how values equal to the overall median are to be handled. The median test computes the median for *varname* by using all observations and then divides the observations into those falling above the median and those falling below the median. When values for an observation are equal to the sample median, they can be dropped from the analysis by specifying `medianties(drop)`; added to the group above or below the median by specifying `medianties(above)` or `medianties(below)`, respectively; or if there is more than 1 observation with values equal to the median, they can be equally divided into the two groups by specifying `medianties(split)`. If this option is not specified, `medianties(below)` is assumed.

Remarks

▷ Example 1

We are testing the effectiveness of a new fuel additive. We run an experiment with 24 cars: 12 cars with the fuel treatment and 12 cars without. We input these data by creating a dataset with 24 observations. `mpg` records the mileage rating, and `treat` records 0 if the mileage corresponds to untreated fuel and 1 if it corresponds to treated fuel.

```
. use http://www.stata-press.com/data/r12/fuel2
. ranksum mpg, by(treat)
Two-sample Wilcoxon rank-sum (Mann-Whitney) test
      treat |       obs    rank sum    expected
------------+---------------------------------
          0 |        12         128         150
          1 |        12         172         150
------------+---------------------------------
   combined |        24         300         300
```

```
unadjusted variance      300.00
adjustment for ties       -4.04
                        ---------
adjusted variance        295.96
Ho: mpg(treat==0) = mpg(treat==1)
             z =  -1.279
    Prob > |z| =   0.2010
```

These results indicate that the medians are not statistically different at any level smaller than 20.1%. Similarly, the median test,

```
. median mpg, by(treat) exact
Median test
```

Greater than the median	treat 0	1	Total
no	7	5	12
yes	5	7	12
Total	12	12	24

```
          Pearson chi2(1) =   0.6667   Pr = 0.414
           Fisher's exact =                 0.684
   1-sided Fisher's exact =                 0.342
   Continuity corrected:
          Pearson chi2(1) =   0.1667   Pr = 0.683
```

fails to reject the null hypothesis that there is no difference between the two fuel additives.

Compare these results from these two tests with those obtained from the `signrank` and `signtest` where we found significant differences; see [R] **signrank**. An experiment run on 24 different cars is not as powerful as a before-and-after comparison using the same 12 cars.

◁

Saved results

`ranksum` saves the following in `r()`:

Scalars

`r(N_1)`	sample size n_1
`r(N_2)`	sample size n_2
`r(z)`	z statistic
`r(Var_a)`	adjusted variance
`r(group1)`	value of variable for first group
`r(sum_obs)`	actual sum of ranks for first group
`r(sum_exp)`	expected sum of ranks for first group
`r(porder)`	probability that draw from first population is larger than draw from second population

`median` saves the following in `r()`:

Scalars

`r(N)`	sample size
`r(chi2)`	Pearson's χ^2
`r(p)`	significance of Pearson's χ^2
`r(p_exact)`	Fisher's exact p
`r(groups)`	number of groups compared
`r(chi2_cc)`	continuity-corrected Pearson's χ^2
`r(p_cc)`	continuity-corrected significance
`r(p1_exact)`	one-sided Fisher's exact p

Methods and formulas

`ranksum` and `median` are implemented as ado-files.

For a practical introduction to these techniques with an emphasis on examples rather than theory, see Acock (2010), Bland (2000), or Sprent and Smeeton (2007). For a summary of these tests, see Snedecor and Cochran (1989).

Methods and formulas are presented under the following headings:

ranksum
median

ranksum

For the Wilcoxon rank-sum test, there are two independent random variables, X_1 and X_2, and we test the null hypothesis that $X_1 \sim X_2$. We have a sample of size n_1 from X_1 and another of size n_2 from X_2.

The data are then ranked without regard to the sample to which they belong. If the data are tied, averaged ranks are used. Wilcoxon's test statistic (1945) is the sum of the ranks for the observations in the first sample:

$$T = \sum_{i=1}^{n_1} R_{1i}$$

Mann and Whitney's U statistic (1947) is the number of pairs (X_{1i}, X_{2j}) such that $X_{1i} > X_{2j}$. These statistics differ only by a constant:

$$U = T - \frac{n_1(n_1+1)}{2}$$

Again Fisher's principle of randomization provides a method for calculating the distribution of the test statistic, ties or not. The randomization distribution consists of the $\binom{n}{n_1}$ ways to choose n_1 ranks from the set of all $n = n_1 + n_2$ ranks and assign them to the first sample.

It is a straightforward exercise to verify that

$$E(T) = \frac{n_1(n+1)}{2} \qquad \text{and} \qquad \mathrm{Var}(T) = \frac{n_1 n_2 s^2}{n}$$

where s is the standard deviation of the combined ranks, r_i, for both groups:

$$s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(r_i - \overline{r})^2$$

This formula for the variance is exact and holds both when there are no ties and when there are ties and we use averaged ranks. (Indeed, the variance formula holds for the randomization distribution of choosing n_1 numbers from any set of n numbers.)

Using a normal approximation, we calculate

$$z = \frac{T - E(T)}{\sqrt{\mathrm{Var}(T)}}$$

When the `porder` option is specified, the probability

$$p = \frac{U}{n_1 n_2}$$

is computed.

median

The median test examines whether it is likely that two or more samples came from populations with the same median. The null hypothesis is that the samples were drawn from populations with the same median. The alternative hypothesis is that at least one sample was drawn from a population with a different median. The test should be used only with ordinal or interval data.

Assume that there are score values for k independent samples to be compared. The median test is performed by first computing the median score for all observations combined, regardless of the sample group. Each score is compared with this computed grand median and is classified as being above the grand median, below the grand median, or equal to the grand median. Observations with scores equal to the grand median can be dropped, added to the "above" group, added to the "below" group, or split between the two groups.

Once all observations are classified, the data are cast into a $2 \times k$ contingency table, and a Pearson's chi-squared test or Fisher's exact test is performed.

Henry Berthold Mann (1905–2000) was born in Vienna, Austria, where he completed a doctorate in algebraic number theory. He moved to the United States in 1938 and for several years made his livelihood by tutoring in New York. During this time, he proved a celebrated conjecture in number theory and studied statistics at Columbia with Abraham Wald, with whom he wrote three papers. After the war, he taught at Ohio State and the Universities of Wisconsin and Arizona. In addition to his work in number theory and statistics, he made major contributions to algebra and combinatorics.

Donald Ransom Whitney (1915–2007) studied at Oberlin, Princeton, and Ohio State Universities and worked at the latter throughout his career. His PhD thesis under Henry Mann was on nonparametric statistics. It was this work that produced the test that bears their names.

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Also see

[R] **signrank** — Equality tests on matched data

[R] **ttest** — Mean-comparison tests

Title

ratio — Estimate ratios

Syntax

Basic syntax

```
ratio [name:] varname [/] varname
```

Full syntax

```
ratio ([name:] varname [/] varname)
      [([name:] varname [/] varname) ...] [if] [in] [weight] [, options]
```

options	Description
Model	
`stdize(`*varname*`)`	variable identifying strata for standardization
`stdweight(`*varname*`)`	weight variable for standardization
`nostdrescale`	do not rescale the standard weight variable
if/in/over	
`over(`*varlist*`[ , nolabel])`	group over subpopulations defined by *varlist*; optionally, suppress group labels
SE/Cluster	
`vce(`*vcetype*`)`	*vcetype* may be `linearized`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noheader`	suppress table header
`nolegend`	suppress table legend
display_options	control column formats and line width
`coeflegend`	display legend instead of statistics

`bootstrap`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Ratios

Description

`ratio` produces estimates of ratios, along with standard errors.

Options

Model

`stdize(`*varname*`)` specifies that the point estimates be adjusted by direct standardization across the strata identified by *varname*. This option requires the `stdweight()` option.

`stdweight(`*varname*`)` specifies the weight variable associated with the standard strata identified in the `stdize()` option. The standardization weights must be constant within the standard strata.

`nostdrescale` prevents the standardization weights from being rescaled within the `over()` groups. This option requires `stdize()` but is ignored if the `over()` option is not specified.

if/in/over

`over(`*varlist* [`, nolabel`]`)` specifies that estimates be computed for multiple subpopulations, which are identified by the different values of the variables in *varlist*.

When this option is supplied with one variable name, such as `over(`*varname*`)`, the value labels of *varname* are used to identify the subpopulations. If *varname* does not have labeled values (or there are unlabeled values), the values themselves are used, provided that they are nonnegative integers. Noninteger values, negative values, and labels that are not valid Stata names are substituted with a default identifier.

When `over()` is supplied with multiple variable names, each subpopulation is assigned a unique default identifier.

`nolabel` requests that value labels attached to the variables identifying the subpopulations be ignored.

SE/Cluster

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(linearized)`, the default, uses the linearized or sandwich estimator of variance.

Reporting

`level(#)`; see [R] **estimation options**.

`noheader` prevents the table header from being displayed. This option implies `nolegend`.

`nolegend` prevents the table legend identifying the subpopulations from being displayed.

display_options: `cformat(%`*fmt*`)` and `nolstretch`; see [R] **estimation options**.

The following option is available with `ratio` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Example 1

Using the fuel data from example 2 of [R] **ttest**, we estimate the ratio of mileage for the cars without the fuel treatment (mpg1) to those with the fuel treatment (mpg2).

```
. use http://www.stata-press.com/data/r12/fuel
. ratio myratio: mpg1/mpg2
Ratio estimation                 Number of obs    =       12
      myratio: mpg1/mpg2
```

	Ratio	Linearized Std. Err.	[95% Conf.	Interval]
myratio	.9230769	.032493	.8515603	.9945936

Using these results, we can test to see if this ratio is significantly different from one.

```
. test _b[myratio] = 1
 ( 1)  myratio = 1
       F(  1,    11) =    5.60
            Prob > F =    0.0373
```

We find that the ratio is different from one at the 5% significance level but not at the 1% significance level.

◁

Example 2

Using state-level census data, we want to test whether the marriage rate is equal to the death rate.

```
. use http://www.stata-press.com/data/r12/census2
(1980 Census data by state)
. ratio (deathrate: death/pop) (marrate: marriage/pop)
Ratio estimation                 Number of obs    =       50
    deathrate: death/pop
      marrate: marriage/pop
```

	Ratio	Linearized Std. Err.	[95% Conf.	Interval]
deathrate	.0087368	.0002052	.0083244	.0091492
marrate	.0105577	.0006184	.009315	.0118005

```
. test _b[deathrate]  =  _b[marrate]
 ( 1)  deathrate - marrate = 0
       F(  1,    49) =    6.93
            Prob > F =    0.0113
```

◁

Saved results

`ratio` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_over)`	number of subpopulations
`e(N_stdize)`	number of standard strata
`e(N_clust)`	number of clusters
`e(k_eq)`	number of equations in `e(b)`
`e(df_r)`	sample degrees of freedom
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`ratio`
`e(cmdline)`	command as typed
`e(varlist)`	*varlist*
`e(stdize)`	*varname* from `stdize()`
`e(stdweight)`	*varname* from `stdweight()`
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(cluster)`	name of cluster variable
`e(over)`	*varlist* from `over()`
`e(over_labels)`	labels from `over()` variables
`e(over_namelist)`	names from `e(over_labels)`
`e(namelist)`	ratio identifiers
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(properties)`	`b V`
`e(estat_cmd)`	program used to implement `estat`
`e(marginsnotok)`	predictions disallowed by `margins`

Matrices

`e(b)`	vector of mean estimates
`e(V)`	(co)variance estimates
`e(_N)`	vector of numbers of nonmissing observations
`e(_N_stdsum)`	number of nonmissing observations within the standard strata
`e(_p_stdize)`	standardizing proportions
`e(error)`	error code corresponding to `e(b)`

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`ratio` is implemented as an ado-file.

Methods and formulas are presented under the following headings:

The ratio estimator
Survey data
The survey ratio estimator
The standardized ratio estimator
The poststratified ratio estimator
The standardized poststratified ratio estimator
Subpopulation estimation

The ratio estimator

Let $R = Y/X$ be the ratio to be estimated, where Y and X are totals; see [R] **total**. The estimate for R is $\widehat{R} = \widehat{Y}/\widehat{X}$ (the ratio of the sample totals). From the delta method (that is, a first-order Taylor expansion), the approximate variance of the sampling distribution of the linearized $\widehat{R}$ is

$$V(\widehat{R}) \approx \frac{1}{X^2}\left\{V(\widehat{Y}) - 2R\mathrm{Cov}(\widehat{Y},\widehat{X}) + R^2V(\widehat{X})\right\}$$

Direct substitution of $\widehat{X}$, $\widehat{R}$, and the estimated variances and covariance of $\widehat{X}$ and $\widehat{Y}$ leads to the following variance estimator:

$$\widehat{V}(\widehat{R}) = \frac{1}{\widehat{X}^2}\left\{\widehat{V}(\widehat{Y}) - 2\widehat{R}\widehat{\mathrm{Cov}}(\widehat{Y},\widehat{X}) + \widehat{R}^2\widehat{V}(\widehat{X})\right\} \tag{1}$$

Survey data

See [SVY] **variance estimation**, [SVY] **direct standardization**, and [SVY] **poststratification** for discussions that provide background information for the following formulas.

The survey ratio estimator

Let Y_j and X_j be survey items for the jth individual in the population, where $j = 1, \ldots, M$ and M is the size of the population. The associated population ratio for the items of interest is $R = Y/X$ where

$$Y = \sum_{j=1}^{M} Y_j \qquad \text{and} \qquad X = \sum_{j=1}^{M} X_j$$

Let y_j and x_j be the corresponding survey items for the jth sampled individual from the population, where $j = 1, \ldots, m$ and m is the number of observations in the sample.

The estimator $\widehat{R}$ for the population ratio R is $\widehat{R} = \widehat{Y}/\widehat{X}$, where

$$\widehat{Y} = \sum_{j=1}^{m} w_j y_j \qquad \text{and} \qquad \widehat{X} = \sum_{j=1}^{m} w_j x_j$$

and w_j is a sampling weight. The score variable for the ratio estimator is

$$z_j(\widehat{R}) = \frac{y_j - \widehat{R}x_j}{\widehat{X}} = \frac{\widehat{X}y_j - \widehat{Y}x_j}{\widehat{X}^2}$$

The standardized ratio estimator

Let D_g denote the set of sampled observations that belong to the gth standard stratum and define $I_{D_g}(j)$ to indicate if the jth observation is a member of the gth standard stratum; where $g = 1, \ldots, L_D$ and L_D is the number of standard strata. Also, let π_g denote the fraction of the population that belongs to the gth standard stratum, thus $\pi_1 + \cdots + \pi_{L_D} = 1$. Note that π_g is derived from the `stdweight()` option.

The estimator for the standardized ratio is

$$\widehat{R}^D = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g}{\widehat{X}_g}$$

where

$$\widehat{Y}_g = \sum_{j=1}^{m} I_{D_g}(j)\, w_j y_j$$

and $\widehat{X}_g$ is similarly defined. The score variable for the standardized ratio is

$$z_j(\widehat{R}^D) = \sum_{g=1}^{L_D} \pi_g I_{D_g}(j) \frac{\widehat{X}_g y_j - \widehat{Y}_g x_j}{\widehat{X}_g^2}$$

The poststratified ratio estimator

Let P_k denote the set of sampled observations that belong to poststratum k, and define $I_{P_k}(j)$ to indicate if the jth observation is a member of poststratum k, where $k = 1, \ldots, L_P$ and L_P is the number of poststrata. Also, let M_k denote the population size for poststratum k. P_k and M_k are identified by specifying the `poststrata()` and `postweight()` options on `svyset`; see [SVY] **svyset**.

The estimator for the poststratified ratio is

$$\widehat{R}^P = \frac{\widehat{Y}^P}{\widehat{X}^P}$$

where

$$\widehat{Y}^P = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{Y}_k = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j)\, w_j y_j$$

and $\widehat{X}^P$ is similarly defined. The score variable for the poststratified ratio is

$$z_j(\widehat{R}^P) = \frac{z_j(\widehat{Y}^P) - \widehat{R}^P z_j(\widehat{X}^P)}{\widehat{X}^P} = \frac{\widehat{X}^P z_j(\widehat{Y}^P) - \widehat{Y}^P z_j(\widehat{X}^P)}{(\widehat{X}^P)^2}$$

where

$$z_j(\widehat{Y}^P) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left(y_j - \frac{\widehat{Y}_k}{\widehat{M}_k} \right)$$

and $z_j(\widehat{X}^P)$ is similarly defined.

The standardized poststratified ratio estimator

The estimator for the standardized poststratified ratio is

$$\widehat{R}^{DP} = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g^P}{\widehat{X}_g^P}$$

where

$$\widehat{Y}_g^P = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \widehat{Y}_{g,k} = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{D_g}(j) I_{P_k}(j)\, w_j y_j$$

and $\widehat{X}_g^P$ is similarly defined. The score variable for the standardized poststratified ratio is

$$z_j(\widehat{R}^{DP}) = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{X}_g^P z_j(\widehat{Y}_g^P) - \widehat{Y}_g^P z_j(\widehat{X}_g^P)}{(\widehat{X}_g^P)^2}$$

where

$$z_j(\widehat{Y}_g^P) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_{D_g}(j) y_j - \frac{\widehat{Y}_{g,k}}{\widehat{M}_k} \right\}$$

and $z_j(\widehat{X}_g^P)$ is similarly defined.

Subpopulation estimation

Let S denote the set of sampled observations that belong to the subpopulation of interest, and define $I_S(j)$ to indicate if the jth observation falls within the subpopulation.

The estimator for the subpopulation ratio is $\widehat{R}^S = \widehat{Y}^S / \widehat{X}^S$, where

$$\widehat{Y}^S = \sum_{j=1}^{m} I_S(j)\, w_j y_j \qquad \text{and} \qquad \widehat{X}^S = \sum_{j=1}^{m} I_S(j)\, w_j x_j$$

Its score variable is

$$z_j(\widehat{R}^S) = I_S(j) \frac{y_j - \widehat{R}^S x_j}{\widehat{X}^S} = I_S(j) \frac{\widehat{X}^S y_j - \widehat{Y}^S x_j}{(\widehat{X}^S)^2}$$

The estimator for the standardized subpopulation ratio is

$$\widehat{R}^{DS} = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g^S}{\widehat{X}_g^S}$$

where

$$\widehat{Y}_g^S = \sum_{j=1}^{m} I_{D_g}(j) I_S(j)\, w_j y_j$$

and $\widehat{X}_g^S$ is similarly defined. Its score variable is

$$z_j(\widehat{R}^{DS}) = \sum_{g=1}^{L_D} \pi_g I_{D_g}(j) I_S(j) \frac{\widehat{X}_g^S y_j - \widehat{Y}_g^S x_j}{(\widehat{X}_g^S)^2}$$

The estimator for the poststratified subpopulation ratio is

$$\widehat{R}^{PS} = \frac{\widehat{Y}^{PS}}{\widehat{X}^{PS}}$$

where

$$\widehat{Y}^{PS} = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{Y}_k^S = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j) I_S(j)\, w_j y_j$$

and $\widehat{X}^{PS}$ is similarly defined. Its score variable is

$$z_j(\widehat{R}^{PS}) = \frac{\widehat{X}^{PS} z_j(\widehat{Y}^{PS}) - \widehat{Y}^{PS} z_j(\widehat{X}^{PS})}{(\widehat{X}^{PS})^2}$$

where

$$z_j(\widehat{Y}^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_S(j)\, y_j - \frac{\widehat{Y}_k^S}{\widehat{M}_k} \right\}$$

and $z_j(\widehat{X}^{PS})$ is similarly defined.

The estimator for the standardized poststratified subpopulation ratio is

$$\widehat{R}^{DPS} = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{Y}_g^{PS}}{\widehat{X}_g^{PS}}$$

where

$$\widehat{Y}_g^{PS} = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \widehat{Y}_{g,k}^S = \sum_{k=1}^{L_p} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{D_g}(j) I_{P_k}(j) I_S(j)\, w_j y_j$$

and $\widehat{X}_g^{PS}$ is similarly defined. Its score variable is

$$z_j(\widehat{R}^{DPS}) = \sum_{g=1}^{L_D} \pi_g \frac{\widehat{X}_g^{PS} z_j(\widehat{Y}_g^{PS}) - \widehat{Y}_g^{PS} z_j(\widehat{X}_g^{PS})}{(\widehat{X}_g^{PS})^2}$$

where

$$z_j(\widehat{Y}_g^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_{D_g}(j) I_S(j)\, y_j - \frac{\widehat{Y}_{g,k}^S}{\widehat{M}_k} \right\}$$

and $z_j(\widehat{X}_g^{PS})$ is similarly defined.

References

Cochran, W. G. 1977. *Sampling Techniques.* 3rd ed. New York: Wiley.

Stuart, A., and J. K. Ord. 1994. *Kendall's Advanced Theory of Statistics: Distribution Theory, Vol I.* 6th ed. London: Arnold.

Also see

[R] **ratio postestimation** — Postestimation tools for ratio

[R] **mean** — Estimate means

[R] **proportion** — Estimate proportions

[R] **total** — Estimate totals

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **poststratification** — Poststratification for survey data

[SVY] **subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **variance estimation** — Variance estimation for survey data

[U] **20 Estimation and postestimation commands**

Title

ratio postestimation — Postestimation tools for ratio

Description

The following postestimation commands are available after `ratio`:

Command	Description
`estat`	VCE
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Remarks

For examples of the use of `test` after `ratio`, see [R] **ratio**.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **ratio** — Estimate ratios

[SVY] **svy postestimation** — Postestimation tools for svy

[U] **20 Estimation and postestimation commands**

Title

reg3 — Three-stage estimation for systems of simultaneous equations

Syntax

Basic syntax

```
reg3 (depvar1 varlist1) (depvar2 varlist2) ... (depvarN varlistN) [if] [in] [weight]
```

Full syntax

```
reg3 ([eqname1:]depvar1a [depvar1b ...=] varlist1 [, noconstant])
    ([eqname2:]depvar2a [depvar2b ...=] varlist2 [, noconstant])
    ...
    ([eqnameN:]depvarNa [depvarNb ...=] varlistN [, noconstant])
    [if] [in] [weight] [, options]
```

options	Description
Model	
ireg3	iterate until estimates converge
constraints(*constraints*)	apply specified linear constraints
Model 2	
exog(*varlist*)	exogenous variables not specified in system equations
endog(*varlist*)	additional right-hand-side endogenous variables
inst(*varlist*)	full list of exogenous variables
allexog	all right-hand-side variables are exogenous
noconstant	suppress constant from instrument list
Est. method	
3sls	three-stage least squares; the default
2sls	two-stage least squares
ols	ordinary least squares (OLS)
sure	seemingly unrelated regression estimation (SURE)
mvreg	sure with OLS degrees-of-freedom adjustment
corr(*correlation*)	unstructured or independent correlation structure; default is unstructured
df adj.	
small	report small-sample statistics
dfk	use small-sample adjustment
dfk2	use alternate adjustment

Reporting	
level(#)	set confidence level; default is level(95)
first	report first-stage regression
nocnsreport	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Optimization	
optimization_options	control the optimization process; seldom used
noheader	suppress display of header
notable	suppress display of coefficient table
nofooter	suppress display of footer
coeflegend	display legend instead of statistics

varlist$_1$, ..., *varlist*$_N$ and the exog() and the inst() varlist may contain factor variables; see [U] **11.4.3 Factor variables**. You must have the same levels of factor variables in all equations that have factor variables.

depvar and *varlist* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, jackknife, rolling, and statsby are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

aweights are not allowed with the jackknife prefix; see [R] **jackknife**.

aweights and fweights are allowed; see [U] **11.1.6 weight**.

noheader, notable, nofooter, and coeflegend do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Explicit equation naming (*eqname*:) cannot be combined with multiple dependent variables in an equation specification.

Menu

Statistics > Endogenous covariates > Three-stage least squares

Description

reg3 estimates a system of structural equations, where some equations contain endogenous variables among the explanatory variables. Estimation is via three-stage least squares (3SLS); see Zellner and Theil (1962). Typically, the endogenous explanatory variables are dependent variables from other equations in the system. reg3 supports iterated GLS estimation and linear constraints.

reg3 can also estimate systems of equations by seemingly unrelated regression estimation (SURE), multivariate regression (MVREG), and equation-by-equation ordinary least squares (OLS) or two-stage least squares (2SLS).

Nomenclature

Under 3SLS or 2SLS estimation, a *structural equation* is defined as one of the equations specified in the system. A *dependent variable* will have its usual interpretation as the left-hand-side variable in an equation with an associated disturbance term. All dependent variables are explicitly taken to be *endogenous* to the system and are treated as correlated with the disturbances in the system's equations. Unless specified in an endog() option, all other variables in the system are treated as *exogenous* to the system and uncorrelated with the disturbances. The exogenous variables are taken to be *instruments* for the endogenous variables.

Options

Model

`ireg3` causes `reg3` to iterate over the estimated disturbance covariance matrix and parameter estimates until the parameter estimates converge. Although the iteration is usually successful, there is no guarantee that it will converge to a stable point. Under SURE, this iteration converges to the maximum likelihood estimates.

`constraints(`*constraints*`)`; see [R] **estimation options**.

Model 2

`exog(`*varlist*`)` specifies additional exogenous variables that are included in none of the system equations. This can occur when the system contains identities that are not estimated. If implicitly exogenous variables from the equations are listed here, `reg3` will just ignore the additional information. Specified variables will be added to the exogenous variables in the system and used in the first stage as instruments for the endogenous variables. By specifying dependent variables from the structural equations, you can use `exog()` to override their endogeneity.

`endog(`*varlist*`)` identifies variables in the system that are not dependent variables but are endogenous to the system. These variables must appear in the variable list of at least one equation in the system. Again the need for this identification often occurs when the system contains identities. For example, a variable that is the sum of an exogenous variable and a dependent variable may appear as an explanatory variable in some equations.

`inst(`*varlist*`)` specifies a full list of all exogenous variables and may not be used with the `endog()` or `exog()` options. It must contain a full list of variables to be used as instruments for the endogenous regressors. Like `exog()`, the list may contain variables not specified in the system of equations. This option can be used to achieve the same results as the `endog()` and `exog()` options, and the choice is a matter of convenience. Any variable not specified in the *varlist* of the `inst()` option is assumed to be endogenous to the system. As with `exog()`, including the dependent variables from the structural equations will override their endogeneity.

`allexog` indicates that all right-hand-side variables are to be treated as exogenous—even if they appear as the dependent variable of another equation in the system. This option can be used to enforce a SURE or MVREG estimation even when some dependent variables appear as regressors.

`noconstant`; see [R] **estimation options**.

Est. method

`3sls` specifies the full 3SLS estimation of the system and is the default for `reg3`.

`2sls` causes `reg3` to perform equation-by-equation 2SLS on the full system of equations. This option implies `dfk`, `small`, and `corr(independent)`.

Cross-equation testing should not be performed after estimation with this option. With `2sls`, no covariance is estimated between the parameters of the equations. For cross-equation testing, use `3sls`.

`ols` causes `reg3` to perform equation-by-equation OLS on the system—even if dependent variables appear as regressors or the regressors differ for each equation; see [R] **mvreg**. `ols` implies `allexog`, `dfk`, `small`, and `corr(independent)`; `nodfk` and `nosmall` may be specified to override `dfk` and `small`.

The covariance of the coefficients between equations is not estimated under this option, and cross-equation tests should not be performed after estimation with `ols`. For cross-equation testing, use `sure` or `3sls` (the default).

`sure` causes `reg3` to perform a SURE of the system—even if dependent variables from some equations appear as regressors in other equations; see [R] **sureg**. `sure` is a synonym for `allexog`.

`mvreg` is identical to `sure`, except that the disturbance covariance matrix is estimated with an OLS degrees-of-freedom adjustment—the `dfk` option. If the regressors are identical for all equations, the parameter point estimates will be the standard MVREG results. If any of the regressors differ, the point estimates are those for SURE with an OLS degrees-of-freedom adjustment in computing the covariance matrix. `nodfk` and `nosmall` may be specified to override `dfk` and `small`.

`corr(`*correlation*`)` specifies the assumed form of the correlation structure of the equation disturbances and is rarely requested explicitly. For the family of models fit by `reg3`, the only two allowable correlation structures are `unstructured` and `independent`. The default is `unstructured`.

This option is used almost exclusively to estimate a system of equations by 2SLS or to perform OLS regression with `reg3` on multiple equations. In these cases, the correlation is set to `independent`, forcing `reg3` to treat the covariance matrix of equation disturbances as diagonal in estimating model parameters. Thus a set of two-stage coefficient estimates can be obtained if the system contains endogenous right-hand-side variables, or OLS regression can be imposed, even if the regressors differ across equations. Without imposing independent disturbances, `reg3` would estimate the former by 3SLS and the latter by SURE.

Any tests performed after estimation with the `independent` option will treat coefficients in different equations as having no covariance; cross-equation tests should not be used after specifying `corr(independent)`.

df adj.

`small` specifies that small-sample statistics be computed. It shifts the test statistics from χ^2 and z statistics to F statistics and t statistics. This option is intended primarily to support MVREG. Although the standard errors from each equation are computed using the degrees of freedom for the equation, the degrees of freedom for the t statistics are all taken to be those for the first equation. This approach poses no problem under MVREG because the regressors are the same across equations.

`dfk` specifies the use of an alternative divisor in computing the covariance matrix for the equation residuals. As an asymptotically justified estimator, `reg3` by default uses the number of sample observations n as a divisor. When the `dfk` option is set, a small-sample adjustment is made, and the divisor is taken to be $\sqrt{(n-k_i)(n-k_j)}$, where k_i and k_j are the numbers of parameters in equations i and j, respectively.

`dfk2` specifies the use of an alternative divisor in computing the covariance matrix for the equation errors. When the `dfk2` option is set, the divisor is taken to be the mean of the residual degrees of freedom from the individual equations.

Reporting

`level(#)`; see [R] **estimation options**.

`first` requests that the first-stage regression results be displayed during estimation.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Optimization

optimization_options control the iterative process that minimizes the sum of squared errors when `ireg3` is specified. These options are seldom used.

`iterate(#)` specifies the maximum number of iterations. When the number of iterations equals #, the optimizer stops and presents the current results, even if the convergence tolerance has not been reached. The default value of `iterate()` is the current value of `set maxiter` (see [R] **maximize**), which is `iterate(16000)` if `maxiter` has not been changed.

`trace` adds to the iteration log a display of the current parameter vector.

`nolog` suppresses the display of the iteration log.

`tolerance(#)` specifies the tolerance for the coefficient vector. When the relative change in the coefficient vector from one iteration to the next is less than or equal to #, the optimization process is stopped. `tolerance(1e-6)` is the default.

The following options are available with `reg3` but are not shown in the dialog box:

`noheader` suppresses display of the header reporting the estimation method and the table of equation summary statistics.

`notable` suppresses display of the coefficient table.

`nofooter` suppresses display of the footer reporting the list of endogenous and exogenous variables in the model.

`coeflegend`; see [R] **estimation options**.

Remarks

`reg3` estimates systems of structural equations where some equations contain endogenous variables among the explanatory variables. Generally, these endogenous variables are the dependent variables of other equations in the system, though not always. The disturbance is correlated with the endogenous variables—violating the assumptions of OLS. Further, because some of the explanatory variables are the dependent variables of other equations in the system, the error terms among the equations are expected to be correlated. `reg3` uses an instrumental-variables approach to produce consistent estimates and generalized least squares (GLS) to account for the correlation structure in the disturbances across the equations. Good general references on three-stage estimation include Davidson and MacKinnon (1993, 651–661) and Greene (2012, 331–334).

Three-stage least squares can be thought of as producing estimates from a three-step process.

Step 1. Develop instrumented values for all endogenous variables. These instrumented values can simply be considered as the predicted values resulting from a regression of each endogenous variable on all exogenous variables in the system. This stage is identical to the first step in 2SLS and is critical for the consistency of the parameter estimates.

Step 2. Obtain a consistent estimate for the covariance matrix of the equation disturbances. These estimates are based on the residuals from a 2SLS estimation of each structural equation.

Step 3. Perform a GLS-type estimation using the covariance matrix estimated in the second stage and with the instrumented values in place of the right-hand-side endogenous variables.

❑ Technical note

The estimation and use of the covariance matrix of disturbances in three-stage estimation is almost identical to the SURE method—`sureg`. As with SURE, using this covariance matrix improves the efficiency of the three-stage estimator. Even without the covariance matrix, the estimates would be consistent. (They would be 2SLS estimates.) This improvement in efficiency comes with a caveat. All the parameter estimates now depend on the consistency of the covariance matrix estimates. If one equation in the system is misspecified, the disturbance covariance estimates will be inconsistent, and the resulting coefficients will be biased and inconsistent. Alternatively, if each equation is estimated separately by 2SLS ([R] **regress**), only the coefficients in the misspecified equation are affected.

❑

❑ Technical note

If an equation is just identified, the 3SLS point estimates for that equation are identical to the 2SLS estimates. However, as with `sureg`, even if all equations are just identified, fitting the model via `reg3` has at least one advantage over fitting each equation separately via `ivregress`; by using `reg3`, tests involving coefficients in different equations can be performed easily using `test` or `testnl`.

❑

▷ Example 1

A simple macroeconomic model relates consumption (`consump`) to private and government wages paid (`wagepriv` and `wagegovt`). Simultaneously, private wages depend on consumption, total government expenditures (`govt`), and the lagged stock of capital in the economy (`capital1`). Although this is not a plausible model, it does meet the criterion of being simple. This model could be written as

$$\texttt{consump} = \beta_0 + \beta_1\,\texttt{wagepriv} + \beta_2\,\texttt{wagegovt} + \epsilon_1$$

$$\texttt{wagepriv} = \beta_3 + \beta_4\,\texttt{consump} + \beta_5\,\texttt{govt} + \beta_6\,\texttt{capital1} + \epsilon_2$$

If we assume that this is the full system, `consump` and `wagepriv` will be endogenous variables, with `wagegovt`, `govt`, and `capital1` exogenous. Data for the U.S. economy on these variables are taken from Klein (1950). This model can be fit with `reg3` by typing

```
. use http://www.stata-press.com/data/r12/klein
. reg3 (consump wagepriv wagegovt) (wagepriv consump govt capital1)
Three-stage least-squares regression
```

Equation	Obs	Parms	RMSE	"R-sq"	chi2	P
consump	22	2	1.776297	0.9388	208.02	0.0000
wagepriv	22	3	2.372443	0.8542	80.04	0.0000

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
consump						
wagepriv	.8012754	.1279329	6.26	0.000	.5505314	1.052019
wagegovt	1.029531	.3048424	3.38	0.001	.432051	1.627011
_cons	19.3559	3.583772	5.40	0.000	12.33184	26.37996
wagepriv						
consump	.4026076	.2567312	1.57	0.117	-.1005764	.9057916
govt	1.177792	.5421253	2.17	0.030	.1152461	2.240338
capital1	-.0281145	.0572111	-0.49	0.623	-.1402462	.0840173
_cons	14.63026	10.26693	1.42	0.154	-5.492552	34.75306

```
Endogenous variables:  consump wagepriv
Exogenous variables:   wagegovt govt capital1
```

Without showing the 2SLS results, we note that the consumption function in this system falls under the conditions noted earlier. That is, the 2SLS and 3SLS coefficients for the equation are identical.

◁

▷ Example 2

Some of the most common simultaneous systems encountered are supply-and-demand models. A simple system could be specified as

$$\texttt{qDemand} = \beta_0 + \beta_1\,\texttt{price} + \beta_2\,\texttt{pcompete} + \beta_3\,\texttt{income} + \epsilon_1$$
$$\texttt{qSupply} = \beta_4 + \beta_5\,\texttt{price} + \beta_6\,\texttt{praw} + \epsilon_2$$
$$\texttt{Equilibrium condition: quantity} = \texttt{qDemand} = \texttt{qSupply}$$

where

`quantity` is the quantity of a product produced and sold,
`price` is the price of the product,
`pcompete` is the price of a competing product,
`income` is the average income level of consumers, and
`praw` is the price of raw materials used to produce the product.

In this system, price is assumed to be determined simultaneously with demand. The important statistical implications are that price is not a predetermined variable and that it is correlated with the disturbances of both equations. The system is somewhat unusual: quantity is associated with two disturbances. This fact really poses no problem because the disturbances are specified on the behavioral demand and supply equations—two separate entities. Often one of the two equations is rewritten to place price on the left-hand side, making this endogeneity explicit in the specification.

To provide a concrete illustration of the effects of simultaneous equations, we can simulate data for the above system by using known coefficients and disturbance properties. Specifically, we will simulate the data as

$$\texttt{qDemand} = 40 - 1.0\,\texttt{price} + 0.25\,\texttt{pcompete} + 0.5\,\texttt{income} + \epsilon_1$$

$$\texttt{qSupply} = 0.5\,\texttt{price} - 0.75\,\texttt{praw} + \epsilon_2$$

where

$$\epsilon_1 \sim N(0, 2.4)$$

$$\epsilon_2 \sim N(0, 3.8)$$

For comparison, we can estimate the supply and demand equations separately by OLS. The estimates for the demand equation are

```
. use http://www.stata-press.com/data/r12/supDem
. regress quantity price pcompete income
      Source |       SS       df       MS              Number of obs =      49
-------------+------------------------------           F(  3,    45) =    1.00
       Model |  23.1579302     3  7.71931008            Prob > F      =  0.4004
    Residual |  346.459313    45  7.69909584            R-squared     =  0.0627
-------------+------------------------------           Adj R-squared =  0.0002
       Total |  369.617243    48  7.70035923            Root MSE      =  2.7747

------------------------------------------------------------------------------
    quantity |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       price |   .1186265   .1716014     0.69   0.493    -.2269965    .4642496
    pcompete |   .0946416   .1200815     0.79   0.435    -.1472149    .3364981
      income |   .0785339   .1159867     0.68   0.502    -.1550754    .3121432
       _cons |   7.563261   5.019479     1.51   0.139     -2.54649    17.67301
------------------------------------------------------------------------------
```

The OLS estimates for the supply equation are

```
. regress quantity price praw
      Source |       SS       df       MS              Number of obs =      49
-------------+------------------------------           F(  2,    46) =   35.71
       Model |  224.819549     2  112.409774            Prob > F      =  0.0000
    Residual |  144.797694    46  3.14777596            R-squared     =  0.6082
-------------+------------------------------           Adj R-squared =  0.5912
       Total |  369.617243    48  7.70035923            Root MSE      =  1.7742

------------------------------------------------------------------------------
    quantity |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       price |    .724675   .1095657     6.61   0.000     .5041307    .9452192
        praw |  -.8674796   .1066114    -8.14   0.000    -1.082077    -.652882
       _cons |   -6.97291   3.323105    -2.10   0.041    -13.66197    -.283847
------------------------------------------------------------------------------
```

Examining the coefficients from these regressions, we note that they are not close to the known parameters used to generate the simulated data. In particular, the positive coefficient on `price` in the demand equation stands out. We constructed our simulated data to be consistent with economic theory—people demand less of a product if its price rises and more if their personal income rises. Although the `price` coefficient is statistically insignificant, the positive value contrasts starkly with what is predicted from economic price theory and the -1.0 value that we used in the simulation. Likewise, we are disappointed with the insignificance and level of the coefficient on average `income`. The supply equation has correct signs on the two main parameters, but their levels are different from the known values. In fact, the coefficient on `price` (0.724675) is different from the simulated parameter (0.5) at the 5% level of significance.

All these problems are to be expected. We explicitly constructed a simultaneous system of equations that violated one of the assumptions of least squares. Specifically, the disturbances were correlated with one of the regressors—`price`.

Two-stage least squares can be used to address the correlation between regressors and disturbances. Using instruments for the endogenous variable, `price`, 2SLS will produce consistent estimates of the parameters in the system. Let's use `ivregress` (see [R] **ivregress**) to see how our simulated system behaves when fit using 2SLS.

```
. ivregress 2sls quantity (price = praw) pcompete income
Instrumental variables (2SLS) regression              Number of obs =      49
                                                      Wald chi2(3)  =    8.77
                                                      Prob > chi2   =  0.0326
                                                      R-squared     =       .
                                                      Root MSE      =  3.7333

------------------------------------------------------------------------------
    quantity |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       price |  -1.015817   .374209    -2.71   0.007    -1.749253   -.282381
    pcompete |   .3319504   .172912     1.92   0.055    -.0069508   .6708517
      income |   .5090607   .1919482    2.65   0.008     .1328491   .8852723
       _cons |   39.89988   10.77378    3.70   0.000     18.78366   61.01611
------------------------------------------------------------------------------
Instrumented:  price
Instruments:   pcompete income praw
. ivregress 2sls quantity (price = pcompete income) praw
Instrumental variables (2SLS) regression              Number of obs =      49
                                                      Wald chi2(2)  =   39.25
                                                      Prob > chi2   =  0.0000
                                                      R-squared     =  0.5928
                                                      Root MSE      =  1.7525

------------------------------------------------------------------------------
    quantity |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       price |   .5773133   .1749974     3.30   0.001     .2343247    .9203019
        praw |  -.7835496   .1312414    -5.97   0.000    -1.040778   -.5263213
       _cons |  -2.550694   5.273067    -0.48   0.629    -12.88571    7.784327
------------------------------------------------------------------------------
Instrumented:  price
Instruments:   praw pcompete income
```

We are now much happier with the estimation results. All the coefficients from both equations are close to the true parameter values for the system. In particular, the coefficients are all well within 95% confidence intervals for the parameters. The missing R-squared in the demand equation seems unusual; we will discuss that more later.

Finally, this system could be estimated using 3SLS. To demonstrate how large systems might be handled and to avoid multiline commands, we will use global macros (see [P] **macro**) to hold the specifications for our equations.

```
. global demand "(qDemand: quantity price pcompete income)"
. global supply "(qSupply: quantity price praw)"
. reg3 $demand $supply, endog(price)
```

We must specify `price` as endogenous because it does not appear as a dependent variable in either equation. Without this option, `reg3` would assume that there are no endogenous variables in the system and produce seemingly unrelated regression (`sureg`) estimates. The `reg3` output from our series of commands is

```
Three-stage least-squares regression
------------------------------------------------------------------------------
Equation           Obs  Parms        RMSE    "R-sq"       chi2         P
------------------------------------------------------------------------------
qDemand             49      3    3.739686   -0.8540       8.68    0.0338
qSupply             49      2    1.752501    0.5928      39.25    0.0000
------------------------------------------------------------------------------

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
qDemand      |
       price |  -1.014345   .3742036    -2.71   0.007    -1.74777   -.2809194
    pcompete |   .2647206   .1464194     1.81   0.071    -.0222561    .5516973
      income |   .5299146   .1898161     2.79   0.005     .1578819    .9019472
       _cons |   40.08749   10.77072     3.72   0.000     18.97726    61.19772
-------------+----------------------------------------------------------------
qSupply      |
       price |   .5773133   .1749974     3.30   0.001     .2343247    .9203019
        praw |  -.7835496   .1312414    -5.97   0.000    -1.040778   -.5263213
       _cons |  -2.550694   5.273067    -0.48   0.629    -12.88571    7.784327
------------------------------------------------------------------------------
Endogenous variables:  quantity price
Exogenous variables:   pcompete income praw
------------------------------------------------------------------------------
```

The use of 3SLS over 2SLS is essentially an efficiency issue. The coefficients of the demand equation from 3SLS are close to the coefficients from two-stage least squares, and those of the supply equation are identical. The latter case was mentioned earlier for systems with some exactly identified equations. However, even for the demand equation, we do not expect the coefficients to change systematically. What we do expect from three-stage least squares are more precise estimates of the parameters given the validity of our specification and `reg3`'s use of the covariances among the disturbances.

Let's summarize the results. With OLS, we got obviously biased estimates of the parameters. No amount of data would have improved the OLS estimates—they are inconsistent in the face of the violated OLS assumptions. With 2SLS, we obtained consistent estimates of the parameters, and these would have improved with more data. With 3SLS, we obtained consistent estimates of the parameters that are more efficient than those obtained by 2SLS.

◁

❑ Technical note

We noted earlier that the R-squared was missing from the two-stage estimates of the demand equation. Now we see that the R-squared is negative for the three-stage estimates of the same equation. How can we have a negative R-squared?

In most estimators, other than least squares, the R-squared is no more than a summary measure of the overall in-sample predictive power of the estimator. The computational formula for R-squared is $R\text{-squared} = 1 - \text{RSS}/\text{TSS}$, where RSS is the residual sum of squares (sum of squared residuals) and TSS is the total sum of squared deviations about the mean of the dependent variable. In a standard linear model with a constant, the model from which the TSS is computed is nested within the full model from which RSS is computed—they both have a constant term based on the same data. Thus it must be that $\text{TSS} \geq \text{RSS}$ and R-squared is constrained between 0 and 1.

For 2SLS and 3SLS, some of the regressors enter the model as instruments when the parameters are estimated. However, because our goal is to fit the structural model, the actual values, not the instruments for the endogenous right-hand-side variables, are used to determine R-squared. The model residuals are computed over a different set of regressors from those used to fit the model. The two-

or three-stage estimates are no longer nested within a constant-only model of the dependent variable, and the residual sum of squares is no longer constrained to be smaller than the total sum of squares.

A negative R-squared in 3SLS should be taken for exactly what it is—an indication that the structural model predicts the dependent variable worse than a constant-only model. Is this a problem? It depends on the application. Three-stage least squares applied to our contrived supply-and-demand example produced good estimates of the known true parameters. Still, the demand equation produced an R-squared of -0.854. How do we feel about our parameter estimates? This should be determined by the estimates themselves, their associated standard errors, and the overall model significance. On this basis, negative R-squared and all, we feel pretty good about all the parameter estimates for both the supply and demand equations. Would we want to make predictions about equilibrium quantity by using the demand equation alone? Probably not. Would we want to make these quantity predictions by using the supply equation? Possibly, because based on in-sample predictions, they seem better than those from the demand equations. However, both the supply and demand estimates are based on limited information. If we are interested in predicting quantity, a reduced-form equation containing all our independent variables would usually be preferred.

❑

❑ Technical note

As a matter of syntax, we could have specified the supply-and-demand model on one line without using global macros.

```
. reg3 (quantity price pcompete income) (quantity price praw), endog(price)
Three-stage least-squares regression
```

Equation	Obs	Parms	RMSE	"R-sq"	chi2	P
quantity	49	3	3.739686	-0.8540	8.68	0.0338
2quantity	49	2	1.752501	0.5928	39.25	0.0000

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
quantity						
price	-1.014345	.3742036	-2.71	0.007	-1.74777	-.2809194
pcompete	.2647206	.1464194	1.81	0.071	-.0222561	.5516973
income	.5299146	.1898161	2.79	0.005	.1578819	.9019472
_cons	40.08749	10.77072	3.72	0.000	18.97726	61.19772
2quantity						
price	.5773133	.1749974	3.30	0.001	.2343247	.9203019
praw	-.7835496	.1312414	-5.97	0.000	-1.040778	-.5263213
_cons	-2.550694	5.273067	-0.48	0.629	-12.88571	7.784327

```
Endogenous variables:  quantity price
Exogenous variables:   pcompete income praw
```

However, here `reg3` has been forced to create a unique equation name for the supply equation—`2quantity`. Both the supply and demand equations could not be designated as `quantity`, so a number was prefixed to the name for the supply equation.

We could have specified

```
. reg3 (qDemand: quantity price pcompete income) (qSupply: quantity price praw),
> endog(price)
```

and obtained the same results and equation labeling as when we used global macros to hold the equation specifications.

Without explicit equation names, `reg3` always assumes that the dependent variable should be used to name equations. When each equation has a different dependent variable, this rule causes no problems and produces easily interpreted result tables. If the same dependent variable appears in more than one equation, however, `reg3` will create a unique equation name based on the dependent variable name. Because equation names must be used for cross-equation tests, you have more control in this situation if explicit names are placed on the equations.

❑

▷ Example 3: Using the full syntax of reg3

Klein's (1950) model of the U.S. economy is often used to demonstrate system estimators. It contains several common features that will serve to demonstrate the full syntax of `reg3`. The Klein model is defined by the following seven relationships:

$$\mathtt{c} = \beta_0 + \beta_1\mathtt{p} + \beta_2\mathtt{p1} + \beta_3\mathtt{w} + \epsilon_1 \tag{1}$$
$$\mathtt{i} = \beta_4 + \beta_5\mathtt{p} + \beta_6\mathtt{p1} + \beta_7\mathtt{k1} + \epsilon_2 \tag{2}$$
$$\mathtt{wp} = \beta_8 + \beta_9\mathtt{y} + \beta_{10}\mathtt{y1} + \beta_{11}\mathtt{yr} + \epsilon_3 \tag{3}$$
$$\mathtt{y} = \mathtt{c} + \mathtt{i} + \mathtt{g} \tag{4}$$
$$\mathtt{p} = \mathtt{y} - \mathtt{t} - \mathtt{wp} \tag{5}$$
$$\mathtt{k} = \mathtt{k1} + \mathtt{i} \tag{6}$$
$$\mathtt{w} = \mathtt{wg} + \mathtt{wp} \tag{7}$$

The variables in the model are listed below. Two sets of variable names are shown. The concise first name uses traditional economics mnemonics, whereas the second name provides more guidance for everyone else. The concise names serve to keep the specification of the model small (and quite understandable to economists).

Short name	Long name	Variable definition	Type
c	consump	Consumption	endogenous
p	profits	Private industry profits	endogenous
p1	profits1	Last year's private industry profits	exogenous
wp	wagepriv	Private wage bill	endogenous
wg	wagegovt	Government wage bill	exogenous
w	wagetot	Total wage bill	endogenous
i	invest	Investment	endogenous
k1	capital1	Last year's level of capital stock	exogenous
y	totinc	Total income/demand	endogenous
y1	totinc1	Last year's total income	exogenous
g	govt	Government spending	exogenous
t	taxnetx	Indirect bus. taxes + net exports	exogenous
yr	year	Year—1931	exogenous

Equations (1)–(3) are behavioral and contain explicit disturbances (ϵ_1, ϵ_2, and ϵ_3). The remaining equations are identities that specify additional variables in the system and their accounting relationships with the variables in the behavioral equations. Some variables are explicitly endogenous by appearing as dependent variables in (1)–(3). Others are implicitly endogenous as linear combinations that contain other endogenous variables (for example, `w` and `p`). Still other variables are implicitly exogenous by appearing in the identities but not in the behavioral equations (for example, `wg` and `g`).

Using the concise names, we can fit Klein's model with the following command:

```
. use http://www.stata-press.com/data/r12/kleinAbr
. reg3 (c p p1 w) (i p p1 k1) (wp y y1 yr), endog(w p y) exog(t wg g)
Three-stage least-squares regression
```

Equation	Obs	Parms	RMSE	"R-sq"	chi2	P
c	21	3	.9443305	0.9801	864.59	0.0000
i	21	3	1.446736	0.8258	162.98	0.0000
wp	21	3	.7211282	0.9863	1594.75	0.0000

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
c						
p	.1248904	.1081291	1.16	0.248	-.0870387	.3368194
p1	.1631439	.1004382	1.62	0.104	-.0337113	.3599992
w	.790081	.0379379	20.83	0.000	.715724	.8644379
_cons	16.44079	1.304549	12.60	0.000	13.88392	18.99766
i						
p	-.0130791	.1618962	-0.08	0.936	-.3303898	.3042316
p1	.7557238	.1529331	4.94	0.000	.4559805	1.055467
k1	-.1948482	.0325307	-5.99	0.000	-.2586072	-.1310893
_cons	28.17785	6.793768	4.15	0.000	14.86231	41.49339
wp						
y	.4004919	.0318134	12.59	0.000	.3381388	.462845
y1	.181291	.0341588	5.31	0.000	.1143411	.2482409
yr	.149674	.0279352	5.36	0.000	.094922	.2044261
_cons	1.797216	1.115854	1.61	0.107	-.3898181	3.984251

```
Endogenous variables:  c i wp w p y
Exogenous variables:   p1 k1 y1 yr t wg g
```

We used the `exog()` option to identify `t`, `wg`, and `g` as exogenous variables in the system. These variables must be identified because they are part of the system but appear directly in none of the behavioral equations. Without this option, `reg3` would not know they were part of the system. The `endog()` option specifying `w`, `p`, and `y` is also required. Without this information, `reg3` would be unaware that these variables are linear combinations that include endogenous variables.

❑ Technical note

Rather than listing additional endogenous and exogenous variables, we could specify the full list of exogenous variables in an `inst()` option,

```
. reg3 (c p p1 w) (i p p1 k1) (wp y y1 yr), inst(g t wg yr p1 k1 y1)
```

or equivalently,

```
. global conseqn "(c p p1 w)"
. global inveqn  "(i p p1 k1)"
. global wageqn  "(wp y y1 yr)"
. global inlist  "g t wg yr p1 k1 y1"
. reg3 $conseqn $inveqn $wageqn, inst($inlist)
```

Macros and explicit equations can also be mixed in the specification

```
. reg3 $conseqn (i p p1 k1) $wageqn, endog(w p y) exog(t wg g)
```

or

```
. reg3 (c p p1 w) $inveqn (wp y y1 yr), endog(w p y) exog(t wg g)
```

Placing the equation-binding parentheses in the global macros was also arbitrary. We could have used

```
. global consump  "c p p1 w"
. global invest   "i p p1 k1"
. global wagepriv "wp y y1 yr"
. reg3 ($consump) ($invest) ($wagepriv), endog(w p y) exog(t wg g)
```

`reg3` is tolerant of all combinations, and these commands will produce identical output.

❑

Switching to the full variable names, we can fit Klein's model with the commands below. We will use global macros to store the lists of endogenous and exogenous variables. Again this is not necessary: these lists could have been typed directly on the command line. However, assigning the lists to local macros makes additional processing easier if alternative models are to be fit. We will also use the `ireg3` option to produce the iterated estimates.

```
. use http://www.stata-press.com/data/r12/klein
. global conseqn "(consump profits profits1 wagetot)"
. global inveqn  "(invest profits profits1 capital1)"
. global wageqn "(wagepriv totinc totinc1 year)"
. global enlist "wagetot profits totinc"
. global exlist "taxnetx wagegovt govt"
. reg3 $conseqn $inveqn $wageqn, endog($enlist) exog($exlist) ireg3
Iteration 1:   tolerance =  .3712549
Iteration 2:   tolerance =  .1894712
Iteration 3:   tolerance =  .1076401
  (output omitted)
Iteration 24:   tolerance =  7.049e-07
Three-stage least-squares regression, iterated
```

Equation	Obs	Parms	RMSE	"R-sq"	chi2	P
consump	21	3	.9565088	0.9796	970.31	0.0000
invest	21	3	2.134327	0.6209	56.78	0.0000
wagepriv	21	3	.7782334	0.9840	1312.19	0.0000

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
consump						
profits	.1645096	.0961979	1.71	0.087	-.0240348	.3530539
profits1	.1765639	.0901001	1.96	0.050	-.0000291	.3531569
wagetot	.7658011	.0347599	22.03	0.000	.6976729	.8339294
_cons	16.55899	1.224401	13.52	0.000	14.15921	18.95877
invest						
profits	-.3565316	.2601568	-1.37	0.171	-.8664296	.1533664
profits1	1.011299	.2487745	4.07	0.000	.5237098	1.498888
capital1	-.2602	.0508694	-5.12	0.000	-.3599022	-.1604978
_cons	42.89629	10.59386	4.05	0.000	22.13271	63.65987
wagepriv						
totinc	.3747792	.0311027	12.05	0.000	.3138191	.4357394
totinc1	.1936506	.0324018	5.98	0.000	.1301443	.257157
year	.1679262	.0289291	5.80	0.000	.1112263	.2246261
_cons	2.624766	1.195559	2.20	0.028	.2815124	4.968019

Endogenous variables: consump invest wagepriv wagetot profits totinc
Exogenous variables: profits1 capital1 totinc1 year taxnetx wagegovt govt

◁

▷ Example 4: Constraints with reg3

As a simple example of constraints, (1) above may be rewritten with both wages explicitly appearing (rather than as a variable containing the sum). Using the longer variable names, we have

$$\texttt{consump} = \beta_0 + \beta_1\,\texttt{profits} + \beta_2\,\texttt{profits1} + \beta_3\,\texttt{wagepriv} + \beta_{12}\,\texttt{wagegovt} + \epsilon_1$$

To retain the effect of the identity in (7), we need $\beta_3 = \beta_{12}$ as a constraint on the system. We obtain this result by defining the constraint in the usual way and then specifying its use in `reg3`. Because `reg3` is a system estimator, we will need to use the full equation syntax of `constraint`. The assumption that the following commands are entered after the model above has been estimated. We are simply changing the definition of the consumption equation (`consump`) and adding a constraint on two of its parameters. The rest of the model definition is carried forward.

```
. global conseqn "(consump profits profits1 wagepriv wagegovt)"
. constraint 1 [consump]wagepriv = [consump]wagegovt
. reg3 $conseqn $inveqn $wageqn, endog($enlist) exog($exlist) constr(1) ireg3
note:  additional endogenous variables not in the system have no effect
       and are ignored:  wagetot
Iteration 1:   tolerance =   .3712547
Iteration 2:   tolerance =    .189471
Iteration 3:   tolerance =     .10764
  (output omitted)
Iteration 24:   tolerance =  7.049e-07
```

```
Three-stage least-squares regression, iterated
------------------------------------------------------------------------------
Equation           Obs  Parms        RMSE    "R-sq"       chi2         P
------------------------------------------------------------------------------
consump             21      3    .9565086    0.9796     970.31    0.0000
invest              21      3    2.134326    0.6209      56.78    0.0000
wagepriv            21      3    .7782334    0.9840    1312.19    0.0000
------------------------------------------------------------------------------

 ( 1)  [consump]wagepriv - [consump]wagegovt = 0

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
consump      |
     profits |   .1645097   .0961978     1.71   0.087    -.0240346     .353054
    profits1 |   .1765639   .0901001     1.96   0.050    -.0000291    .3531568
    wagepriv |   .7658012   .0347599    22.03   0.000     .6976729    .8339294
    wagegovt |   .7658012   .0347599    22.03   0.000     .6976729    .8339294
       _cons |   16.55899   1.224401    13.52   0.000      14.1592    18.95877
-------------+----------------------------------------------------------------
invest       |
     profits |  -.3565311   .2601567    -1.37   0.171    -.8664288    .1533666
    profits1 |   1.011298   .2487744     4.07   0.000     .5237096    1.498887
    capital1 |  -.2601999   .0508694    -5.12   0.000     -.359902   -.1604977
       _cons |   42.89626   10.59386     4.05   0.000     22.13269    63.65984
-------------+----------------------------------------------------------------
wagepriv     |
      totinc |   .3747792   .0311027    12.05   0.000      .313819    .4357394
     totinc1 |   .1936506   .0324018     5.98   0.000     .1301443     .257157
        year |   .1679262   .0289291     5.80   0.000     .1112263    .2246261
       _cons |   2.624766   1.195559     2.20   0.028      .281512    4.968019
------------------------------------------------------------------------------
Endogenous variables:  consump invest wagepriv wagetot profits totinc
Exogenous variables:   profits1 wagegovt capital1 totinc1 year taxnetx govt
------------------------------------------------------------------------------
```

As expected, none of the parameter or standard error estimates has changed from the previous estimates (before the seventh significant digit). We have simply decomposed the total wage variable into its two parts and constrained the coefficients on these parts. The warning about additional endogenous variables was just `reg3`'s way of letting us know that we had specified some information that was irrelevant to the estimation of the system. We had left the `wagetot` variable in our `endog` macro. It does not mean anything to the system to specify `wagetot` as endogenous because it is no longer in the system. That's fine with `reg3` and fine for our current purposes.

We can also impose constraints across the equations. For example, the admittedly meaningless constraint of requiring `profits` to have the same effect in both the consumption and investment equations could be imposed. Retaining the constraint on the wage coefficients, we would estimate this constrained system.

```
. constraint 2 [consump]profits = [invest]profits

. reg3 $conseqn $inveqn $wageqn, endog($enlist) exog($exlist) constr(1 2) ireg3
note:  additional endogenous variables not in the system have no effect
       and are ignored:  wagetot

Iteration 1:   tolerance =   .1427927
Iteration 2:   tolerance =    .032539
Iteration 3:   tolerance =  .00307811
Iteration 4:   tolerance =  .00016903
Iteration 5:   tolerance =  .00003409
Iteration 6:   tolerance =  7.763e-06
Iteration 7:   tolerance =  9.240e-07
```

```
Three-stage least-squares regression, iterated
------------------------------------------------------------------------------
Equation           Obs  Parms        RMSE    "R-sq"       chi2         P
------------------------------------------------------------------------------
consump             21      3    .9504669    0.9798    1019.54    0.0000
invest              21      3    1.247066    0.8706     144.57    0.0000
wagepriv            21      3    .7225276    0.9862    1537.45    0.0000
------------------------------------------------------------------------------

 ( 1)  [consump]wagepriv - [consump]wagegovt = 0
 ( 2)  [consump]profits - [invest]profits = 0

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
consump      |
     profits |   .1075413   .0957767     1.12   0.262    -.0801777    .2952602
    profits1 |   .1712756   .0912613     1.88   0.061    -.0075932    .3501444
    wagepriv |    .798484   .0340876    23.42   0.000     .7316734    .8652946
    wagegovt |    .798484   .0340876    23.42   0.000     .7316734    .8652946
       _cons |   16.2521    1.212157    13.41   0.000     13.87631    18.62788
-------------+----------------------------------------------------------------
invest       |
     profits |   .1075413   .0957767     1.12   0.262    -.0801777    .2952602
    profits1 |   .6443378   .1058682     6.09   0.000        .43684    .8518356
    capital1 |  -.1766669   .0261889    -6.75   0.000    -.2279962   -.1253375
       _cons |   24.31931   5.284325     4.60   0.000     13.96222     34.6764
-------------+----------------------------------------------------------------
wagepriv     |
      totinc |   .4014106   .0300552    13.36   0.000     .3425035    .4603177
     totinc1 |   .1775359   .0321583     5.52   0.000     .1145068     .240565
        year |   .1549211   .0282291     5.49   0.000      .099593    .2102492
       _cons |   1.959788    1.14467     1.71   0.087    -.2837242    4.203299
------------------------------------------------------------------------------
Endogenous variables:  consump invest wagepriv wagetot profits totinc
Exogenous variables:   profits1 wagegovt capital1 totinc1 year taxnetx govt
------------------------------------------------------------------------------
```

◁

❑ Technical note

Identification in a system of simultaneous equations involves the notion that there is enough information to estimate the parameters of the model given the specified functional form. Underidentification usually manifests itself as one matrix in the 3SLS computations. The most commonly violated order condition for 2SLS or 3SLS involves the number of endogenous and exogenous variables. There must be at least as many noncollinear exogenous variables in the remaining system as there are endogenous right-hand-side variables in an equation. This condition must hold for each structural equation in the system.

Put as a set of rules the following:

1. Count the number of right-hand-side endogenous variables in an equation and call this m_i.
2. Count the number of exogenous variables in the same equation and call this k_i.
3. Count the total number of exogenous variables in all the structural equations plus any additional variables specified in an `exog()` or `inst()` option and call this K.
4. If $m_i > (K - k_i)$ for any structural equation (i), then the system is underidentified and cannot be estimated by 3SLS.

We are also possibly in trouble if any of the exogenous variables are linearly dependent. We must have m_i linearly independent variables among the exogenous variables represented by $(K - k_i)$.

The complete conditions for identification involve rank-order conditions on several matrices. For a full treatment, see Theil (1971) or Greene (2012, 331–334).

❑

Saved results

reg3 saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(mss_#)	model sum of squares for equation #
e(df_m#)	model degrees of freedom for equation #
e(rss_#)	residual sum of squares for equation #
e(df_r)	residual degrees of freedom (small)
e(r2_#)	R-squared for equation #
e(F_#)	F statistic for equation # (small)
e(rmse_#)	root mean squared error for equation #
e(dfk2_adj)	divisor used with VCE when dfk2 specified
e(ll)	log likelihood
e(chi2_#)	χ^2 for equation #
e(p_#)	significance for equation #
e(cons_#)	1 when equation # has a constant, 0 otherwise
e(rank)	rank of e(V)
e(ic)	number of iterations

Macros

e(cmd)	reg3
e(cmdline)	command as typed
e(depvar)	names of dependent variables
e(exog)	names of exogenous variables
e(endog)	names of endogenous variables
e(eqnames)	names of equations
e(corr)	correlation structure
e(wtype)	weight type
e(wexp)	weight expression
e(method)	3sls, 2sls, ols, sure, or mvreg
e(small)	small
e(dfk)	dfk, if specified
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(Sigma)	$\widehat{\Sigma}$ matrix
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

`reg3` is implemented as an ado-file.

The most concise way to represent a system of equations for 3SLS requires thinking of the individual equations and their associated data as being stacked. `reg3` does not expect the data in this format, but it is a convenient shorthand. The system could then be formulated as

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \vdots \\ \mathbf{y}_M \end{bmatrix} = \begin{bmatrix} \mathbf{Z}_1 & 0 & \dots & 0 \\ 0 & \mathbf{Z}_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & \mathbf{Z}_M \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \vdots \\ \beta_M \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_M \end{bmatrix}$$

In full matrix notation, this is just

$$\mathbf{y} = \mathbf{Z}\,\mathbf{B} + \epsilon$$

The $\mathbf{Z}$ elements in these matrices represent both the endogenous and the exogenous right-hand-side variables in the equations.

Also assume that there will be correlation between the disturbances of the equations so that

$$E(\epsilon\epsilon') = \mathbf{\Sigma}$$

where the disturbances are further assumed to have an expected value of 0; $E(\epsilon) = 0$.

The first stage of 3SLS regression requires developing instrumented values for the endogenous variables in the system. These values can be derived as the predictions from a linear regression of each endogenous regressor on all exogenous variables in the system or, more succinctly, as the projection of each regressor through the projection matrix of all exogenous variables onto the regressors. Designating the set of all exogenous variables as $\mathbf{X}$ results in

$$\widehat{\mathbf{z}}_i = \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{z}_i \quad \text{for each } i$$

Taken collectively, these $\widehat{\mathbf{Z}}$ contain the instrumented values for all the regressors. They take on the actual values for the exogenous variables and first-stage predictions for the endogenous variables. Given these instrumented variables, a generalized least squares (GLS) or Aitken (1935) estimator can be formed for the parameters of the system

$$\widehat{\mathbf{B}} = \left\{\widehat{\mathbf{Z}}'(\mathbf{\Sigma}^{-1} \otimes \mathbf{I})\widehat{\mathbf{Z}}\right\}^{-1} \widehat{\mathbf{Z}}'(\mathbf{\Sigma}^{-1} \otimes \mathbf{I})\mathbf{y}$$

All that remains is to obtain a consistent estimator for $\mathbf{\Sigma}$. This estimate can be formed from the residuals of 2SLS estimates of each equation in the system. Alternately, and identically, the residuals can be computed from the estimates formed by taking $\mathbf{\Sigma}$ to be an identity matrix. This maintains the full system of coefficients and allows constraints to be applied when the residuals are computed.

If we take $\mathbf{E}$ to be the matrix of residuals from these estimates, a consistent estimate of $\mathbf{\Sigma}$ is

$$\widehat{\mathbf{\Sigma}} = \frac{\mathbf{E}'\mathbf{E}}{n}$$

where n is the number of observations in the sample. An alternative divisor for this estimate can be obtained with the `dfk` option as outlined under options.

With the estimate of $\widehat{\mathbf{\Sigma}}$ placed into the GLS estimating equation,

$$\widehat{\mathbf{B}} = \left\{\widehat{\mathbf{Z}}'(\widehat{\mathbf{\Sigma}}^{-1} \otimes \mathbf{I})\widehat{\mathbf{Z}}\right\}^{-1} \widehat{\mathbf{Z}}'(\widehat{\mathbf{\Sigma}}^{-1} \otimes \mathbf{I})\mathbf{y}$$

is the 3SLS estimates of the system parameters.

The asymptotic variance–covariance matrix of the estimator is just the standard formulation for a GLS estimator

$$\mathbf{V}_{\widehat{\mathbf{B}}} = \left\{\widehat{\mathbf{Z}}'(\widehat{\mathbf{\Sigma}}^{-1} \otimes \mathbf{I})\widehat{\mathbf{Z}}\right\}^{-1}$$

Iterated 3SLS estimates can be obtained by computing the residuals from the three-stage parameter estimates, using these to formulate a new $\widehat{\mathbf{\Sigma}}$, and recomputing the parameter estimates. This process is repeated until the estimates $\widehat{\mathbf{B}}$ converge—if they converge. Convergence is not guaranteed. When estimating a system by SURE, these iterated estimates will be the maximum likelihood estimates for the system. The iterated solution can also be used to produce estimates that are invariant to choice of system and restriction parameterization for many linear systems under full 3SLS.

The exposition above follows the parallel developments in Greene (2012) and Davidson and MacKinnon (1993).

Henri Theil (1924–2000) was born in Amsterdam and awarded a PhD in 1951 by the University of Amsterdam. He researched and taught econometric theory, statistics, microeconomics, macroeconomic modeling, and economic forecasting, and policy at (what is now) Erasmus University Rotterdam, the University of Chicago, and the University of Florida. Theil's many specific contributions include work on 2SLS and 3SLS, inequality and concentration, and consumer demand.

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Also see

[R] **reg3 postestimation** — Postestimation tools for reg3

[R] **ivregress** — Single-equation instrumental-variables regression

[R] **mvreg** — Multivariate regression

[R] **nlsur** — Estimation of nonlinear systems of equations

[R] **regress** — Linear regression

[R] **sureg** — Zellner's seemingly unrelated regression

Stata Structural Equation Modeling Reference Manual

[U] **20 Estimation and postestimation commands**

Title

reg3 postestimation — Postestimation tools for reg3

Description

The following postestimation commands are available after `reg3`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
*`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

*`estat ic` is not appropriate after `reg3, 2sls`.

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`, equation(`*eqno*[`,`*eqno*]`)` *statistic*]

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`residuals`	residuals
`difference`	difference between the linear predictions of two equations
`stddp`	standard error of the difference in linear predictions

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`equation(`*eqno*`[ ,`*eqno*`])` specifies to which equation you are referring.

`equation()` is filled in with one *eqno* for the `xb`, `stdp`, and `residuals` options. `equation(#1)` would mean the calculation is to be made for the first equation, `equation(#2)` would mean the second, and so on. You could also refer to the equations by their names. `equation(income)` would refer to the equation named income and `equation(hours)` to the equation named hours.

If you do not specify `equation()`, results are the same as if you specified `equation(#1)`.

`difference` and `stddp` refer to between-equation concepts. To use these options, you must specify two equations, for example, `equation(#1,#2)` or `equation(income,hours)`. When two equations must be specified, `equation()` is required.

`xb`, the default, calculates the linear prediction (fitted values)—the prediction of $\mathbf{x}_j\mathbf{b}$ for the specified equation.

`stdp` calculates the standard error of the prediction for the specified equation. It can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`residuals` calculates the residuals.

`difference` calculates the difference between the linear predictions of two equations in the system. With `equation(#1,#2)`, `difference` computes the prediction of `equation(#1)` minus the prediction of `equation(#2)`.

`stddp` is allowed only after you have previously fit a multiple-equation model. The standard error of the difference in linear predictions $(\mathbf{x}_{1j}\mathbf{b} - \mathbf{x}_{2j}\mathbf{b})$ between equations 1 and 2 is calculated.

For more information on using `predict` after multiple-equation estimation commands, see [R] **predict**.

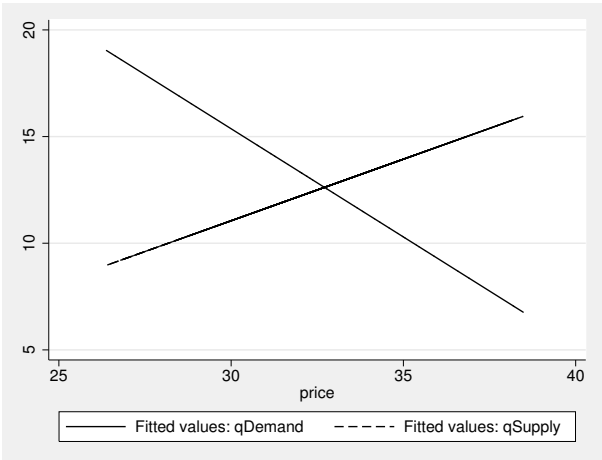
Remarks

▷ Example 1

In example 2 of [R] **reg3**, we fit a simple supply-and-demand model. Here we obtain the fitted supply and demand curves assuming that the exogenous regressors equal their sample means. We first `replace` each of the three exogenous regressors with their sample means, then we call `predict` to obtain the predictions.

```
. use http://www.stata-press.com/data/r12/supDem
. global demand "(qDemand: quantity price pcompete income)"
. global supply "(qSupply: quantity price praw)"
. reg3 $demand $supply, endog(price)
  (output omitted)
. summarize pcompete, meanonly
. replace pcompete = r(mean)
(49 real changes made)
```

```
. summarize income, meanonly
. replace income = r(mean)
(49 real changes made)
. summarize praw, meanonly
. replace praw = r(mean)
(49 real changes made)
. predict demand, equation(qDemand)
(option xb assumed; fitted values)
. predict supply, equation(qSupply)
(option xb assumed; fitted values)
. graph twoway line demand price, sort || line supply price
```



As we would expect based on economic theory, the demand curve slopes downward while the supply curve slopes upward. With the exogenous variables at their mean levels, the equilibrium price and quantity are slightly less than 33 and 13, respectively.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

The computational formulas for the statistics produced by `predict` can be found in [R] **predict** and [R] **regress postestimation**.

Also see

[R] **reg3** — Three-stage estimation for systems of simultaneous equations

[U] **20 Estimation and postestimation commands**

Title

regress — Linear regression

Syntax

```
regress depvar [indepvars] [if] [in] [weight] [, options]
```

options	Description
Model	
noconstant	suppress constant term
hascons	has user-supplied constant
tsscons	compute total sum of squares with constant; seldom used
SE/Robust	
vce(*vcetype*)	*vcetype* may be ols, robust, cluster *clustvar*, bootstrap, jackknife, hc2, or hc3
Reporting	
level(#)	set confidence level; default is level(95)
beta	report standardized beta coefficients
eform(*string*)	report exponentiated coefficients and label as *string*
depname(*varname*)	substitute dependent variable name; programmer's option
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
noheader	suppress output header
notable	suppress coefficient table
plus	make table extendable
mse1	force mean squared error to 1
coeflegend	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

bootstrap, by, fracpoly, jackknife, mfp, mi estimate, nestreg, rolling, statsby, stepwise, and svy are allowed; see [U] **11.1.10 Prefix commands**.

vce(bootstrap) and vce(jackknife) are not allowed with the mi estimate prefix; see [MI] **mi estimate**.

Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.

aweights are not allowed with the jackknife prefix; see [R] **jackknife**.

hascons, tsscons, vce(), beta, noheader, notable, plus, depname(), mse1, and weights are not allowed with the svy prefix; see [SVY] **svy**.

aweights, fweights, iweights, and pweights are allowed; see [U] **11.1.6 weight**.

noheader, notable, plus, mse1, and coeflegend do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Linear regression

Description

`regress` fits a model of *depvar* on *indepvars* using linear regression.

Here is a short list of other regression commands that may be of interest. See [I] **estimation commands** for a complete list.

Command	Entry	Description
`areg`	[R] **areg**	an easier way to fit regressions with many dummy variables
`arch`	[TS] **arch**	regression models with ARCH errors
`arima`	[TS] **arima**	ARIMA models
`boxcox`	[R] **boxcox**	Box–Cox regression models
`cnsreg`	[R] **cnsreg**	constrained linear regression
`eivreg`	[R] **eivreg**	errors-in-variables regression
`frontier`	[R] **frontier**	stochastic frontier models
`gmm`	[R] **gmm**	generalized method of moments estimation
`heckman`	[R] **heckman**	Heckman selection model
`intreg`	[R] **intreg**	interval regression
`ivregress`	[R] **ivregress**	single-equation instrumental-variables regression
`ivtobit`	[R] **ivtobit**	tobit regression with endogenous variables
`newey`	[TS] **newey**	regression with Newey–West standard errors
`nl`	[R] **nl**	nonlinear least-squares estimation
`nlsur`	[R] **nlsur**	estimation of nonlinear systems of equations
`qreg`	[R] **qreg**	quantile (including median) regression
`reg3`	[R] **reg3**	three-stage least-squares (3SLS) regression
`rreg`	[R] **rreg**	a type of robust regression
`sureg`	[R] **sureg**	seemingly unrelated regression
`tobit`	[R] **tobit**	tobit regression
`treatreg`	[R] **treatreg**	treatment-effects model
`truncreg`	[R] **truncreg**	truncated regression
`xtabond`	[XT] **xtabond**	Arellano–Bond linear dynamic panel-data estimation
`xtdpd`	[XT] **xtdpd**	linear dynamic panel-data estimation
`xtfrontier`	[XT] **xtfrontier**	panel-data stochastic frontier models
`xtgls`	[XT] **xtgls**	panel-data GLS models
`xthtaylor`	[XT] **xthtaylor**	Hausman–Taylor estimator for error-components models
`xtintreg`	[XT] **xtintreg**	panel-data interval regression models
`xtivreg`	[XT] **xtivreg**	panel-data instrumental-variables (2SLS) regression
`xtpcse`	[XT] **xtpcse**	linear regression with panel-corrected standard errors
`xtreg`	[XT] **xtreg**	fixed- and random-effects linear models
`xtregar`	[XT] **xtregar**	fixed- and random-effects linear models with an AR(1) disturbance
`xttobit`	[XT] **xttobit**	panel-data tobit models
	[SEM] *Stata Structural Equation Modeling Reference Manual*	

Options

Model

`noconstant`; see [R] **estimation options**.

`hascons` indicates that a user-defined constant or its equivalent is specified among the independent variables in *indepvars*. Some caution is recommended when specifying this option, as resulting estimates may not be as accurate as they otherwise would be. Use of this option requires "sweeping" the constant last, so the moment matrix must be accumulated in absolute rather than deviation form. This option may be safely specified when the means of the dependent and independent variables are all reasonable and there is not much collinearity between the independent variables. The best procedure is to view `hascons` as a reporting option—estimate with and without `hascons` and verify that the coefficients and standard errors of the variables not affected by the identity of the constant are unchanged.

`tsscons` forces the total sum of squares to be computed as though the model has a constant, that is, as deviations from the mean of the dependent variable. This is a rarely used option that has an effect only when specified with `noconstant`. It affects the total sum of squares and all results derived from the total sum of squares.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(ols)`, the default, uses the standard variance estimator for ordinary least-squares regression.

`regress` also allows the following:

`vce(hc2)` and `vce(hc3)` specify an alternative bias correction for the robust variance calculation. `vce(hc2)` and `vce(hc3)` may not be specified with `svy` prefix. In the unclustered case, `vce(robust)` uses $\widehat{\sigma}_j^2 = \{n/(n-k)\}u_j^2$ as an estimate of the variance of the jth observation, where u_j is the calculated residual and $n/(n-k)$ is included to improve the overall estimate's small-sample properties.

`vce(hc2)` instead uses $u_j^2/(1-h_{jj})$ as the observation's variance estimate, where h_{jj} is the diagonal element of the hat (projection) matrix. This estimate is unbiased if the model really is homoskedastic. `vce(hc2)` tends to produce slightly more conservative confidence intervals.

`vce(hc3)` uses $u_j^2/(1-h_{jj})^2$ as suggested by Davidson and MacKinnon (1993), who report that this method tends to produce better results when the model really is heteroskedastic. `vce(hc3)` produces confidence intervals that tend to be even more conservative.

See Davidson and MacKinnon (1993, 554–556) and Angrist and Pischke (2009, 294–308) for more discussion on these two bias corrections.

Reporting

`level(#)`; see [R] **estimation options**.

`beta` asks that standardized beta coefficients be reported instead of confidence intervals. The beta coefficients are the regression coefficients obtained by first standardizing all variables to have a mean of 0 and a standard deviation of 1. `beta` may not be specified with `vce(cluster` *clustvar*`)` or the `svy` prefix.

`eform(`*string*`)` is used only in programs and ado-files that use `regress` to fit models other than linear regression. `eform()` specifies that the coefficient table be displayed in exponentiated form as defined in [R] **maximize** and that *string* be used to label the exponentiated coefficients in the table.

`depname(`*varname*`)` is used only in programs and ado-files that use `regress` to fit models other than linear regression. `depname()` may be specified only at estimation time. *varname* is recorded as the identity of the dependent variable, even though the estimates are calculated using *depvar*. This method affects the labeling of the output—not the results calculated—but could affect subsequent calculations made by `predict`, where the residual would be calculated as deviations from *varname* rather than *depvar*. `depname()` is most typically used when *depvar* is a temporary variable (see [P] **macro**) used as a proxy for *varname*.

`depname()` is not allowed with the `svy` prefix.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following options are available with `regress` but are not shown in the dialog box:

`noheader` suppresses the display of the ANOVA table and summary statistics at the top of the output; only the coefficient table is displayed. This option is often used in programs and ado-files.

`notable` suppresses display of the coefficient table.

`plus` specifies that the output table be made extendable. This option is often used in programs and ado-files.

`mse1` is used only in programs and ado-files that use `regress` to fit models other than linear regression and is not allowed with the `svy` prefix. `mse1` sets the mean squared error to `1`, forcing the variance–covariance matrix of the estimators to be $(\mathbf{X}'\mathbf{D}\mathbf{X})^{-1}$ (see *Methods and formulas* below) and affecting calculated standard errors. Degrees of freedom for t statistics are calculated as n rather than $n-k$.

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Ordinary least squares
Treatment of the constant
Robust standard errors
Weighted regression
Instrumental variables and two-stage least-squares regression

`regress` performs linear regression, including ordinary least squares and weighted least squares. For a general discussion of linear regression, see Draper and Smith (1998), Greene (2012), or Kmenta (1997).

See Wooldridge (2009) for an excellent treatment of estimation, inference, interpretation, and specification testing in linear regression models. This presentation stands out for its clarification of the statistical issues, as opposed to the algebraic issues. See Wooldridge (2010, chap. 4) for a more advanced discussion along the same lines.

See Hamilton (2009, chap. 6) and Cameron and Trivedi (2010, chap. 3) for an introduction to linear regression using Stata. Dohoo, Martin, and Stryhn (2010) discuss linear regression using examples from epidemiology, and Stata datasets and do-files used in the text are available. Cameron and Trivedi (2010) discuss linear regression using econometric examples with Stata.

Chatterjee and Hadi (2006) explain regression analysis by using examples containing typical problems that you might encounter when performing exploratory data analysis. We also recommend Weisberg (2005), who emphasizes the importance of the assumptions of linear regression and problems resulting from these assumptions. Angrist and Pischke (2009) approach regression as a tool for exploring relationships, estimating treatment effects, and providing answers to public policy questions. For a discussion of model-selection techniques and exploratory data analysis, see Mosteller and Tukey (1977). For a mathematically rigorous treatment, see Peracchi (2001, chap. 6). Finally, see Plackett (1972) if you are interested in the history of regression. Least squares, which dates back to the 1790s, was discovered independently by Legendre and Gauss.

Ordinary least squares

▷ Example 1

Suppose that we have data on the mileage rating and weight of 74 automobiles. The variables in our data are `mpg`, `weight`, and `foreign`. The last variable assumes the value 1 for foreign and 0 for domestic automobiles. We wish to fit the model

$$\texttt{mpg} = \beta_0 + \beta_1\texttt{weight} + \beta_2\texttt{weight}^2 + \beta_3\texttt{foreign} + \epsilon$$

We include `c.weight#c.weight` in our model for the weight-squared term (see [U] **11.4.3 Factor variables**):

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight c.weight#c.weight foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  3,    70) =   52.25
       Model |  1689.15372     3  563.05124              Prob > F      =  0.0000
    Residual |   754.30574    70  10.7757963            R-squared     =  0.6913
-------------+------------------------------           Adj R-squared =  0.6781
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.2827

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0165729   .0039692    -4.18   0.000    -.0244892   -.0086567
             |
c.weight#    |
c.weight     |   1.59e-06   6.25e-07     2.55   0.013     3.45e-07    2.84e-06
             |
     foreign |     -2.2035   1.059246    -2.08   0.041      -4.3161   -.0909002
       _cons |    56.53884   6.197383     9.12   0.000     44.17855    68.89913
------------------------------------------------------------------------------
```

◁

`regress` produces a variety of summary statistics along with the table of regression coefficients. At the upper left, `regress` reports an analysis-of-variance (ANOVA) table. The column headings `SS`, `df`, and `MS` stand for "sum of squares", "degrees of freedom", and "mean square", respectively. In the previous example, the total sum of squares is 2,443.5: 1,689.2 accounted for by the model and 754.3 left unexplained. Because the regression included a constant, the total sum reflects the sum after removal of means, as does the sum of squares due to the model. The table also reveals that there are 73 total degrees of freedom (counted as 74 observations less 1 for the mean removal), of which 3 are consumed by the model, leaving 70 for the residual.

To the right of the ANOVA table are presented other summary statistics. The F statistic associated with the ANOVA table is 52.25. The statistic has 3 numerator and 70 denominator degrees of freedom. The F statistic tests the hypothesis that all coefficients *excluding the constant* are zero. The chance of observing an F statistic that large or larger is reported as 0.0000, which is Stata's way of indicating a number smaller than 0.00005. The R-squared (R^2) for the regression is 0.6913, and the R-squared adjusted for degrees of freedom (R^2_a) is 0.6781. The root mean squared error, labeled `Root MSE`, is 3.2827. It is the square root of the mean squared error reported for the residual in the ANOVA table.

Finally, Stata produces a table of the estimated coefficients. The first line of the table indicates that the left-hand-side variable is `mpg`. Thereafter follow the four estimated coefficients. Our fitted model is

$$\texttt{mpg\_hat} = 56.54 - 0.0166\,\texttt{weight} + 1.59 \times 10^{-6}\,\texttt{c.weight\#c.weight} - 2.20\,\texttt{foreign}$$

Reported to the right of the coefficients in the output are the standard errors. For instance, the standard error for the coefficient on `weight` is 0.0039692. The corresponding t statistic is -4.18, which has a two-sided significance level of 0.000. This number indicates that the significance is less than 0.0005. The 95% confidence interval for the coefficient is $[-0.024, -0.009]$.

▷ Example 2

`regress` shares the features of all estimation commands. Among other things, this means that after running a regression, we can use `test` to test hypotheses about the coefficients, `estat vce` to examine the covariance matrix of the estimators, and `predict` to obtain predicted values, residuals, and influence statistics. See [U] **20 Estimation and postestimation commands**. Options that affect how estimates are displayed, such as `beta` or `level()`, can be used when replaying results.

Suppose that we meant to specify the `beta` option to obtain beta coefficients (regression coefficients normalized by the ratio of the standard deviation of the regressor to the standard deviation of the dependent variable). Even though we forgot, we can specify the option now:

```
. regress, beta
```

Source	SS	df	MS		
Model	1689.15372	3	563.05124	Number of obs	= 74
Residual	754.30574	70	10.7757963	F(3, 70)	= 52.25
				Prob > F	= 0.0000
				R-squared	= 0.6913
				Adj R-squared	= 0.6781
Total	2443.45946	73	33.4720474	Root MSE	= 3.2827

mpg	Coef.	Std. Err.	t	P>|t|	Beta
weight	-.0165729	.0039692	-4.18	0.000	-2.226321
c.weight# c.weight	1.59e-06	6.25e-07	2.55	0.013	1.32654
foreign	-2.2035	1.059246	-2.08	0.041	-.17527
_cons	56.53884	6.197383	9.12	0.000	.

◁

Treatment of the constant

By default, regress includes an intercept (constant) term in the model. The noconstant option suppresses it, and the hascons option tells regress that the model already has one.

▷ Example 3

We wish to fit a regression of the weight of an automobile against its length, and we wish to impose the constraint that the weight is zero when the length is zero.

If we simply type regress weight length, we are fitting the model

$$\texttt{weight} = \beta_0 + \beta_1\,\texttt{length} + \epsilon$$

Here a length of zero corresponds to a weight of β_0. We want to force β_0 to be zero or, equivalently, estimate an equation that does not include an intercept:

$$\texttt{weight} = \beta_1\,\texttt{length} + \epsilon$$

We do this by specifying the noconstant option:

```
. regress weight length, noconstant
```

Source	SS	df	MS	Number of obs =	74
				F(1, 73) =	3450.13
Model	703869302	1	703869302	Prob > F =	0.0000
Residual	14892897.8	73	204012.299	R-squared =	0.9793
				Adj R-squared =	0.9790
Total	718762200	74	9713002.7	Root MSE =	451.68

weight	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
length	16.29829	.2774752	58.74	0.000	15.74528	16.8513

In our data, length is measured in inches and weight in pounds. We discover that each inch of length adds 16 pounds to the weight.

◁

Sometimes there is no need for Stata to include a constant term in the model. Most commonly, this occurs when the model contains a set of mutually exclusive indicator variables. hascons is a variation of the noconstant option—it tells Stata not to add a constant to the regression because the regression specification already has one, either directly or indirectly.

For instance, we now refit our model of weight as a function of length and include separate constants for foreign and domestic cars by specifying bn.foreign. bn.foreign is factor-variable notation for "no base for foreign" or "include all levels of variable foreign in the model"; see [U] **11.4.3 Factor variables**.

```
. regress weight length bn.foreign, hascons
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =  316.54
       Model |  39647744.7     2  19823872.3            Prob > F      =  0.0000
    Residual |   4446433.7    71  62625.8268            R-squared     =  0.8992
-------------+------------------------------           Adj R-squared =  0.8963
       Total |  44094178.4    73  604029.841            Root MSE      =  250.25

------------------------------------------------------------------------------
      weight |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      length |   31.44455   1.601234    19.64   0.000     28.25178    34.63732
             |
     foreign |
           0 |   -2850.25   315.9691    -9.02   0.000    -3480.274   -2220.225
           1 |  -2983.927   275.1041   -10.85   0.000    -3532.469   -2435.385
------------------------------------------------------------------------------
```

❑ Technical note

There is a subtle distinction between the `hascons` and `noconstant` options. We can most easily reveal it by refitting the last regression, specifying `noconstant` rather than `hascons`:

```
. regress weight length bn.foreign, noconstant
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  3,    71) = 3802.03
       Model |  714315766     3   238105255            Prob > F      =  0.0000
    Residual |   4446433.7    71  62625.8268            R-squared     =  0.9938
-------------+------------------------------           Adj R-squared =  0.9936
       Total |  718762200    74   9713002.7            Root MSE      =  250.25

------------------------------------------------------------------------------
      weight |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      length |   31.44455   1.601234    19.64   0.000     28.25178    34.63732
             |
     foreign |
           0 |   -2850.25   315.9691    -9.02   0.000    -3480.274   -2220.225
           1 |  -2983.927   275.1041   -10.85   0.000    -3532.469   -2435.385
------------------------------------------------------------------------------
```

Comparing this output with that produced by the previous `regress` command, we see that they are almost, but not quite, identical. The parameter estimates and their associated statistics—the second half of the output—are identical. The overall summary statistics and the ANOVA table—the first half of the output—are different, however.

In the first case, the R^2 is shown as 0.8992; here it is shown as 0.9938. In the first case, the F statistic is 316.54; now it is 3,802.03. The numerator degrees of freedom are different as well. In the first case, the numerator degrees of freedom are 2; now they are 3. Which is correct?

Both are. Specifying the `hascons` option causes `regress` to adjust the ANOVA table and its associated statistics for the explanatory power of the constant. The regression in effect has a constant; it is just written in such a way that a separate constant is unnecessary. No such adjustment is made with the `noconstant` option.

❑

❑ Technical note

When the hascons option is specified, regress checks to make sure that the model does in fact have a constant term. If regress cannot find a constant term, it automatically adds one. Fitting a model of weight on length and specifying the hascons option, we obtain

```
. regress weight length, hascons
(note: hascons false)
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =  613.27
       Model |  39461306.8     1  39461306.8            Prob > F      =  0.0000
    Residual |  4632871.55    72  64345.4382            R-squared     =  0.8949
-------------+------------------------------           Adj R-squared =  0.8935
       Total |  44094178.4    73  604029.841            Root MSE      =  253.66

------------------------------------------------------------------------------
      weight |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      length |   33.01988   1.333364    24.76   0.000     30.36187    35.67789
       _cons |  -3186.047   252.3113   -12.63   0.000     -3689.02   -2683.073
------------------------------------------------------------------------------
```

Even though we specified hascons, regress included a constant, anyway. It also added a note to our output: "note: hascons false".

❑

❑ Technical note

Even if the model specification effectively includes a constant term, we need not specify the hascons option. regress is always on the lookout for collinear variables and omits them from the model. For instance,

```
. regress weight length bn.foreign
note: 1.foreign omitted because of collinearity
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =  316.54
       Model |  39647744.7     2  19823872.3            Prob > F      =  0.0000
    Residual |  4446433.7     71  62625.8268            R-squared     =  0.8992
-------------+------------------------------           Adj R-squared =  0.8963
       Total |  44094178.4    73  604029.841            Root MSE      =  250.25

------------------------------------------------------------------------------
      weight |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      length |   31.44455   1.601234    19.64   0.000     28.25178    34.63732
             |
     foreign |
           0 |   133.6775   77.47615     1.73   0.089    -20.80555    288.1605
           1 |          0  (omitted)
             |
       _cons |  -2983.927   275.1041   -10.85   0.000    -3532.469   -2435.385
------------------------------------------------------------------------------
```

❑

Robust standard errors

regress with the vce(robust) option substitutes a robust variance matrix calculation for the conventional calculation, or if vce(cluster *clustvar*) is specified, allows relaxing the assumption of independence within groups. How this method works is explained in [U] **20.20 Obtaining robust variance estimates**. Below we show how well this approach works.

▷ Example 4

Specifying the vce(robust) option is equivalent to requesting White-corrected standard errors in the presence of heteroskedasticity. We use the automobile data and, in the process of looking at the energy efficiency of cars, analyze a variable with considerable heteroskedasticity.

We will examine the amount of energy—measured in gallons of gasoline—that the cars in the data need to move 1,000 pounds of their weight 100 miles. We are going to examine the relative efficiency of foreign and domestic cars.

```
. gen gpmw = ((1/mpg)/weight)*100*1000
. summarize gpmw
    Variable |      Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
        gpmw |       74    1.682184    .2426311    1.09553    2.30521
```

In these data, the engines consume between 1.10 and 2.31 gallons of gas to move 1,000 pounds of the car's weight 100 miles. If we ran a regression with conventional standard errors of gpmw on foreign, we would obtain

```
. regress gpmw foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =   20.07
       Model |  .936705572     1  .936705572            Prob > F      =  0.0000
    Residual |  3.36079459    72  .046677703            R-squared     =  0.2180
-------------+------------------------------           Adj R-squared =  0.2071
       Total |  4.29750017    73  .058869865            Root MSE      =  .21605

------------------------------------------------------------------------------
        gpmw |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     foreign |   .2461526   .0549487     4.48   0.000     .1366143    .3556909
       _cons |   1.609004   .0299608    53.70   0.000     1.549278     1.66873
------------------------------------------------------------------------------
```

regress with the vce(robust) option, on the other hand, reports

```
. regress gpmw foreign, vce(robust)
Linear regression                               Number of obs =      74
                                                F(  1,    72) =   13.13
                                                Prob > F      =  0.0005
                                                R-squared     =  0.2180
                                                Root MSE      =  .21605

------------------------------------------------------------------------------
             |               Robust
        gpmw |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     foreign |   .2461526   .0679238     3.62   0.001     .1107489    .3815563
       _cons |   1.609004   .0234535    68.60   0.000      1.56225    1.655758
------------------------------------------------------------------------------
```

The point estimates are the same (foreign cars need one-quarter gallon more gas), but the standard errors differ by roughly 20%. Conventional regression reports the 95% confidence interval as $[0.14, 0.36]$, whereas the robust standard errors make the interval $[0.11, 0.38]$.

Which is right? Notice that `gpmw` is a variable with considerable heteroskedasticity:

```
. tabulate foreign, summarize(gpmw)
```

Car type	Summary of gpmw Mean	Std. Dev.	Freq.
Domestic	1.6090039	.16845182	52
Foreign	1.8551565	.30186861	22
Total	1.6821844	.24263113	74

Thus here we favor the robust standard errors. In [U] **20.20 Obtaining robust variance estimates**, we show another example using linear regression where it makes little difference whether we specify `vce(robust)`. The linear-regression assumptions were true, and we obtained nearly linear-regression results. The advantage of the robust estimate is that in neither case did we have to check assumptions.

◁

❑ Technical note

`regress` purposefully suppresses displaying the ANOVA table when `vce(robust)` is specified, as it is no longer appropriate in a statistical sense, even though, mechanically, the numbers would be unchanged. That is, sums of squares remain unchanged, but the meaning of those sums is no longer relevant. The F statistic, for instance, is no longer based on sums of squares; it becomes a Wald test based on the robustly estimated variance matrix. Nevertheless, `regress` continues to report the R^2 and the root MSE even though both numbers are based on sums of squares and are, strictly speaking, irrelevant. In this, the root MSE is more in violation of the spirit of the robust estimator than is R^2. As a goodness-of-fit statistic, R^2 is still fine; just do not use it in formulas to obtain F statistics because those formulas no longer apply. The root MSE is valid in a literal sense—it is the square root of the mean squared error, but it is no longer an estimate of σ because there is no single σ; the variance of the residual varies observation by observation.

❑

▷ Example 5

The `vce(hc2)` and `vce(hc3)` options modify the robust variance calculation. In the context of linear regression without clustering, the idea behind the robust calculation is somehow to measure σ_j^2, the variance of the residual associated with the jth observation, and then to use that estimate to improve the estimated variance of $\widehat{\boldsymbol{\beta}}$. Because residuals have (theoretically and practically) mean 0, one estimate of σ_j^2 is the observation's squared residual itself—u_j^2. A finite-sample correction could improve that by multiplying u_j^2 by $n/(n-k)$, and, as a matter of fact, `vce(robust)` uses $\{n/(n-k)\}u_j^2$ as its estimate of the residual's variance.

`vce(hc2)` and `vce(hc3)` use alternative estimators of the observation-specific variances. For instance, if the residuals are homoskedastic, we can show that the expected value of u_j^2 is $\sigma^2(1-h_{jj})$, where h_{jj} is the jth diagonal element of the projection (hat) matrix. h_{jj} has average value k/n, so $1-h_{jj}$ has average value $1-k/n = (n-k)/n$. Thus the default robust estimator $\widehat{\sigma}_j = \{n/(n-k)\}u_j^2$ amounts to dividing u_j^2 by the average of the expectation.

vce(hc2) divides u_j^2 by $1 - h_{jj}$ itself, so it should yield better estimates if the residuals really are homoskedastic. vce(hc3) divides u_j^2 by $(1 - h_{jj})^2$ and has no such clean interpretation. Davidson and MacKinnon (1993) show that $u_j^2/(1 - h_{jj})^2$ approximates a more complicated estimator that they obtain by jackknifing (MacKinnon and White 1985). Angrist and Pischke (2009) also illustrate the relative merits of these adjustments.

Here are the results of refitting our efficiency model using vce(hc2) and vce(hc3):

```
. regress gpmw foreign, vce(hc2)
Linear regression                               Number of obs =      74
                                                F(  1,    72) =   12.93
                                                Prob > F      =  0.0006
                                                R-squared     =  0.2180
                                                Root MSE      =  .21605
```

gpmw	Coef.	Robust HC2 Std. Err.	t	P>|t|	[95% Conf.	Interval]
foreign	.2461526	.0684669	3.60	0.001	.1096662	.3826389
_cons	1.609004	.0233601	68.88	0.000	1.562437	1.655571

```
. regress gpmw foreign, vce(hc3)
Linear regression                               Number of obs =      74
                                                F(  1,    72) =   12.38
                                                Prob > F      =  0.0008
                                                R-squared     =  0.2180
                                                Root MSE      =  .21605
```

gpmw	Coef.	Robust HC3 Std. Err.	t	P>|t|	[95% Conf.	Interval]
foreign	.2461526	.069969	3.52	0.001	.1066719	.3856332
_cons	1.609004	.023588	68.21	0.000	1.561982	1.656026

◁

▷ Example 6

The vce(cluster *clustvar*) option relaxes the assumption of independence. Below we have 28,534 observations on 4,711 women aged 14–46 years. Data were collected on these women between 1968 and 1988. We are going to fit a classic earnings model, and we begin by ignoring that each woman appears an average of 6.056 times in the data.

```
. use http://www.stata-press.com/data/r12/regsmpl, clear
(NLS Women 14-26 in 1968)
. regress ln_wage age c.age#c.age tenure
      Source |       SS       df       MS              Number of obs =   28101
-------------+------------------------------           F(  3, 28097) = 1842.45
       Model |  1054.52501     3  351.508335            Prob > F      =  0.0000
    Residual |  5360.43962 28097  .190783344            R-squared     =  0.1644
-------------+------------------------------           Adj R-squared =  0.1643
       Total |  6414.96462 28100  .228290556            Root MSE      =  .43679

------------------------------------------------------------------------------
     ln_wage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0752172   .0034736    21.65   0.000     .0684088    .0820257
             |
 c.age#c.age |  -.0010851   .0000575   -18.86   0.000    -.0011979   -.0009724
             |
      tenure |   .0390877   .0007743    50.48   0.000     .0375699    .0406054
       _cons |   .3339821   .0504413     6.62   0.000     .2351148    .4328495
------------------------------------------------------------------------------
```

The number of observations in our model is 28,101 because Stata drops observations that have a missing value for one or more of the variables in the model. We can be reasonably certain that the standard errors reported above are meaningless. Without a doubt, a woman with higher-than-average wages in one year typically has higher-than-average wages in other years, and so the residuals are not independent. One way to deal with this would be to fit a random-effects model—and we are going to do that—but first we fit the model using `regress` specifying `vce(cluster id)`, which treats only observations with different person `id`s as truly independent:

```
. regress ln_wage age c.age#c.age tenure, vce(cluster id)
Linear regression                               Number of obs =   28101
                                                F(  3,  4698) =  748.82
                                                Prob > F      =  0.0000
                                                R-squared     =  0.1644
                                                Root MSE      =  .43679

                                  (Std. Err. adjusted for 4699 clusters in idcode)
------------------------------------------------------------------------------
             |               Robust
     ln_wage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0752172   .0045711    16.45   0.000     .0662557    .0841788
             |
 c.age#c.age |  -.0010851   .0000778   -13.94   0.000    -.0012377   -.0009325
             |
      tenure |   .0390877   .0014425    27.10   0.000     .0362596    .0419157
       _cons |   .3339821   .0641918     5.20   0.000      .208136    .4598282
------------------------------------------------------------------------------
```

For comparison, we focus on the tenure coefficient, which in economics jargon can be interpreted as the rate of return for keeping your job. The 95% confidence interval we previously estimated—an interval we do not believe—is $[0.038, 0.041]$. The robust interval is twice as wide, being $[0.036, 0.042]$.

As we said, one correct way to fit this model is by random-effects regression. Here is the random-effects result:

```
. xtreg ln_wage age c.age#c.age tenure, re
Random-effects GLS regression                   Number of obs      =     28101
Group variable: idcode                          Number of groups   =      4699

R-sq:  within  = 0.1370                         Obs per group: min =         1
       between = 0.2154                                        avg =       6.0
       overall = 0.1608                                        max =        15

Random effects u_i ~ Gaussian                   Wald chi2(3)       =   4717.05
corr(u_i, X)       = 0 (assumed)                Prob > chi2        =    0.0000

------------------------------------------------------------------------------
     ln_wage |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0568296   .0026958    21.08   0.000     .0515459    .0621132
             |
 c.age#c.age |  -.0007566   .0000447   -16.93   0.000    -.0008441   -.000669
             |
      tenure |   .0260135   .0007477    34.79   0.000     .0245481    .0274789
       _cons |   .6136792   .0394611    15.55   0.000     .5363368    .6910216
-------------+----------------------------------------------------------------
     sigma_u |  .33542449
     sigma_e |  .29674679
         rho |  .56095413   (fraction of variance due to u_i)
------------------------------------------------------------------------------
```

Robust regression estimated the 95% interval $[0.036, 0.042]$, and `xtreg` (see [XT] **xtreg**) estimates $[0.025, 0.027]$. Which is better? The random-effects regression estimator assumes a lot. We can check some of these assumptions by performing a Hausman test. Using `estimates` (see [R] **estimates store**), we save the random-effects estimation results, and then we run the required fixed-effects regression to perform the test.

```
. estimates store random
. xtreg ln_wage age c.age#c.age tenure, fe
Fixed-effects (within) regression               Number of obs      =     28101
Group variable: idcode                          Number of groups   =      4699

R-sq:  within  = 0.1375                         Obs per group: min =         1
       between = 0.2066                                        avg =       6.0
       overall = 0.1568                                        max =        15

                                                F(3,23399)         =   1243.00
corr(u_i, Xb)  = 0.1380                         Prob > F           =    0.0000

------------------------------------------------------------------------------
     ln_wage |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         age |   .0522751    .002783    18.78   0.000     .0468202     .05773
             |
 c.age#c.age |  -.0006717   .0000461   -14.56   0.000    -.0007621   -.0005813
             |
      tenure |    .021738    .000799    27.21   0.000      .020172    .023304
       _cons |    .687178   .0405944    16.93   0.000     .6076103    .7667456
-------------+----------------------------------------------------------------
     sigma_u |  .38743138
     sigma_e |  .29674679
         rho |   .6302569   (fraction of variance due to u_i)
------------------------------------------------------------------------------
F test that all u_i=0:     F(4698, 23399) =     7.98         Prob > F = 0.0000
```

```
. hausman . random
                 ---- Coefficients ----
                |      (b)          (B)            (b-B)     sqrt(diag(V_b-V_B))
                |        .       random       Difference          S.E.
----------------+----------------------------------------------------------------
            age |    .0522751    .0568296       -.0045545        .0006913
  c.age#c.age   |   -.0006717   -.0007566        .0000849        .0000115
         tenure |     .021738    .0260135       -.0042756        .0002816
------------------------------------------------------------------------------
                           b = consistent under Ho and Ha; obtained from xtreg
            B = inconsistent under Ha, efficient under Ho; obtained from xtreg

    Test:  Ho:  difference in coefficients not systematic

                  chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                          =      336.62
                Prob>chi2 =      0.0000
```

The Hausman test casts grave suspicions on the random-effects model we just fit, so we should be careful in interpreting those results.

Meanwhile, our robust regression results still stand, as long as we are careful about the interpretation. The correct interpretation is that, if the data collection were repeated (on women sampled the same way as in the original sample), and if we were to refit the model, 95% of the time we would expect the estimated coefficient on tenure to be in the range $[0.036, 0.042]$.

Even with robust regression, we must be careful about going beyond that statement. Here the Hausman test is probably picking up something that differs within and between person, which would cast doubt on our robust regression model in terms of interpreting $[0.036, 0.042]$ to contain the rate of return for keeping a job, economywide, for all women, without exception. ◁

Weighted regression

`regress` can perform weighted and unweighted regression. We indicate the weight by specifying the [*weight*] qualifier. By default, `regress` assumes analytic weights; see the technical note below.

▷ Example 7

We have census data recording the death rate (`drate`) and median age (`medage`) for each state. The data also record the region of the country in which each state is located and the overall population of the state:

```
. use http://www.stata-press.com/data/r12/census9
(1980 Census data by state)
. describe
Contains data from http://www.stata-press.com/data/r12/census9.dta
  obs:            50                          1980 Census data by state
 vars:             6                          6 Apr 2011 15:43
 size:         1,450
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
state           str14  %-14s                  State
state2          str2   %-2s                   Two-letter state abbreviation
drate           float  %9.0g                  Death Rate
pop             long   %12.0gc                Population
medage          float  %9.2f                  Median age
region          byte   %-8.0g      cenreg      Census region
-------------------------------------------------------------------------------
Sorted by:
```

We can use factor variables to include dummy variables for region. Because the variables in the regression reflect means rather than individual observations, the appropriate method of estimation is analytically weighted least squares (Davidson and MacKinnon 2004, 261–262), where the weight is total population:

```
. regress drate medage i.region [w=pop]
(analytic weights assumed)
(sum of wgt is   2.2591e+08)
```

Source	SS	df	MS	Number of obs =	50
				F(4, 45) =	37.21
Model	4096.6093	4	1024.15232	Prob > F =	0.0000
Residual	1238.40987	45	27.5202192	R-squared =	0.7679
				Adj R-squared =	0.7472
Total	5335.01916	49	108.877942	Root MSE =	5.246

drate	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
medage	4.283183	.5393329	7.94	0.000	3.196911	5.369455
region						
2	.3138738	2.456431	0.13	0.899	-4.633632	5.26138
3	-1.438452	2.320244	-0.62	0.538	-6.111663	3.234758
4	-10.90629	2.681349	-4.07	0.000	-16.30681	-5.505777
_cons	-39.14727	17.23613	-2.27	0.028	-73.86262	-4.431915

To weight the regression by population, we added the qualifier `[w=pop]` to the end of the `regress` command. Our qualifier was vague (we did not say `[aweight=pop]`), but unless told otherwise, Stata assumes analytic weights for `regress`. Stata informed us that the sum of the weight is 2.2591×10^8; there were approximately 226 million people residing in the United States according to our 1980 data. ◁

❑ Technical note

Once we fit a weighted regression, we can obtain the appropriately weighted variance–covariance matrix of the estimators using `estat vce` and perform appropriately weighted hypothesis tests using `test`.

In the weighted regression in the previous example, we see that `4.region` is statistically significant but that `2.region` and `3.region` are not. We use `test` to test the joint significance of the region variables:

```
. test 2.region 3.region 4.region
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    45) =    9.84
            Prob > F =    0.0000
```

The results indicate that the region variables are jointly significant.

❑

`regress` also accepts frequency weights (`fweight`s). Frequency weights are appropriate when the data do not reflect cell means, but instead represent replicated observations. Specifying `aweight`s or `fweight`s will not change the parameter estimates, but it will change the corresponding significance levels.

For instance, if we specified [fweight=pop] in the weighted regression example above—which would be statistically incorrect—Stata would treat the data as if the data represented 226 million independent observations on death rates and median age. The data most certainly do not represent that—they represent 50 observations on state averages.

With aweights, Stata treats the number of observations on the process as the number of observations in the data. When we specify fweights, Stata treats the number of observations as if it were equal to the sum of the weights; see *Methods and formulas* below.

❑ Technical note

A popular request on the help line is to describe the effect of specifying [aweight=*exp*] with regress in terms of transformation of the dependent and independent variables. The mechanical answer is that typing

```
. regress y x1 x2 [aweight=n]
```

is equivalent to fitting the model

$$y_j\sqrt{n_j} = \beta_0\sqrt{n_j} + \beta_1 x_{1j}\sqrt{n_j} + \beta_2 x_{2j}\sqrt{n_j} + u_j\sqrt{n_j}$$

This regression will reproduce the coefficients and covariance matrix produced by the aweighted regression. The mean squared errors (estimates of the variance of the residuals) will, however, be different. The transformed regression reports s_t^2, an estimate of $\mathrm{Var}(u_j\sqrt{n_j})$. The aweighted regression reports s_a^2, an estimate of $\mathrm{Var}(u_j\sqrt{n_j}\sqrt{N/\sum_k n_k})$, where N is the number of observations. Thus

$$s_a^2 = \frac{N}{\sum_k n_k} s_t^2 = \frac{s_t^2}{\overline{n}} \tag{1}$$

The logic for this adjustment is as follows: Consider the model

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + u$$

Assume that, were this model fit on individuals, $\mathrm{Var}(u) = \sigma_u^2$, a constant. Assume that individual data are not available; what is available are averages $(\overline{y}_j, \overline{x}_{1j}, \overline{x}_{2j})$ for $j = 1, \ldots, N$, and each average is calculated over n_j observations. Then it is still true that

$$\overline{y}_j = \beta_0 + \beta_1\overline{x}_{1j} + \beta_2\overline{x}_{2j} + \overline{u}_j$$

where $\overline{u}_j$ is the average of n_j mean 0, variance σ_u^2 deviates and has variance $\sigma_{\overline{u}}^2 = \sigma_u^2/n_j$. Thus multiplying through by $\sqrt{n_j}$ produces

$$\overline{y}_j\sqrt{n_j} = \beta_0\sqrt{n_j} + \beta_1\overline{x}_{1j}\sqrt{n_j} + \beta_2\overline{x}_{2j}\sqrt{n_j} + \overline{u}_j\sqrt{n_j}$$

and $\mathrm{Var}(\overline{u}_j\sqrt{n_j}) = \sigma_u^2$. The mean squared error, s_t^2, reported by fitting this transformed regression is an estimate of σ_u^2. The coefficients and covariance matrix could also be obtained by aweighted regress. The only difference would be in the reported mean squared error, which from (1) is $\sigma_u^2/\overline{n}$. On average, each observation in the data reflects the averages calculated over $\overline{n} = \sum_k n_k/N$ individuals, and thus this reported mean squared error is the average variance of an observation in the dataset. We can retrieve the estimate of σ_u^2 by multiplying the reported mean squared error by $\overline{n}$.

More generally, aweights are used to solve general heteroskedasticity problems. In these cases, we have the model

$$y_j = \beta_0 + \beta_1 x_{1j} + \beta_2 x_{2j} + u_j$$

and the variance of u_j is thought to be proportional to a_j. If the variance is proportional to a_j, it is also proportional to αa_j, where α is any positive constant. Not quite arbitrarily, but with no loss of generality, we could choose $\alpha = \sum_k (1/a_k)/N$, the average value of the inverse of a_j. We can then write $\mathrm{Var}(u_j) = k\alpha a_j \sigma^2$, where k is the constant of proportionality that is no longer a function of the scale of the weights.

Dividing this regression through by the $\sqrt{a_j}$,

$$y_j/\sqrt{a_j} = \beta_0/\sqrt{a_j} + \beta_1 x_{1j}/\sqrt{a_j} + \beta_2 x_{2j}/\sqrt{a_j} + u_j/\sqrt{a_j}$$

produces a model with $\mathrm{Var}(u_j/\sqrt{a_j}) = k\alpha\sigma^2$, which is the constant part of $\mathrm{Var}(u_j)$. This variance is a function of α, the average of the reciprocal weights; if the weights are scaled arbitrarily, then so is this variance.

We can also fit this model by typing

```
. regress y x1 x2 [aweight=1/a]
```

This input will produce the same estimates of the coefficients and covariance matrix; the reported mean squared error is, from (1), $\{N/\sum_k (1/a_k)\} k\alpha\sigma^2 = k\sigma^2$. This variance is independent of the scale of a_j.

❑

Instrumental variables and two-stage least-squares regression

An alternate syntax for `regress` can be used to produce instrumental-variables (two-stage least squares) estimates.

`regress` *depvar* [*varlist*$_1$ [`(`*varlist*$_2$`)`]] [*if*] [*in*] [*weight*] [`,` *regress_options*]

This syntax is used mainly by programmers developing estimators using the instrumental-variables estimates as intermediate results. `ivregress` is normally used to directly fit these models; see [R] **ivregress**.

With this syntax, `regress` fits a structural equation of *depvar* on *varlist*$_1$ using instrumental variables regression; `(`*varlist*$_2$`)` indicates the list of instrumental variables. With the exception of `vce(hc2)` and `vce(hc3)`, all standard `regress` options are allowed.

Saved results

`regress` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(mss)`	model sum of squares
`e(df_m)`	model degrees of freedom
`e(rss)`	residual sum of squares
`e(df_r)`	residual degrees of freedom
`e(r2)`	R-squared
`e(r2_a)`	adjusted R-squared
`e(F)`	F statistic
`e(rmse)`	root mean squared error
`e(ll)`	log likelihood under additional assumption of i.i.d. normal errors
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`regress`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(model)`	`ols` or `iv`
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output when `vce()` is not `ols`
`e(clustvar)`	name of cluster variable
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(properties)`	`b V`
`e(estat_cmd)`	program used to implement `estat`
`e(predict)`	program used to implement `predict`
`e(marginsok)`	predictions allowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators
`e(V_modelbased)`	model-based variance

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`regress` is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Coefficient estimation and ANOVA table
A general notation for the robust variance calculation
Robust calculation for regress

Coefficient estimation and ANOVA table

Variables printed in lowercase and not boldfaced (for example, x) are scalars. Variables printed in lowercase and boldfaced (for example, $\mathbf{x}$) are column vectors. Variables printed in uppercase and boldfaced (for example, $\mathbf{X}$) are matrices.

Let $\mathbf{v}$ be a column vector of weights specified by the user. If no weights are specified, $\mathbf{v} = \mathbf{1}$. Let $\mathbf{w}$ be a column vector of normalized weights. If no weights are specified or if the user specified `fweights` or `iweights`, $\mathbf{w} = \mathbf{v}$. Otherwise, $\mathbf{w} = \{\mathbf{v}/(\mathbf{1}'\mathbf{v})\}(\mathbf{1}'\mathbf{1})$.

The *number of observations*, n, is defined as $\mathbf{1}'\mathbf{w}$. For `iweights`, this is truncated to an integer. The *sum of the weights* is $\mathbf{1}'\mathbf{v}$. Define $c = 1$ if there is a constant in the regression and zero otherwise. Define k as the number of right-hand-side variables (including the constant).

Let $\mathbf{X}$ denote the matrix of observations on the right-hand-side variables, $\mathbf{y}$ the vector of observations on the left-hand-side variable, and $\mathbf{Z}$ the matrix of observations on the instruments. If the user specifies no instruments, then $\mathbf{Z} = \mathbf{X}$. In the following formulas, if the user specifies weights, then $\mathbf{X}'\mathbf{X}$, $\mathbf{X}'\mathbf{y}$, $\mathbf{y}'\mathbf{y}$, $\mathbf{Z}'\mathbf{Z}$, $\mathbf{Z}'\mathbf{X}$, and $\mathbf{Z}'\mathbf{y}$ are replaced by $\mathbf{X}'\mathbf{D}\mathbf{X}$, $\mathbf{X}'\mathbf{D}\mathbf{y}$, $\mathbf{y}'\mathbf{D}\mathbf{y}$, $\mathbf{Z}'\mathbf{D}\mathbf{Z}$, $\mathbf{Z}'\mathbf{D}\mathbf{X}$, and $\mathbf{Z}'\mathbf{D}\mathbf{y}$, respectively, where $\mathbf{D}$ is a diagonal matrix whose diagonal elements are the elements of $\mathbf{w}$. We suppress the $\mathbf{D}$ below to simplify the notation.

If no instruments are specified, define $\mathbf{A}$ as $\mathbf{X}'\mathbf{X}$ and $\mathbf{a}$ as $\mathbf{X}'\mathbf{y}$. Otherwise, define $\mathbf{A}$ as $\mathbf{X}'\mathbf{Z}(\mathbf{Z}'\mathbf{Z})^{-1}(\mathbf{X}'\mathbf{Z})'$ and $\mathbf{a}$ as $\mathbf{X}'\mathbf{Z}(\mathbf{Z}'\mathbf{Z})^{-1}\mathbf{Z}'\mathbf{y}$.

The coefficient vector $\mathbf{b}$ is defined as $\mathbf{A}^{-1}\mathbf{a}$. Although not shown in the notation, unless `hascons` is specified, $\mathbf{A}$ and $\mathbf{a}$ are accumulated in deviation form and the constant is calculated separately. This comment applies to all statistics listed below.

The *total sum of squares*, TSS, equals $\mathbf{y}'\mathbf{y}$ if there is no intercept and $\mathbf{y}'\mathbf{y} - \{(\mathbf{1}'\mathbf{y})^2/n\}$ otherwise. The *degrees of freedom* is $n - c$.

The *error sum of squares*, ESS, is defined as $\mathbf{y}'\mathbf{y} - 2\mathbf{b}\mathbf{X}'\mathbf{y} + \mathbf{b}'\mathbf{X}'\mathbf{X}\mathbf{b}$ if there are instruments and as $\mathbf{y}'\mathbf{y} - \mathbf{b}'\mathbf{X}'\mathbf{y}$ otherwise. The *degrees of freedom* is $n - k$.

The *model sum of squares*, MSS, equals TSS − ESS. The *degrees of freedom* is $k - c$.

The *mean squared error*, s^2, is defined as ESS$/(n - k)$. The *root mean squared error* is s, its square root.

The F statistic with $k - c$ and $n - k$ degrees of freedom is defined as

$$F = \frac{\text{MSS}}{(k-c)s^2}$$

if no instruments are specified. If instruments are specified and $c = 1$, then F is defined as

$$F = \frac{(\mathbf{b}-\mathbf{c})'\mathbf{A}(\mathbf{b}-\mathbf{c})}{(k-1)s^2}$$

where $\mathbf{c}$ is a vector of $k-1$ zeros and kth element $\mathbf{1}'\mathbf{y}/n$. Otherwise, F is defined as *missing*. (Here you may use the `test` command to construct any F test that you wish.)

The *R-squared*, R^2, is defined as $R^2 = 1 - \text{ESS}/\text{TSS}$.

The *adjusted R-squared*, R_a^2, is $1 - (1 - R^2)(n - c)/(n - k)$.

If `vce(robust)` is not specified, the conventional estimate of variance is $s^2\mathbf{A}^{-1}$. The handling of `vce(robust)` is described below.

A general notation for the robust variance calculation

Put aside all context of linear regression and the notation that goes with it—we will return to it. First, we are going to establish a notation for describing robust variance calculations.

The calculation formula for the robust variance calculation is

$$\widehat{\mathcal{V}} = q_c \widehat{\mathbf{V}} \Big(\sum_{k=1}^{M} \mathbf{u}_k^{(G)\prime} \mathbf{u}_k^{(G)} \Big) \widehat{\mathbf{V}}$$

where

$$\mathbf{u}_k^{(G)} = \sum_{j \in G_k} w_j \mathbf{u}_j$$

$G_1, G_2, \ldots, G_M$ are the clusters specified by `vce(cluster` *clustvar*`)`, and w_j are the user-specified weights, normalized if `aweight`s or `pweight`s are specified and equal to 1 if no weights are specified.

For `fweight`s without clusters, the variance formula is

$$\widehat{\mathcal{V}} = q_c \widehat{\mathbf{V}} \Big(\sum_{j=1}^{N} w_j \mathbf{u}_j' \mathbf{u}_j \Big) \widehat{\mathbf{V}}$$

which is the same as expanding the dataset and making the calculation on the unweighted data.

If `vce(cluster` *clustvar*`)` is not specified, $M = N$, and each cluster contains 1 observation. The inputs into this calculation are

- $\widehat{\mathbf{V}}$, which is typically a conventionally calculated variance matrix;
- $\mathbf{u}_j$, $j = 1, \ldots, N$, a row vector of scores; and
- q_c, a constant finite-sample adjustment.

Thus we can now describe how estimators apply the robust calculation formula by defining $\widehat{\mathbf{V}}$, $\mathbf{u}_j$, and q_c.

Two definitions are popular enough for q_c to deserve a name. The regression-like formula for q_c (Fuller et al. 1986) is

$$q_c = \frac{N-1}{N-k} \frac{M}{M-1}$$

where M is the number of clusters and N is the number of observations. For weights, N refers to the sum of the weights if weights are frequency weights and the number of observations in the dataset (ignoring weights) in all other cases. Also note that, weighted or not, $M = N$ when `vce(cluster` *clustvar*`)` is not specified, and then $q_c = N/(N-k)$.

The asymptotic-like formula for q_c is

$$q_c = \frac{M}{M-1}$$

where $M = N$ if `vce(cluster` *clustvar*`)` is not specified.

See [U] **20.20 Obtaining robust variance estimates** and [P] **_robust** for a discussion of the robust variance estimator and a development of these formulas.

Robust calculation for regress

For `regress`, $\widehat{\mathbf{V}} = \mathbf{A}^{-1}$. The other terms are

No instruments, `vce(robust)`, but not `vce(hc2)` or `vce(hc3)`,

$$\mathbf{u}_j = (y_j - \mathbf{x}_j\mathbf{b})\mathbf{x}_j$$

and q_c is given by its regression-like definition.

No instruments, `vce(hc2)`,

$$\mathbf{u}_j = \frac{1}{\sqrt{1-h_{jj}}}(y_j - \mathbf{x}_j\mathbf{b})\mathbf{x}_j$$

where $q_c = 1$ and $h_{jj} = \mathbf{x}_j(\mathbf{X}'\mathbf{X})^{-1}\mathbf{x}_j'$.

No instruments, `vce(hc3)`,

$$\mathbf{u}_j = \frac{1}{1-h_{jj}}(y_j - \mathbf{x}_j\mathbf{b})\mathbf{x}_j$$

where $q_c = 1$ and $h_{jj} = \mathbf{x}_j(\mathbf{X}'\mathbf{X})^{-1}\mathbf{x}_j'$.

Instrumental variables,

$$\mathbf{u}_j = (y_j - \mathbf{x}_j\mathbf{b})\widehat{\mathbf{x}}_j$$

where q_c is given by its regression-like definition, and

$$\widehat{\mathbf{x}}_j' = \mathbf{P}\mathbf{z}_j'$$

where $\mathbf{P} = (\mathbf{X}'\mathbf{Z})(\mathbf{Z}'\mathbf{Z})^{-1}$.

Acknowledgments

The robust estimate of variance was first implemented in Stata by Mead Over, Center for Global Development; Dean Jolliffe, World Bank; and Andrew Foster, Department of Economics, Brown University (Over, Jolliffe, and Foster 1996).

The history of regression is long and complicated: the books by Stigler (1986) and Hald (1998) are devoted largely to the story. Legendre published first on least squares in 1805. Gauss published later in 1809, but he had the idea earlier. Gauss, and especially Laplace, tied least squares to a normal errors assumption. The idea of the normal distribution can itself be traced back to De Moivre in 1733. Laplace discussed a variety of other estimation methods and error assumptions over his long career, while linear models long predate either innovation. Most of this work was linked to problems in astronomy and geodesy.

A second wave of ideas started when Galton used graphical and descriptive methods on data bearing on heredity to develop what he called regression. His term reflects the common phenomenon that characteristics of offspring are positively correlated with those of parents but with regression slope such that offspring "regress toward the mean". Galton's work was rather intuitive: contributions from Pearson, Edgeworth, Yule, and others introduced more formal machinery, developed related ideas on correlation, and extended application into the biological and social sciences. So most of the elements of regression as we know it were in place by 1900.

Pierre-Simon Laplace (1749–1827) was born in Normandy and was early recognized as a remarkable mathematician. He weathered a changing political climate well enough to rise to Minister of the Interior under Napoleon in 1799 (although only for 6 weeks) and to be made a Marquis by Louis XVIII in 1817. He made many contributions to mathematics and physics, his two main interests being theoretical astronomy and probability theory (including statistics). Laplace transforms are named for him.

Adrien-Marie Legendre (1752–1833) was born in Paris (or possibly in Toulouse) and educated in mathematics and physics. He worked in number theory, geometry, differential equations, calculus, function theory, applied mathematics, and geodesy. The Legendre polynomials are named for him. His main contribution to statistics is as one of the discoverers of least squares. He died in poverty, having refused to bow to political pressures.

Johann Carl Friedrich Gauss (1777–1855) was born in Braunschweig (Brunswick), now in Germany. He studied there and at Göttingen. His doctoral dissertation at the University of Helmstedt was a discussion of the fundamental theorem of algebra. He made many fundamental contributions to geometry, number theory, algebra, real analysis, differential equations, numerical analysis, statistics, astronomy, optics, geodesy, mechanics, and magnetism. An outstanding genius, Gauss worked mostly in isolation in Göttingen.

Francis Galton (1822–1911) was born in Birmingham, England, into a well-to-do family with many connections: he and Charles Darwin were first cousins. After an unsuccessful foray into medicine, he became independently wealthy at the death of his father. Galton traveled widely in Europe, the Middle East, and Africa, and became celebrated as an explorer and geographer. His pioneering work on weather maps helped in the identification of anticyclones, which he named. From about 1865, most of his work was centered on quantitative problems in biology, anthropology, and psychology. In a sense, Galton (re)invented regression, and he certainly named it. Galton also promoted the normal distribution, correlation approaches, and the use of median and selected quantiles as descriptive statistics. He was knighted in 1909.

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Also see

[R] **regress postestimation** — Postestimation tools for regress

[R] **regress postestimation time series** — Postestimation tools for regress with time series

[R] **anova** — Analysis of variance and covariance

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

Stata Structural Equation Modeling Reference Manual

[U] **20 Estimation and postestimation commands**

Title

regress postestimation — Postestimation tools for regress

Description

The following postestimation commands are of special interest after `regress`:

Command	Description
`dfbeta`	DFBETA influence statistics
`estat hettest`	tests for heteroskedasticity
`estat imtest`	information matrix test
`estat ovtest`	Ramsey regression specification-error test for omitted variables
`estat szroeter`	Szroeter's rank test for heteroskedasticity
`estat vif`	variance inflation factors for the independent variables
`acprplot`	augmented component-plus-residual plot
`avplot`	added-variable plot
`avplots`	all added-variables plots in one image
`cprplot`	component-plus-residual plot
`lvr2plot`	leverage-versus-squared-residual plot
`rvfplot`	residual-versus-fitted plot
`rvpplot`	residual-versus-predictor plot

These commands are not appropriate after the `svy` prefix.

For information about these commands, see below.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

For postestimation tests specific to time series, see [R] **regress postestimation time series**.

Special-interest postestimation commands

These commands provide tools for diagnosing sensitivity to individual observations, analyzing residuals, and assessing specification.

`dfbeta` will calculate one, more than one, or all the DFBETAs after `regress`. Although `predict` will also calculate DFBETAs, `predict` can do this for only one variable at a time. `dfbeta` is a convenience tool for those who want to calculate DFBETAs for multiple variables. The names for the new variables created are chosen automatically and begin with the letters `_dfbeta_`.

`estat hettest` performs three versions of the Breusch–Pagan (1979) and Cook–Weisberg (1983) test for heteroskedasticity. All three versions of this test present evidence against the null hypothesis that $\mathbf{t} = \mathbf{0}$ in $\mathrm{Var}(e) = \sigma^2\exp(\mathbf{zt})$. In the `normal` version, performed by default, the null hypothesis also includes the assumption that the regression disturbances are independent-normal draws with variance σ^2. The normality assumption is dropped from the null hypothesis in the `iid` and `fstat` versions, which respectively produce the score and F tests discussed in *Methods and formulas*. If *varlist* is not specified, the fitted values are used for $\mathbf{z}$. If *varlist* or the `rhs` option is specified, the variables specified are used for $\mathbf{z}$.

`estat imtest` performs an information matrix test for the regression model and an orthogonal decomposition into tests for heteroskedasticity, skewness, and kurtosis due to Cameron and Trivedi (1990);

White's test for homoskedasticity against unrestricted forms of heteroskedasticity (1980) is available as an option. White's test is usually similar to the first term of the Cameron–Trivedi decomposition.

`estat ovtest` performs two versions of the Ramsey (1969) regression specification-error test (RESET) for omitted variables. This test amounts to fitting $y = \mathbf{xb} + \mathbf{zt} + u$ and then testing $\mathbf{t} = \mathbf{0}$. If the `rhs` option is not specified, powers of the fitted values are used for $\mathbf{z}$. If `rhs` is specified, powers of the individual elements of $\mathbf{x}$ are used.

`estat szroeter` performs Szroeter's rank test for heteroskedasticity for each of the variables in *varlist* or for the explanatory variables of the regression if `rhs` is specified.

`estat vif` calculates the centered or uncentered variance inflation factors (VIFs) for the independent variables specified in a linear regression model.

`acprplot` graphs an augmented component-plus-residual plot (a.k.a. augmented partial residual plot) as described by Mallows (1986). This seems to work better than the component-plus-residual plot for identifying nonlinearities in the data.

`avplot` graphs an added-variable plot (a.k.a. partial-regression leverage plot, partial regression plot, or adjusted partial residual plot) after `regress`. *indepvar* may be an independent variable (a.k.a. predictor, carrier, or covariate) that is currently in the model or not.

`avplots` graphs all the added-variable plots in one image.

`cprplot` graphs a component-plus-residual plot (a.k.a. partial residual plot) after `regress`. *indepvar* must be an independent variable that is currently in the model.

`lvr2plot` graphs a leverage-versus-squared-residual plot (a.k.a. L-R plot).

`rvfplot` graphs a residual-versus-fitted plot, a graph of the residuals against the fitted values.

`rvpplot` graphs a residual-versus-predictor plot (a.k.a. independent variable plot or carrier plot), a graph of the residuals against the specified predictor.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic]
```

statistic	Description
Main	
`xb`	linear prediction; the default
`residuals`	residuals
`score`	score; equivalent to `residuals`
`rstandard`	standardized residuals
`rstudent`	Studentized (jackknifed) residuals
`cooksd`	Cook's distance
`leverage` | `hat`	leverage (diagonal elements of hat matrix)
`pr(`*a*`,`*b*`)`	$\Pr(y_j \mid a < y_j < b)$
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$
* `dfbeta(`*varname*`)`	DFBETA for *varname*
`stdp`	standard error of the linear prediction
`stdf`	standard error of the forecast
`stdr`	standard error of the residual
* `covratio`	COVRATIO
* `dfits`	DFITS
* `welsch`	Welsch distance

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

`rstandard`, `rstudent`, `cooksd`, `leverage`, `dfbeta()`, `stdf`, `stdr`, `covratio`, `dfits`, and `welsch` are not available if any `vce()` other than `vce(ols)` was specified with `regress`.

`xb`, `residuals`, `score`, and `stdp` are the only options allowed with `svy` estimation results.

where *a* and *b* may be numbers or variables; *a* missing ($a \geq .$) means $-\infty$, and *b* missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`residuals` calculates the residuals.

`score` is equivalent to `residuals` in linear regression.

`rstandard` calculates the standardized residuals.

`rstudent` calculates the Studentized (jackknifed) residuals.

`cooksd` calculates the Cook's D influence statistic (Cook 1977).

`leverage` or `hat` calculates the diagonal elements of the projection hat matrix.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \mid a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated.
a and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`dfbeta(`*varname*`)` calculates the DFBETA for *varname*, the difference between the regression coefficient when the jth observation is included and excluded, said difference being scaled by the estimated standard error of the coefficient. *varname* must have been included among the regressors in the previously fitted model. The calculation is automatically restricted to the estimation subsample.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas*.

`stdr` calculates the standard error of the residuals.

`covratio` calculates COVRATIO (Belsley, Kuh, and Welsch 1980), a measure of the influence of the jth observation based on considering the effect on the variance–covariance matrix of the estimates. The calculation is automatically restricted to the estimation subsample.

`dfits` calculates DFITS (Welsch and Kuh 1977) and attempts to summarize the information in the leverage versus residual-squared plot into one statistic. The calculation is automatically restricted to the estimation subsample.

`welsch` calculates Welsch distance (Welsch 1982) and is a variation on `dfits`. The calculation is automatically restricted to the estimation subsample.

Syntax for dfbeta

`dfbeta` [*indepvar* [*indepvar* [...]]] [`, stub(`*name*`)`]

Menu

Statistics > Linear models and related > Regression diagnostics > DFBETAs

Option for dfbeta

`stub(`*name*`)` specifies the leading characters `dfbeta` uses to name the new variables to be generated. The default is `stub(_dfbeta_)`.

Syntax for estat hettest

`estat hettest` [*varlist*] [`, rhs` [`normal` | `iid` | `fstat`] `mtest` [`(`*spec*`)`]]

Menu

Statistics > Postestimation > Reports and statistics

Options for estat hettest

`rhs` specifies that tests for heteroskedasticity be performed for the right-hand-side (explanatory) variables of the fitted regression model. The `rhs` option may be combined with a *varlist*.

`normal`, the default, causes `estat hettest` to compute the original Breusch–Pagan/Cook–Weisberg test, which assumes that the regression disturbances are normally distributed.

`iid` causes `estat hettest` to compute the $N * R^2$ version of the score test that drops the normality assumption.

`fstat` causes `estat hettest` to compute the F-statistic version that drops the normality assumption.

`mtest` [`(`*spec*`)`] specifies that multiple testing be performed. The argument specifies how p-values are adjusted. The following specifications, *spec*, are supported:

`bonferroni`	Bonferroni's multiple testing adjustment
`holm`	Holm's multiple testing adjustment
`sidak`	Šidák's multiple testing adjustment
`noadjust`	no adjustment is made for multiple testing

`mtest` may be specified without an argument. This is equivalent to specifying `mtest(noadjust)`; that is, tests for the individual variables should be performed with unadjusted p-values. By default, `estat hettest` does not perform multiple testing. `mtest` may not be specified with `iid` or `fstat`.

Syntax for estat imtest

`estat imtest` [`, preserve white`]

Menu

Statistics > Postestimation > Reports and statistics

Options for estat imtest

`preserve` specifies that the data in memory be preserved, all variables and cases that are not needed in the calculations be dropped, and at the conclusion the original data be restored. This option is costly for large datasets. However, because `estat imtest` has to perform an auxiliary regression on $k(k+1)/2$ temporary variables, where k is the number of regressors, it may not be able to perform the test otherwise.

`white` specifies that White's original heteroskedasticity test also be performed.

Syntax for estat ovtest

```
estat ovtest [ , rhs ]
```

Menu

Statistics > Postestimation > Reports and statistics

Option for estat ovtest

`rhs` specifies that powers of the right-hand-side (explanatory) variables be used in the test rather than powers of the fitted values.

Syntax for estat szroeter

```
estat szroeter [ varlist ] [ , rhs mtest(spec) ]
```

Either *varlist* or `rhs` must be specified.

Menu

Statistics > Postestimation > Reports and statistics

Options for estat szroeter

`rhs` specifies that tests for heteroskedasticity be performed for the right-hand-side (explanatory) variables of the fitted regression model. Option `rhs` may be combined with a *varlist*.

`mtest(`*spec*`)` specifies that multiple testing be performed. The argument specifies how p-values are adjusted. The following specifications, *spec*, are supported:

`bonferroni`	Bonferroni's multiple testing adjustment
`holm`	Holm's multiple testing adjustment
`sidak`	Šidák's multiple testing adjustment
`noadjust`	no adjustment is made for multiple testing

`estat szroeter` always performs multiple testing. By default, it does not adjust the p-values.

Syntax for estat vif

```
estat vif [, uncentered]
```

Menu

Statistics > Postestimation > Reports and statistics

Option for estat vif

`uncentered` requests that the computation of the uncentered variance inflation factors. This option is often used to detect the collinearity of the regressors with the constant. `estat vif, uncentered` may be used after regression models fit without the constant term.

Syntax for acprplot

```
acprplot indepvar [, acprplot_options]
```

acprplot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Options	
`lowess`	add a lowess smooth of the plotted points
`lsopts(`*lowess_options*`)`	affect rendition of the lowess smooth
`mspline`	add median spline of the plotted points
`msopts(`*mspline_options*`)`	affect rendition of the spline
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Augmented component-plus-residual plot

Options for acprplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line. See [G-3] ***cline_options***.

Options

`lowess` adds a lowess smooth of the plotted points to assist in detecting nonlinearities.

`lsopts(`*lowess_options*`)` affects the rendition of the lowess smooth. For an explanation of these options, especially the `bwidth()` option, see [R] **lowess**. Specifying `lsopts()` implies the `lowess` option.

`mspline` adds a median spline of the plotted points to assist in detecting nonlinearities.

`msopts(`*mspline_options*`)` affects the rendition of the spline. For an explanation of these options, especially the `bands()` option, see [G-2] **graph twoway mspline**. Specifying `msopts()` implies the `mspline` option.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for avplot

`avplot` *indepvar* [`,` *avplot_options*]

avplot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Added-variable plot

Options for avplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line. See [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for avplots

`avplots` [`,` *avplots_options*]

avplots_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
combine_options	any of the options documented in [G-2] **graph combine**
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Added-variable plot

Options for avplots

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

combine_options are any of the options documented in [G-2] **graph combine**. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line. See [G-3] ***cline_options***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for cprplot

`cprplot` *indepvar* [`,` *cprplot_options*]

cprplot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Options	
`lowess`	add a lowess smooth of the plotted points
`lsopts(`*lowess_options*`)`	affect rendition of the lowess smooth
`mspline`	add median spline of the plotted points
`msopts(`*mspline_options*`)`	affect rendition of the spline
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Component-plus-residual plot

Options for cprplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line. See [G-3] ***cline_options***.

Options

`lowess` adds a lowess smooth of the plotted points to assist in detecting nonlinearities.

`lsopts(`*lowess_options*`)` affects the rendition of the lowess smooth. For an explanation of these options, especially the `bwidth()` option, see [R] **lowess**. Specifying `lsopts()` implies the `lowess` option.

`mspline` adds a median spline of the plotted points to assist in detecting nonlinearities.

`msopts(`*mspline_options*`)` affects the rendition of the spline. For an explanation of these options, especially the `bands()` option, see [G-2] **graph twoway mspline**. Specifying `msopts()` implies the `mspline` option.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for lvr2plot

`lvr2plot` [`,` *lvr2plot_options*]

lvr2plot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Leverage-versus-squared-residual plot

Options for lvr2plot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for rvfplot

`rvfplot` [`,` *rvfplot_options*]

rvfplot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Add plots	
`addplot(`*plot*`)`	add plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Residual-versus-fitted plot

Options for rvfplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Add plots

`addplot(`*plot*`)` provides a way to add plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Syntax for rvpplot

`rvpplot` *indepvar* [`,` *rvpplot_options*]

rvpplot_options	Description
Plot	
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Linear models and related > Regression diagnostics > Residual-versus-predictor plot

Options for rvpplot

Plot

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

marker_label_options specify if and how the markers are to be labeled; see [G-3] ***marker_label_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Remarks are presented under the following headings:

Fitted values and residuals
Prediction standard errors
Prediction with weighted data
Residual-versus-fitted plots
Added-variable plots
Component-plus-residual plots
Residual-versus-predictor plots
Leverage statistics
L-R plots
Standardized and Studentized residuals
DFITS, Cook's Distance, and Welsch Distance
COVRATIO
DFBETAs
Formal tests for violations of assumptions
Variance inflation factors

Many of these commands concern identifying influential data in linear regression. This is, unfortunately, a field that is dominated by jargon, codified and partially begun by Belsley, Kuh, and Welsch (1980). In the words of Chatterjee and Hadi (1986, 416), "Belsley, Kuh, and Welsch's book, *Regression Diagnostics*, was a very valuable contribution to the statistical literature, but it unleashed on an unsuspecting statistical community a computer speak (à la Orwell), the likes of which we have never seen." Things have only gotten worse since then. Chatterjee and Hadi's (1986, 1988) own attempts to clean up the jargon did not improve matters (see Hoaglin and Kempthorne [1986], Velleman [1986], and Welsch [1986]). We apologize for the jargon, and for our contribution to the jargon in the form of inelegant command names, we apologize most of all.

Model *sensitivity* refers to how estimates are affected by subsets of our data. Imagine data on y and x, and assume that the data are to be fit by the regression $y_i = \alpha + \beta x_i + \epsilon_i$. The regression estimates of α and β are a and b, respectively. Now imagine that the estimated a and b would be different if a small portion of the dataset, perhaps even one observation, were deleted. As a data analyst, you would like to think that you are summarizing tendencies that apply to all the data, but you have just been told that the model you fit is unduly influenced by one point or just a few points and that, as a matter of fact, there is another model that applies to the rest of the data—a model that you have ignored. The search for subsets of the data that, if deleted, would change the results markedly is a predominant theme of this entry.

There are three key issues in identifying model sensitivity to individual observations, which go by the names *residuals*, *leverage*, and *influence*. In our $y_i = a + bx_i + e_i$ regression, the residuals are, of course, e_i—they reveal how much our fitted value $\widehat{y}_i = a + bx_i$ differs from the observed y_i. A point (x_i, y_i) with a corresponding large residual is called an outlier. Say that you are interested in outliers because you somehow think that such points will exert undue influence on your estimates. Your feelings are generally right, but there are exceptions. A point might have a huge residual and yet not affect the estimated b at all. Nevertheless, studying observations with large residuals almost always pays off.

(x_i, y_i) can be an outlier in another way—just as y_i can be far from $\widehat{y}_i$, x_i can be far from the center of mass of the other x's. Such an "outlier" should interest you just as much as the more traditional outliers. Picture a scatterplot of y against x with thousands of points in some sort of mass at the lower left of the graph and one point at the upper right of the graph. Now run a regression line through the points—the regression line will come close to the point at the upper right of the graph and may in fact, go through it. That is, this isolated point will not appear as an outlier as measured by residuals because its residual will be small. Yet this point might have a dramatic effect on our resulting estimates in the sense that, were you to delete the point, the estimates would change

markedly. Such a point is said to have high leverage. Just as with traditional outliers, a high leverage point does not necessarily have an undue effect on regression estimates, but if it does not, it is more the exception than the rule.

Now all this is a most unsatisfactory state of affairs. Points with large residuals may, but need not, have a large effect on our results, and points with small residuals may still have a large effect. Points with high leverage may, but need not, have a large effect on our results, and points with low leverage may still have a large effect. Can you not identify the influential points and simply have the computer list them for you? You can, but you will have to define what you mean by "influential".

"Influential" is defined with respect to some statistic. For instance, you might ask which points in your data have a large effect on your estimated a, which points have a large effect on your estimated b, which points have a large effect on your estimated standard error of b, and so on, but do not be surprised when the answers to these questions are different. In any case, obtaining such measures is not difficult—all you have to do is fit the regression excluding each observation one at a time and record the statistic of interest which, in the day of the modern computer, is not too onerous. Moreover, you can save considerable computer time by doing algebra ahead of time and working out formulas that will calculate the same answers as if you ran each of the regressions. (Ignore the question of pairs of observations that, together, exert undue influence, and triples, and so on, which remains largely unsolved and for which the brute force fit-every-possible-regression procedure is not a viable alternative.)

Fitted values and residuals

Typing `predict` *newvar* with no options creates *newvar* containing the fitted values. Typing `predict` *newvar*`, resid` creates *newvar* containing the residuals.

▷ Example 1

Continuing with example 1 from [R] **regress**, we wish to fit the following model:

$$\texttt{mpg} = \beta_0 + \beta_1\texttt{weight} + \beta_2\texttt{weight}^2 + \beta_3\texttt{foreign} + \epsilon$$

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight c.weight#c.weight foreign
```

Source	SS	df	MS		
Model	1689.15372	3	563.05124	Number of obs	= 74
Residual	754.30574	70	10.7757963	F(3, 70)	= 52.25
				Prob > F	= 0.0000
				R-squared	= 0.6913
				Adj R-squared	= 0.6781
Total	2443.45946	73	33.4720474	Root MSE	= 3.2827

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0165729	.0039692	-4.18	0.000	-.0244892	-.0086567
c.weight# c.weight	1.59e-06	6.25e-07	2.55	0.013	3.45e-07	2.84e-06
foreign	-2.2035	1.059246	-2.08	0.041	-4.3161	-.0909002
_cons	56.53884	6.197383	9.12	0.000	44.17855	68.89913

That done, we can now obtain the predicted values from the regression. We will store them in a new variable called pmpg by typing predict pmpg. Because predict produces no output, we will follow that by summarizing our predicted and observed values.

```
. predict pmpg
(option xb assumed; fitted values)
. summarize pmpg mpg
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
        pmpg |         74     21.2973    4.810311   13.59953   31.86288
         mpg |         74     21.2973    5.785503         12         41
```

◁

▷ Example 2: Out-of-sample predictions

We can just as easily obtain predicted values from the model by using a wholly different dataset from the one on which the model was fit. The only requirement is that the data have the necessary variables, which here are weight and foreign.

Using the data on two new cars (the Pontiac Sunbird and the Volvo 260) from the newautos.dta dataset, we can obtain out-of-sample predictions (or forecasts) by typing

```
. use http://www.stata-press.com/data/r12/newautos, clear
(New Automobile Models)
. predict pmpg
(option xb assumed; fitted values)
. list, divider
```

	make	weight	foreign	pmpg
1.	Pont. Sunbird	2690	Domestic	23.47137
2.	Volvo 260	3170	Foreign	17.78846

The Pontiac Sunbird has a predicted mileage rating of 23.5 mpg, whereas the Volvo 260 has a predicted rating of 17.8 mpg. In comparison, the actual mileage ratings are 24 for the Pontiac and 17 for the Volvo.

◁

Prediction standard errors

predict can calculate the standard error of the forecast (stdf option), the standard error of the prediction (stdp option), and the standard error of the residual (stdr option). It is easy to confuse stdf and stdp because both are often called the prediction error. Consider the prediction $\widehat{y}_j = \mathbf{x}_j\mathbf{b}$, where $\mathbf{b}$ is the estimated coefficient (column) vector and $\mathbf{x}_j$ is a (row) vector of independent variables for which you want the prediction. First, $\widehat{y}_j$ has a variance due to the variance of the estimated coefficient vector $\mathbf{b}$,

$$\mathrm{Var}(\widehat{y}_j) = \mathrm{Var}(\mathbf{x}_j\mathbf{b}) = s^2 h_j$$

where $h_j = \mathbf{x}_j(\mathbf{X}'\mathbf{X})^{-1}\mathbf{x}_j'$ and s^2 is the mean squared error of the regression. Do not panic over the algebra—just remember that $\mathrm{Var}(\widehat{y}_j) = s^2 h_j$, whatever s^2 and h_j are. stdp calculates this quantity. This is the error in the prediction due to the uncertainty about $\mathbf{b}$.

If you are about to hand this number out as your forecast, however, there is another error. According to your model, the true value of y_j is given by

$$y_j = \mathbf{x}_j\mathbf{b} + \epsilon_j = \widehat{y}_j + \epsilon_j$$

and thus the $\mathrm{Var}(y_j) = \mathrm{Var}(\widehat{y}_j) + \mathrm{Var}(\epsilon_j) = s^2h_j + s^2$, which is the square of `stdf`. `stdf`, then, is the sum of the error in the prediction plus the residual error.

`stdr` has to do with an analysis-of-variance decomposition of s^2, the estimated variance of y. The standard error of the prediction is s^2h_j, and therefore $s^2h_j + s^2(1 - h_j) = s^2$ decomposes s^2 into the prediction and residual variances.

▷ Example 3: standard error of the forecast

Returning to our model of `mpg` on `weight`, `weight`^{2}, and `foreign`, we previously predicted the mileage rating for the Pontiac Sunbird and Volvo 260 as 23.5 and 17.8 mpg, respectively. We now want to put a standard error around our forecast. Remember, the data for these two cars were in `newautos.dta`:

```
. use http://www.stata-press.com/data/r12/newautos, clear
(New Automobile Models)
. predict pmpg
(option xb assumed; fitted values)
. predict se_pmpg, stdf
. list, divider
```

	make	weight	foreign	pmpg	se_pmpg
1.	Pont. Sunbird	2690	Domestic	23.47137	3.341823
2.	Volvo 260	3170	Foreign	17.78846	3.438714

Thus an approximate 95% confidence interval for the mileage rating of the Volvo 260 is $17.8 \pm 2 \cdot 3.44 = [\,10.92, 24.68\,]$.

◁

Prediction with weighted data

`predict` can be used after frequency-weighted (`fweight`) estimation, just as it is used after unweighted estimation. The technical note below concerns the use of `predict` after analytically weighted (`aweight`) estimation.

❑ Technical note

After analytically weighted estimation, `predict` is willing to calculate only the prediction (no options), residual (`residual` option), standard error of the prediction (`stdp` option), and diagonal elements of the projection matrix (`hat` option). Moreover, the results produced by `hat` need to be adjusted, as will be described. For analytically weighted estimation, the standard error of the forecast and residuals, the standardized and Studentized residuals, and Cook's D are not statistically well-defined concepts.

To obtain the correct values of the diagonal elements of the hat matrix, you can use `predict` with the `hat` option to make a first, partially adjusted calculation, and then follow that by completing the adjustment. Assume that you are fitting a linear regression model weighting the data with the variable `w` (`[aweight=w]`). Begin by creating a new variable, `w0`:

```
. predict resid if e(sample), resid
. summarize w if resid < . & e(sample)
. gen w0=w/r(mean)
```

Some caution is necessary at this step—the `summarize w` must be performed on the same sample that was used to fit the model, which means that you must include `if e(sample)` to restrict the prediction to the estimation sample. You created the residual and then included the modifier '`if resid < .`' so that if the dependent variable or any of the independent variables is missing, the corresponding observations will be excluded from the calculation of the average value of the original weight.

To correct `predict`'s `hat` calculation, multiply the result by `w0`:

```
. predict myhat, hat
. replace myhat = w0 * myhat
```

❑

Residual-versus-fitted plots

▷ Example 4: rvfplot

Using the automobile dataset described in [U] **1.2.2 Example datasets**, we will use `regress` to fit a model of `price` on `weight`, `mpg`, `foreign`, and the interaction of `foreign` with `mpg`. We specify `foreign##c.mpg` to obtain the interaction of `foreign` with `mpg`; see [U] **11.4.3 Factor variables**.

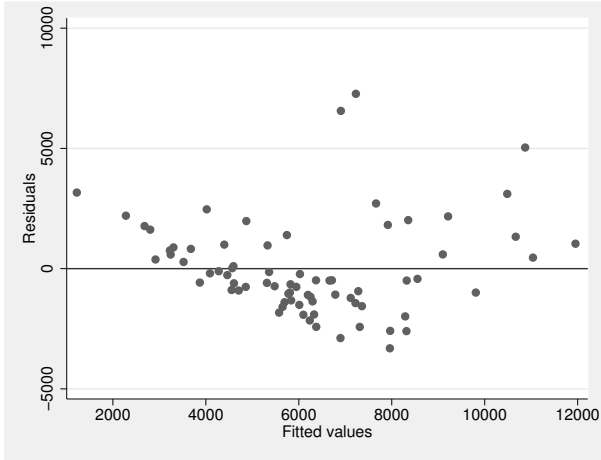
```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. regress price weight foreign##c.mpg
```

Source	SS	df	MS	Number of obs =	74
				F(4, 69) =	21.22
Model	350319665	4	87579916.3	Prob > F =	0.0000
Residual	284745731	69	4126749.72	R-squared =	0.5516
				Adj R-squared =	0.5256
Total	635065396	73	8699525.97	Root MSE =	2031.4

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	4.613589	.7254961	6.36	0.000	3.166263	6.060914
1.foreign	11240.33	2751.681	4.08	0.000	5750.878	16729.78
mpg	263.1875	110.7961	2.38	0.020	42.15527	484.2197
foreign# c.mpg 1	-307.2166	108.5307	-2.83	0.006	-523.7294	-90.70368
_cons	-14449.58	4425.72	-3.26	0.002	-23278.65	-5620.51

Once we have fit a model, we may use any of the regression diagnostics commands. `rvfplot` (read residual-versus-fitted plot) graphs the residuals against the fitted values:

```
. rvfplot, yline(0)
```



All the diagnostic plot commands allow the `graph twoway` and `graph twoway scatter` options; we specified a `yline(0)` to draw a line across the graph at $y = 0$; see [G-2] **graph twoway scatter**.

In a well-fitted model, there should be no pattern to the residuals plotted against the fitted values—something not true of our model. Ignoring the two outliers at the top center of the graph, we see curvature in the pattern of the residuals, suggesting a violation of the assumption that `price` is linear in our independent variables. We might also have seen increasing or decreasing variation in the residuals—heteroskedasticity. Any pattern whatsoever indicates a violation of the least-squares assumptions.

◁

Added-variable plots

▷ Example 5: avplot

We continue with our price model, and another diagnostic graph is provided by `avplot` (read added-variable plot, also known as the partial-regression leverage plot).

One of the wonderful features of one-regressor regressions (regressions of y on one x) is that we can graph the data and the regression line. There is no easier way to understand the regression than to examine such a graph. Unfortunately, we cannot do this when we have more than one regressor. With two regressors, it is still theoretically possible—the graph must be drawn in three dimensions, but with three or more regressors no graph is possible.

The added-variable plot is an attempt to project multidimensional data back to the two-dimensional world for each of the original regressors. This is, of course, impossible without making some concessions. Call the coordinates on an added-variable plot y and x. The added-variable plot has the following properties:

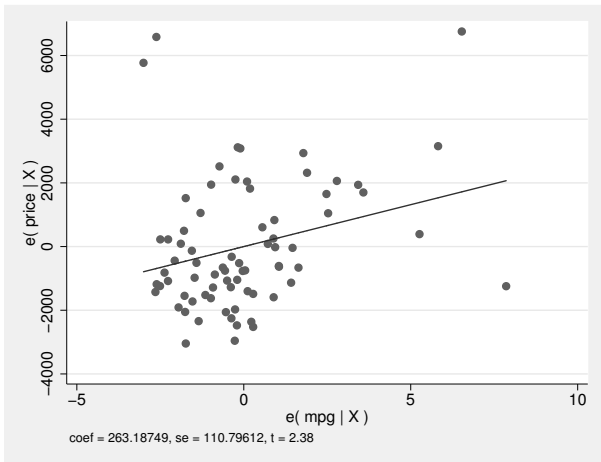
- There is a one-to-one correspondence between (x_i, y_i) and the ith observation used in the original regression.
- A regression of y on x has the same coefficient and standard error (up to a degree-of-freedom adjustment) as the estimated coefficient and standard error for the regressor in the original regression.

- The "outlierness" of each observation in determining the slope is in some sense preserved.

It is equally important to note the properties that are not listed. The y and x coordinates of the added-variable plot cannot be used to identify functional form, or, at least, not well (see Mallows [1986]). In the construction of the added-variable plot, the relationship between y and x is forced to be linear.

Let's examine the added-variable plot for `mpg` in our regression of `price` on `weight` and `foreign##c.mpg`:

```
. avplot mpg
```



This graph suggests a problem in determining the coefficient on `mpg`. Were this a one-regressor regression, the two points at the top-left corner and the one at the top right would cause us concern, and so it does in our more complicated multiple-regressor case. To identify the problem points, we retyped our command, modifying it to read `avplot mpg, mlabel(make)`, and discovered that the two cars at the top left are the Cadillac Eldorado and the Lincoln Versailles; the point at the top right is the Cadillac Seville. These three cars account for 100% of the luxury cars in our data, suggesting that our model is misspecified. By the way, the point at the lower right of the graph, also cause for concern, is the Plymouth Arrow, our data-entry error.

◁

❑ Technical note

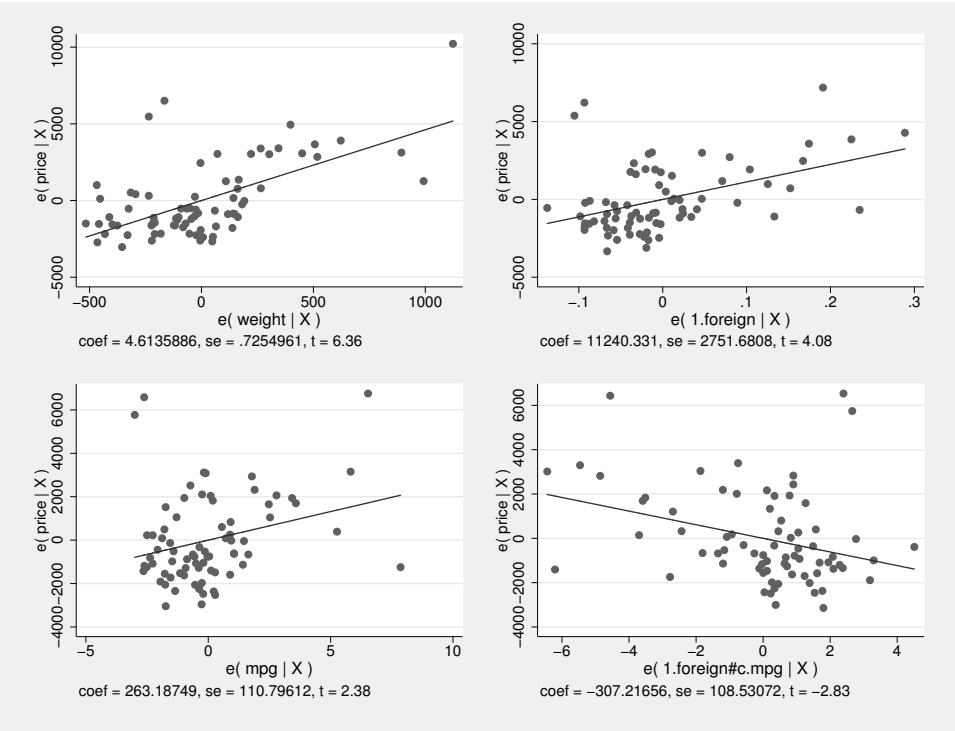
Stata's `avplot` command can be used with regressors already in the model, as we just did, or with potential regressors not yet in the model. In either case, `avplot` will produce the correct graph. The name "added-variable plot" is unfortunate in the case when the variable is already among the list of regressors but is, we think, still preferable to the name "partial-regression leverage plot" assigned by Belsley, Kuh, and Welsch (1980, 30) and more in the spirit of the original use of such plots by Mosteller and Tukey (1977, 271–279). Welsch (1986, 403), however, disagrees: "I am sorry to see that Chatterjee and Hadi [1986] endorse the term 'added-variable plot' when X_j is part of the original model" and goes on to suggest the name "adjusted partial residual plot".

❑

▷ Example 6: avplots

Added-variable plots are so useful that we should look at them for every regressor in the data. `avplots` makes this easy:

```
. avplots
```



◁

Component-plus-residual plots

Added-variable plots are successful at identifying outliers, but they cannot be used to identify functional form. The component-plus-residual plot (Ezekiel 1924; Larsen and McCleary 1972) is another attempt at projecting multidimensional data into a two-dimensional form, but with different properties. Although the added-variable plot can identify outliers, the component-plus-residual plot cannot. It can, however, be used to examine the functional-form assumptions of the model. Both plots have the property that a regression line through the coordinates has a slope equal to the estimated coefficient in the regression model.

▷ Example 7: cprplot and acprplot

To illustrate these plots, we begin with a different model:

```
. use http://www.stata-press.com/data/r12/auto1, clear
(Automobile Models)

. regress price mpg weight
```

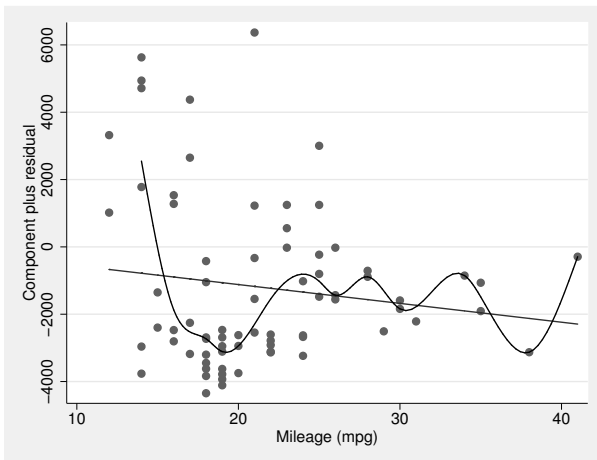
Source	SS	df	MS	Number of obs =	74
				F(2, 71) =	14.90
Model	187716578	2	93858289	Prob > F =	0.0000
Residual	447348818	71	6300687.58	R-squared =	0.2956
				Adj R-squared =	0.2757
Total	635065396	73	8699525.97	Root MSE =	2510.1

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
mpg	-55.9393	75.24136	-0.74	0.460	-205.9663	94.08771
weight	1.710992	.5861682	2.92	0.005	.5422063	2.879779
_cons	2197.9	3190.768	0.69	0.493	-4164.311	8560.11

In fact, we know that the effects of `mpg` in this model are nonlinear—if we added `mpg` squared to the model, its coefficient would have a t statistic of 2.38, the t statistic on `mpg` would become -2.48, and `weight`'s effect would become about one-third of its current value and become statistically insignificant. Pretend that we do not know this.

The component-plus-residual plot for `mpg` is

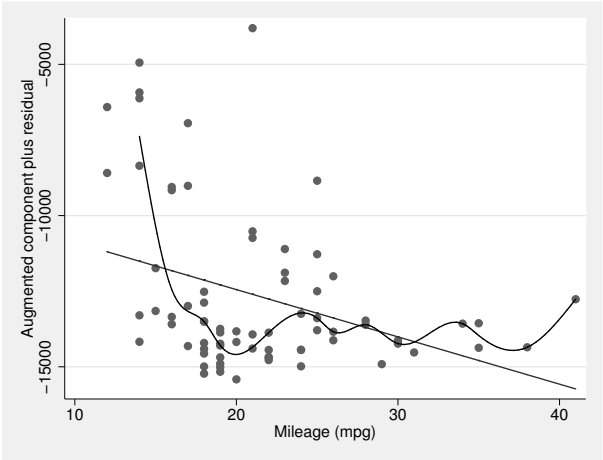
```
. cprplot mpg, mspline msopts(bands(13))
```



We are supposed to examine the above graph for nonlinearities or, equivalently, ask if the regression line, which has slope equal to the estimated effect of `mpg` in the original model, fits the data adequately. To assist our eyes, we added a median spline. Perhaps some people may detect nonlinearity from this graph, but we assert that if we had not previously revealed the nonlinearity of `mpg` and if we had not added the median spline, the graph would not overly bother us.

Mallows (1986) proposed an augmented component-plus-residual plot that is often more sensitive to detecting nonlinearity:

```
. acprplot mpg, mspline msopts(bands(13))
```



It does do somewhat better.

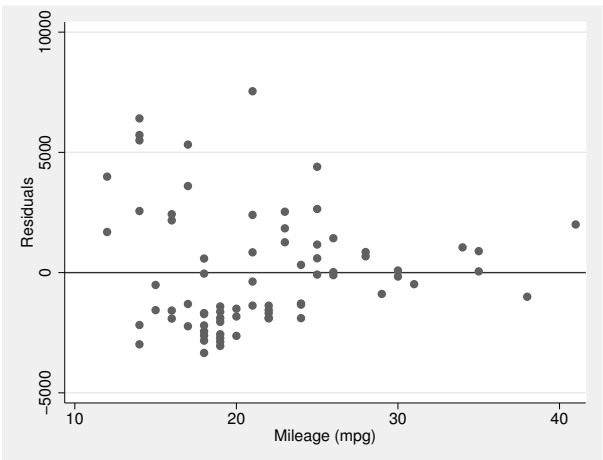
◁

Residual-versus-predictor plots

▷ Example 8: rvpplot

The residual-versus-predictor plot is a simple way to look for violations of the regression assumptions. If the assumptions are correct, there should be no pattern in the graph. Using our `price` on `mpg` and `weight` model, we type

```
. rvpplot mpg, yline(0)
```



Remember, any pattern counts as a problem, and in this graph, we see that the variation in the residuals decreases as `mpg` increases.

◁

Leverage statistics

In addition to providing fitted values and the associated standard errors, the `predict` command can also be used to generate various statistics used to detect the influence of individual observations. This section provides a brief introduction to leverage (hat) statistics, and some of the following subsections discuss other influence statistics produced by `predict`.

▷ Example 9: diagonal elements of projection matrix

The diagonal elements of the projection matrix, obtained by the `hat` option, are a measure of distance in explanatory variable space. `leverage` is a synonym for `hat`.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight c.weight#c.weight foreign
  (output omitted)
. predict xdist, hat
. summarize xdist, detail
                        Leverage
-------------------------------------------------------------
      Percentiles      Smallest
 1%     .0251334       .0251334
 5%     .0255623       .0251334
10%     .0259213       .0253883       Obs                  74
25%     .0278442       .0255623       Sum of Wgt.          74
50%       .04103                      Mean           .0540541
                       Largest        Std. Dev.      .0459218
75%     .0631279       .1593606
90%     .0854584       .1593606       Variance       .0021088
95%     .1593606       .2326124       Skewness       3.440809
99%     .3075759       .3075759       Kurtosis       16.95135
```

Some 5% of our sample has an `xdist` measure in excess of 0.15. Let's force them to reveal their identities:

```
. list foreign make mpg if xdist>.15, divider
```

	foreign	make	mpg
24.	Domestic	Ford Fiesta	28
26.	Domestic	Linc. Continental	12
27.	Domestic	Linc. Mark V	12
43.	Domestic	Plym. Champ	34

To understand why these cars are on this list, we must remember that the explanatory variables in our model are `weight` and `foreign` and that `xdist` measures distance in this metric. The Ford Fiesta and the Plymouth Champ are the two lightest domestic cars in our data. The Lincolns are the two heaviest domestic cars.

◁

L-R plots

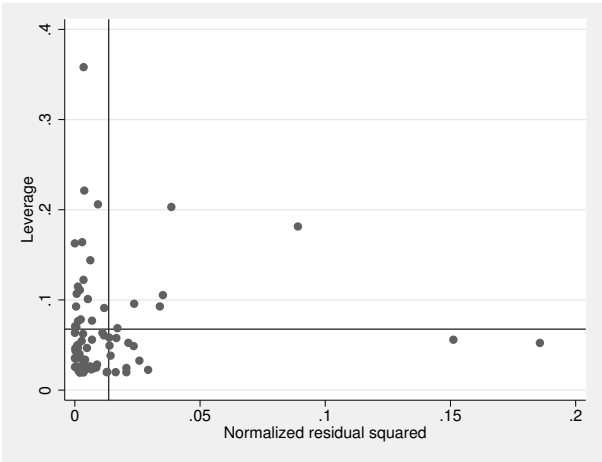
▷ Example 10: lvr2plot

One of the most useful diagnostic graphs is provided by `lvr2plot` (leverage-versus-residual-squared plot), a graph of leverage against the (normalized) residuals squared.

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. regress price weight foreign##c.mpg
```

(*output omitted*)

```
. lvr2plot
```

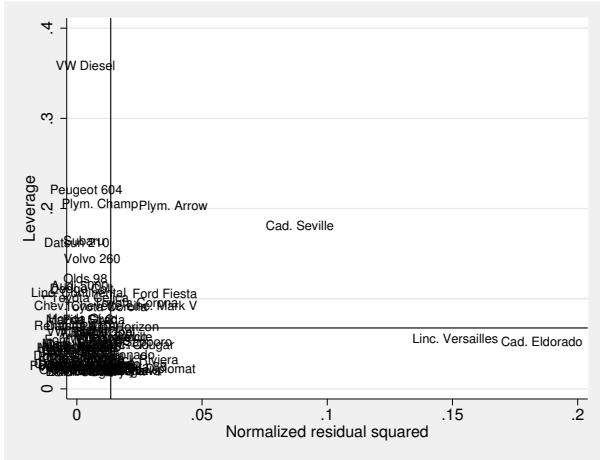


The lines on the chart show the average values of leverage and the (normalized) residuals squared. Points above the horizontal line have higher-than-average leverage; points to the right of the vertical line have larger-than-average residuals.

One point immediately catches our eye, and four more make us pause. The point at the top of the graph has high leverage and a smaller-than-average residual. The other points that bother us all have higher-than-average leverage, two with smaller-than-average residuals and two with larger-than-average residuals.

A less pretty but more useful version of the above graph specifies that `make` be used as the symbol (see [G-3] ***marker_label_options***):

```
. lvr2plot, mlabel(make) mlabp(0) m(none) mlabsize(small)
```



The VW Diesel, Plymouth Champ, Plymouth Arrow, and Peugeot 604 are the points that cause us the most concern. When we further examine our data, we discover that the VW Diesel is the only diesel in our data and that the data for the Plymouth Arrow were entered incorrectly into the computer. No such simple explanations were found for the Plymouth Champ and Peugeot 604.

◁

Standardized and Studentized residuals

The terms standardized and Studentized residuals have meant different things to different authors. In Stata, `predict` defines the standardized residual as $\widehat{e}_i = e_i/(s\sqrt{1-h_i})$ and the Studentized residual as $r_i = e_i/(s_{(i)}\sqrt{1-h_i})$, where $s_{(i)}$ is the root mean squared error of a regression with the ith observation removed. Stata's definition of the Studentized residual is the same as the one given in Bollen and Jackman (1990, 264) and is what Chatterjee and Hadi (1988, 74) call the "externally Studentized" residual. Stata's "standardized" residual is the same as what Chatterjee and Hadi (1988, 74) call the "internally Studentized" residual.

Standardized and Studentized residuals are attempts to adjust residuals for their standard errors. Although the ϵ_i theoretical residuals are homoskedastic by assumption (that is, they all have the same variance), the calculated e_i are not. In fact,

$$\mathrm{Var}(e_i) = \sigma^2(1-h_i)$$

where h_i are the leverage measures obtained from the diagonal elements of hat matrix. Thus observations with the greatest leverage have corresponding residuals with the smallest variance.

Standardized residuals use the root mean squared error of the regression for σ. Studentized residuals use the root mean squared error of a regression omitting the observation in question for σ. In general, Studentized residuals are preferable to standardized residuals for purposes of outlier identification. Studentized residuals can be interpreted as the t statistic for testing the significance of a dummy variable equal to 1 in the observation in question and 0 elsewhere (Belsley, Kuh, and Welsch 1980). Such a dummy variable would effectively absorb the observation and so remove its influence in determining the other coefficients in the model. Caution must be exercised here, however, because of the simultaneous testing problem. You cannot simply list the residuals that would be individually significant at the 5% level—their joint significance would be far less (their joint significance *level* would be far greater).

▷ Example 11: standardized and Studentized residuals

In the opening remarks for this entry, we distinguished residuals from leverage and speculated on the impact of an observation with a small residual but large leverage. If we had adjusted the residuals for their standard errors, however, the adjusted residual would have been (relatively) larger and perhaps large enough so that we could simply examine the adjusted residuals. Taking our `price` on `weight` and `foreign##c.mpg` model, we can obtain the in-sample standardized and Studentized residuals by typing

```
. predict esta if e(sample), rstandard
. predict estu if e(sample), rstudent
```

In *L-R plots*, we discovered that the VW Diesel has the highest leverage in our data, but a corresponding small residual. The standardized and Studentized residuals for the VW Diesel are

```
. list make price esta estu if make=="VW Diesel"
```

	make	price	esta	estu
74.	VW Diesel	5,397	.6142691	.6114758

The Studentized residual of 0.611 can be interpreted as the t statistic for including a dummy variable for VW Diesel in our regression. Such a variable would not be significant.

◁

DFITS, Cook's Distance, and Welsch Distance

DFITS (Welsch and Kuh 1977), Cook's Distance (Cook 1977), and Welsch Distance (Welsch 1982) are three attempts to summarize the information in the leverage versus residual-squared plot into one statistic. That is, the goal is to create an index that is affected by the size of the residuals—outliers—and the size of h_i—leverage. Viewed mechanically, one way to write DFITS (Bollen and Jackman 1990, 265) is

$$\text{DFITS}_i = r_i\sqrt{\frac{h_i}{1-h_i}}$$

where r_i are the Studentized residuals. Thus large residuals increase the value of DFITS, as do large values of h_i. Viewed more traditionally, DFITS is a scaled difference between predicted values for the ith case when the regression is fit with and without the ith observation, hence the name.

The mechanical relationship between DFITS and Cook's Distance, D_i (Bollen and Jackman 1990, 266), is

$$D_i = \frac{1}{k}\frac{s^2_{(i)}}{s^2}\text{DFITS}_i^2$$

where k is the number of variables (including the constant) in the regression, s is the root mean squared error of the regression, and $s_{(i)}$ is the root mean squared error when the ith observation is omitted. Viewed more traditionally, D_i is a scaled measure of the distance between the coefficient vectors when the ith observation is omitted.

The mechanical relationship between DFITS and Welsch's Distance, W_i (Chatterjee and Hadi 1988, 123), is

$$W_i = \text{DFITS}_i\sqrt{\frac{n-1}{1-h_i}}$$

The interpretation of W_i is more difficult, as it is based on the empirical influence curve. Although DFITS and Cook's distance are similar, the Welsch distance measure includes another normalization by leverage.

Belsley, Kuh, and Welsch (1980, 28) suggest that DFITS values greater than $2\sqrt{k/n}$ deserve more investigation, and so values of Cook's distance greater than $4/n$ should also be examined (Bollen and Jackman 1990, 265–266). Through similar logic, the cutoff for Welsch distance is approximately $3\sqrt{k}$ (Chatterjee and Hadi 1988, 124).

▷ Example 12: DFITS influence measure

Using our model of `price` on `weight` and `foreign##c.mpg`, we can obtain the DFITS influence measure:

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. regress price weight foreign##c.mpg
  (output omitted)
. predict e if e(sample), resid
. predict dfits, dfits
```

We did not specify `if e(sample)` in computing the DFITS statistic. DFITS is available only over the estimation sample, so specifying `if e(sample)` would have been redundant. It would have done no harm, but it would not have changed the results.

Our model has $k = 5$ independent variables (k includes the constant) and $n = 74$ observations; following the $2\sqrt{k/n}$ cutoff advice, we type

```
. list make price e dfits if abs(dfits) > 2*sqrt(5/74), divider
```

	make	price	e	dfits
12.	Cad. Eldorado	14,500	7271.96	.9564455
13.	Cad. Seville	15,906	5036.348	1.356619
24.	Ford Fiesta	4,389	3164.872	.5724172
27.	Linc. Mark V	13,594	3109.193	.5200413
28.	Linc. Versailles	13,466	6560.912	.8760136
42.	Plym. Arrow	4,647	-3312.968	-.9384231

We calculate Cook's distance and list the observations greater than the suggested $4/n$ cutoff:

```
. predict cooksd if e(sample), cooksd
. list make price e cooksd if cooksd > 4/74, divider
```

	make	price	e	cooksd
12.	Cad. Eldorado	14,500	7271.96	.1492676
13.	Cad. Seville	15,906	5036.348	.3328515
24.	Ford Fiesta	4,389	3164.872	.0638815
28.	Linc. Versailles	13,466	6560.912	.1308004
42.	Plym. Arrow	4,647	-3312.968	.1700736

Here we used `if e(sample)` because Cook's distance is not restricted to the estimation sample by default. It is worth comparing this list with the preceding one.

Finally, we use Welsch distance and the suggested $3\sqrt{k}$ cutoff:

```
. predict wd, welsch
. list make price e wd if abs(wd) > 3*sqrt(5), divider
```

	make	price	e	wd
12.	Cad. Eldorado	14,500	7271.96	8.394372
13.	Cad. Seville	15,906	5036.348	12.81125
28.	Linc. Versailles	13,466	6560.912	7.703005
42.	Plym. Arrow	4,647	-3312.968	-8.981481

Here we did not need to specify `if e(sample)` because `welsch` automatically restricts the prediction to the estimation sample.

◁

COVRATIO

COVRATIO (Belsley, Kuh, and Welsch 1980) measures the influence of the ith observation by considering the effect on the variance–covariance matrix of the estimates. The measure is the ratio of the determinants of the covariances matrix, with and without the ith observation. The resulting formula is

$$\text{COVRATIO}_i = \frac{1}{1-h_i}\left(\frac{n-k-\widehat{e}_i^2}{n-k-1}\right)^k$$

where $\widehat{e}_i$ is the standardized residual.

For noninfluential observations, the value of COVRATIO is approximately 1. Large values of the residuals or large values of leverage will cause deviations from 1, although if both are large, COVRATIO may tend back toward 1 and therefore not identify such observations (Chatterjee and Hadi 1988, 139).

Belsley, Kuh, and Welsch (1980) suggest that observations for which

$$|\text{COVRATIO}_i - 1| \geq \frac{3k}{n}$$

are worthy of further examination.

▷ Example 13: COVRATIO influence measure

Using our model of `price` on `weight` and `foreign##c.mpg`, we can obtain the COVRATIO measure and list the observations outside the suggested cutoff by typing

```
. predict covr, covratio
. list make price e covr if abs(covr-1) >= 3*5/74, divider
```

	make	price	e	covr
12.	Cad. Eldorado	14,500	7271.96	.3814242
13.	Cad. Seville	15,906	5036.348	.7386969
28.	Linc. Versailles	13,466	6560.912	.4761695
43.	Plym. Champ	4,425	1621.747	1.27782
53.	Audi 5000	9,690	591.2883	1.206842
57.	Datsun 210	4,589	19.81829	1.284801
64.	Peugeot 604	12,990	1037.184	1.348219
66.	Subaru	3,798	-909.5894	1.264677
71.	VW Diesel	5,397	999.7209	1.630653
74.	Volvo 260	11,995	1327.668	1.211888

The `covratio` option automatically restricts the prediction to the estimation sample.

◁

DFBETAs

DFBETAs are perhaps the most direct influence measure of interest to model builders. DFBETAs focus on one coefficient and measure the difference between the regression coefficient when the ith observation is included and excluded, the difference being scaled by the estimated standard error of the coefficient. Belsley, Kuh, and Welsch (1980, 28) suggest observations with $|\text{DFBETA}_i| > 2/\sqrt{n}$ as deserving special attention, but it is also common practice to use 1 (Bollen and Jackman 1990, 267), meaning that the observation shifted the estimate at least one standard error.

▷ Example 14: DFBETAs influence measure; the dfbeta() option

Using our model of `price` on `weight` and `foreign##c.mpg`, let's first ask which observations have the greatest impact on the determination of the coefficient on `1.foreign`. We will use the suggested $2/\sqrt{n}$ cutoff:

```
. sort foreign make
. predict dfor, dfbeta(1.foreign)
. list make price foreign dfor if abs(dfor) > 2/sqrt(74), divider
```

	make	price	foreign	dfor
12.	Cad. Eldorado	14,500	Domestic	-.5290519
13.	Cad. Seville	15,906	Domestic	.8243419
28.	Linc. Versailles	13,466	Domestic	-.5283729
42.	Plym. Arrow	4,647	Domestic	-.6622424
43.	Plym. Champ	4,425	Domestic	.2371104
64.	Peugeot 604	12,990	Foreign	.2552032
69.	Toyota Corona	5,719	Foreign	-.256431

The Cadillac Seville shifted the coefficient on `1.foreign` 0.82 standard deviations!

Now let us ask which observations have the greatest effect on the mpg coefficient:

```
. predict dmpg, dfbeta(mpg)
. list make price mpg dmpg if abs(dmpg) > 2/sqrt(74), divider
```

	make	price	mpg	dmpg
12.	Cad. Eldorado	14,500	14	-.5970351
13.	Cad. Seville	15,906	21	1.134269
28.	Linc. Versailles	13,466	14	-.6069287
42.	Plym. Arrow	4,647	28	-.8925859
43.	Plym. Champ	4,425	34	.3186909

Once again we see the Cadillac Seville heading the list, indicating that our regression results may be dominated by this one car.

◁

▷ Example 15: DFBETAs influence measure; the dfbeta command

We can use `predict, dfbeta()` or the `dfbeta` command to generate the DFBETAs. `dfbeta` makes up names for the new variables automatically and, without arguments, generates the DFBETAs for all the variables in the regression:

```
. dfbeta
                        _dfbeta_1: dfbeta(weight)
                        _dfbeta_2: dfbeta(1.foreign)
                        _dfbeta_3: dfbeta(mpg)
                        _dfbeta_4: dfbeta(1.foreign#c.mpg)
```

`dfbeta` created four new variables in our dataset: `_dfbeta_1`, containing the DFBETAs for `weight`; `_dfbeta_2`, containing the DFBETAs for `mpg`; and so on. Had we wanted only the DFBETAs for `mpg` and `weight`, we might have typed

```
. dfbeta mpg weight
                        _dfbeta_5: dfbeta(weight)
                        _dfbeta_6: dfbeta(mpg)
```

In the example above, we typed `dfbeta mpg weight` instead of `dfbeta`; if we had typed `dfbeta` followed by `dfbeta mpg weight`, here is what would have happened:

```
. dfbeta
                        _dfbeta_7: dfbeta(weight)
                        _dfbeta_8: dfbeta(1.foreign)
                        _dfbeta_9: dfbeta(mpg)
                       _dfbeta_10: dfbeta(1.foreign#c.mpg)
. dfbeta mpg weight
                       _dfbeta_11: dfbeta(weight)
                       _dfbeta_12: dfbeta(mpg)
```

`dfbeta` would have made up different names for the new variables. `dfbeta` never replaces existing variables—it instead makes up a different name, so we need to pay attention to `dfbeta`'s output.

◁

Formal tests for violations of assumptions

This section introduces some regression diagnostic commands that are designed to test for certain violations that `rvfplot` less formally attempts to detect. `estat ovtest` provides Ramsey's test for omitted variables—a pattern in the residuals. `estat hettest` provides a test for heteroskedasticity—the increasing or decreasing variation in the residuals with fitted values, with respect to the explanatory variables, or with respect to yet other variables. The score test implemented in `estat hettest` (Breusch and Pagan 1979; Cook and Weisberg 1983) performs a score test of the null hypothesis that $b = 0$ against the alternative hypothesis of multiplicative heteroskedasticity. `estat szroeter` provides a rank test for heteroskedasticity, which is an alternative to the score test computed by `estat hettest`. Finally, `estat imtest` computes an information matrix test, including an orthogonal decomposition into tests for heteroskedasticity, skewness, and kurtosis (Cameron and Trivedi 1990). The heteroskedasticity test computed by `estat imtest` is similar to the general test for heteroskedasticity that was proposed by White (1980). Cameron and Trivedi (2010, chap. 3) discuss most of these tests and provides more examples.

▷ Example 16: estat ovtest, estat hettest, estat szroeter, and estat imtest

We run these commands just mentioned on our model:

```
. estat ovtest
Ramsey RESET test using powers of the fitted values of price
       Ho:  model has no omitted variables
                  F(3, 66) =      7.77
                  Prob > F =      0.0002
. estat hettest
Breusch-Pagan / Cook-Weisberg tests for heteroskedasticity
         Ho: Constant variance
         variables: fitted values of price
         chi2(1)      =     6.50
         Prob > chi2  =   0.0108
```

Testing for heteroskedasticity in the right-hand-side variables is requested by specifying the `rhs` option. By specifying the `mtest(bonferroni)` option, we request that tests be conducted for each of the variables, with a Bonferroni adjustment for the p-values to accommodate our testing multiple hypotheses.

```
. estat hettest, rhs mtest(bonf)
Breusch-Pagan / Cook-Weisberg test for heteroskedasticity
         Ho: Constant variance
```

Variable	chi2	df	p	
weight	15.24	1	0.0004	#
1.foreign	6.15	1	0.0525	#
mpg	9.04	1	0.0106	#
foreign# c.mpg				
1	6.02	1	0.0566	#
simultaneous	15.60	4	0.0036	

 # Bonferroni-adjusted p-values

```
. estat szroeter, rhs mtest(holm)
Szroeter's test for homoskedasticity
    Ho: variance constant
    Ha: variance monotonic in variable
```

Variable	chi2	df	p	
weight	17.07	1	0.0001	#
1.foreign	6.15	1	0.0131	#
mpg	11.45	1	0.0021	#
foreign# c.mpg				
1	6.17	1	0.0260	#

 # Holm adjusted p-values

Finally, we request the information matrix test, which is a conditional moments test with second-, third-, and fourth-order moment conditions.

```
. estat imtest
Cameron & Trivedi's decomposition of IM-test
```

Source	chi2	df	p
Heteroskedasticity	18.86	10	0.0420
Skewness	11.69	4	0.0198
Kurtosis	2.33	1	0.1273
Total	32.87	15	0.0049

We find evidence for omitted variables, heteroskedasticity, and nonnormal skewness.

So, why bother with the various graphical commands when the tests seem so much easier to interpret? In part, it is a matter of taste: both are designed to uncover the same problem, and both are, in fact, going about it in similar ways. One is based on a formal calculation, whereas the other is based on personal judgment in evaluating a graph. On the other hand, the tests are seeking evidence of specific problems, whereas judgment is more general. The careful analyst will use both.

We performed the omitted-variable test first. Omitted variables are a more serious problem than heteroskedasticity or the violations of higher moment conditions tested by `estat imtest`. If this were not a manual, having found evidence of omitted variables, we would never have run the `estat hettest`, `estat szroeter`, and `estat imtest` commands, at least not until we solved the omitted-variable problem.

◁

❑ Technical note

`estat ovtest` and `estat hettest` both perform two flavors of their respective tests. By default, `estat ovtest` looks for evidence of omitted variables by fitting the original model augmented by $\widehat{y}^2$, $\widehat{y}^3$, and $\widehat{y}^4$, which are the fitted values from the original model. Under the assumption of no misspecification, the coefficients on the powers of the fitted values will be zero. With the `rhs` option, `estat ovtest` instead augments the original model with powers (second through fourth) of the explanatory variables (except for dummy variables).

`estat hettest`, by default, looks for heteroskedasticity by modeling the variance as a function of the fitted values. If, however, we specify a variable or variables, the variance will be modeled as a function of the specified variables. In our example, if we had, a priori, some reason to suspect heteroskedasticity and that the heteroskedasticity is a function of a car's weight, then using a test that focuses on weight would be more powerful than the more general tests such as White's test or the first term in the Cameron–Trivedi decomposition test.

`estat hettest`, by default, computes the original Breusch–Pagan/Cook–Weisberg test, which includes the assumption of normally distributed errors. Koenker (1981) derived an $N * R^2$ version of this test that drops the normality assumption. Wooldridge (2009) gives an F-statistic version that does not require the normality assumption.

❑

Variance inflation factors

Problems arise in regression when the predictors are highly correlated. In this situation, there may be a significant change in the regression coefficients if you add or delete an independent variable. The estimated standard errors of the fitted coefficients are inflated, or the estimated coefficients may not be statistically significant even though a statistical relation exists between the dependent and independent variables.

Data analysts rely on these facts to check informally for the presence of multicollinearity. `estat vif`, another command for use after `regress`, calculates the variance inflation factors and tolerances for each of the independent variables.

The output shows the variance inflation factors together with their reciprocals. Some analysts compare the reciprocals with a predetermined tolerance. In the comparison, if the reciprocal of the VIF is smaller than the tolerance, the associated predictor variable is removed from the regression model. However, most analysts rely on informal rules of thumb applied to the VIF; see Chatterjee and Hadi (2006). According to these rules, there is evidence of multicollinearity if

1. The largest VIF is greater than 10 (some choose a more conservative threshold value of 30).
2. The mean of all the VIFs is considerably larger than 1.

▷ Example 17: estat vif

We examine a regression model fit using the ubiquitous automobile dataset:

```
. regress price mpg rep78 trunk headroom length turn displ gear_ratio
```

Source	SS	df	MS	Number of obs =	69
				F(8, 60) =	6.33
Model	264102049	8	33012756.2	Prob > F =	0.0000
Residual	312694909	60	5211581.82	R-squared =	0.4579
				Adj R-squared =	0.3856
Total	576796959	68	8482308.22	Root MSE =	2282.9

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
mpg	-144.84	82.12751	-1.76	0.083	-309.1195	19.43948
rep78	727.5783	337.6107	2.16	0.035	52.25638	1402.9
trunk	44.02061	108.141	0.41	0.685	-172.2935	260.3347
headroom	-807.0996	435.5802	-1.85	0.069	-1678.39	64.19061
length	-8.688914	34.89848	-0.25	0.804	-78.49626	61.11843
turn	-177.9064	137.3455	-1.30	0.200	-452.6383	96.82551
displacement	30.73146	7.576952	4.06	0.000	15.5753	45.88762
gear_ratio	1500.119	1110.959	1.35	0.182	-722.1303	3722.368
_cons	6691.976	7457.906	0.90	0.373	-8226.057	21610.01

```
. estat vif
    Variable |       VIF       1/VIF
-------------+----------------------
      length |      8.22    0.121614
displacement |      6.50    0.153860
        turn |      4.85    0.205997
  gear_ratio |      3.45    0.290068
         mpg |      3.03    0.330171
       trunk |      2.88    0.347444
    headroom |      1.80    0.554917
      rep78 |      1.46    0.686147
-------------+----------------------
    Mean VIF |      4.02
```

The results are mixed. Although we have no VIFs greater than 10, the mean VIF is greater than 1, though not considerably so. We could continue the investigation of collinearity, but given that other authors advise that collinearity is a problem only when VIFs exist that are greater than 30 (contradicting our rule above), we will not do so here.

◁

▷ Example 18: estat vif, with strong evidence of multicollinearity

This example comes from a dataset described in Kutner, Nachtsheim, and Neter (2004, 257) that examines body fat as modeled by caliper measurements on the triceps, midarm, and thigh.

```
. use http://www.stata-press.com/data/r12/bodyfat, clear
(Body Fat)
. regress bodyfat tricep thigh midarm
      Source |       SS       df       MS              Number of obs =      20
-------------+------------------------------           F(  3,    16) =   21.52
       Model |  396.984607     3  132.328202            Prob > F      =  0.0000
    Residual |  98.4049068    16  6.15030667            R-squared     =  0.8014
-------------+------------------------------           Adj R-squared =  0.7641
       Total |  495.389513    19  26.0731323            Root MSE      =    2.48

------------------------------------------------------------------------------
     bodyfat |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     triceps |   4.334085   3.015511     1.44   0.170    -2.058512    10.72668
       thigh |  -2.856842   2.582015    -1.11   0.285    -8.330468    2.616785
     midarm |  -2.186056   1.595499    -1.37   0.190    -5.568362     1.19625
       _cons |   117.0844   99.78238     1.17   0.258    -94.44474    328.6136
------------------------------------------------------------------------------
. estat vif
    Variable |       VIF       1/VIF
-------------+----------------------
     triceps |    708.84    0.001411
       thigh |    564.34    0.001772
     midarm |    104.61    0.009560
-------------+----------------------
    Mean VIF |    459.26
```

Here we see strong evidence of multicollinearity in our model. More investigation reveals that the measurements on the thigh and the triceps are highly correlated:

```
. corr triceps thigh midarm
(obs=20)
```

	triceps	thigh	midarm
triceps	1.0000		
thigh	0.9238	1.0000	
midarm	0.4578	0.0847	1.0000

If we remove the predictor `tricep` from the model (because it had the highest VIF), we get

```
. regress bodyfat thigh midarm
```

Source	SS	df	MS		
Model	384.279748	2	192.139874	Number of obs	= 20
Residual	111.109765	17	6.53586854	F(2, 17)	= 29.40
				Prob > F	= 0.0000
Total	495.389513	19	26.0731323	R-squared	= 0.7757
				Adj R-squared	= 0.7493
				Root MSE	= 2.5565

bodyfat	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
thigh	.8508818	.1124482	7.57	0.000	.6136367	1.088127
midarm	.0960295	.1613927	0.60	0.560	-.2444792	.4365383
_cons	-25.99696	6.99732	-3.72	0.002	-40.76001	-11.2339

```
. estat vif
```

Variable	VIF	1/VIF
midarm	1.01	0.992831
thigh	1.01	0.992831
Mean VIF	1.01	

Note how the coefficients change and how the estimated standard errors for each of the regression coefficients become much smaller. The calculated value of R^2 for the overall regression for the subset model does not appreciably decline when we remove the correlated predictor. Removing an independent variable from the model is one way to deal with multicollinearity. Other methods include ridge regression, weighted least squares, and restricting the use of the fitted model to data that follow the same pattern of multicollinearity. In economic studies, it is sometimes possible to estimate the regression coefficients from different subsets of the data by using cross-section and time series.

◁

All examples above demonstrated the use of centered VIFs. As pointed out by Belsley (1991), the centered VIFs may fail to discover collinearity involving the constant term. One solution is to use the uncentered VIFs instead. According to the definition of the uncentered VIFs, the constant is viewed as a legitimate explanatory variable in a regression model, which allows one to obtain the VIF value for the constant term.

▷ Example 19: estat vif, with strong evidence of collinearity with the constant term

Consider the extreme example in which one of the regressors is highly correlated with the constant. We simulate the data and examine both centered and uncentered VIF diagnostics after fitted regression model as follows.

```
. use http://www.stata-press.com/data/r12/extreme_collin
. summarize
  (output omitted)
. regress y one x z
```

Source	SS	df	MS	Number of obs = 100
Model	223801.985	3	74600.6617	F(3, 96) = 2710.27
Residual	2642.42124	96	27.5252213	Prob > F = 0.0000
				R-squared = 0.9883
Total	226444.406	99	2287.31723	Adj R-squared = 0.9880
				Root MSE = 5.2464

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
one	-3.278582	10.5621	-0.31	0.757	-24.24419	17.68702
x	2.038696	.0242673	84.01	0.000	1.990526	2.086866
z	4.863137	.2681036	18.14	0.000	4.330956	5.395319
_cons	9.760075	10.50935	0.93	0.355	-11.10082	30.62097

```
. estat vif
```

Variable	VIF	1/VIF
z	1.03	0.968488
x	1.03	0.971307
one	1.00	0.995425
Mean VIF	1.02	

```
. estat vif, uncentered
```

Variable	VIF	1/VIF
one	402.94	0.002482
intercept	401.26	0.002492
z	2.93	0.341609
x	1.13	0.888705
Mean VIF	202.06	

According to the values of the centered VIFs (1.03, 1.03, 1.00), no harmful collinearity is detected in the model. However, by the construction of these simulated data, we know that `one` is highly collinear with the constant term. As such, the large values of uncentered VIFs for `one` (402.94) and `intercept` (401.26) reveal high collinearity of the variable `one` with the constant term.

◁

Saved results

`estat hettest` saves the following results for the (multivariate) score test in `r()`:

Scalars

`r(chi2)`	χ^2 test statistic
`r(df)`	#df for the asymptotic χ^2 distribution under H_0
`r(p)`	p-value

`estat hettest, fstat` saves results for the (multivariate) score test in `r()`:

Scalars

`r(F)`	test statistic
`r(df_m)`	#df of the test for the F distribution under H_0
`r(df_r)`	#df of the residuals for the F distribution under H_0
`r(p)`	p-value

`estat hettest` (if `mtest` is specified) and `estat szroeter` save the following in `r()`:

Matrices

`r(mtest)`	a matrix of test results, with rows corresponding to the univariate tests
	`mtest[.,1]` χ^2 test statistic
	`mtest[.,2]` #df
	`mtest[.,3]` unadjusted p-value
	`mtest[.,4]` adjusted p-value (if an `mtest()` adjustment method is specified)

Macros

`r(mtmethod)`	adjustment method for p-values

`estat imtest` saves the following in `r()`:

Scalars

`r(chi2_t)`	IM-test statistic $\big(=$ `r(chi2_h)` $+$ `r(chi2_s)` $+$ `r(chi2_k)`$\big)$
`r(df_t)`	df for limiting χ^2 distribution under H_0 $\big(=$ `r(df_h)` $+$ `r(df_s)` $+$ `r(df_k)`$\big)$
`r(chi2_h)`	heteroskedasticity test statistic
`r(df_h)`	df for limiting χ^2 distribution under H_0
`r(chi2_s)`	skewness test statistic
`r(df_s)`	df for limiting χ^2 distribution under H_0
`r(chi2_k)`	kurtosis test statistic
`r(df_k)`	df for limiting χ^2 distribution under H_0
`r(chi2_w)`	White's heteroskedasticity test (if `white` specified)
`r(df_w)`	df for limiting χ^2 distribution under H_0

`estat ovtest` saves the following in `r()`:

Scalars

`r(p)`	two-sided p-value
`r(F)`	F statistic
`r(df)`	degrees of freedom
`r(df_r)`	residual degrees of freedom

Methods and formulas

All regression fit and diagnostic commands are implemented as ado-files.

See Hamilton (2009, chap. 7), Kohler and Kreuter (2009, sec. 8.3), or Baum (2006, chap. 5) for an overview of using Stata to perform regression diagnostics. See Peracchi (2001, chap. 8) for a mathematically rigorous discussion of diagnostics.

Methods and formulas are presented under the following headings:

predict
Special-interest postestimation commands

predict

Assume that you have already fit the regression model

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{e}$$

where $\mathbf{X}$ is $n \times k$.

Denote the previously estimated coefficient vector by $\mathbf{b}$ and its estimated variance matrix by $\mathbf{V}$. `predict` works by recalling various aspects of the model, such as $\mathbf{b}$, and combining that information with the data currently in memory. Let $\mathbf{x}_j$ be the jth observation currently in memory, and let s^2 be the mean squared error of the regression.

Let $\mathbf{V} = s^2(\mathbf{X}'\mathbf{X})^{-1}$. Let k be the number of independent variables including the intercept, if any, and let y_j be the observed value of the dependent variable.

The *predicted value* (`xb` option) is defined as $\widehat{y}_j = \mathbf{x}_j\mathbf{b}$.

Let ℓ_j represent a lower bound for an observation j and u_j represent an upper bound. The probability that $y_j|\mathbf{x}_j$ would be observed in the interval (ℓ_j, u_j)—the `pr(`ℓ`, `u`)` option—is

$$P(\ell_j, u_j) = \Pr(\ell_j < \mathbf{x}_j\mathbf{b} + e_j < u_j) = \Phi\left(\frac{u_j - \widehat{y}_j}{s}\right) - \Phi\left(\frac{\ell_j - \widehat{y}_j}{s}\right)$$

where for the `pr(`ℓ`, `u`)`, `e(`ℓ`, `u`)`, and `ystar(`ℓ`, `u`)` options, ℓ_j and u_j can be anywhere in the range $(-\infty, +\infty)$.

The option `e(`ℓ`, `u`)` computes the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (ℓ_j, u_j), that is, when $y_j|\mathbf{x}_j$ is truncated. It can be expressed as

$$E(\ell_j, u_j) = E(\mathbf{x}_j\mathbf{b} + e_j \mid \ell_j < \mathbf{x}_j\mathbf{b} + e_j < u_j) = \widehat{y}_j - s\frac{\phi\left(\frac{u_j - \widehat{y}_j}{s}\right) - \phi\left(\frac{\ell_j - \widehat{y}_j}{s}\right)}{\Phi\left(\frac{u_j - \widehat{y}_j}{s}\right) - \Phi\left(\frac{\ell_j - \widehat{y}_j}{s}\right)}$$

where ϕ is the normal density and Φ is the cumulative normal.

You can also compute `ystar(`ℓ, u`)`—the expected value of $y_j|\mathbf{x}_j$, where y_j is assumed censored at ℓ_j and u_j:

$$y_j^* = \begin{cases} \ell_j & \text{if } \mathbf{x}_j\mathbf{b} + e_j \le \ell_j \\ \mathbf{x}_j\mathbf{b} + u & \text{if } \ell_j < \mathbf{x}_j\mathbf{b} + e_j < u_j \\ u_j & \text{if } \mathbf{x}_j\mathbf{b} + e_j \ge u_j \end{cases}$$

This computation can be expressed in several ways, but the most intuitive formulation involves a combination of the two statistics just defined:

$$y_j^* = P(-\infty, \ell_j)\ell_j + P(\ell_j, u_j)E(\ell_j, u_j) + P(u_j, +\infty)u_j$$

A diagonal element of the projection matrix (`hat`) or (`leverage`) is given by

$$h_j = \mathbf{x}_j(\mathbf{X}'\mathbf{X})^{-1}\mathbf{x}_j'$$

The *standard error of the prediction* (the `stdp` option) is defined as $s_{p_j} = \sqrt{\mathbf{x}_j\mathbf{V}\mathbf{x}_j'}$

and can also be written as $s_{p_j} = s\sqrt{h_j}$.

The *standard error of the forecast* (`stdf`) is defined as $s_{f_j} = s\sqrt{1 + h_j}$.

The *standard error of the residual* (`stdr`) is defined as $s_{r_j} = s\sqrt{1 - h_j}$.

The *residuals* (`residuals`) are defined as $\widehat{e}_j = y_j - \widehat{y}_j$.

The *standardized residuals* (`rstandard`) are defined as $\widehat{e}_{s_j} = \widehat{e}_j / s_{r_j}$.

The *Studentized residuals* (`rstudent`) are defined as

$$r_j = \frac{\widehat{e}_j}{s_{(j)}\sqrt{1 - h_j}}$$

where $s_{(j)}$ represents the root mean squared error with the jth observation removed, which is given by

$$s^2_{(j)} = \frac{s^2(T - k)}{T - k - 1} - \frac{\widehat{e}_j^2}{(T - k - 1)(1 - h_j)}$$

Cook's D (`cooksd`) is given by

$$D_j = \frac{\widehat{e}_{s_j}^2 (s_{p_j}/s_{r_j})^2}{k} = \frac{h_j \widehat{e}_j^2}{k s^2 (1 - h_j)^2}$$

DFITS (`dfits`) is given by

$$\text{DFITS}_j = r_j \sqrt{\frac{h_j}{1 - h_j}}$$

Welsch distance (`welsch`) is given by

$$W_j = \frac{r_j \sqrt{h_j (n - 1)}}{1 - h_j}$$

COVRATIO (`covratio`) is given by

$$\text{COVRATIO}_j = \frac{1}{1 - h_j} \left(\frac{n - k - \widehat{e}_j^2}{n - k - 1} \right)^k$$

The DFBETAs (`dfbeta`) for a particular regressor x_i are given by

$$\text{DFBETA}_j = \frac{r_j u_j}{\sqrt{U^2 (1 - h_j)}}$$

where u_j are the residuals obtained from a regression of x_i on the remaining x's and $U^2 = \sum_j u_j^2$.

Special-interest postestimation commands

The `lvr2plot` command plots leverage against the squares of the normalized residuals. The normalized residuals are defined as $\widehat{e}_{n_j} = \widehat{e}_j/(\sum_i \widehat{e}_i^2)^{1/2}$.

The omitted-variable test (Ramsey 1969) reported by `estat ovtest` fits the regression $y_i = \mathbf{x}_i\mathbf{b} + \mathbf{z}_i\mathbf{t} + u_i$ and then performs a standard F test of $\mathbf{t} = \mathbf{0}$. The default test uses $\mathbf{z}_i = (\widehat{y}_i^2, \widehat{y}_i^3, \widehat{y}_i^4)$. If `rhs` is specified, $\mathbf{z}_i = (x_{1i}^2, x_{1i}^3, x_{1i}^4, x_{2i}^2, \ldots, x_{mi}^4)$. In either case, the variables are normalized to have minimum 0 and maximum 1 before powers are calculated.

The test for heteroskedasticity (Breusch and Pagan 1979; Cook and Weisberg 1983) models $\mathrm{Var}(e_i) = \sigma^2 \exp(\mathbf{zt})$, where $\mathbf{z}$ is a variable list specified by the user, the list of right-hand-side variables, or the fitted values $\mathbf{x}\widehat{\beta}$. The test is of $\mathbf{t} = \mathbf{0}$. Mechanically, `estat hettest` fits the augmented regression $\widehat{e}_i^2/\widehat{\sigma}^2 = a + \mathbf{z}_i\mathbf{t} + v_i$.

The original Breusch–Pagan/Cook–Weisberg version of the test assumes that the e_i are normally distributed under the null hypothesis which implies that the score test statistic S is equal to the model sum of squares from the augmented regression divided by 2. Under the null hypothesis, S has the χ^2 distribution with m degrees of freedom, where m is the number of columns of $\mathbf{z}$.

Koenker (1981) derived a score test of the null hypothesis that $\mathbf{t} = \mathbf{0}$ under the assumption that the e_i are independent and identically distributed (i.i.d.). Koenker showed that $S = N * R^2$ has a large-sample χ^2 distribution with m degrees of freedom, where N is the number of observations and R^2 is the R-squared in the augmented regression and m is the number of columns of $\mathbf{z}$. `estat hettest, iid` produces this version of the test.

Wooldridge (2009) showed that an F test of $\mathbf{t} = \mathbf{0}$ in the augmented regression can also be used under the assumption that the e_i are i.i.d. `estat hettest, fstat` produces this version of the test.

Szroeter's class of tests for homoskedasticity against the alternative that the residual variance increases in some variable x is defined in terms of

$$H = \frac{\sum_{i=1}^{n} h(x_i)e_i^2}{\sum_{i=1}^{n} e_i^2}$$

where $h(x)$ is some weight function that increases in x (Szroeter 1978). H is a weighted average of the $h(x)$, with the squared residuals serving as weights. Under homoskedasticity, H should be approximately equal to the unweighted average of $h(x)$. Large values of H suggest that e_i^2 tends to be large where $h(x)$ is large; that is, the variance indeed increases in x, whereas small values of H suggest that the variance actually decreases in x. `estat szroeter` uses $h(x_i) = \mathrm{rank}(x_i \text{ in } x_1 \ldots x_n)$; see Judge et al. [1985, 452] for details. `estat szroeter` displays a normalized version of H,

$$Q = \sqrt{\frac{6n}{n^2 - 1}}H$$

which is approximately $N(0, 1)$ distributed under the null (homoskedasticity).

`estat hettest` and `estat szroeter` provide adjustments of p-values for multiple testing. The supported methods are described in [R] **test**.

`estat imtest` performs the information matrix test for the regression model, as well as an orthogonal decomposition into tests for heteroskedasticity δ_1, nonnormal skewness δ_2, and nonnormal kurtosis δ_3 (Cameron and Trivedi 1990; Long and Trivedi 1993). The decomposition is obtained via three auxiliary regressions. Let e be the regression residuals, $\widehat{\sigma}^2$ be the maximum likelihood estimate of σ^2 in the regression, n be the number of observations, X be the set of k variables specified with `estat imtest`, and R^2_{un} be the uncentered R^2 from a regression. δ_1 is obtained as nR^2_{un} from a

regression of $e^2 - \widehat{\sigma}^2$ on the cross-products of the variables in X. δ_2 is computed as nR^2_{un} from a regression of $e^3 - 3\widehat{\sigma}^2 e$ on X. Finally, δ_3 is obtained as nR^2_{un} from a regression of $e^4 - 6\widehat{\sigma}^2 e^2 - 3\widehat{\sigma}^4$ on X. δ_1, δ_2, and δ_3 are asymptotically χ^2 distributed with $1/2k(k+1)$, K, and 1 degree of freedom. The information test statistic $\delta = \delta_1 + \delta_2 + \delta_3$ is asymptotically χ^2 distributed with $1/2k(k+3)$ degrees of freedom. White's test for heteroskedasticity is computed as nR^2 from a regression of $\widehat{u}^2$ on X and the cross-products of the variables in X. This test statistic is usually close to δ_1.

`estat vif` calculates the centered variance inflation factor (VIF_c) (Chatterjee and Hadi 2006, 235–239) for x_j, given by

$$\text{VIF}_c(x_j) = \frac{1}{1 - \widehat{R}^2_j}$$

where $\widehat{R}^2_j$ is the square of the centered multiple correlation coefficient that results when x_j is regressed with intercept against all the other explanatory variables.

The uncentered variance inflation factor (VIF_{uc}) (Belsley 1991, 28–29) for x_j is given by

$$\text{VIF}_{uc}(x_j) = \frac{1}{1 - \widetilde{R}^2_j}$$

where $\widetilde{R}^2_j$ is the square of the uncentered multiple correlation coefficient that results when x_j is regressed without intercept against all the other explanatory variables including the constant term.

Acknowledgments

`estat ovtest` and `estat hettest` are based on programs originally written by Richard Goldstein (1991, 1992). `estat imtest`, `estat szroeter`, and the current version of `estat hettest` were written by Jeroen Weesie, Department of Sociology, Utrecht University, The Netherlands; `estat imtest` is based in part on code written by J. Scott Long, Department of Sociology, Indiana University.

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Also see

[R] **regress** — Linear regression

[R] **regress postestimation time series** — Postestimation tools for regress with time series

[U] **20 Estimation and postestimation commands**

Title

regress postestimation time series — Postestimation tools for regress with time series

Description

The following postestimation commands for time series are available for `regress`:

Command	Description
`estat archlm`	test for ARCH effects in the residuals
`estat bgodfrey`	Breusch–Godfrey test for higher-order serial correlation
`estat durbinalt`	Durbin's alternative test for serial correlation
`estat dwatson`	Durbin–Watson d statistic to test for first-order serial correlation

These commands provide regression diagnostic tools specific to time series. You must `tsset` your data before using these commands; see [TS] **tsset**.

`estat archlm` tests for time-dependent volatility. `estat bgodfrey`, `estat durbinalt`, and `estat dwatson` test for serial correlation in the residuals of a linear regression. For non–time-series regression diagnostic tools, see [R] **regress postestimation**.

`estat archlm` performs Engle's Lagrange multiplier (LM) test for the presence of autoregressive conditional heteroskedasticity.

`estat bgodfrey` performs the Breusch–Godfrey test for higher-order serial correlation in the disturbance. This test does not require that all the regressors be strictly exogenous.

`estat durbinalt` performs Durbin's alternative test for serial correlation in the disturbance. This test does not require that all the regressors be strictly exogenous.

`estat dwatson` computes the Durbin–Watson d statistic (Durbin and Watson 1950) to test for first-order serial correlation in the disturbance when all the regressors are strictly exogenous.

Syntax for estat archlm

`estat archlm` [`,` *archlm_options*]

archlm_options	Description
`lags(`*numlist*`)`	test *numlist* lag orders
`force`	allow test after `regress, vce(robust)`

Options for estat archlm

`lags(`*numlist*`)` specifies a list of numbers, indicating the lag orders to be tested. The test will be performed separately for each order. The default is order one.

`force` allows the test to be run after `regress, vce(robust)`. The command will not work if the `vce(cluster` *clustvar*`)` option is specified with `regress`; see [R] **regress**.

Syntax for estat bgodfrey

```
estat bgodfrey [ , bgodfrey_options ]
```

bgodfrey_options	Description
lags(*numlist*)	test *numlist* lag orders
nomiss0	do not use Davidson and MacKinnon's approach
small	obtain p-values using the F or t distribution

Options for estat bgodfrey

lags(*numlist*) specifies a list of numbers, indicating the lag orders to be tested. The test will be performed separately for each order. The default is order one.

nomiss0 specifies that Davidson and MacKinnon's approach (1993, 358), which replaces the missing values in the initial observations on the lagged residuals in the auxiliary regression with zeros, not be used.

small specifies that the p-values of the test statistics be obtained using the F or t distribution instead of the default chi-squared or normal distribution.

Syntax for estat durbinalt

```
estat durbinalt [ , durbinalt_options ]
```

durbinalt_options	Description
lags(*numlist*)	test *numlist* lag orders
nomiss0	do not use Davidson and MacKinnon's approach
robust	compute standard errors using the robust/sandwich estimator
small	obtain p-values using the F or t distribution
force	allow test after `regress, vce(robust)` or after `newey`

Options for estat durbinalt

lags(*numlist*) specifies a list of numbers, indicating the lag orders to be tested. The test will be performed separately for each order. The default is order one.

nomiss0 specifies that Davidson and MacKinnon's approach (1993, 358), which replaces the missing values in the initial observations on the lagged residuals in the auxiliary regression with zeros, not be used.

robust specifies that the Huber/White/sandwich robust estimator of the variance–covariance matrix be used in Durbin's alternative test.

small specifies that the p-values of the test statistics be obtained using the F or t distribution instead of the default chi-squared or normal distribution. This option may not be specified with robust, which always uses an F or t distribution.

`force` allows the test to be run after `regress, vce(robust)` and after `newey` (see [R] **regress** and [TS] **newey**). The command will not work if the `vce(cluster` *clustvar*`)` option is specified with `regress`.

Syntax for estat dwatson

```
estat dwatson
```

Remarks

The Durbin–Watson test is used to determine whether the error term in a linear regression model follows an AR(1) process. For the linear model

$$y_t = \mathbf{x}_t\boldsymbol{\beta} + u_t$$

the AR(1) process can be written as

$$u_t = \rho u_{t-1} + \epsilon_t$$

In general, an AR(1) process requires only that ϵ_t be independent and identically distributed (i.i.d.). The Durbin–Watson test, however, requires ϵ_t to be distributed $N(0, \sigma^2)$ for the statistic to have an exact distribution. Also, the Durbin–Watson test can be applied only when the regressors are strictly exogenous. A regressor x is strictly exogenous if $\text{Corr}(x_s, u_t) = 0$ for all s and t, which precludes the use of the Durbin–Watson statistic with models where lagged values of the dependent variable are included as regressors.

The null hypothesis of the test is that there is no first-order autocorrelation. The Durbin–Watson d statistic can take on values between 0 and 4 and under the null d is equal to 2. Values of d less than 2 suggest positive autocorrelation ($\rho > 0$), whereas values of d greater than 2 suggest negative autocorrelation ($\rho < 0$). Calculating the exact distribution of the d statistic is difficult, but empirical upper and lower bounds have been established based on the sample size and the number of regressors. Extended tables for the d statistic have been published by Savin and White (1977). For example, suppose you have a model with 30 observations and three regressors (including the constant term). For a test of the null hypothesis of no autocorrelation versus the alternative of positive autocorrelation, the lower bound of the d statistic is 1.284, and the upper bound is 1.567 at the 5% significance level. You would reject the null if $d < 1.284$, and you would fail to reject if $d > 1.567$. A value falling within the range (1.284, 1.567) leads to no conclusion about whether or not to reject the null hypothesis.

When lagged dependent variables are included among the regressors, the past values of the error term are correlated with those lagged variables at time t, implying that they are not strictly exogenous regressors. The inclusion of covariates that are not strictly exogenous causes the d statistic to be biased toward the acceptance of the null hypothesis. Durbin (1970) suggested an alternative test for models with lagged dependent variables and extended that test to the more general AR(p) serial correlation process

$$u_t = \rho_1 u_{t-1} + \cdots + \rho_p u_{t-p} + \epsilon_t$$

where ϵ_t is i.i.d. with variance σ^2 but is not assumed or required to be normal for the test.

The null hypothesis of Durbin's alternative test is

$$H_0 : \rho_1 = 0, \ldots, \rho_p = 0$$

and the alternative is that at least one of the ρ's is nonzero. Although the null hypothesis was originally derived for an AR(p) process, this test turns out to have power against MA(p) processes as well. Hence, the actual null of this test is that there is no serial correlation up to order p because the MA(p) and the AR(p) models are locally equivalent alternatives under the null. See Godfrey (1988, 113–115) for a discussion of this result.

Durbin's alternative test is in fact a LM test, but it is most easily computed with a Wald test on the coefficients of the lagged residuals in an auxiliary OLS regression of the residuals on their lags and all the covariates in the original regression. Consider the linear regression model

$$y_t = \beta_1 x_{1t} + \cdots + \beta_k x_{kt} + u_t \tag{1}$$

in which the covariates x_1 through x_k are not assumed to be strictly exogenous and u_t is assumed to be i.i.d. and to have finite variance. The process is also assumed to be stationary. (See Wooldridge [2009] for a discussion of stationarity.) Estimating the parameters in (1) by OLS obtains the residuals $\widehat{u}_t$. Next another OLS regression is performed of $\widehat{u}_t$ on $\widehat{u}_{t-1}, \ldots, \widehat{u}_{t-p}$ and the other regressors,

$$\widehat{u}_t = \gamma_1 \widehat{u}_{t-1} + \cdots + \gamma_p \widehat{u}_{t-p} + \beta_1 x_{1t} + \cdots + \beta_k x_{kt} + \epsilon_t \tag{2}$$

where ϵ_t stands for the random-error term in this auxiliary OLS regression. Durbin's alternative test is then obtained by performing a Wald test that $\gamma_1, \ldots, \gamma_p$ are jointly zero. The test can be made robust to an unknown form of heteroskedasticity by using a robust VCE estimator when estimating the regression in (2). When there are only strictly exogenous regressors and $p = 1$, this test is asymptotically equivalent to the Durbin–Watson test.

The Breusch–Godfrey test is also an LM test of the null hypothesis of no autocorrelation versus the alternative that u_t follows an AR(p) or MA(p) process. Like Durbin's alternative test, it is based on the auxiliary regression (2), and it is computed as NR^2, where N is the number of observations and R^2 is the simple R^2 from the regression. This test and Durbin's alternative test are asymptotically equivalent. The test statistic NR^2 has an asymptotic χ^2 distribution with p degrees of freedom. It is valid with or without the strict exogeneity assumption but is not robust to conditional heteroskedasticity, even if a robust VCE is used when fitting (2).

In fitting (2), the values of the lagged residuals will be missing in the initial periods. As noted by Davidson and MacKinnon (1993), the residuals will not be orthogonal to the other covariates in the model in this restricted sample, which implies that the R^2 from the auxiliary regression will not be zero when the lagged residuals are left out. Hence, Breusch and Godfrey's NR^2 version of the test may overreject in small samples. To correct this problem, Davidson and MacKinnon (1993) recommend setting the missing values of the lagged residuals to zero and running the auxiliary regression in (2) over the full sample used in (1). This small-sample correction has become conventional for both the Breusch–Godfrey and Durbin's alternative test, and it is the default for both commands. Specifying the `nomiss0` option overrides this default behavior and treats the initial missing values generated by regressing on the lagged residuals as missing. Hence, `nomiss0` causes these initial observations to be dropped from the sample of the auxiliary regression.

Durbin's alternative test and the Breusch–Godfrey test were originally derived for the case covered by `regress` without the `vce(robust)` option. However, after `regress, vce(robust)` and `newey`, Durbin's alternative test is still valid and can be invoked if the `robust` and `force` options are specified.

Example 1: tests for serial correlation

Using data from Klein (1950), we first fit an OLS regression of consumption on the government wage bill:

```
. use http://www.stata-press.com/data/r12/klein
. tsset yr
        time variable:  yr, 1920 to 1941
                delta:  1 unit
. regress consump wagegovt
```

Source	SS	df	MS	Number of obs =	22
				F(1, 20) =	17.72
Model	532.567711	1	532.567711	Prob > F =	0.0004
Residual	601.207167	20	30.0603584	R-squared =	0.4697
				Adj R-squared =	0.4432
Total	1133.77488	21	53.9892799	Root MSE =	5.4827

consump	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
wagegovt	2.50744	.5957173	4.21	0.000	1.264796	3.750085
_cons	40.84699	3.192183	12.80	0.000	34.18821	47.50577

If we assume that `wagegov` is a strictly exogenous variable, we can use the Durbin–Watson test to check for first-order serial correlation in the errors.

```
. estat dwatson
Durbin-Watson d-statistic(  2,    22) =  .3217998
```

The Durbin–Watson d statistic, 0.32, is far from the center of its distribution ($d = 2.0$). Given 22 observations and two regressors (including the constant term) in the model, the lower 5% bound is about 0.997, much greater than the computed d statistic. Assuming that `wagegov` is strictly exogenous, we can reject the null of no first-order serial correlation. Rejecting the null hypothesis does not necessarily mean an AR process; other forms of misspecification may also lead to a significant test statistic. If we are willing to assume that the errors follow an AR(1) process and that `wagegov` is strictly exogenous, we could refit the model using `arima` or `prais` and model the error process explicitly; see [TS] **arima** and [TS] **prais**.

If we are not willing to assume that `wagegov` is strictly exogenous, we could instead use Durbin's alternative test or the Breusch–Godfrey to test for first-order serial correlation. Because we have only 22 observations, we will use the `small` option.

```
. estat durbinalt, small
Durbin's alternative test for autocorrelation
```

lags(*p*)	F	df	Prob > F
1	35.035	(1, 19)	0.0000

H0: no serial correlation

```
. estat bgodfrey, small
Breusch-Godfrey LM test for autocorrelation
```

lags(*p*)	F	df	Prob > F
1	14.264	(1, 19)	0.0013

H0: no serial correlation

Both tests strongly reject the null of no first-order serial correlation, so we decide to refit the model with two lags of `consump` included as regressors and then rerun `estat durbinalt` and `estat bgodfrey`. Because the revised model includes lagged values of the dependent variable, the Durbin–Watson test is not applicable.

```
. regress consump wagegovt L.consump L2.consump
```

Source	SS	df	MS		
Model	702.660311	3	234.220104	Number of obs	= 20
Residual	85.1596011	16	5.32247507	F(3, 16)	= 44.01
				Prob > F	= 0.0000
				R-squared	= 0.8919
				Adj R-squared	= 0.8716
Total	787.819912	19	41.4642059	Root MSE	= 2.307

consump	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
wagegovt	.6904282	.3295485	2.10	0.052	-.0081835	1.38904
consump						
L1.	1.420536	.197024	7.21	0.000	1.002864	1.838208
L2.	-.650888	.1933351	-3.37	0.004	-1.06074	-.241036
_cons	9.209073	5.006701	1.84	0.084	-1.404659	19.82281

```
. estat durbinalt, small lags(1/2)
Durbin's alternative test for autocorrelation
```

lags(p)	F	df	Prob > F
1	0.080	(1, 15)	0.7805
2	0.260	(2, 14)	0.7750

H0: no serial correlation

```
. estat bgodfrey, small lags(1/2)
Breusch-Godfrey LM test for autocorrelation
```

lags(p)	F	df	Prob > F
1	0.107	(1, 15)	0.7484
2	0.358	(2, 14)	0.7056

H0: no serial correlation

Although `wagegov` and the constant term are no longer statistically different from zero at the 5% level, the output from `estat durbinalt` and `estat bgodfrey` indicates that including the two lags of `consump` has removed any serial correlation from the errors.

◁

Engle (1982) suggests an LM test for checking for autoregressive conditional heteroskedasticity (ARCH) in the errors. The pth-order ARCH model can be written as

$$\begin{aligned}\sigma_t^2 &= E(u_t^2|u_{t-1},\ldots,u_{t-p}) \\ &= \gamma_0 + \gamma_1 u_{t-1}^2 + \cdots + \gamma_p u_{t-p}^2\end{aligned}$$

To test the null hypothesis of no autoregressive conditional heteroskedasticity (that is, $\gamma_1 = \cdots = \gamma_p = 0$), we first fit the OLS model (1), obtain the residuals $\widehat{u}_t$, and run another OLS regression on the lagged residuals:

$$\widehat{u}_t^2 = \gamma_0 + \gamma_1 \widehat{u}_{t-1}^2 + \cdots + \gamma_p \widehat{u}_{t-p}^2 + \epsilon \tag{3}$$

The test statistic is NR^2, where N is the number of observations in the sample and R^2 is the R^2 from the regression in (3). Under the null hypothesis, the test statistic follows a χ^2_p distribution.

▷ Example 2: estat archlm

We refit the original model that does not include the two lags of `consump` and then use `estat archlm` to see if there is any evidence that the errors are autoregressive conditional heteroskedastic.

```
. regress consump wagegovt
```

Source	SS	df	MS		
Model	532.567711	1	532.567711	Number of obs	= 22
Residual	601.207167	20	30.0603584	F(1, 20)	= 17.72
				Prob > F	= 0.0004
				R-squared	= 0.4697
				Adj R-squared	= 0.4432
Total	1133.77488	21	53.9892799	Root MSE	= 5.4827

consump	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
wagegovt	2.50744	.5957173	4.21	0.000	1.264796	3.750085
_cons	40.84699	3.192183	12.80	0.000	34.18821	47.50577

```
. estat archlm, lags(1 2 3)
LM test for autoregressive conditional heteroskedasticity (ARCH)
```

lags(p)	chi2	df	Prob > chi2
1	5.543	1	0.0186
2	9.431	2	0.0090
3	9.039	3	0.0288

H0: no ARCH effects *vs.* H1: ARCH(*p*) disturbance

`estat archlm` shows the results for tests of ARCH(1), ARCH(2), and ARCH(3) effects, respectively. At the 5% significance level, all three tests reject the null hypothesis that the errors are not autoregressive conditional heteroskedastic. See [TS] **arch** for information on fitting ARCH models.

◁

Saved results

`estat archlm` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(N_gaps)`	number of gaps
`r(k)`	number of regressors		

Macros

`r(lags)`	lag order

Matrices

`r(arch)`	test statistic for each lag order	`r(p)`	two-sided p-values
`r(df)`	degrees of freedom		

`estat bgodfrey` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(N_gaps)`	number of gaps
`r(k)`	number of regressors		

Macros

`r(lags)`	lag order

Matrices

`r(chi2)`	χ^2 statistic for each lag order	`r(p)`	two-sided p-values
`r(F)`	F statistic for each lag order (`small` only)	`r(df)`	degrees of freedom
`r(df_r)`	residual degrees of freedom (`small` only)		

`estat durbinalt` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(N_gaps)`	number of gaps
`r(k)`	number of regressors		

Macros

`r(lags)`	lag order

Matrices

`r(chi2)`	χ^2 statistic for each lag order	`r(p)`	two-sided p-values
`r(F)`	F statistic for each lag order (`small` only)	`r(df)`	degrees of freedom
`r(df_r)`	residual degrees of freedom (`small` only)		

`estat dwatson` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(N_gaps)`	number of gaps
`r(k)`	number of regressors	`r(dw)`	Durbin–Watson statistic

Methods and formulas

`estat archlm`, `estat bgodfrey`, `estat durbinalt`, and `estat dwatson` are implemented as ado-files.

Consider the regression

$$y_t = \beta_1 x_{1t} + \cdots + \beta_k x_{kt} + u_t \tag{4}$$

in which some of the covariates are not strictly exogenous. In particular, some of the x_{it} may be lags of the dependent variable. We are interested in whether the u_t are serially correlated.

The Durbin–Watson d statistic reported by `estat dwatson` is

$$d = \frac{\sum_{t=1}^{n-1} (\widehat{u}_{t+1} - \widehat{u}_t)^2}{\sum_{t=1}^{n} \widehat{u}_t^2}$$

where $\widehat{u}_t$ represents the residual of the tth observation.

To compute Durbin's alternative test and the Breusch–Godfrey test against the null hypothesis that there is no pth order serial correlation, we fit the regression in (4), compute the residuals, and then fit the following auxiliary regression of the residuals $\widehat{u}_t$ on p lags of $\widehat{u}_t$ and on all the covariates in the original regression in (4):

$$\widehat{u}_t = \gamma_1 \widehat{u}_{t-1} + \cdots + \gamma_p \widehat{u}_{t-p} + \beta_1 x_{1t} + \cdots + \beta_k x_{kt} + \epsilon \tag{5}$$

Durbin's alternative test is computed by performing a Wald test to determine whether the coefficients of $\widehat{u}_{t-1}, \ldots, \widehat{u}_{t-p}$ are jointly different from zero. By default, the statistic is assumed to be distributed $\chi^2(\mathrm{p})$. When `small` is specified, the statistic is assumed to follow an $F(p, N-p-k)$ distribution. The reported p-value is a two-sided p-value. When `robust` is specified, the Wald test is performed using the Huber/White/sandwich estimator of the variance–covariance matrix, and the test is robust to an unspecified form of heteroskedasticity.

The Breusch–Godfrey test is computed as NR^2, where N is the number of observations in the auxiliary regression (5) and R^2 is the R^2 from the same regression (5). Like Durbin's alternative test, the Breusch–Godfrey test is asymptotically distributed $\chi^2(p)$, but specifying `small` causes the p-value to be computed using an $F(p, N-p-k)$.

By default, the initial missing values of the lagged residuals are replaced with zeros, and the auxiliary regression is run over the full sample used in the original regression of (4). Specifying the `nomiss0` option causes these missing values to be treated as missing values, and the observations are dropped from the sample.

Engle's LM test for ARCH(p) effects fits an OLS regression of $\widehat{u}_t^2$ on $\widehat{u}_{t-1}^2, \ldots, \widehat{u}_{t-p}^2$:

$$\widehat{u}_t^2 = \gamma_0 + \gamma_1 \widehat{u}_{t-1}^2 + \cdots + \gamma_p \widehat{u}_{t-p}^2 + \epsilon$$

The test statistic is nR^2 and is asymptotically distributed $\chi^2(p)$.

Acknowledgment

The original versions of `estat archlm`, `estat bgodfrey`, and `estat durbinalt` were written by Christopher F. Baum, Boston College.

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James Durbin (1923–) is a British statistician who was born in Wigan, near Manchester. He studied mathematics at Cambridge and after military service and various research posts joined the London School of Economics in 1950. His many contributions to statistics have centered on serial correlation, time series, sample survey methodology, goodness-of-fit tests, and sample distribution functions, with emphasis on applications in the social sciences.

Geoffrey Stuart Watson (1921–1998) was born in Victoria, Australia, and earned degrees at Melbourne University and North Carolina State University. After a visit to the University of Cambridge, he returned to Australia, working at Melbourne and then the Australian National University. Following periods at Toronto and Johns Hopkins, he settled at Princeton. Throughout his wide-ranging career, he made many notable accomplishments and important contributions, including the Durbin–Watson test for serial correlation, the Nadaraya–Watson estimator in nonparametric regression, and methods for analyzing directional data.

Leslie G. Godfrey (1946–) was born in London and earned degrees at the Universities of Exeter and London. He is now a professor of econometrics at the University of York. His interests center on implementation and interpretation of tests of econometric models, including nonnested models.

Trevor Stanley Breusch (1949–) was born in Queensland and earned degrees at the University of Queensland and Australian National University (ANU). After a post at the University of Southampton, he returned to work at ANU. His background is in econometric methods and his recent interests include political values and social attitudes, earnings and income, and measurement of underground economic activity.

Also see

[R] **regress** — Linear regression

[TS] **tsset** — Declare data to be time-series data

[R] **regress postestimation** — Postestimation tools for regress

Title

#review — Review previous commands

Syntax

```
#review  [ #1 [ #2 ] ]
```

Description

The `#review` command displays the last few lines typed at the terminal.

Remarks

`#review` (pronounced *pound-review*) is a Stata preprocessor command. `#`*command*s do not generate a return code or generate ordinary Stata errors. The only error message associated with `#`*command*s is "unrecognized #command".

The `#review` command displays the last few lines typed at the terminal. If no arguments follow `#review`, the last five lines typed at the terminal are displayed. The first argument specifies the number of lines to be reviewed, so `#review 10` displays the last 10 lines typed. The second argument specifies the number of lines to be displayed, so `#review 10 5` displays five lines, starting at the 10th previous line.

Stata reserves a buffer for `#review` lines and stores as many previous lines in the buffer as will fit, rolling out the oldest line to make room for the newest. Requests to `#review` lines no longer stored will be ignored. Only lines typed at the terminal are placed in the `#review` buffer. See [U] **10.5 Editing previous lines in Stata**.

▷ Example 1

Typing `#review` by itself will show the last five lines you typed at the terminal:

```
. #review
5 use mydata
4 * comments go into the #review buffer, too
3 describe
2 tabulate marriage educ [freq=number]
1 tabulate marriage educ [freq=number], chi2
. _
```

Typing `#review 15 2` shows the 15th and 14th previous lines:

```
. #review 15 2
15 replace x=. if x<200
14 summarize x
. _
```

◁

Title

roc — Receiver operating characteristic (ROC) analysis

Description

ROC analysis quantifies the accuracy of diagnostic tests or other evaluation modalities used to discriminate between two states or conditions, which are here referred to as normal and abnormal or control and case. The discriminatory accuracy of a diagnostic test is measured by its ability to correctly classify known normal and abnormal subjects. For this reason, we often refer to the diagnostic test as a classifier. The analysis uses the ROC curve, a graph of the sensitivity versus 1 − specificity of the diagnostic test. The sensitivity is the fraction of positive cases that are correctly classified by the diagnostic test, whereas the specificity is the fraction of negative cases that are correctly classified. Thus the sensitivity is the true-positive rate, and the specificity is the true-negative rate.

There are six ROC commands:

Command	Entry	Description
`roccomp`	[R] **roccomp**	Tests of equality of ROC areas
`rocgold`	[R] **roccomp**	Tests of equality of ROC areas against a standard ROC curve
`rocfit`	[R] **rocfit**	Parametric ROC models
`rocreg`	[R] **rocreg**	Nonparametric and parametric ROC regression models
`rocregplot`	[R] **rocregplot**	Plot marginal and covariate-specific ROC curves
`roctab`	[R] **roctab**	Nonparametric ROC analysis

Postestimation commands are available after `rocfit` and `rocreg`; see [R] **rocfit postestimation** and [R] **rocreg postestimation**.

Both nonparametric and parametric (semiparametric) methods have been suggested for generating the ROC curve. The `roctab` command performs nonparametric ROC analysis for a single classifier. `roccomp` extends the nonparametric ROC analysis function of `roctab` to situations where we have multiple diagnostic tests of interest to be compared and tested. The `rocgold` command also provides ROC analysis for multiple classifiers. `rocgold` compares each classifier's ROC curve to a "gold standard" ROC curve and makes adjustments for multiple comparisons in the analysis. Both `rocgold` and `roccomp` also allow parametric estimation of the ROC curve through a binormal fit. In a binormal fit, both the control and the case populations are normal.

The `rocfit` command also estimates the ROC curve of a classifier through a binormal fit. Unlike `roctab`, `roccomp`, and `rocgold`, `rocfit` is an estimation command. In postestimation, graphs of the ROC curve and confidence bands can be produced. Additional tests on the parameters can also be conducted.

ROC analysis can be interpreted as a two-stage process. First, the control distribution of the classifier is estimated, assuming a normal model or using a distribution-free estimation technique. The classifier is standardized using the control distribution to 1 − percentile value, the false-positive rate. Second, the ROC curve is estimated as the case distribution of the standardized classifier values.

Covariates may affect both stages of ROC analysis. The first stage may be affected, yielding a covariate-adjusted ROC curve. The second stage may also be affected, producing multiple covariate-specific ROC curves.

The `rocreg` command performs ROC analysis under both types of covariate effects. Both parametric (semiparametric) and nonparametric methods may be used by `rocreg`. Like `rocfit`, `rocreg` is an estimation command and provides many postestimation capabilities.

The global performance of a diagnostic test is commonly summarized by the area under the ROC curve (AUC). This area can be interpreted as the probability that the result of a diagnostic test of a randomly selected abnormal subject will be greater than the result of the same diagnostic test from a randomly selected normal subject. The greater the AUC, the better the global performance of the diagnostic test. Each of the ROC commands provides computation of the AUC.

Citing a lack of clinical relevance for the AUC, other ROC summary measures have been suggested. These include the partial area under the ROC curve for a given false-positive rate t [pAUC(t)]. This is the area under the ROC curve from the false-positive rate of 0 to t. The ROC value at a particular false-positive rate and the false-positive rate for a particular ROC value are also useful summary measures for the ROC curve. These three measures are directly estimated by `rocreg` during the model fit or postestimation stages. Point estimates of ROC value are computed by the other ROC commands, but no standard errors are reported.

See Pepe (2003) for a discussion of ROC analysis. Pepe has posted Stata datasets and programs used to reproduce results presented in the book (http://www.stata.com/bookstore/pepe.html).

Reference

Pepe, M. S. 2003. *The Statistical Evaluation of Medical Tests for Classification and Prediction*. New York: Oxford University Press.

Title

roccomp — Tests of equality of ROC areas

Syntax

Test equality of ROC areas

`roccomp` *refvar classvar* [*classvars*] [*if*] [*in*] [*weight*] [`,` *roccomp_options*]

Test equality of ROC area against a standard ROC curve

`rocgold` *refvar goldvar classvar* [*classvars*] [*if*] [*in*] [*weight*] [`,` *rocgold_options*]

roccomp_options	Description
Main	
`by(`*varname*`)`	split into groups by variable
`test(`*matname*`)`	use contrast matrix for comparing ROC areas
`graph`	graph the ROC curve
`norefline`	suppress plotting the 45-degree reference line
`separate`	place each ROC curve on its own graph
`summary`	report the area under the ROC curve
`binormal`	estimate areas by using binormal distribution assumption
`line#opts(`*cline_options*`)`	affect rendition of the #th binormal fit line
`level(#)`	set confidence level; default is `level(95)`
Plot	
`plot#opts(`*plot_options*`)`	affect rendition of the #th ROC curve
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

`fweights` are allowed; see [U] **11.1.6 weight**.

rocgold_options	Description
Main	
`sidak`	adjust the significance probability by using Šidák's method
`test(`*matname*`)`	use contrast matrix for comparing ROC areas
`graph`	graph the ROC curve
`norefline`	suppress plotting the 45-degree reference line
`separate`	place each ROC curve on its own graph
`summary`	report the area under the ROC curve
`binormal`	estimate areas by using binormal distribution assumption
`line#opts(`*cline_options*`)`	affect rendition of the #th binormal fit line
`level(#)`	set confidence level; default is `level(95)`
Plot	
`plot#opts(`*plot_options*`)`	affect rendition of the #th ROC curve; plot 1 is the "gold standard"
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

`fweights` are allowed; see [U] **11.1.6 weight**.

plot_options	Description
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
cline_options	change the look of the line

Menu

roccomp

Statistics > Epidemiology and related > ROC analysis > Test equality of two or more ROC areas

rocgold

Statistics > Epidemiology and related > ROC analysis > Test equality of ROC area against gold standard

Description

The above commands are used to perform receiver operating characteristic (ROC) analyses with rating and discrete classification data.

The two variables *refvar* and *classvar* must be numeric. The reference variable indicates the true state of the observation, such as diseased and nondiseased or normal and abnormal, and must be coded as 0 and 1. The rating or outcome of the diagnostic test or test modality is recorded in *classvar*, which must be at least ordinal, with higher values indicating higher risk.

`roccomp` tests the equality of two or more ROC areas obtained from applying two or more test modalities to the same sample or to independent samples. `roccomp` expects the data to be in wide form when comparing areas estimated from the same sample and in long form for areas estimated from independent samples.

`rocgold` independently tests the equality of the ROC area of each of several test modalities, specified by *classvar*, against a "gold standard" ROC curve, *goldvar*. For each comparison, `rocgold` reports the raw and the Bonferroni-adjusted significance probability. Optionally, Šidák's adjustment for multiple comparisons can be obtained.

See [R] **rocfit** and [R] **rocreg** for commands that fit maximum-likelihood ROC models.

Options

Main

`by(`*varname*`)` (`roccomp` only) is required when comparing independent ROC areas. The `by()` variable identifies the groups to be compared.

`sidak` (`rocgold` only) requests that the significance probability be adjusted for the effect of multiple comparisons by using Šidák's method. Bonferroni's adjustment is reported by default.

`test(`*matname*`)` specifies the contrast matrix to be used when comparing ROC areas. By default, the null hypothesis that all areas are equal is tested.

`graph` produces graphical output of the ROC curve.

`norefline` suppresses plotting the 45-degree reference line from the graphical output of the ROC curve.

`separate` is meaningful only with `roccomp` and specifies that each ROC curve be placed on its own graph rather than one curve on top of the other.

`summary` reports the area under the ROC curve, its standard error, and its confidence interval. This option is needed only when also specifying `graph`.

`binormal` specifies that the areas under the ROC curves to be compared should be estimated using the binormal distribution assumption. By default, areas to be compared are computed using the trapezoidal rule.

`line#opts(`*cline_options*`)` affects the rendition of the line representing the #th ROC curve drawn using the binormal distribution assumption; see [G-3] ***cline_options***. These lines are drawn only if the `binormal` option is specified.

`level(#)` specifies the confidence level, as a percentage, for the confidence intervals. The default is `level(95)` or as set by `set level`; see [R] **level**.

Plot

`plot#opts(`*plot_options*`)` affects the rendition of the #th ROC curve—the curve's plotted points connected by lines. The *plot_options* can affect the size and color of markers, whether and how the markers are labeled, and whether and how the points are connected; see [G-3] ***marker_options***, [G-3] ***marker_label_options***, and [G-3] ***cline_options***.

For `rocgold`, `plot1opts()` are applied to the ROC for the gold standard.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line; see [G-3] ***cline_options***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***. These include options for titling the graph (see [G-3] ***title_options***), options for saving the graph to disk (see [G-3] ***saving_option***), and the `by()` option (see [G-3] ***by_option***).

Remarks

Remarks are presented under the following headings:

Introduction
Comparing areas under the ROC curve
Correlated data
Independent data
Comparing areas with a gold standard

Introduction

`roccomp` provides comparison of the ROC curves of multiple classifiers. `rocgold` compares the ROC curves of multiple classifiers with a single "gold standard" classifier. Adjustment of inference for multiple comparisons is also provided by `rocgold`.

See Pepe (2003) for a discussion of ROC analysis. Pepe has posted Stata datasets and programs used to reproduce results presented in the book (http://www.stata.com/bookstore/pepe.html).

Comparing areas under the ROC curve

The area under multiple ROC curves can be compared by using `roccomp`. The command syntax is slightly different if the ROC curves are correlated (that is, different diagnostic tests are applied to the same sample) or independent (that is, diagnostic tests are applied to different samples).

Correlated data

▷ Example 1

Hanley and McNeil (1983) presented data from an evaluation of two computer algorithms designed to reconstruct CT images from phantoms. We will call these two algorithms' modalities 1 and 2. A sample of 112 phantoms was selected; 58 phantoms were considered normal, and the remaining 54 were abnormal. Each of the two modalities was applied to each phantom, and the resulting images were rated by a reviewer using a six-point scale: 1 = definitely normal, 2 = probably normal, 3 = possibly normal, 4 = possibly abnormal, 5 = probably abnormal, and 6 = definitely abnormal. Because each modality was applied to the same sample of phantoms, the two sets of outcomes are correlated.

We list the first 7 observations:

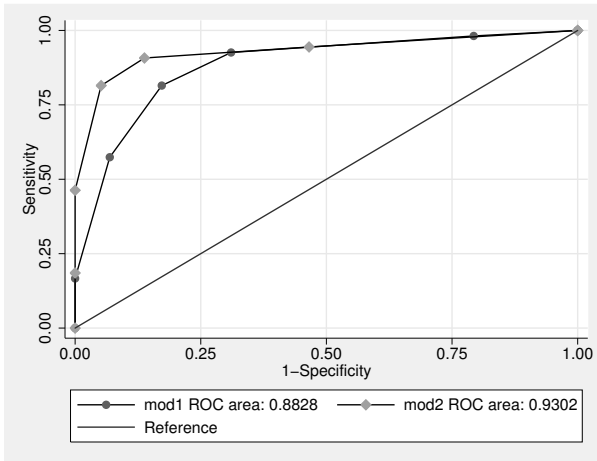
```
. use http://www.stata-press.com/data/r12/ct
. list in 1/7, sep(0)
```

	mod1	mod2	status
1.	2	1	0
2.	5	5	1
3.	2	1	0
4.	2	3	0
5.	5	6	1
6.	2	2	0
7.	3	2	0

The data are in wide form, which is required when dealing with correlated data. Each observation corresponds to one phantom. The variable `mod1` identifies the rating assigned for the first modality, and `mod2` identifies the rating assigned for the second modality. The true status of the phantoms is given by `status=0` if they are normal and `status=1` if they are abnormal. The observations with at least one missing rating were dropped from the analysis.

We plot the two ROC curves and compare their areas.

```
. roccomp status mod1 mod2, graph summary
```



	Obs	ROC Area	Std. Err.	−Asymptotic Normal− [95% Conf.	Interval]
mod1	112	0.8828	0.0317	0.82067	0.94498
mod2	112	0.9302	0.0256	0.88005	0.98042

```
Ho: area(mod1) = area(mod2)
    chi2(1) =     2.31       Prob>chi2 =   0.1282
```

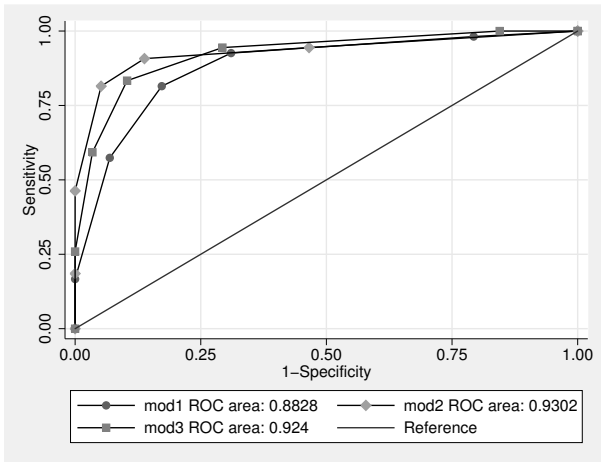
By default, `roccomp`, with the `graph` option specified, plots the ROC curves on the same graph. Optionally the curves can be plotted side by side, each on its own graph, by also specifying `separate`.

For each curve, `roccomp` reports summary statistics and provides a test for the equality of the area under the curves, using an algorithm suggested by DeLong, DeLong, and Clarke-Pearson (1988).

Although the area under the ROC curve for modality 2 is larger than that of modality 1, the chi-squared test yielded a significance probability of 0.1282, suggesting that there is no significant difference between these two areas.

The `roccomp` command can also be used to compare more than two ROC areas. To illustrate this, we modified the previous dataset by including a fictitious third modality.

```
. use http://www.stata-press.com/data/r12/ct2
. roccomp status mod1 mod2 mod3, graph summary
```



	Obs	ROC Area	Std. Err.	−Asymptotic Normal− [95% Conf.	Interval]
mod1	112	0.8828	0.0317	0.82067	0.94498
mod2	112	0.9302	0.0256	0.88005	0.98042
mod3	112	0.9240	0.0241	0.87670	0.97132

```
Ho: area(mod1) = area(mod2) = area(mod3)
    chi2(2) =     6.54       Prob>chi2 =   0.0381
```

By default, `roccomp` tests whether the areas under the ROC curves are all equal. Other comparisons can be tested by creating a contrast matrix and specifying `test(`*matname*`)`, where *matname* is the name of the contrast matrix.

For example, assume that we are interested in testing whether the area under the ROC for `mod1` is equal to that of `mod3`. To do this, we can first create an appropriate contrast matrix and then specify its name with the `test()` option.

Of course, this is a trivial example because we could have just specified

```
. roccomp status mod1 mod3
```

without including `mod2` to obtain the same test results. However, for illustration, we will continue with this example.

The contrast matrix must have its number of columns equal to the number of *classvars* (that is, the total number of ROC curves) and a number of rows less than or equal to the number of *classvars*, and the elements of each row must add to zero.

```
. matrix C=(1,0,-1)
. roccomp status mod1 mod2 mod3, test(C)
                              ROC                    -Asymptotic Normal--
                    Obs       Area     Std. Err.      [95% Conf. Interval]
---------------------------------------------------------------------------
mod1                112     0.8828       0.0317        0.82067     0.94498
mod2                112     0.9302       0.0256        0.88005     0.98042
mod3                112     0.9240       0.0241        0.87670     0.97132
---------------------------------------------------------------------------
Ho: Comparison as defined by contrast matrix: C
    chi2(1) =     5.25       Prob>chi2 =    0.0220
```

Although all three areas are reported, the comparison is made using the specified contrast matrix.

Perhaps more interesting would be a comparison of the area from `mod1` and the average area of `mod2` and `mod3`.

```
. matrix C=(1,-.5,-.5)
. roccomp status mod1 mod2 mod3, test(C)
                              ROC                    -Asymptotic Normal--
                    Obs       Area     Std. Err.      [95% Conf. Interval]
---------------------------------------------------------------------------
mod1                112     0.8828       0.0317        0.82067     0.94498
mod2                112     0.9302       0.0256        0.88005     0.98042
mod3                112     0.9240       0.0241        0.87670     0.97132
---------------------------------------------------------------------------
Ho: Comparison as defined by contrast matrix: C
    chi2(1) =     3.43       Prob>chi2 =    0.0642
```

Other contrasts could be made. For example, we could test if `mod3` is different from at least one of the other two by first creating the following contrast matrix:

```
. matrix C=(-1, 0, 1 \ 0, -1, 1)
. matrix list C
C[2,3]
    c1  c2  c3
r1  -1   0   1
r2   0  -1   1
```

◁

Independent data

▷ Example 2

In example 1, we noted that because each test modality was applied to the same sample of phantoms, the classification outcomes were correlated. Now assume that we have collected the same data presented by Hanley and McNeil (1983), except that we applied the first test modality to one sample of phantoms and the second test modality to a different sample of phantoms. The resulting measurements are now considered independent.

Here are a few of the observations.

```
. use http://www.stata-press.com/data/r12/ct3
. list in 1/7, sep(0)
```

	pop	status	rating	mod
1.	12	0	1	1
2.	31	0	1	2
3.	1	1	1	1
4.	3	1	1	2
5.	28	0	2	1
6.	19	0	2	2
7.	3	1	2	1

The data are in long form, which is required when dealing with independent data. The data consist of 24 observations: 6 observations corresponding to abnormal phantoms and 6 to normal phantoms evaluated using the first modality, and similarly 6 observations corresponding to abnormal phantoms and 6 to normal phantoms evaluated using the second modality. The number of phantoms corresponding to each observation is given by the `pop` variable. Once again we have frequency-weighted data. The variable `mod` identifies the modality, and `rating` is the assigned classification.

We can better view our data by using the `table` command.

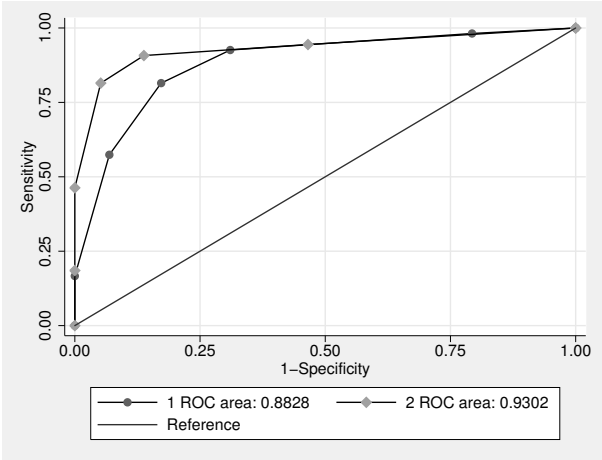
```
. table status rating [fw=pop], by(mod) row col
```

mod and status	rating						
	1	2	3	4	5	6	Total
1							
0	12	28	8	6	4		58
1	1	3	6	13	22	9	54
Total	13	31	14	19	26	9	112
2							
0	31	19	5	3			58
1	3	2	5	19	15	10	54
Total	34	21	10	22	15	10	112

The `status` variable indicates the true status of the phantoms: `status` $= 0$ if they are normal and `status` $= 1$ if they are abnormal.

We now compare the areas under the two ROC curves.

```
. roccomp status rating [fw=pop], by(mod) graph summary
```



mod	Obs	ROC Area	Std. Err.	-Asymptotic Normal— [95% Conf.	Interval]
1	112	0.8828	0.0317	0.82067	0.94498
2	112	0.9302	0.0256	0.88005	0.98042

```
Ho: area(1) = area(2)
    chi2(1) =     1.35       Prob>chi2 =   0.2447
```

Comparing areas with a gold standard

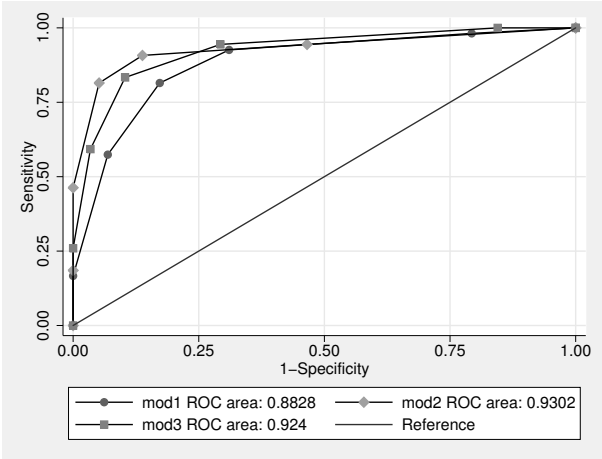
The area under multiple ROC curves can be compared with a gold standard using `rocgold`. The command syntax is similar to that of `roccomp`. The tests are corrected for the effect of multiple comparisons.

▷ Example 3

We will use the same data (presented by Hanley and McNeil [1983]) as in the `roccomp` examples. Let's assume that the first modality is considered to be the standard against which both the second and third modalities are compared.

We want to plot and compare both the areas of the ROC curves of `mod2` and `mod3` with `mod1`. Because we consider `mod1` to be the gold standard, it is listed first after the reference variable in the `rocgold` command line.

```
. use http://www.stata-press.com/data/r12/ct2
. rocgold status mod1 mod2 mod3, graph summary
```



	ROC Area	Std. Err.	chi2	df	Pr>chi2	Bonferroni Pr>chi2
mod1 (standard)	0.8828	0.0317				
mod2	0.9302	0.0256	2.3146	1	0.1282	0.2563
mod3	0.9240	0.0241	5.2480	1	0.0220	0.0439

Equivalently, we could have done this in two steps by using the `roccomp` command.

```
. roccomp status mod1 mod2, graph summary
. roccomp status mod1 mod3, graph summary
```

◁

Saved results

`roccomp` saves the following in `r()`:

Scalars

`r(N_g)`	number of groups	`r(df)`	χ^2 degrees of freedom
`r(p)`	significance probability	`r(chi2)`	χ^2

Matrices

`r(V)`	variance–covariance matrix

`rocgold` saves the following in `r()`:

Scalars

`r(N_g)`	number of groups

Matrices

`r(V)`	variance–covariance matrix	`r(p)`	significance-probability vector
`r(chi2)`	χ^2 vector	`r(p_adj)`	adjusted significance-probability vector
`r(df)`	χ^2 degrees-of-freedom vector		

Methods and formulas

`roccomp` and `rocgold` are implemented as ado-files.

Assume that we applied a diagnostic test to each of N_n normal and N_a abnormal subjects. Further assume that the higher the outcome value of the diagnostic test, the higher the risk of the subject being abnormal. Let $\widehat{\theta}$ be the estimated area under the curve, and let $X_i, i = 1, 2, \ldots, N_a$ and $Y_j, j = 1, 2, \ldots, N_n$ be the values of the diagnostic test for the abnormal and normal subjects, respectively.

Areas under ROC curves are compared using an algorithm suggested by DeLong, DeLong, and Clarke-Pearson (1988). Let $\widehat{\theta} = (\widehat{\theta^1}, \widehat{\theta^2}, \ldots, \widehat{\theta^k})$ be a vector representing the areas under k ROC curves. See *Methods and formulas* in [R] **roctab** for the definition of these area estimates.

For the rth area, define

$$V_{10}^r(X_i) = \frac{1}{N_n} \sum_{j=1}^{N_n} \psi(X_i^r, Y_j^r)$$

and for each normal subject, j, define

$$V_{01}^r(Y_j) = \frac{1}{N_a} \sum_{i=1}^{N_a} \psi(X_i^r, Y_j^r)$$

where

$$\psi(X^r, Y^r) = \begin{cases} 1 & Y^r < X^r \\ \frac{1}{2} & Y^r = X^r \\ 0 & Y^r > X^r \end{cases}$$

Define the $k \times k$ matrix $\mathbf{S_{10}}$ such that the (r, s)th element is

$$S_{10}^{r,s} = \frac{1}{N_a - 1} \sum_{i=1}^{N_a} \{V_{10}^r(X_i) - \widehat{\theta^r}\}\{V_{10}^s(X_i) - \widehat{\theta^s}\}$$

and $\mathbf{S_{01}}$ such that the (r, s)th element is

$$S_{01}^{r,s} = \frac{1}{N_n - 1} \sum_{j=1}^{N_n} \{V_{01}^r(Y_i) - \widehat{\theta^r}\}\{V_{01}^s(Y_i) - \widehat{\theta^s}\}$$

Then the covariance matrix is

$$S = \frac{1}{N_a} S_{10} + \frac{1}{N_n} S_{01}$$

Let $\mathbf{L}$ be a contrast matrix defining the comparison, so that

$$(\widehat{\theta} - \theta)' \mathbf{L}' \left(\mathbf{LSL}'\right)^{-1} \mathbf{L} (\widehat{\theta} - \theta)$$

has a chi-squared distribution with degrees of freedom equal to the rank of $\mathbf{LSL}'$.

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Also see

[R] **logistic postestimation** — Postestimation tools for logistic

[R] **roc** — Receiver operating characteristic (ROC) analysis

[R] **rocfit** — Parametric ROC models

[R] **rocreg** — Receiver operating characteristic (ROC) regression

[R] **roctab** — Nonparametric ROC analysis

Title

rocfit — Parametric ROC models

Syntax

`rocfit` *refvar classvar* [*if*] [*in*] [*weight*] [`,` *rocfit_options*]

rocfit_options	Description
Model	
`continuous(#)`	divide *classvar* into # groups of approximately equal length
`generate(`*newvar*`)`	create *newvar* containing classification groups
SE	
`vce(`*vcetype*`)`	*vcetype* may be `oim` or `opg`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
Maximization	
maximize_options	control the maximization process; seldom used

`fweights` are allowed; see [U] **11.1.6 weight**.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Epidemiology and related > ROC analysis > Parametric ROC analysis without covariates

Description

`rocfit` fits maximum-likelihood ROC models assuming a binormal distribution of the latent variable.

The two variables *refvar* and *classvar* must be numeric. The reference variable indicates the true state of the observation, such as diseased and nondiseased or normal and abnormal, and must be coded as 0 and 1. The rating or outcome of the diagnostic test or test modality is recorded in *classvar*, which must be at least ordinal, with higher values indicating higher risk.

See [R] **roc** for other commands designed to perform receiver operating characteristic (ROC) analyses with rating and discrete classification data.

Options

Model

`continuous(#)` specifies that the continuous *classvar* be divided into # groups of approximately equal length. This option is required when *classvar* takes on more than 20 distinct values.

`continuous(.)` may be specified to indicate that *classvar* be used as it is, even though it could have more than 20 distinct values.

`generate(`*newvar*`)` specifies the new variable that is to contain the values indicating the groups produced by `continuous(#)`. `generate()` may be specified only with `continuous()`.

SE

`vce(`*vcetype*`)` specifies the type of standard error reported. *vcetype* may be either `oim` or `opg`; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

Remarks

Dorfman and Alf (1969) developed a generalized approach for obtaining maximum likelihood estimates of the parameters for a smooth fitting ROC curve. The most commonly used method for ordinal data, and the one implemented here, is based upon the binormal model; see Pepe (2003), Pepe, Longton, and Janes (2009), and Janes, Longton, and Pepe (2009) for methods of ROC analysis for continuous data, including methods for adjusting for covariates.

The model assumes the existence of an unobserved, continuous, latent variable that is normally distributed (perhaps after a monotonic transformation) in both the normal and abnormal populations with means μ_n and μ_a and variances σ_n^2 and σ_a^2, respectively. The model further assumes that the K categories of the rating variable result from partitioning the unobserved latent variable by $K-1$ fixed boundaries. The method fits a straight line to the empirical ROC points plotted using normal probability scales on both axes. Maximum likelihood estimates of the line's slope and intercept and the $K-1$ boundaries are obtained simultaneously. See *Methods and formulas* for details.

The intercept from the fitted line is a measurement of $(\mu_a - \mu_n)/\sigma_a$, and the slope measures σ_n/σ_a.

Thus the intercept is the standardized difference between the two latent population means, and the slope is the ratio of the two standard deviations. The null hypothesis that there is no difference between the two population means is evaluated by testing that the intercept $= 0$, and the null hypothesis that the variances in the two populations are equal is evaluated by testing that the slope $= 1$.

▷ Example 1

We use Hanley and McNeil's (1982) dataset, described in example 1 of [R] **roctab**, to fit a smooth ROC curve assuming a binormal model.

```
. use http://www.stata-press.com/data/r12/hanley
. rocfit disease rating
Fitting binormal model:
Iteration 0:   log likelihood = -123.68069
Iteration 1:   log likelihood = -123.64867
Iteration 2:   log likelihood = -123.64855
Iteration 3:   log likelihood = -123.64855
Binormal model of disease on rating              Number of obs   =       109
Goodness-of-fit chi2(2) =        0.21
Prob > chi2             =      0.9006
Log likelihood          =  -123.64855
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
intercept	1.656782	0.310456	5.34	0.000	1.048300	2.265265
slope (*)	0.713002	0.215882	-1.33	0.092	0.289881	1.136123
/cut1	0.169768	0.165307	1.03	0.152	-0.154227	0.493764
/cut2	0.463215	0.167235	2.77	0.003	0.135441	0.790990
/cut3	0.766860	0.174808	4.39	0.000	0.424243	1.109477
/cut4	1.797938	0.299581	6.00	0.000	1.210770	2.385106

	Indices from binormal fit			
Index	Estimate	Std. Err.	[95% Conf.	Interval]
ROC area	0.911331	0.029506	0.853501	0.969161
delta(m)	2.323671	0.502370	1.339044	3.308298
d(e)	1.934361	0.257187	1.430284	2.438438
d(a)	1.907771	0.259822	1.398530	2.417012

```
(*) z test for slope==1
```

`rocfit` outputs the MLE for the intercept and slope of the fitted regression line along with, here, four boundaries (because there are five ratings) labeled `/cut1` through `/cut4`. Also `rocfit` computes and reports four indices based on the fitted ROC curve: the area under the curve (labeled `ROC area`), $\delta(m)$ (labeled `delta(m)`), d_e (labeled `d(e)`), and d_a (labeled `d(a)`). More information about these indices can be found in *Methods and formulas* and in Erdreich and Lee (1981).

◁

Saved results

rocfit saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(chi2_gf)	goodness-of-fit χ^2
e(df_gf)	goodness-of-fit degrees of freedom
e(p_gf)	χ^2 goodness-of-fit significance probability
e(area)	area under the ROC curve
e(se_area)	standard error for the area under the ROC curve
e(deltam)	delta(m)
e(se_delm)	standard area for delta(m)
e(de)	d(e) index
e(se_de)	standard error for d(e) index
e(da)	d(a) index
e(se_da)	standard error for d(a) index
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	rocfit
e(cmdline)	command as typed
e(depvar)	*refvar* and *classvar*
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(chi2type)	GOF; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V

Matrices

e(b)	coefficient vector
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators

Functions

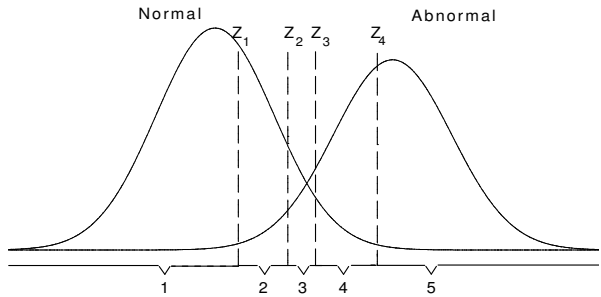
e(sample)	marks estimation sample

Methods and formulas

`rocfit` is implemented as an ado-file.

Dorfman and Alf (1969) developed a general procedure for obtaining maximum likelihood estimates of the parameters of a smooth-fitting ROC curve. The most common method, and the one implemented in Stata, is based upon the binormal model.

The model assumes that there is an unobserved continuous latent variable that is normally distributed in both the normal and abnormal populations. The idea is better explained with the following illustration:



The latent variable is assumed to be normally distributed for both the normal and abnormal subjects, perhaps after a monotonic transformation, with means μ_n and μ_a and variances σ_n^2 and σ_a^2, respectively.

This latent variable is assumed to be partitioned into the k categories of the rating variable by $k-1$ fixed boundaries. In the above figure, the $k=5$ categories of the rating variable identified on the bottom result from the partition of the four boundaries Z_1 through Z_4.

Let R_j for $j=1,2,\ldots,k$ indicate the categories of the rating variable, let $i=1$ if the subject belongs to the normal group, and let $i=2$ if the subject belongs to the abnormal group.

Then

$$p(R_j|i=1) = F(Z_j) - F(Z_{j-1})$$

where $Z_k = (x_k - \mu_n)/\sigma_n$, F is the cumulative normal distribution, $F(Z_0)=0$, and $F(Z_k)=1$. Also,

$$p(R_j|i=2) = F(bZ_j - a) - F(bZ_{j-1} - a)$$

where $b = \sigma_n/\sigma_a$ and $a = (\mu_a - \mu_n)/\sigma_a$.

The parameters a, b and the $k-1$ fixed boundaries Z_j are simultaneously estimated by maximizing the log-likelihood function

$$\log L = \sum_{i=1}^{2}\sum_{j=1}^{k} r_{ij}\log\{p(R_j|i)\}$$

where r_{ij} is the number of R_js in group i.

The area under the fitted ROC curve is computed as

$$\Phi\left(\frac{a}{\sqrt{1+b^2}}\right)$$

where Φ is the standard normal cumulative distribution function.

Point estimates for the ROC curve indices are as follows:

$$\delta(m) = \frac{a}{b} \qquad d_e = \frac{2a}{b+1} \qquad d_a = \frac{a\sqrt{2}}{\sqrt{1+b^2}}$$

Variances for these indices are computed using the delta method.

The $\delta(m)$ estimates $(\mu_a - \mu_n)/\sigma_n$, d_e estimates $2(\mu_a - \mu_n)/(\sigma_a - \sigma_n)$, and d_a estimates $\sqrt{2}(\mu_a - \mu_n)/(\sigma_a^2 - \sigma_n^2)^2$.

Simultaneous confidence bands for the entire curve are obtained, as suggested by Ma and Hall (1993), by first obtaining Working–Hotelling (1929) confidence bands for the fitted straight line in normal probability coordinates and then transforming them back to ROC coordinates.

References

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Also see

[R] **rocfit postestimation** — Postestimation tools for rocfit

[R] **roc** — Receiver operating characteristic (ROC) analysis

[R] **rocreg** — Receiver operating characteristic (ROC) regression

[U] **20 Estimation and postestimation commands**

Title

rocfit postestimation — Postestimation tools for rocfit

Description

The following command is of special interest after `rocfit`:

Command	Description
`rocplot`	plot the fitted ROC curve and simultaneous confidence bands

For information about `rocplot`, see below.

The following standard postestimation commands are also available:

Command	Description
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
* `lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
* `test`	Wald tests of simple and composite linear hypotheses

*See *Using lincom and test* below.

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation command

`rocplot` plots the fitted ROC curve and simultaneous confidence bands.

Syntax for rocplot

```
rocplot [ , rocplot_options ]
```

rocplot_options	Description
Main	
confband	display confidence bands
norefline	suppress plotting the reference line
level(#)	set confidence level; default is level(95)
Plot	
plotopts(*plot_options*)	affect rendition of the ROC points
Fit line	
lineopts(*cline_options*)	affect rendition of the fitted ROC line
CI plot	
ciopts(*area_options*)	affect rendition of the confidence bands
Reference line	
rlopts(*cline_options*)	affect rendition of the reference line
Add plots	
addplot(*plot*)	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than by() documented in [G-3] ***twoway_options***

plot_options	Description
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
cline_options	change the look of the line

Menu

Statistics > Epidemiology and related > ROC analysis > ROC curves after rocfit

Options for rocplot

Main

confband specifies that simultaneous confidence bands be plotted around the ROC curve.

norefline suppresses plotting the 45-degree reference line from the graphical output of the ROC curve.

level(#) specifies the confidence level, as a percentage, for the confidence bands. The default is level(95) or as set by set level; see [R] **level**.

Plot

`plotopts(`*plot_options*`)` affects the rendition of the plotted ROC points, including the size and color of markers, whether and how the markers are labeled, and whether and how the points are connected. For the full list of available *plot_options*, see [G-3] ***marker_options***, [G-3] ***marker_label_options***, and [G-3] ***cline_options***.

Fit line

`lineopts(`*cline_options*`)` affects the rendition of the fitted ROC line; see [G-3] ***cline_options***.

CI plot

`ciopts(`*area_options*`)` affects the rendition of the confidence bands; see [G-3] ***area_options***.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Remarks are presented under the following headings:

Using lincom and test
Using rocplot

Using lincom and test

`intercept`, `slope`, and `cut#`, shown in example 1 of [R] **rocfit**, are equation names and not variable names, so they need to be referenced as described in *Special syntaxes after multiple-equation estimation* of [R] **test**. For example, instead of typing

```
. test intercept
intercept not found
r(111);
```

you should type

```
. test [intercept]_cons
 ( 1)  [intercept]_cons = 0
           chi2(  1) =   28.48
         Prob > chi2 =    0.0000
```

Using rocplot

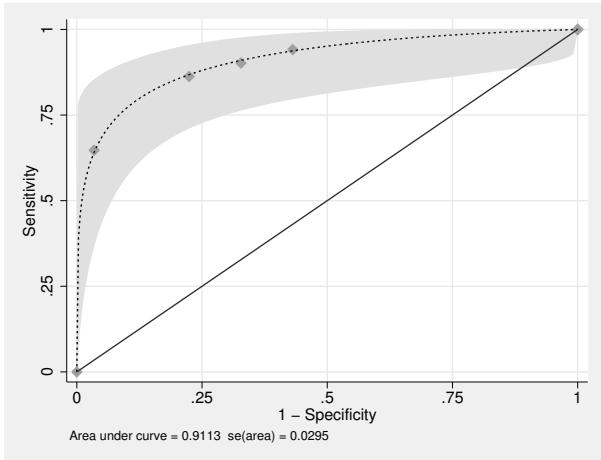
▷ Example 1

In example 1 of [R] **rocfit**, we fit a ROC curve by typing `rocfit disease rating`.

In the output table for our model, we are testing whether the variances of the two latent populations are equal by testing that the slope = 1.

We plot the fitted ROC curve.

```
. rocplot, confband
```



◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **rocfit** — Parametric ROC models

[U] **20 Estimation and postestimation commands**

Title

rocreg — Receiver operating characteristic (ROC) regression

Syntax

Perform nonparametric analysis of ROC curve under covariates, using bootstrap

```
rocreg refvar classvar [classvars] [if] [in] [, np_options boot_options]
```

Perform parametric analysis of ROC curve under covariates, using bootstrap

```
rocreg refvar classvar [classvars] [if] [in], probit
    [probit_options boot_options]
```

Perform parametric analysis of ROC curve under covariates, using maximum likelihood

```
rocreg refvar classvar [classvars] [if] [in] [weight], probit ml
    [probit_ml_options]
```

np_options	Description
Model	
`auc`	estimate total area under the ROC curve; the default
`roc(`*numlist*`)`	estimate ROC for given false-positive rates
`invroc(`*numlist*`)`	estimate false-positive rates for given ROC values
`pauc(`*numlist*`)`	estimate partial area under the ROC curve (pAUC) up to each false-positive rate
`cluster(`*varname*`)`	variable identifying resampling clusters
`ctrlcov(`*varlist*`)`	adjust control distribution for covariates in *varlist*
`ctrlmodel(strata|linear)`	stratify or regress on covariates; default is `ctrlmodel(strata)`
`pvc(empirical|normal)`	use empirical or normal distribution percentile value estimates; default is `pvc(empirical)`
`tiecorrected`	adjust for tied observations; not allowed with `pvc(normal)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`

probit_options	Description
Model	
* probit	fit the probit model
roccov(*varlist*)	covariates affecting ROC curve
fprpts(#)	number of false-positive rate points to use in fitting ROC curve; default is fprpts(10)
ctrlfprall	fit ROC curve at each false-positive rate in control population
cluster(*varname*)	variable identifying resampling clusters
ctrlcov(*varlist*)	adjust control distribution for covariates in *varlist*
ctrlmodel(strata | linear)	stratify or regress on covariates; default is ctrlmodel(strata)
pvc(empirical | normal)	use empirical or normal distribution percentile value estimates; default is pvc(empirical)
tiecorrected	adjust for tied observations; not allowed with pvc(normal)
Reporting	
level(#)	set confidence level; default is level(95)

*probit is required.

probit_ml_options	Description
Model	
* probit	fit the probit model
* ml	fit the probit model by maximum likelihood estimation
roccov(*varlist*)	covariates affecting ROC curve
cluster(*varname*)	variable identifying clusters
ctrlcov(*varlist*)	adjust control distribution for covariates in *varlist*
Reporting	
level(#)	set confidence level; default is level(95)
display_options	control column formats, line width, and display of omitted variables
Maximization	
maximize_options	control the maximization process; seldom used

*probit and ml are required.

fweights, iweights, and pweights are allowed with maximum likelihood estimation; see [U] **11.1.6 weight**.

boot_options	Description
Bootstrap	
nobootstrap	do not perform bootstrap, just output point estimates
bseed(#)	random-number seed for bootstrap
breps(#)	number of bootstrap replications; default is breps(1000)
bootcc	perform case–control (stratified on *refvar*) sampling rather than cohort sampling in bootstrap
nobstrata	ignore covariate stratification in bootstrap sampling
nodots	suppress bootstrap replication dots
* bsave(*filename*, ...)	save bootstrap replicates from parametric estimation
* bfile(*filename*)	use bootstrap replicates dataset for estimation replay

* bsave() and bfile() are allowed only when the probit option is also specified.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Epidemiology and related > ROC analysis > ROC regression models

Description

The rocreg command is used to perform receiver operating characteristic (ROC) analyses with rating and discrete classification data under the presence of covariates.

The two variables *refvar* and *classvar* must be numeric. The reference variable indicates the true state of the observation—such as diseased and nondiseased or normal and abnormal—and must be coded as 0 and 1. The *refvar* coded as 0 can also be called the control population, while the *refvar* coded as 1 comprises the case population. The rating or outcome of the diagnostic test or test modality is recorded in *classvar*, which must be ordinal, with higher values indicating higher risk.

rocreg can fit three models: a nonparametric model, a parametric probit model that uses the bootstrap for inference, and a parametric probit model fit using maximum likelihood.

Options for nonparametric ROC estimation, using bootstrap

Model

auc estimates the total area under the ROC curve. This is the default summary statistic.

roc(*numlist*) estimates the ROC corresponding to each of the false-positive rates in *numlist*. The values of *numlist* must be in the range (0,1).

invroc(*numlist*) estimates the false-positive rates corresponding to each of the ROC values in *numlist*. The values of *numlist* must be in the range (0,1).

pauc(*numlist*) estimates the partial area under the ROC curve up to each false-positive rate in *numlist*. The values of *numlist* must in the range (0,1].

cluster(*varname*) specifies the variable identifying resampling clusters.

ctrlcov(*varlist*) specifies the covariates to be used to adjust the control population.

`ctrlmodel(strata|linear)` specifies how to model the control population of classifiers on `ctrlcov()`. When `ctrlmodel(linear)` is specified, linear regression is used. The default is `ctrlmodel(strata)`; that is, the control population of classifiers is stratified on the control variables.

`pvc(empirical|normal)` determines how the percentile values of the control population will be calculated. When `pvc(normal)` is specified, the standard normal cumulative distribution function (CDF) is used for calculation. Specifying `pvc(empirical)` will use the empirical CDFs of the control population classifiers for calculation. The default is `pvc(empirical)`.

`tiecorrected` adjusts the percentile values for ties. For each value of the classifier, one half the probability that the classifier equals that value under the control population is added to the percentile value. `tiecorrected` is not allowed with `pvc(normal)`.

Reporting

`level(#)`; see [R] **estimation options**.

Also see *Options for rocreg, using bootstrap*.

Options for parametric ROC estimation, using bootstrap

Model

`probit` fits the probit model. This option is required and implies parametric estimation.

`roccov(`*varlist*`)` specifies the covariates that will affect the ROC curve.

`fprpts(#)` sets the number of false-positive rate points to use in modeling the ROC curve. These points form an equispaced grid on (0,1). The default is `fprpts(10)`.

`ctrlfprall` models the ROC curve at each false-positive rate in the control population.

`cluster(`*varname*`)` specifies the variable identifying resampling clusters.

`ctrlcov(`*varlist*`)` specifies the covariates to be used to adjust the control population.

`ctrlmodel(strata|linear)` specifies how to model the control population of classifiers on `ctrlcov()`. When `ctrlmodel(linear)` is specified, linear regression is used. The default is `ctrlmodel(strata)`; that is, the control population of classifiers is stratified on the control variables.

`pvc(empirical|normal)` determines how the percentile values of the control population will be calculated. When `pvc(normal)` is specified, the standard normal CDF is used for calculation. Specifying `pvc(empirical)` will use the empirical CDFs of the control population classifiers for calculation. The default is `pvc(empirical)`.

`tiecorrected` adjusts the percentile values for ties. For each value of the classifier, one half the probability that the classifier equals that value under the control population is added to the percentile value. `tiecorrected` is not allowed with `pvc(normal)`.

Reporting

`level(#)`; see [R] **estimation options**.

Also see *Options for rocreg, using bootstrap*.

Options for parametric ROC estimation, using maximum likelihood

Model

`probit` fits the probit model. This option is required and implies parametric estimation.

`ml` fits the probit model by maximum likelihood estimation. This option is required and must be specified with `probit`.

`roccov(`*varlist*`)` specifies the covariates that will affect the ROC curve.

`cluster(`*varname*`)` specifies the variable used for clustering.

`ctrlcov(`*varlist*`)` specifies the covariates to be used to adjust the control population.

Reporting

`level(#)`; see [R] **estimation options**.

display_options: `noomitted`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used. The `technique(bhhh)` option is not allowed.

Options for rocreg, using bootstrap

Bootstrap

`nobootstrap` specifies that bootstrap standard errors not be calculated.

`bseed(#)` specifies the random-number seed to be used in the bootstrap.

`breps(#)` sets the number of bootstrap replications. The default is `breps(1000)`.

`bootcc` performs case–control (stratified on *refvar*) sampling rather than cohort bootstrap sampling.

`nobstrata` ignores covariate stratification in bootstrap sampling.

`nodots` suppresses bootstrap replicate dots.

`bsave(`*filename*`, ...)` saves bootstrap replicates from parametric estimation in the given *filename* with specified options (that is, `replace`). `bsave()` is only allowed with parametric analysis using bootstrap.

`bfile(`*filename*`)` specifies to use the bootstrap replicates dataset for estimation replay. `bfile()` is only allowed with parametric analysis using bootstrap.

Remarks

Remarks are presented under the following headings:

Introduction
ROC statistics
Covariate-adjusted ROC curves
Parametric ROC curves: Estimating equations
Parametric ROC curves: Maximum likelihood

Introduction

Receiver operating characteristic (ROC) analysis provides a quantitative measure of the accuracy of diagnostic tests to discriminate between two states or conditions. These conditions may be referred to as normal and abnormal, nondiseased and diseased, or control and case. We will use these terms interchangeably. The discriminatory accuracy of a diagnostic test is measured by its ability to correctly classify known control and case subjects.

The analysis uses the ROC curve, a graph of the sensitivity versus 1 − specificity of the diagnostic test. The sensitivity is the fraction of positive cases that are correctly classified by the diagnostic test, whereas the specificity is the fraction of negative cases that are correctly classified. Thus the sensitivity is the true-positive rate, and the specificity is the true-negative rate. We also call 1 − specificity the false-positive rate.

These rates are functions of the possible outcomes of the diagnostic test. At each outcome, a decision will be made by the user of the diagnostic test to classify the tested subject as either normal or abnormal. The true-positive and false-positive rates measure the probability of correct classification or incorrect classification of the subject as abnormal. Given the classification role of the diagnostic test, we will refer to it as the classifier.

Using this basic definition of the ROC curve, Pepe (2000) and Pepe (2003) describe how ROC analysis can be performed as a two-stage process. In the first stage, the control distribution of the classifier is estimated. The specificity is then determined as the percentiles of the classifier values calculated based on the control population. The false-positive rates are calculated as 1 − specificity. In the second stage, the ROC curve is estimated as the cumulative distribution of the case population's "false-positive" rates, also known as the survival function under the case population of the previously calculated percentiles. We use the terms ROC value and true-positive value interchangeably.

This formulation of ROC curve analysis provides simple, nonparametric estimates of several ROC curve summary parameters: area under the ROC curve, partial area under the ROC curve, ROC value for a given false-positive rate, and false-positive rate (also known as invROC) for a given ROC value. In the next section, we will show how to use `rocreg` to compute these estimates with bootstrap inference. There we will also show how `rocreg` complements the other nonparametric Stata ROC commands `roctab` and `roccomp`.

Other factors beyond condition status and the diagnostic test may affect both stages of ROC analysis. For example, a test center may affect the control distribution of the diagnostic test. Disease severity may affect the distribution of the standardized diagnostic test under the case population. Our analysis of the ROC curve in these situations will be more accurate if we take these covariates into account.

In a nonparametric ROC analysis, covariates may only affect the first stage of estimation; that is, they may be used to adjust the control distribution of the classifier. In a parametric ROC analysis, it is assumed that ROC follows a normal distribution, and thus covariates may enter the model at both stages; they may be used to adjust the control distribution and to model ROC as a function of these covariates and the false-positive rate. In parametric models, both sets of covariates need not be distinct but, in fact, they are often the same.

To model covariate effects on the first stage of ROC analysis, Janes and Pepe (2009) propose a covariate-adjusted ROC curve. We will demonstrate the covariate adjustment capabilities of `rocreg` in *Covariate-adjusted ROC curves*.

To account for covariate effects at the second stage, we assume a parametric model. Particularly, the ROC curve is a generalized linear model of the covariates. We will thus have a separate ROC curve for each combination of the relevant covariates. In *Parametric ROC curves: Estimating equations*, we show how to fit the model with estimating equations and bootstrap inference using `rocreg`.

This method, documented as the "pdf" approach in Alonzo and Pepe (2002), works well with weak assumptions about the control distribution.

Also in *Parametric ROC curves: Estimating equations*, we show how to fit a constant-only parametric model (involving no covariates) of the ROC curve with weak assumptions about the control distribution. The constant-only model capabilities of `rocreg` in this context will be compared with those of `rocfit`. `roccomp` has the `binormal` option, which will allow it to compute area under the ROC curve according to a normal ROC curve, equivalent to that obtained by `rocfit`. We will compare this functionality with that of `rocreg`.

In *Parametric ROC curves: Maximum likelihood*, we demonstrate maximum likelihood estimation of the ROC curve model with `rocreg`. There we assume a normal linear model for the classifier on the covariates and case–control status. This method is documented in Pepe (2003). We will also demonstrate how to use this method with no covariates, and we will compare `rocreg` under the constant-only model with `rocfit` and `roccomp`.

The `rocregplot` command is used repeatedly in this entry. This command provides graphical output for `rocreg` and is documented in [R] **rocregplot**.

ROC statistics

`roctab` computes the ROC curve by calculating the false-positive rate and true-positive rate empirically at every value of the input classifier. It makes no distributional assumptions about the case or control distributions. We can get identical behavior from `rocreg` by using the default option settings.

▷ Example 1: Nonparametric ROC, AUC

Hanley and McNeil (1982) presented data from a study in which a reviewer was asked to classify, using a five-point scale, a random sample of 109 tomographic images from patients with neurological problems. The rating scale was as follows: 1 is definitely normal, 2 is probably normal, 3 is questionable, 4 is probably abnormal, and 5 is definitely abnormal. The true disease status was normal for 58 of the patients and abnormal for the remaining 51 patients.

Here we list 9 of the 109 observations:

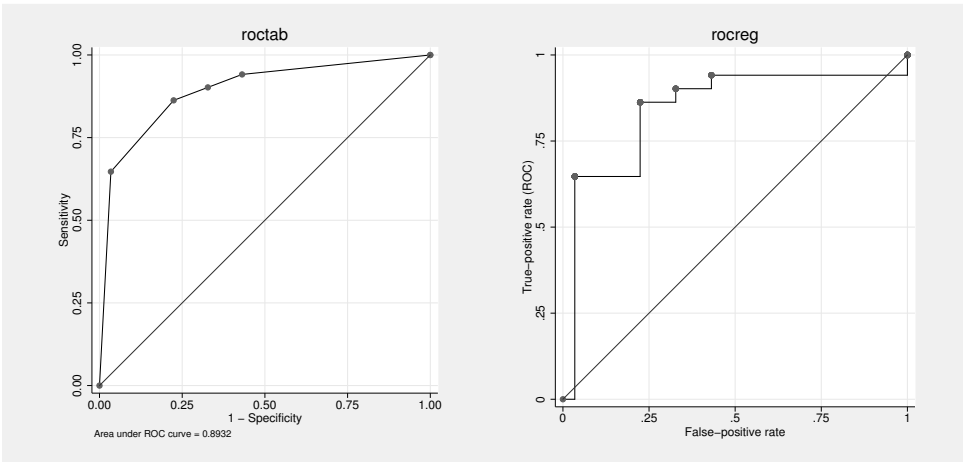
```
. use http://www.stata-press.com/data/r12/hanley
. list disease rating in 1/9
```

	disease	rating
1.	1	5
2.	0	1
3.	1	5
4.	0	4
5.	0	1
6.	0	3
7.	1	5
8.	0	5
9.	0	1

For each observation, `disease` identifies the true disease status of the subject (`0` is normal, `1` is abnormal), and `rating` contains the classification value assigned by the reviewer.

We run `roctab` on these data, specifying the `graph` option so that the ROC curve is rendered. We then calculate the false-positive and true-positive rates of the ROC curve by using `rocreg`. We graph the rates with `rocregplot`. Because we focus on `rocreg` output later, for now we use the `quietly` prefix to omit the output of `rocreg`. Both graphs are combined using `graph combine` (see [G-2] **graph combine**) for comparison. To ease the comparison, we specify the `aspectratio(1)` option in `roctab`; this is the default aspect ratio in `rocregplot`.

```
. roctab disease rating, graph aspectratio(1) name(a) nodraw title("roctab")
. quietly rocreg disease rating
. rocregplot, name(b) nodraw legend(off) title("rocreg")
. graph combine a b
```



Both `roctab` and `rocreg` compute the same false-positive rate and ROC values. The stairstep line connection style of the graph on the right emphasizes the empirical nature of its estimates. The control distribution of the classifier is estimated using the empirical CDF estimate. Similarly, the ROC curve, the distribution of the resulting case observation false-positive rate values, is estimated using the empirical CDF. Note the footnote in the `roctab` plot. By default, `roctab` will estimate the area under the ROC curve (AUC) using a trapezoidal approximation to the estimated false-positive rate and true-positive rate points.

The AUC can be interpreted as the probability that a randomly selected member of the case population will have a larger classifier value than a randomly selected member of the control population. It can also be viewed as the average ROC value, averaged uniformly over the (0,1) false-positive rate domain (Pepe 2003).

The nonparametric estimator of the AUC (DeLong, DeLong, and Clarke-Pearson 1988; Hanley and Hajian-Tilaki 1997) used by `rocreg` is equivalent to the sample mean of the percentile values of the case observations. Thus to calculate the nonparametric AUC estimate, we only need to calculate the percentile values of the case observations with respect to the control distribution.

This estimate can differ from the trapezoidal approximation estimate. Under discrete classification data, like we have here, there may be ties between classifier values from case to control. The trapezoidal approximation uses linear interpolation between the classifier values to correct for ties. Correcting the nonparametric estimator involves adding a correction term to each observation's percentile value, which measures the probability that the classifier is equal to (instead of less than) the observation's classifier value.

The tie-corrected nonparametric estimate (trapezoidal approximation) is used when we think the true ROC curve is smooth. This means that the classifier we measure is a discretized approximation of a true latent and a continuous classifier.

We now recompute the ROC curve of `rating` for classifying `disease` and calculate the AUC. Specifying the `tiecorrected` option allows tie correction to be used in the `rocreg` calculation. Under nonparametric estimation, `rocreg` bootstraps to obtain standard errors and confidence intervals for requested statistics. We use the default 1,000 bootstrap replications to obtain confidence intervals for our parameters. This is a reasonable lower bound to the number of replications (Mooney and Duval 1993) required for estimating percentile confidence intervals. By specifying the `summary` option in `roctab`, we will obtain output showing the trapezoidal approximation of the AUC estimate, along with standard error and confidence-interval estimates for the trapezoidal approximation suggested by DeLong, DeLong, and Clarke-Pearson (1988).

```
. roctab disease rating, summary
                    ROC                    -Asymptotic Normal--
          Obs       Area     Std. Err.      [95% Conf. Interval]
-------------------------------------------------------------------
          109     0.8932       0.0307        0.83295     0.95339

. rocreg disease rating, auc tiecorrected bseed(29092)
(running rocregstat on estimation sample)

Bootstrap replications (1000)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
..................................................   100
  (output omitted)
..................................................   950
..................................................  1000

Bootstrap results                                 Number of obs      =       109
                                                  Replications       =      1000

Nonparametric ROC estimation

Control standardization: empirical, corrected for ties
ROC method             : empirical

Area under the ROC curve

   Status    : disease
   Classifier: rating

------------------------------------------------------------------------------
             |    Observed                 Bootstrap
         AUC |       Coef.       Bias      Std. Err.      [95% Conf. Interval]
-------------+----------------------------------------------------------------
             |   .8931711    .000108      .0292028      .8359347   .9504075  (N)
             |                                          .8290958   .9457951  (P)
             |                                          .8280714   .9450642 (BC)
------------------------------------------------------------------------------
```

The estimates of AUC match well. The standard error from `roctab` is close to the bootstrap standard error calculated by `rocreg`. The bootstrap standard error generalizes to the more complex models that we consider later, whereas the `roctab` standard-error calculation does not.

◁

The AUC can be used to compare different classifiers. It is the most popular summary statistic for comparisons (Pepe, Longton, and Janes 2009). `roccomp` will compute the trapezoidal approximation of the AUC and graph the ROC curves of multiple classifiers. Using the DeLong, DeLong, and Clarke-Pearson (1988) covariance estimates for the AUC estimate, `roccomp` performs a Wald test of the null hypothesis that all classifier AUC values are equal. `rocreg` has similar capabilities.

Example 2: Nonparametric ROC, AUC, multiple classifiers

Hanley and McNeil (1983) presented data from an evaluation of two computer algorithms designed to reconstruct CT images from phantoms. We will call these two algorithms modalities 1 and 2. A sample of 112 phantoms was selected; 58 phantoms were considered normal, and the remaining 54 were abnormal. Each of the two modalities was applied to each phantom, and the resulting images were rated by a reviewer using a six-point scale: 1 is definitely normal, 2 is probably normal, 3 is possibly normal, 4 is possibly abnormal, 5 is probably abnormal, and 6 is definitely abnormal. Because each modality was applied to the same sample of phantoms, the two sets of outcomes are correlated.

We list the first seven observations:

```
. use http://www.stata-press.com/data/r12/ct, clear
. list in 1/7, sep(0)
```

	mod1	mod2	status
1.	2	1	0
2.	5	5	1
3.	2	1	0
4.	2	3	0
5.	5	6	1
6.	2	2	0
7.	3	2	0

Each observation corresponds to one phantom. The `mod1` variable identifies the rating assigned for the first modality, and the `mod2` variable identifies the rating assigned for the second modality. The true status of the phantoms is given by `status==0` if they are normal and `status==1` if they are abnormal. The observations with at least one missing rating were dropped from the analysis.

A fictitious dataset was created from this true dataset, adding a third test modality. We will use `roccomp` to compute the AUC statistic for each modality in these data and compare the AUC of the three modalities. We obtain the same behavior from `rocreg`. As before, the `tiecorrected` option is specified so that the AUC is calculated with the trapezoidal approximation.

```
. use http://www.stata-press.com/data/r12/ct2
. roccomp status mod1 mod2 mod3, summary
```

	Obs	ROC Area	Std. Err.	−Asymptotic Normal− [95% Conf.	Interval]
mod1	112	0.8828	0.0317	0.82067	0.94498
mod2	112	0.9302	0.0256	0.88005	0.98042
mod3	112	0.9240	0.0241	0.87670	0.97132

```
Ho: area(mod1) = area(mod2) = area(mod3)
    chi2(2) =     6.54       Prob>chi2 =   0.0381
```

```
. rocreg status mod1 mod2 mod3, tiecorrected bseed(38038) nodots
Bootstrap results                                 Number of obs      =       112
                                                  Replications       =      1000

Nonparametric ROC estimation

Control standardization: empirical, corrected for ties
ROC method             : empirical

Area under the ROC curve

   Status    : status
   Classifier: mod1
```

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.8828225	-.0006367	.0322291	.8196546	.9459903	(N)
				.8147518	.9421572	(P)
				.8124397	.9394085	(BC)

```
   Status    : status
   Classifier: mod2
```

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.9302363	-.0015402	.0259593	.8793569	.9811156	(N)
				.8737522	.9737432	(P)
				.8739467	.9737768	(BC)

```
   Status    : status
   Classifier: mod3
```

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.9240102	-.0003528	.0247037	.8755919	.9724286	(N)
				.8720036	.9674485	(P)
				.8693548	.965	(BC)

```
Ho: All classifiers have equal AUC values.
Ha: At least one classifier has a different AUC value.

P-value:     .0389797                 Test based on bootstrap (N) assumptions.
```

We see that the AUC estimates are equivalent, and the standard errors are quite close as well. The p-value for the tests of equal AUC under `rocreg` leads to similar inference as the p-value from `roccomp`. The Wald test performed by `rocreg` uses the joint bootstrap estimate variance matrix of the three AUC estimators rather than the DeLong, DeLong, and Clarke-Pearson (1988) variance estimate used by `roccomp`.

`roccomp` is used here on potentially correlated classifiers that are recorded in wide-format data. It can also be used on long-format data to compare independent classifiers. Further details can be found in [R] **roccomp**.

◁

Citing the AUC's lack of clinical relevance, there is argument against using it as a key summary statistic of the ROC curve (Pepe 2003; Cook 2007). Pepe, Longton, and Janes (2009) suggest using the estimate of the ROC curve itself at a particular point, or the estimate of the false-positive rate at a given ROC value, also known as invROC.

Recall from example 1 how nonparametric rocreg graphs look, with the stairstep pattern in the ROC curve. In an ideal world, the graph would be a smooth one-to-one function, and it would be trivial to map a false-positive rate to its corresponding true-positive rate and vice versa.

However, smooth ROC curves can only be obtained by assuming a parametric model that uses linear interpolation between observed false-positive rates and between observed true-positive rates, and rocreg is certainly capable of that; see example 1 of [R] **rocregplot**. However, under nonparametric estimation, the mapping between false-positive rates and true-positive rates is not one to one, and estimates tend to be less reliable the further you are from an observed data point. This is somewhat mitigated by using tie-corrected rates (the tiecorrected option).

When we examine continuous data, the difference between the tie-corrected estimates and the standard estimates becomes negligible, and the empirical estimate of the ROC curve becomes close to the smooth ROC curve obtained by linear interpolation. So the nonparametric ROC and invROC estimates work well.

Fixing one rate value of interest can be difficult and subjective (Pepe 2003). A compromise measure is the partial area under the ROC curve (pAUC) (McClish 1989; Thompson and Zucchini 1989). This is the integral of the ROC curve from 0 and above to a given false-positive rate (perhaps the largest clinically acceptable value). Like the AUC estimate, the nonparametric estimate of the pAUC can be written as a sample average of the case observation percentiles, but with an adjustment based on the prescribed maximum false-positive rate (Dodd and Pepe 2003). A tie correction may also be applied so that it reflects the trapezoidal approximation.

We cannot compare rocreg with roctab or roccomp on the estimation of pAUC, because pAUC is not computed by the latter two.

▷ Example 3: Nonparametric ROC, other statistics

To see how rocreg estimates ROC, invROC, and pAUC, we will examine a new study. Wieand et al. (1989) examined a pancreatic cancer study with two continuous classifiers, here called y1 (CA 19-9) and y2 (CA 125). This study was also examined in Pepe, Longton, and Janes (2009). The indicator of cancer in a subject is recorded as d. The study was a case–control study, stratifying participants on disease status.

We list the first five observations:

```
. use http://labs.fhcrc.org/pepe/book/data/wiedat2b.dta, clear
(S. Wieand - Pancreatic cancer diagnostic marker data)
. list in 1/5
```

	y1	y2	d
1.	28	13.3	no
2.	15.5	11.1	no
3.	8.2	16.7	no
4.	3.4	12.6	no
5.	17.3	7.4	no

We will estimate the ROC curves at a large value (0.7) and a small value (0.2) of the false-positive rate. These values are specified in roc(). The false-positive rate for ROC or sensitivity value of 0.6 will also be estimated by specifying invroc(). Percentile confidence intervals for these parameters are displayed in the graph obtained by rocregplot after rocreg. The pAUC statistic will be calculated for the false-positive rate of 0.5, which is specified as an argument to the pauc() option. Following Pepe, Longton, and Janes (2009), we use a stratified bootstrap, sampling separately from the case

and control populations by specifying the bootcc option. This reflects the case–control nature of the study.

All four statistics can be estimated simultaneously by rocreg. For clarity, however, we will estimate each statistic with a separate call to rocreg. rocregplot is used after estimation to graph the ROC and false-positive rate estimates. The display of the individual, observation-specific false-positive rate and ROC values will be omitted in the plot. This is accomplished by specifying msymbol(i) in our plot1opts() and plot2opts() options to rocregplot.

```
. rocreg d y1 y2, roc(.7) bseed(8378923) bootcc nodots

Bootstrap results
Number of strata   =         2                  Number of obs      =       141
                                                 Replications       =      1000

Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
ROC curve
   Status    : d
   Classifier: y1
```

ROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.7	.9222222	-.0021889	.0323879	.8587432	.9857013	(N)
				.8444445	.9777778	(P)
				.8555555	.9777778	(BC)

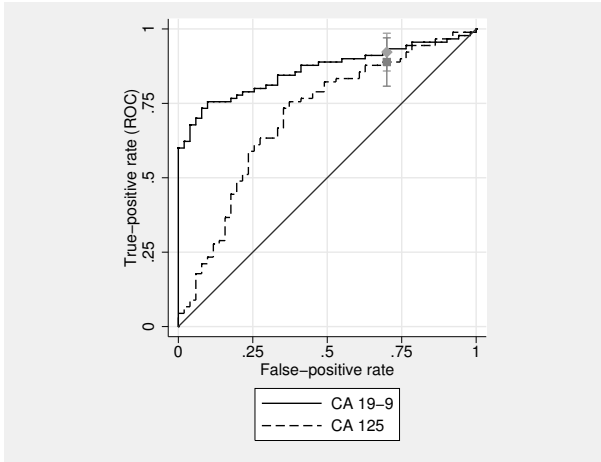
```
   Status    : d
   Classifier: y2
```

ROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.7	.8888889	-.0035556	.0414215	.8077043	.9700735	(N)
				.8	.9611111	(P)
				.7888889	.9555556	(BC)

```
Ho: All classifiers have equal ROC values.
Ha: At least one classifier has a different ROC value.
Test based on bootstrap (N) assumptions.
```

ROC	P-value
.7	.5423044

```
. rocregplot, plot1opts(msymbol(i)) plot2opts(msymbol(i))
```



In this study, we see that classifier `y1` (CA 19-9) is a uniformly better test than is classifier `y2` (CA 125) until high levels of false-positive rate and sensitivity or ROC value are reached. At the high level of false-positive rate, 0.7, the ROC value does not significantly differ between the two classifiers. This can be seen in the plot by the overlapping confidence intervals.

```
. rocreg d y1 y2, roc(.2) bseed(8378923) bootcc nodots
Bootstrap results
Number of strata   =         2                  Number of obs      =       141
                                                Replications       =      1000
Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
ROC curve
   Status    : d
   Classifier: y1
```

ROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.2	.7777778	.0011778	.0483655	.6829831	.8725725	(N)
				.6888889	.8777778	(P)
				.6777778	.8666667	(BC)

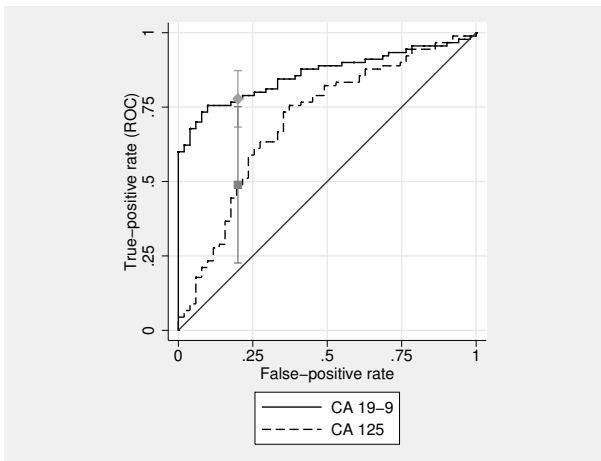
```
   Status    : d
   Classifier: y2
```

ROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.2	.4888889	-.0091667	.1339863	.2262806	.7514971	(N)
				.2222222	.7	(P)
				.2111111	.7	(BC)

```
Ho: All classifiers have equal ROC values.
Ha: At least one classifier has a different ROC value.
Test based on bootstrap (N) assumptions.
```

ROC	P-value
.2	.043234

```
. rocregplot, plot1opts(msymbol(i)) plot2opts(msymbol(i))
```



The sensitivity for the false-positive rate of 0.2 is found to be higher under y1 than under y2, and this difference is significant at the 0.05 level. In the plot, this is shown by the vertical confidence intervals.

```
. rocreg d y1 y2, invroc(.6) bseed(8378923) bootcc nodots
Bootstrap results
Number of strata   =         2                  Number of obs      =       141
                                                 Replications       =      1000
Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
False-positive rate
   Status    : d
   Classifier: y1
```

invROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.6	0	.0158039	.0267288	-.0523874	.0523874	(N)
				0	.0784314	(P)
				0	.1372549	(BC)

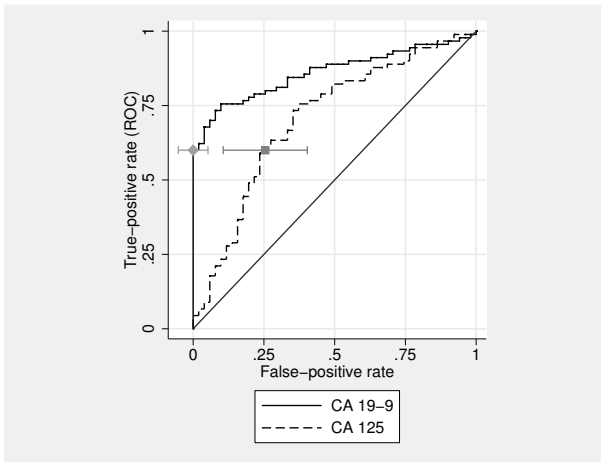
```
   Status    : d
   Classifier: y2
```

invROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.6	.254902	.0101961	.0757902	.1063559	.403448	(N)
				.1372549	.4313726	(P)
				.1176471	.3921569	(BC)

```
Ho: All classifiers have equal invROC values.
Ha: At least one classifier has a different invROC value.
Test based on bootstrap (N) assumptions.
```

invROC	P-value
.6	.0016562

```
. rocregplot, plot1opts(msymbol(i)) plot2opts(msymbol(i))
```



We find significant evidence that false-positive rates corresponding to a sensitivity of 0.6 are different from `y1` to `y2`. This is visually indicated by the horizontal confidence intervals, which are separated from each other.

```
. rocreg d y1 y2, pauc(.5) bseed(8378923) bootcc nodots
Bootstrap results
Number of strata   =         2                  Number of obs      =       141
                                                 Replications       =      1000

Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
Partial area under the ROC curve
   Status    : d
   Classifier: y1
```

pAUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.5	.3932462	-.0000769	.021332	.3514362	.4350562	(N)
				.3492375	.435512	(P)
				.3492375	.435403	(BC)

```
   Status    : d
   Classifier: y2
```

pAUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.5	.2496732	.0019168	.0374973	.1761798	.3231666	(N)
				.177451	.3253268	(P)
				.1738562	.3233115	(BC)

```
Ho: All classifiers have equal pAUC values.
Ha: At least one classifier has a different pAUC value.
Test based on bootstrap (N) assumptions.
```

pAUC	P-value
.5	.0011201

We also find significant evidence supporting the hypothesis that the pAUC for `y1` up to a false-positive rate of 0.5 differs from the area of the same region under the ROC curve of `y2`.

◁

Covariate-adjusted ROC curves

When covariates affect the control distribution of the diagnostic test, thresholds for the test being classified as abnormal may be chosen that vary with the covariate values. These conditional thresholds will be more accurate than the marginal thresholds that would normally be used, because they take into account the specific distribution of the diagnostic test under the given covariate values as opposed to the marginal distribution over all covariate values.

By using these covariate-specific thresholds, we are essentially creating new classifiers for each covariate-value combination, and thus we are creating multiple ROC curves. As explained in Pepe (2003), when the case and control distributions of the covariates are the same, the marginal ROC curve will always be bound above by these covariate-specific ROC curves. So using conditional thresholds will never provide a less powerful test diagnostic in this case.

In the marginal ROC curve calculation, the classifiers are standardized to percentiles according to the control distribution, marginalized over the covariates. Thus the ROC curve is the CDF of the standardized case observations. The covariate-adjusted ROC curve is the CDF of one minus the conditional control percentiles for the case observations, and the marginal ROC curve is the CDF of one minus the marginal control percentiles for the case observations (Pepe and Cai 2004). Thus the standardization of classifier to false-positive rate value is conditioned on the specific covariate values under the covariate-adjusted ROC curve.

The covariate-adjusted ROC curve (Janes and Pepe 2009) at a given false-positive rate t is equivalent to the expected value of the covariate-specific ROC at t over all covariate combinations. When the covariates in question do not affect the case distribution of the classifier, the covariate-specific ROC will have the same value at each covariate combination. So here the covariate-adjusted ROC is equivalent to the covariate-specific ROC, regardless of covariate values.

When covariates do affect the case distribution of the classifier, users of the diagnostic test would likely want to model the covariate-specific ROC curves separately. Tools to do this can be found in the parametric modeling discussion in the following two sections. Regardless, the covariate-adjusted ROC curve can serve as a meaningful summary of covariate-adjusted accuracy.

Also note that the ROC summary statistics defined in the previous section have covariate-adjusted analogs. These analogs are estimated in a similar manner as under the marginal ROC curve (Janes, Longton, and Pepe 2009). The options for their calculation in `rocreg` are identical to those given in the previous section. Further details can be found in *Methods and formulas*.

▷ Example 4: Nonparametric ROC, linear covariate adjustment

Norton et al. (2000) studied data from a neonatal audiology study on three tests to identify hearing impairment in newborns. These data were also studied in Janes, Longton, and Pepe (2009). Here we list 5 of the 5,058 observations.

```
. use http://www.stata-press.com/data/r12/nnhs, clear
(Norton - neonatal audiology data)
. list in 1/5
```

	id	ear	male	currage	d	y1	y2	y3
1.	B0157	R	M	42.42	0	-3.1	-9	-1.5
2.	B0157	L	M	42.42	0	-4.5	-8.7	-2.71
3.	B0158	R	M	40.14	1	-3.2	-13.2	-2.64
4.	B0161	L	F	38.14	0	-22.1	-7.8	-2.59
5.	B0167	R	F	37	0	-10.9	-6.6	-1.42

The classifiers `y1` (DPOAE 65 at 2 kHz), `y2` (TEOAE 80 at 2 kHz), and `y3` (ABR) and the hearing impairment indicator `d` are recorded along with some relevant covariates. The infant's age is recorded in months as `currage`, and the infant's gender is indicated by `male`. Over 90% of the newborns were tested in each ear (`ear`), so we will cluster on infant ID (`id`).

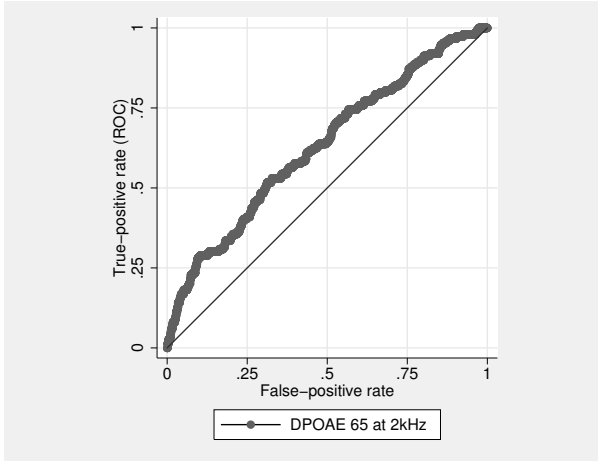
Following the strategy of Janes, Longton, and Pepe (2009), we will first perform ROC analysis for the classifiers while adjusting for the covariate effects of the infant's gender and age. This is done by specifying these variables in the `ctrlcov()` option. We adjust using a linear regression rule, by specifying `ctrlmodel(linear)`. This means that when a user of the diagnostic test chooses a threshold conditional on the age and gender covariates, they assume that the diagnostic test classifier has some linear dependence on age and gender and equal variance as their levels vary. Our cluster adjustment is made by specifying the `cluster()` option.

We will focus on the first classifier. The percentile, or specificity, values are calculated empirically by default, and thus so are the false-positive rates, (1 − specificity). Also by default, the ROC curve values are empirically defined by the false-positive rates. To draw the ROC curve, we again use `rocregplot`.

The AUC is calculated by default. For brevity, we specify the `nobootstrap` option so that bootstrap sampling is not performed. The AUC point estimate will be sufficient for our purposes.

```
. rocreg d y1, ctrlcov(male currage) ctrlmodel(linear) cluster(id) nobootstrap

Nonparametric ROC estimation

Covariate control      : linear regression
Control variables      : male currage
Control standardization: empirical
ROC method             : empirical

Status    : d
Classifier: y1
Covariate control adjustment model:

Linear regression                               Number of obs =    4907
                                                F(  2,  2685) =   13.80
                                                Prob > F      =  0.0000
                                                R-squared     =  0.0081
                                                Root MSE      =  7.7515

                                (Std. Err. adjusted for 2686 clusters in id)
------------------------------------------------------------------------------
             y1 |      Coef.   Robust Std. Err.      t    P>|t|     [95% Conf. Interval]
----------------+-------------------------------------------------------------
           male |   .2471744   .2603598     0.95   0.343    -.2633516    .7577005
       currage |  -.2032456   .0389032    -5.22   0.000    -.2795288   -.1269624
          _cons |  -1.239484   1.487855    -0.83   0.405    -4.156942    1.677973
------------------------------------------------------------------------------

Area under the ROC curve

   Status    : d
   Classifier: y1

------------------------------------------------------------------------------
             |   Observed              Bootstrap
         AUC |      Coef.       Bias    Std. Err.     [95% Conf. Interval]
-------------+----------------------------------------------------------------
             |   .6293994          .           .            .           . (N)
             |                                              .           . (P)
             |                                              .           . (BC)
------------------------------------------------------------------------------
```

```
. rocregplot
```



Our covariate control adjustment model shows that `currage` has a negative effect on `y1` (DPOAE 65 at 2 kHz) under the control population. At the 0.001 significance level, we reject that its contribution to `y1` is zero, and the point estimate has a negative sign. This result does not directly tell us about the effect of `currage` on the ROC curve of `y1` as a classifier of `d`. None of the case observations are used in the linear regression, so information on `currage` for abnormal cases is not used in the model. This result does show us how to calculate false-positive rates for tests that use thresholds conditional on a child's sex and current age. We will see how `currage` affects the ROC curve when `y1` is used as a classifier and conditional thresholds are used based on `male` and `currage` in the following section, *Parametric ROC curves: Estimating equations*.

❑ Technical note

Under this nonparametric estimation, `rocreg` saved the false-positive rate for each observation's `y1` values in the utility variable `_fpr_y1`. The true-positive rates are stored in the utility variable `_roc_y1`. For other models, say with classifier *yname*, these variables would be named `_fpr_`*yname* and `_roc_`*yname*. They will also be overwritten with each call of `rocreg`. The variables `_roc_*` and `_fpr_*` are usually for internal `rocreg` use only and are overwritten with each call of `rocreg`. They are only created for nonparametric models or parametric models that do not involve ROC covariates. In these models, covariates may only affect the first stage of estimation, the control distribution, and not the ROC curve itself. In parametric models that allow ROC covariates, different covariate values would lead to different ROC curves.

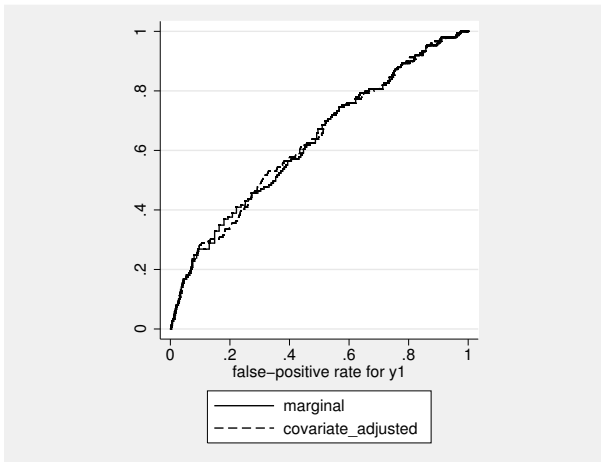
❑

To see how the covariate-adjusted ROC curve estimate differs from the standard marginal estimate, we will reestimate the ROC curve for classifier `y1` without covariate adjustment. We rename these variables before the new estimation and then draw an overlaid `twoway line` (see [G-2] **graph twoway line**) plot to compare the two.

```
. rename _fpr_y1 o_fpr_y1
. rename _roc_y1 o_roc_y1
. label variable o_roc_y1 "covariate_adjusted"
. rocreg d y1, cluster(id) nobootstrap
Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
Area under the ROC curve
   Status    : d
   Classifier: y1
```

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf. Interval]	
	.6279645	.	.	.	. (N)
				.	. (P)
				.	. (BC)

```
. label variable _roc_y1 "marginal"
. twoway line _roc_y1 _fpr_y1, sort(_fpr_y1 _roc_y1) connect(J) ||
     line o_roc_y1 o_fpr_y1, sort(o_fpr_y1 o_roc_y1)
     connect(J) lpattern(dash) aspectratio(1) legend(cols(1))
```



Though they are close, particularly in AUC, there are clearly some points of difference between the estimates. So the covariate-adjusted ROC curve may be useful here.

◁

In our examples thus far, we have used the empirical CDF estimator to estimate the control distribution. `rocreg` allows some flexibility here. The `pvc(normal)` option may be specified to calculate the percentile values according to a Gaussian distribution of the control.

Covariate adjustment in `rocreg` may also be performed with stratification instead of linear regression. Under the stratification method, the unique values of the stratified covariates each define separate parameters for the control distribution of the classifier. A user of the diagnostic test chooses a threshold based on the control distribution conditioned on the unique covariate value parameters.

We will demonstrate the use of normal percentile values and covariate stratification in our next example.

▷ Example 5: Nonparametric ROC, covariate stratification

The hearing test study of Stover et al. (1996) examined the effectiveness of negative signal-to-noise ratio, `nsnr`, as a classifier of hearing loss. The test was administered under nine different settings, corresponding to different frequency, `xf`, and intensity, `xl`, combinations. Here we list 10 of the 1,848 observations.

```
. use http://www.stata-press.com/data/r12/dp, clear
(Stover - DPOAE test data)
. list in 1/10
```

	id	d	nsnr	xf	xl	xd
1.	101	1	18	10.01	5.5	3.5
2.	101	1	19	20.02	5.5	3
3.	101	1	7.6	10.01	6	3.5
4.	101	1	15	20.02	6	3
5.	101	1	16	10.01	6.5	3.5
6.	101	1	5.8	20.02	6.5	3
7.	102	0	-2.6	10.01	5.5	.
8.	102	0	-3	14.16	5.5	.
9.	102	1	10	20.02	5.5	1
10.	102	0	-5.8	10.01	6	.

Hearing loss is represented by `d`. The covariate `xd` is a measure of the degree of hearing loss. We will use this covariate in later analysis, because it only affects the case distribution of the classifier. Multiple measurements are taken for each individual, `id`, so we will cluster by individual.

We evaluate the effectiveness of `nsnr` using `xf` and `xl` as stratification covariates with `rocreg`; the default method of covariate adjustment.

As mentioned before, the default false-positive rate calculation method in `rocreg` estimates the conditional control distribution of the classifiers empirically. For comparison, we will also estimate a separate ROC curve using false-positive rates assuming the conditional control distribution is normal. This behavior is requested by specifying the `pvc(normal)` option. Using the `rocregplot` option `name()` to store the ROC plots and using the `graph combine` command, we are able to compare the Gaussian and empirical ROC curves side by side. As before, for brevity we specify the `nobootstrap` option to suppress bootstrap sampling.

```
. rocreg d nsnr, ctrlcov(xf xl) cluster(id) nobootstrap
Nonparametric ROC estimation
Covariate control      : stratification
Control variables      : xf xl
Control standardization: empirical
ROC method             : empirical
Area under the ROC curve
   Status    : d
   Classifier: nsnr
```

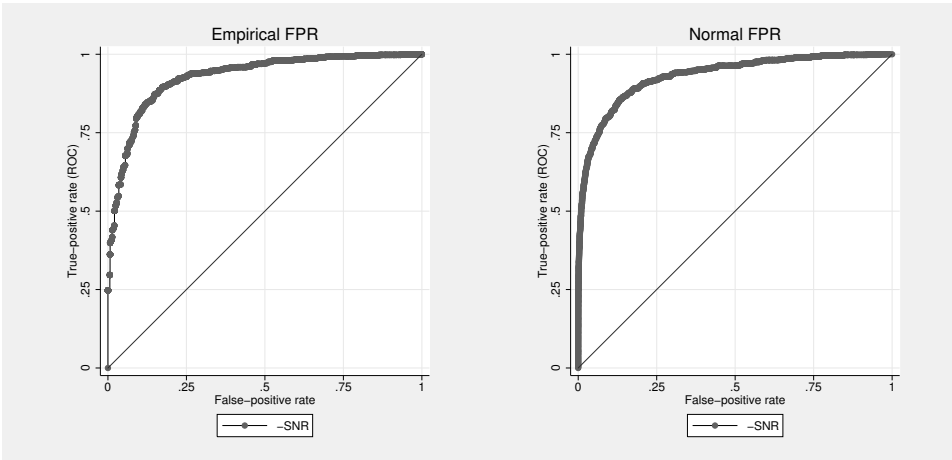
AUC	Observed Coef.	Bootstrap Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.9264192	.	.	.	.	(N)
				.	.	(P)
				.	.	(BC)

```
. rocregplot, title(Empirical FPR) name(a) nodraw
```

```
. rocreg d nsnr, pvc(normal) ctrlcov(xf xl) cluster(id) nobootstrap
Nonparametric ROC estimation
Covariate control      : stratification
Control variables      : xf xl
Control standardization: normal
ROC method             : empirical
Area under the ROC curve
   Status    : d
   Classifier: nsnr
```

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf. Interval]	
	.9309901	.	.	.	. (N)
				.	. (P)
				.	. (BC)

```
. rocregplot, title(Normal FPR) name(b) nodraw
. graph combine a b, xsize(5)
```



On cursory visual inspection, we see little difference between the two curves. The AUC values are close as well. So it is sensible to assume that we have Gaussian percentile values for control standardization. ◁

Parametric ROC curves: Estimating equations

We now assume a parametric model for covariate effects on the second stage of ROC analysis. Particularly, the ROC curve is a probit model of the covariates. We will thus have a separate ROC curve for each combination of the relevant covariates.

Under weak assumptions about the control distribution of the classifier, we can fit this model by using estimating equations as described in Alonzo and Pepe (2002). This method can be also be used without covariate effects in the second stage, assuming a parametric model for the single (constant only) ROC curve. Covariates may still affect the first stage of estimation, so we parametrically model the single covariate-adjusted ROC curve (from the previous section). The marginal ROC curve, involving no covariates in either stage of estimation, can be fit parametrically as well.

In addition to the Alonzo and Pepe (2002) explanation, further details are given in Pepe, Longton, and Janes (2009); Janes, Longton, and Pepe (2009); Pepe (2003); and Janes and Pepe (2009).

The parametric models that we consider assume that the ROC curve is a cumulative distribution function g invoked with input of a linear polynomial in the corresponding quantile function invoked on the false-positive rate u. In this context, we assume that g corresponds to a standard normal cumulative distribution function, Φ. So the corresponding quantile function is Φ^{-1}. The constant intercept of the polynomial may depend on covariates, but the slope term α (the quantile coefficient) may not.

$$\text{ROC}(u) = g\{\mathbf{x}'\boldsymbol{\beta} + \alpha g^{-1}(u)\}$$

The first step of the algorithm involves the choice of false-positive rates to use in the parametric fit. These are typically a set of equispaced points spanning the interval (0,1). Alonzo and Pepe (2002) examined the effect of fitting large and small sets of points, finding that relatively small sets could be used with little loss of efficiency. Alternatively, the set can be formed by using the observed false-positive rates in the data (Pepe 2003). Further details on the algorithm are provided in *Methods and formulas*.

Under parametric estimation, all the summary measures we defined earlier, except the AUC, are not calculated until postestimation. In models with covariates, each covariate combination would yield a different ROC curve and thus different summary parameters, so no summary parameters are initially estimated. In marginal parametric models (where there are no ROC covariates, but there are potentially control covariates), we will calculate the AUC and leave the other measures for postestimation; see [R] **rocreg postestimation**. As with the other parameters, we bootstrap for standard errors and inference.

We will now demonstrate how `rocreg` performs the Alonzo and Pepe (2002) algorithm using the previous section's examples and others.

▷ Example 6: Parametric ROC, linear covariate adjustment

We return to the neonatal audiology study with gender and age covariates (Norton et al. 2000), which we discussed in example 4. Janes, Longton, and Pepe (2009) suspected the current age of the infant would play a role in the case distribution of the classifier `y1` (DPOAE 65 at 2 kHz). They postulated a probit link between the ROC curve and the covariate-adjusted false-positive rates. We follow their investigation and reach similar results.

In example 4, we saw the results of adjusting for the `currage` and `male` variables in the control population for classifier `y1`. Now we see how `currage` affects the ROC curve when `y1` is used with thresholds conditioned on `male` and `currage`.

We specify the covariates that should affect the ROC curve in the `roccov()` option. By default, `rocreg` will choose 10 equally spaced false-positive rates in the (0,1) interval as fitting points. The `fprpts()` option allows the user to specify more or fewer points. We specify the `bsave()` option with the `nnhs2y1` dataset so that we can use the bootstrap resamples in postestimation.

```
. use http://www.stata-press.com/data/r12/nnhs, clear
(Norton - neonatal audiology data)
. rocreg d y1, probit ctrlcov(currage male) ctrlmodel(linear) roccov(currage)
> cluster(id) bseed(56930) bsave(nnhs2y1) nodots
Bootstrap results                                 Number of obs      =      5056
                                                  Replications       =      1000

Parametric ROC estimation

Covariate control      : linear regression
Control variables      : currage male
Control standardization: empirical
ROC method             : parametric               Link: probit

Status    : d
Classifier: y1
Covariate control adjustment model:
Linear regression                                 Number of obs =    4907
                                                  F(  2,  2685) =   13.80
                                                  Prob > F      =  0.0000
                                                  R-squared     =  0.0081
                                                  Root MSE      =  7.7515
                                  (Std. Err. adjusted for 2686 clusters in id)
------------------------------------------------------------------------------
             |               Robust
          y1 |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
     currage |   -.2032456   .0389032    -5.22   0.000    -.2795288   -.1269624
        male |    .2471744   .2603598     0.95   0.343    -.2633516    .7577005
       _cons |   -1.239484   1.487855    -0.83   0.405    -4.156942    1.677973
------------------------------------------------------------------------------

   Status    : d
   Classifier: y1
   ROC Model :
                                  (Replications based on 2741 clusters in id)
------------------------------------------------------------------------------
             |   Observed               Bootstrap
          y1 |      Coef.       Bias    Std. Err.     [95% Conf. Interval]
-------------+----------------------------------------------------------------
       _cons |   -1.272505  -.0566737    1.076706     -3.38281    .8377993  (N)
             |                                      -3.509356    .7178385  (P)
             |                                      -3.487457    .7813575 (BC)
     currage |    .0448228   .0015878    .0280384    -.0101316    .0997771  (N)
             |                                       -.007932    .1033131  (P)
             |                                      -.0102905     .101021 (BC)
-------------+----------------------------------------------------------------
      probit |
-------------+----------------------------------------------------------------
       _cons |    .9372393   .0128376    .0747228     .7907853   1.083693  (N)
             |                                       .8079087   1.101941  (P)
             |                                       .7928988   1.083399 (BC)
------------------------------------------------------------------------------
```

Note how the number of clusters—here infants—changes from the covariate control adjustment model fit to the ROC model. The control fit is limited to control cases and thus fewer infants. The ROC is fit on all the data, so the variance is adjusted for all clustering on all infants.

With a 0.05 level of statistical significance, we cannot reject the null hypothesis that `currage` has no effect on the ROC curve at a given false-positive rate. This is because each of our 95% bootstrap confidence intervals contains 0. This corresponds with the finding in Janes, Longton, and Pepe (2009) where the reported 95% intervals each contained 0. We cannot reject that the intercept parameter β_0, reported as `_cons` in the main table, is 0 at the 0.05 level either. The slope parameter α, reported

as _cons in the probit table, is close to 1 and cannot be rejected as being 1 at the 0.05 level. Under the assumption that the ROC coefficients except α are 0 and that $\alpha = 1$, the ROC curve at false-positive rate u is equal to u. In other words, we cannot reject that the false-positive rate is equal to the true-positive rate, and so the test is noninformative. Further investigation of the results requires postestimation; see [R] **rocreg postestimation**.

◁

The fitting point set can be formed by using the observed false-positive rates (Pepe 2003). Our next example will illustrate this.

▷ Example 7: Parametric ROC, covariate stratification

We return to the hearing test study of Stover et al. (1996), which we discussed in example 5. Pepe (2003) suspected that intensity, xd, would play a role in the case distribution of the negative signal-to-noise ratio (nsnr) classifier. A ROC regression was fit with covariate adjustment for xf and xl with stratification, and for ROC covariates xf, xl, and xd. There is no prohibition against the same covariate being used in the first and second stages of ROC calculation. The false-positive rate fitting point set was composed of all observed false-positive rates in the control data.

We fit the model with rocreg here. Using observed false-positive rates as the fitting point set can make the dataset very large, so fitting the model is computationally intensive. We demonstrate the fitting algorithm without precise confidence intervals, focusing instead on the coefficient estimates and standard errors. We will thus perform only 50 bootstrap replications, a reasonable number to obtain accurate standard error estimates (Mooney and Duval 1993). The number of replications is specified in the breps() option.

The ROC covariates are specified in roccov(). We specify that all observed false-positive rates in the control observations be used as fitting points with the ctrlfprall option. The nobstrata option specifies that the bootstrap is not stratified. The covariate stratification in the first stage of estimation does not affect the resampling. We will return to this example in postestimation, so we save the bootstrap results in the nsnrf dataset with the bsave() option.

```
. use http://www.stata-press.com/data/r12/dp
(Stover - DPOAE test data)

. rocreg d nsnr, probit ctrlcov(xf xl) roccov(xf xl xd) ctrlfprall cluster(id)
> nobstrata bseed(156385) breps(50) bsave(nsnrf)
(running rocregstat on estimation sample)

Bootstrap replications (50)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50

Bootstrap results                                 Number of obs      =      1848
                                                  Replications       =        50

Parametric ROC estimation

Covariate control      : stratification
Control variables      : xf xl
Control standardization: empirical
ROC method             : parametric               Link: probit

   Status    : d
   Classifier: nsnr
   ROC Model :
                                  (Replications based on 208 clusters in id)
```

nsnr	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
_cons	3.247872	-.0846178	.8490006	1.583862	4.911883	(N)
				1.598022	4.690076	(P)
				1.346904	4.690076	(BC)
xf	.0502557	.014478	.0329044	-.0142357	.1147471	(N)
				-.0031814	.1186107	(P)
				-.0053095	.1132185	(BC)
xl	-.4327223	-.0194846	.1116309	-.6515149	-.2139298	(N)
				-.6570321	-.2499706	(P)
				-.6570321	-.231854	(BC)
xd	.4431764	.0086147	.0936319	.2596612	.6266916	(N)
				.330258	.6672749	(P)
				.3487118	.7674865	(BC)
probit						
_cons	1.032657	-.0188887	.1224993	.7925628	1.272751	(N)
				.7815666	1.236179	(P)
				.7815666	1.237131	(BC)

We obtain results similar to those reported in Pepe (2003, 159). Unlike in our previous example, we find that the coefficients for `xl` and `xd` differ from 0 at the 0.05 level of significance. So over certain covariate combinations, we can have a variety of informative tests using `nsnr` as a classifier. ◁

As mentioned before, when there are no covariates, `rocreg` can still fit a parametric model for the ROC curve of a classifier by using the Alonzo and Pepe (2002) method. `roccomp` and `rocfit` can fit marginal probit models as well. We will compare the behavior of `rocreg` with that of `roccomp` and `rocfit` for probit models without covariates.

When the `binormal` option is specified, `roccomp` calculates the AUC for input classifiers according to the maximum likelihood algorithm of `rocfit`. The `rocfit` algorithm expects discrete classifiers but can slice continuous classifiers into discrete partitions. Further, the case and control distributions are both assumed normal. Actually, the observed classification values are taken as discrete indicators

of the latent normally distributed classification values. This method is documented in Dorfman and Alf (1969).

Alonzo and Pepe (2002) compared their estimating equations probability density function method (with empirical estimation of the false-positive rates) to the maximum likelihood approach of Dorfman and Alf (1969) and found that they had similar efficiency and mean squared error. So we should expect `rocfit` and `rocreg` to give similar results when fitting a simple probit model.

▷ Example 8: Parametric ROC, marginal model

We return to the Hanley and McNeil (1982) data. We will fit a probit model to the ROC curve, assuming that the `rating` variable is a discrete indicator of an underlying latent normal random variable in both the case and control populations of `disease`. We invoke `rocfit` with the default options. `rocreg` is invoked with the `probit` option. The percentile values are calculated empirically. Because there are fewer categories than 10, there will be fewer than 10 false-positive rates that trigger a different true-positive rate value. So for efficiency, we invoke `rocreg` with the `ctrlfprall` option.

```
. use http://www.stata-press.com/data/r12/hanley
. rocfit disease rating, nolog
Binormal model of disease on rating              Number of obs   =       109
Goodness-of-fit chi2(2) =       0.21
Prob > chi2             =     0.9006
Log likelihood          =  -123.64855
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
intercept	1.656782	0.310456	5.34	0.000	1.048300	2.265265
slope (*)	0.713002	0.215882	-1.33	0.184	0.289881	1.136123
/cut1	0.169768	0.165307	1.03	0.304	-0.154227	0.493764
/cut2	0.463215	0.167235	2.77	0.006	0.135441	0.790990
/cut3	0.766860	0.174808	4.39	0.000	0.424243	1.109477
/cut4	1.797938	0.299581	6.00	0.000	1.210770	2.385106

	Indices from binormal fit			
Index	Estimate	Std. Err.	[95% Conf.	Interval]
ROC area	0.911331	0.029506	0.853501	0.969161
delta(m)	2.323671	0.502370	1.339044	3.308298
d(e)	1.934361	0.257187	1.430284	2.438438
d(a)	1.907771	0.259822	1.398530	2.417012

(*) z test for slope==1

```
. rocreg disease rating, probit ctrlfprall bseed(8574309) nodots
Bootstrap results                                 Number of obs      =       109
                                                  Replications       =      1000

Parametric ROC estimation

Control standardization: empirical
ROC method             : parametric               Link: probit

   Status    : disease
   Classifier: rating
   ROC Model :
```

rating	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
_cons	1.635041	.0588548	.3609651	.9275621	2.342519	(N)
				1.162363	2.556508	(P)
				1.164204	2.566174	(BC)
probit						
_cons	.6951252	.0572146	.3241451	.0598125	1.330438	(N)
				.3500569	1.430441	(P)
				.3372983	1.411953	(BC)

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.9102903	-.0051749	.0314546	.8486405	.9719402	(N)
				.837113	.9605498	(P)
				.8468336	.9630486	(BC)

We see that the intercept and slope parameter estimates are close. The intercept (`_cons` in the main table) is clearly nonzero. Under `rocreg`, the slope (`_cons` in the `probit` table) and its percentile and bias-corrected confidence intervals are close to those of `rocfit`. The area under the ROC curve for each of the `rocreg` and `rocfit` estimators also matches closely.

◁

Now we will compare the parametric fit of `rocreg` under the constant probit model with `roccomp`.

▷ Example 9: Parametric ROC, marginal model, multiple classifiers

We now use the fictitious dataset generated from Hanley and McNeil (1983). To fit a probit model using `roccomp`, we specify the `binormal` option. Our specification of `rocreg` remains the same as before.

`rocregplot` is used to render the model produced by `rocreg`. We specify several graph options to both `roccomp` and `rocregplot` to ease comparison. When the `binormal` option is specified along with `graph`, `roccomp` will draw the binormal fitted lines in addition to connected line plots of the empirical false-positive and true-positive rates.

In this plot, we overlay scatterplots of the empirical false-positive rates (because percentile value calculation defaulted to `pvc(empirical)`) and the parametric true-positive rates.

```
. use http://www.stata-press.com/data/r12/ct2, clear
. roccomp status mod1 mod2 mod3, summary binormal graph aspectratio(1)
>         plot1opts(connect(i) msymbol(o))
>         plot2opts(connect(i) msymbol(s))
>         plot3opts(connect(i) msymbol(t))
>         legend(label(1 "mod1") label(3 "mod2") label(5 "mod3")
>               label(2 "mod1 fit") label(4 "mod2 fit")
>               label(6 "mod3 fit")  order(1 3 5 2 4 6) cols(1))
>         title(roccomp) name(a) nodraw
Fitting binormal model for: mod1
Fitting binormal model for: mod2
Fitting binormal model for: mod3
```

	Obs	ROC Area	Std. Err.	[95% Conf.	Interval]
mod1	112	0.8945	0.0305	0.83482	0.95422
mod2	112	0.9382	0.0264	0.88647	0.99001
mod3	112	0.9376	0.0223	0.89382	0.98139

```
Ho: area(mod1) = area(mod2) = area(mod3)
    chi2(2) =     8.27       Prob>chi2 =   0.0160
. rocreg status mod1 mod2 mod3, probit ctrlfprall bseed(867340912) nodots
Bootstrap results                                 Number of obs      =       112
                                                  Replications       =      1000
Parametric ROC estimation
Control standardization: empirical
ROC method             : parametric               Link: probit
   Status    : status
   Classifier: mod1
   ROC Model :
```

mod1	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
_cons	1.726034	.1363112	.5636358	.6213277	2.83074	(N)
				1.162477	3.277376	(P)
				1.152112	3.187595	(BC)
probit						
_cons	.9666323	.0872018	.4469166	.0906919	1.842573	(N)
				.518082	2.219548	(P)
				.5568404	2.394036	(BC)

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.8927007	-.0011794	.0313951	.8311675	.954234	(N)
				.8245637	.9466904	(P)
				.8210562	.9432855	(BC)

```
Status    : status
Classifier: mod2
ROC Model :
```

mod2	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
_cons	1.696811	.0918364	.5133386	.6906858	2.702936	(N)
				1.21812	2.973929	(P)
				1.22064	3.068454	(BC)
probit						
_cons	.4553828	.047228	.3345303	-.2002845	1.11105	(N)
				.1054933	1.18013	(P)
				.1267796	1.272523	(BC)

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.938734	-.0037989	.0261066	.8875659	.9899021	(N)
				.8777664	.9778214	(P)
				.8823555	.9792451	(BC)

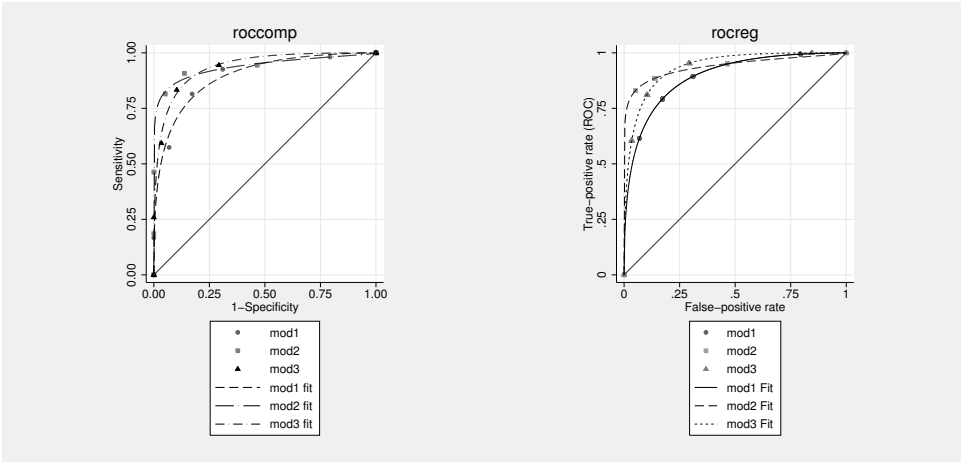
```
Status    : status
Classifier: mod3
ROC Model :
```

mod3	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
_cons	2.281359	.1062846	.6615031	.9848363	3.577881	(N)
				1.637764	4.157873	(P)
				1.666076	4.474779	(BC)
probit						
_cons	1.107736	.0514693	.4554427	.2150843	2.000387	(N)
				.58586	2.28547	(P)
				.6385949	2.671192	(BC)

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.9368321	-.0023853	.0231363	.8914859	.9821784	(N)
				.8844096	.9722485	(P)
				.8836259	.9718463	(BC)

```
Ho: All classifiers have equal AUC values.
Ha: At least one classifier has a different AUC value.

P-value:     .0778556                  Test based on bootstrap (N) assumptions.

. rocregplot, title(rocreg) nodraw name(b) plot1opts(msymbol(o))
> plot2opts(msymbol(s)) plot3opts(msymbol(t))
```

```
. graph combine a b
```



We see differing true-positive rate values in the scattered points, which is expected because `roccomp` gives the empirical estimate and `rocreg` gives the parametric estimate. However, the estimated curves and areas under the ROC curve look similar. Using the Wald test based on the bootstrap covariance, `rocreg` rejects the null hypothesis that each test has the same AUC at the 0.1 significance level. `roccomp` formulates the asymptotic covariance using the `rocfit` estimates of AUC. Examination of its output leads to rejection of the null hypothesis that the AUCs are equal across each test at the 0.05 significance level.

◁

Parametric ROC curves: Maximum likelihood

The Alonzo and Pepe (2002) method of fitting a parametric model to the ROC curve is powerful because it can be generally applied, but that can be a limitation as well. Whenever we invoke the method and want anything other than point estimates of the parameters, we must perform bootstrap resampling.

An alternative is to use maximum likelihood inference to fit the ROC curve. This method can save computational time by avoiding the bootstrap.

`rocreg` implements maximum likelihood estimation for ROC curve analysis when both the case and control populations are normal. Particularly, the classifier is a normal linear model on certain covariates, and the covariate effect and variance of the classifier may change between the case and control populations. This model is defined in Pepe (2003, 145).

$$y = \mathbf{z}'\boldsymbol{\beta_0} + D\mathbf{x}'\boldsymbol{\beta_1} + \sigma\left(D\right)\epsilon$$

Our error term, ϵ, is a standard normal random variable. The variable D is our true status variable, being 1 for the case population observations and 0 for the control population observations. The variance function σ is defined as

$$\sigma\left(D\right) = \sigma_0\left(D=0\right) + \sigma_1\left(D=1\right)$$

This provides two variance parameters in the model and does not depend on covariate values.

Suppose a covariate x_i is present in $\mathbf{z}$ and $\mathbf{x}$. The coefficient β_{1i} represents the interaction effect of the x_i and D. It is the extra effect that x_i has on classifier y under the case population, $D = 1$, beyond the main effect β_{0i}. These $\boldsymbol{\beta_1}$ coefficients are directly related to the ROC curve of y.

Under this model, the ROC curve is derived to be

$$\text{ROC}(u) = \Phi\left[\frac{1}{\sigma_1}\{\mathbf{x}'\boldsymbol{\beta_1} + \sigma_0\Phi^{-1}(u)\}\right]$$

For convenience, we reparameterize the model at this point, creating the parameters $\beta_i = \sigma_1^{-1}\beta_{1i}$ and $\alpha = \sigma_1^{-1}\sigma_0$. We refer to β_0 as the constant intercept, `i_cons`. The parameter α is referred to as the constant slope, `s_cons`.

$$\text{ROC}(u) = \Phi\{\mathbf{x}'\boldsymbol{\beta} + \alpha\Phi^{-1}(u)\}$$

We may interpret the final coefficients as the standardized linear effect of the ROC covariate on the classifier under the case population. The marginal effect of the covariate on the classifier in the control population is removed, and it is rescaled by the case population standard deviation of the classifier when all ROC covariate effects are removed. An appreciable effect on the classifier by a ROC covariate in this measure leads to an appreciable effect on the classifier's ROC curve by the ROC covariate.

The advantage of estimating the control coefficients $\boldsymbol{\beta_0}$ is similar to the gains of estimating the covariate control models in the estimating equations ROC method and nonparametric ROC estimation. This model would similarly apply when evaluating a test that is conditioned on control covariates.

Again we note that under parametric estimation, all the summary measures we defined earlier except the AUC are not calculated until postestimation. In models with covariates, each covariate combination would yield a different ROC curve and thus different summary parameters, so no summary parameters are estimated initially. In marginal parametric models, we will calculate the AUC and leave the other measures for postestimation. There is a simple closed-form formula for the AUC under the probit model. Using this formula, the delta method can be invoked for inference on the AUC. Details on AUC estimation for probit marginal models are found in *Methods and formulas*.

We will demonstrate the maximum likelihood method of `rocreg` by revisiting the models of the previous section.

▷ Example 10: Maximum likelihood ROC, single classifier

Returning to the hearing test study of Stover et al. (1996), we use a similar covariate grouping as before. The frequency `xf` and intensity `xl` are control covariates (`z`), while all three covariates `xf`, `xl`, and hearing loss degree `xd` are case covariates (`x`). In example 7, we fit this model using the Alonzo and Pepe (2002) method. Earlier we stratified on the control covariates and estimated the conditioned control distribution of `nsnr` empirically. Now we assume a normal linear model for `nsnr` on `xf` and `xl` under the control population.

We fit the model by specifying the control covariates in the `ctrlcov()` option and the case covariates in the `roccov()` option. The `ml` option tells `rocreg` to perform maximum likelihood estimation.

```
. use http://www.stata-press.com/data/r12/dp, clear
(Stover - DPOAE test data)
. rocreg d nsnr, ctrlcov(xf xl) roccov(xf xl xd) probit ml cluster(id) nolog
Parametric ROC estimation
Covariate control      : linear regression
Control variables      : xf xl
Control standardization: normal
ROC method             : parametric              Link: probit
  Status     : d
  Classifiers: nsnr
  Classifier : nsnr
  Covariate control adjustment model:
                                  (Std. Err. adjusted for 208 clusters in id)
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
xf	.4690907	.1408683	3.33	0.001	.192994	.7451874
xl	-3.187785	.8976521	-3.55	0.000	-4.947151	-1.42842
xd	3.042998	.3569756	8.52	0.000	2.343339	3.742657
_cons	23.48064	5.692069	4.13	0.000	12.32439	34.63689
casesd						
_cons	7.979708	.354936	22.48	0.000	7.284047	8.67537
ctrlcov						
xf	-.1447499	.0615286	-2.35	0.019	-.2653438	-.0241561
xl	-.8631348	.2871976	-3.01	0.003	-1.426032	-.3002378
_cons	1.109477	1.964004	0.56	0.572	-2.7399	4.958854
ctrlsd						
_cons	7.731203	.3406654	22.69	0.000	7.063511	8.398894

```
   Status     : d
   ROC Model :
                                  (Std. Err. adjusted for 208 clusters in id)
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
nsnr						
i_cons	2.942543	.7569821	3.89	0.000	1.458885	4.426201
xf	.0587854	.0175654	3.35	0.001	.024358	.0932129
xl	-.3994865	.1171914	-3.41	0.001	-.6291775	-.1697955
xd	.381342	.0449319	8.49	0.000	.2932771	.4694068
s_cons	.9688578	.0623476	15.54	0.000	.8466587	1.091057

We find the results are similar to those of example 7. Frequency (`xf`) and intensity (`xl`) have a negative effect on the classifier `nsnr` in the control population.

The negative control effect is mitigated for `xf` in the case population, but the effect for `xl` is even more negative there. Hearing loss severity, `xd`, has a positive effect on `nsnr` in the case population, and it is undefined in the control population.

The ROC coefficients are shown in the `ROC Model` table. Each are different from 0 at the 0.05 level. At this level, we also cannot conclude that the variances differ from case to control populations, because 1 is in the 95% confidence interval for `s_cons`, the ratio of the case to control standard deviation parameters.

Both frequency (xf) and hearing loss severity (xd) make a positive contribution to the ROC curve and thus make the test more powerful. Intensity (xl) has a negative effect on the ROC curve and weakens the test. We previously saw in example 5 that the control distribution appears to be normal, so using maximum likelihood to fit this model is a reasonable approach.

This model was also fit in Pepe (2003, 147). Pepe used separate least-squares estimates for the case and control samples. We obtain similar results for the coefficients, but the maximum likelihood fitting yields slightly different standard deviations by considering both case and control observations concurrently. In addition, a misprint in Pepe (2003, 147) reports a coefficient of −4.91 for xl in the case population instead of −3.19 as reported by Stata.

◁

Inference on multiple classifiers using the Alonzo and Pepe (2002) estimating equation method is performed by fitting each model separately and bootstrapping to determine the dependence of the estimates. Using the maximum likelihood method, we also fit each model separately. We use suest (see [R] **suest**) to estimate the joint variance–covariance of our parameter estimates.

For our models, we can view the score equation for each model as an estimating equation. The estimate that solves the estimating equation (that makes the score 0) is asymptotically normal with a variance matrix that can be estimated using the inverse of the squared scores. By stacking the score equations of the separate models, we can estimate the variance matrix for all the parameter estimates by using this rule. This is an informal explanation; further details can be found in [R] **suest** and in the references Rogers (1993); White (1982 and 1996).

Now we will examine a case with multiple classification variables.

▷ Example 11: Maximum likelihood ROC, multiple classifiers

We return to the neonatal audiology study with gender and age covariates (Norton et al. 2000). In example 6, we fit a model with male and currage as control covariates, and currage as a ROC covariate for the classifier y1 (DPOAE 65 at 2 kHz). We will refit this model, extending it to include the classifier y2 (TEOAE 80 at 2 kHz).

```
. use http://www.stata-press.com/data/r12/nnhs
(Norton - neonatal audiology data)
. rocreg d y1 y2, probit ml ctrlcov(currage male) roccov(currage) cluster(id) nolog
Parametric ROC estimation
Covariate control      : linear regression
Control variables      : currage male
Control standardization: normal
ROC method             : parametric              Link: probit
  Status     : d
  Classifiers: y1 y2
  Classifier : y1
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
currage	.494211	.2126672	2.32	0.020	.077391	.9110311
_cons	-15.00403	8.238094	-1.82	0.069	-31.1504	1.142338
casesd						
_cons	8.49794	.4922792	17.26	0.000	7.533091	9.46279
ctrlcov						
currage	-.2032048	.0323803	-6.28	0.000	-.266669	-.1397406
male	.2369359	.2201391	1.08	0.282	-.1945288	.6684006
_cons	-1.23534	1.252775	-0.99	0.324	-3.690734	1.220055
ctrlsd						
_cons	7.749156	.0782225	99.07	0.000	7.595843	7.902469

```
  Classifier : y2
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
currage	.5729861	.2422662	2.37	0.018	.0981532	1.047819
_cons	-18.2597	9.384968	-1.95	0.052	-36.6539	.1344949
casesd						
_cons	9.723858	.5632985	17.26	0.000	8.619813	10.8279
ctrlcov						
currage	-.1694575	.0291922	-5.80	0.000	-.2266732	-.1122419
male	.7122587	.1993805	3.57	0.000	.3214802	1.103037
_cons	-5.651728	1.129452	-5.00	0.000	-7.865415	-3.438042
ctrlsd						
_cons	6.986167	.0705206	99.07	0.000	6.84795	7.124385

```
Status    : d
ROC Model :
                                (Std. Err. adjusted for 2741 clusters in id)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
y1           |
       i_cons |  -1.765608   1.105393    -1.60   0.110    -3.932138    .4009225
     currage |   .0581566   .0290177     2.00   0.045     .0012828    .1150303
      s_cons |   .9118864   .0586884    15.54   0.000     .7968593    1.026913
-------------+----------------------------------------------------------------
y2           |
       i_cons |  -1.877825    .905174    -2.07   0.038    -3.651933   -.1037167
     currage |   .0589258   .0235849     2.50   0.012     .0127002    .1051514
      s_cons |   .7184563   .0565517    12.70   0.000      .607617    .8292957
------------------------------------------------------------------------------
```

Both classifiers have similar results. The results for `y1` show the same direction as the estimating equation results in example 6. However, we can now reject the null hypothesis that the ROC `currage` coefficient is 0 at the 0.05 level.

In example 6, we could not reject that the slope parameter `s_cons` was 1 and that the constant intercept or ROC coefficient for current age was 0. The resulting ROC curve implied a noninformative test using `y1` as a classifier. This is not the case with our current results. As `currage` increases, we expect a steeper ROC curve and thus a more powerful test, for both classifiers `y1` (DPOAE 65 at 2 kHz) and `y2` (TEOAE 80 at 2 kHz).

In example 10, the clustering of observations within infant `id` was adjusted in the individual fit of `nsnr`. In our current example, the adjustment for the clustering of observations within `id` is performed during concurrent estimation, as opposed to during the individual classifier fits (as in example 10). This adjustment, performed by `suest`, is still accurate.

◁

Now we will fit constant probit models and compare `rocreg` with `rocfit` and `roccomp` with the `binormal` option. Our first applications of `rocfit` and `roccomp` are taken directly from examples 8 and 9. The Dorfman and Alf (1969) algorithm that `rocfit` works with uses discrete classifiers or uses slicing to make a classifier discrete. So we are applying the maximum likelihood method of `rocreg` on discrete classification data here, where it expects continuous data. We expect to see some discrepancies, but we do not find great divergence in the estimates. After revisiting examples 8 and 9, we will fit a probit model with a continuous classifier and no covariates using `rocreg`, and we will compare the results with those from `rocfit`.

▷ Example 12: Maximum likelihood ROC, marginal model

Using the Hanley and McNeil (1982) data, discussed in example 1 and in example 8, we fit a constant probit model of the classifier `rating` with true status `disease`. `rocreg` is invoked with the `ml` option and compared with `rocfit`.

```
. use http://www.stata-press.com/data/r12/hanley, clear
. rocfit disease rating, nolog
Binormal model of disease on rating              Number of obs   =       109
Goodness-of-fit chi2(2) =       0.21
Prob > chi2             =     0.9006
Log likelihood          =  -123.64855
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
intercept	1.656782	0.310456	5.34	0.000	1.048300	2.265265
slope (*)	0.713002	0.215882	-1.33	0.184	0.289881	1.136123
/cut1	0.169768	0.165307	1.03	0.304	-0.154227	0.493764
/cut2	0.463215	0.167235	2.77	0.006	0.135441	0.790990
/cut3	0.766860	0.174808	4.39	0.000	0.424243	1.109477
/cut4	1.797938	0.299581	6.00	0.000	1.210770	2.385106

	Indices from binormal fit			
Index	Estimate	Std. Err.	[95% Conf.	Interval]
ROC area	0.911331	0.029506	0.853501	0.969161
delta(m)	2.323671	0.502370	1.339044	3.308298
d(e)	1.934361	0.257187	1.430284	2.438438
d(a)	1.907771	0.259822	1.398530	2.417012

(*) z test for slope==1

```
. rocreg disease rating, probit ml nolog
Parametric ROC estimation
Control standardization: normal
ROC method             : parametric              Link: probit
  Status     : disease
  Classifiers: rating
  Classifier : rating
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
_cons	2.3357	.2334285	10.01	0.000	1.878188	2.793211
casesd						
_cons	1.117131	.1106124	10.10	0.000	.9003344	1.333927
ctrlcov						
_cons	2.017241	.1732589	11.64	0.000	1.67766	2.356823
ctrlsd						
_cons	1.319501	.1225125	10.77	0.000	1.07938	1.559621

```
   Status    : disease
   ROC Model :
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
rating						
i_cons	2.090802	.2941411	7.11	0.000	1.514297	2.667308
s_cons	1.181151	.1603263	7.37	0.000	.8669177	1.495385
auc	.9116494	.0261658	34.84	0.000	.8603654	.9629333

We compare the estimates for these models:

	rocfit	rocreg, ml
slope	0.7130	1.1812
SE of slope	0.2159	0.1603
intercept	1.6568	2.0908
SE of intercept	0.3105	0.2941
AUC	0.9113	0.9116
SE of AUC	0.0295	0.0262

We find that both the intercept and the slope are estimated as higher with the maximum likelihood method under rocreg than with rocfit. The AUC (ROC area in rocfit) is close for both commands. We find that the standard errors of each of these estimates is slightly lower under rocreg than rocfit as well.

Both rocfit and rocreg suggest that the slope parameter of the ROC curve (slope in rocfit and s_cons in rocreg) is not significantly different from 1. Thus we cannot reject that the classifier has the same variance in both case and control populations. There is, however, significant evidence that the intercepts (i_cons in rocreg and intercept in rocfit) differ from 0. Because of the positive direction of the intercept estimates, the ROC curve for rating as a classifier of disease suggests that rating provides an informative test. This is also suggested by the high AUC, which is significantly different from 0.5, that is, a flip of a coin.

◁

▷ Example 13: Maximum likelihood ROC, marginal model, multiple classifiers

We use the fictitious dataset generated from Hanley and McNeil (1983), which we previously used in example 2 and in example 9. To fit a probit model using roccomp, we specify the binormal option. We perform parametric, maximum likelihood ROC analysis using rocreg. We use rocregplot to plot the ROC curves created by rocreg.

```
. use http://www.stata-press.com/data/r12/ct2, clear
. roccomp status mod1 mod2 mod3, summary binormal graph aspectratio(1)
>         plot1opts(connect(i) msymbol(o))
>         plot2opts(connect(i) msymbol(s))
>         plot3opts(connect(i) msymbol(t))
>         legend(label(1 "mod1") label(3 "mod2") label(5 "mod3")
>                label(2 "mod1 fit") label(4 "mod2 fit") label(6 "mod3 fit")
>         order(1 3 5 2 4 6) cols(1)) title(roccomp) name(a) nodraw
Fitting binormal model for: mod1
Fitting binormal model for: mod2
Fitting binormal model for: mod3
                            ROC
                    Obs     Area     Std. Err.      [95% Conf. Interval]
---------------------------------------------------------------------------
mod1                112   0.8945       0.0305       0.83482     0.95422
mod2                112   0.9382       0.0264       0.88647     0.99001
mod3                112   0.9376       0.0223       0.89382     0.98139
---------------------------------------------------------------------------
Ho: area(mod1) = area(mod2) = area(mod3)
    chi2(2) =     8.27       Prob>chi2 =   0.0160
```

```
. rocreg status mod1 mod2 mod3, probit ml nolog
Parametric ROC estimation
Control standardization: normal
ROC method             : parametric               Link: probit
  Status     : status
  Classifiers: mod1 mod2 mod3
  Classifier : mod1
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
_cons	2.118135	.2165905	9.78	0.000	1.693626	2.542645
casesd						
_cons	1.166078	.1122059	10.39	0.000	.9461589	1.385998
ctrlcov						
_cons	2.344828	.1474147	15.91	0.000	2.0559	2.633755
ctrlsd						
_cons	1.122677	.1042379	10.77	0.000	.9183746	1.32698

```
  Classifier : mod2
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
_cons	2.659642	.2072731	12.83	0.000	2.253395	3.06589
casesd						
_cons	1.288468	.1239829	10.39	0.000	1.045466	1.53147
ctrlcov						
_cons	1.655172	.1105379	14.97	0.000	1.438522	1.871823
ctrlsd						
_cons	.8418313	.0781621	10.77	0.000	.6886365	.9950262

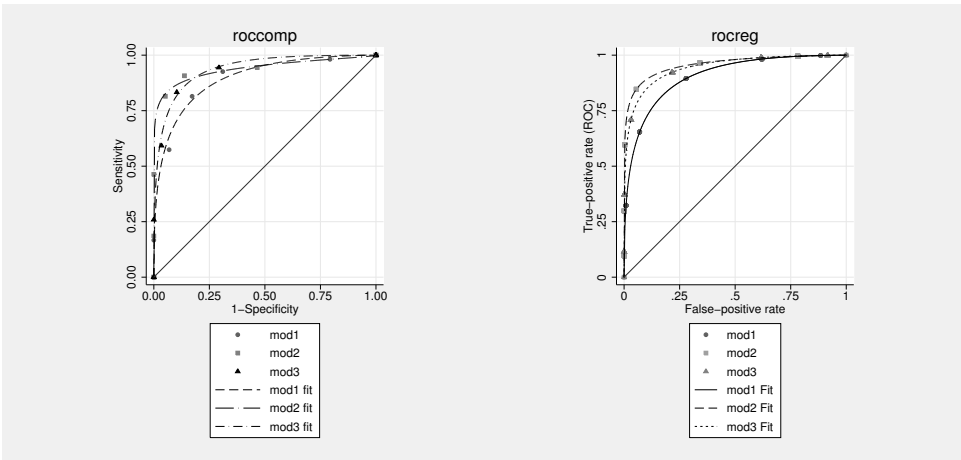
```
  Classifier : mod3
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
_cons	2.353768	.1973549	11.93	0.000	1.966959	2.740576
casesd						
_cons	1.143359	.1100198	10.39	0.000	.9277243	1.358994
ctrlcov						
_cons	2.275862	.1214094	18.75	0.000	2.037904	2.51382
ctrlsd						
_cons	.9246267	.0858494	10.77	0.000	.7563649	1.092888

```
   Status    : status
   ROC Model :
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
mod1						
i_cons	1.81646	.3144804	5.78	0.000	1.20009	2.432831
s_cons	.9627801	.1364084	7.06	0.000	.6954245	1.230136
auc	.904657	.0343518	26.34	0.000	.8373287	.9719853
mod2						
i_cons	2.064189	.3267274	6.32	0.000	1.423815	2.704563
s_cons	.6533582	.1015043	6.44	0.000	.4544135	.8523029
auc	.9580104	.0219713	43.60	0.000	.9149473	1.001073
mod3						
i_cons	2.058643	.2890211	7.12	0.000	1.492172	2.625113
s_cons	.8086932	.1163628	6.95	0.000	.5806262	1.03676
auc	.9452805	.0236266	40.01	0.000	.8989732	.9915877

```
Ho: All classifiers have equal AUC values.
Ha: At least one classifier has a different AUC value.
P-value:     .0808808
. rocregplot, title(rocreg) nodraw name(b)
> plot1opts(msymbol(o)) plot2opts(msymbol(s)) plot3opts(msymbol(t))
. graph combine a b, xsize(5)
```



We compare the AUC estimates for these models:

	roccomp	rocreg, ml
mod1	0.8945	0.9047
mod2	0.9382	0.9580
mod3	0.9376	0.9453

Each classifier has a higher estimated AUC under rocreg than roccomp. Each curve appears to be raised and smoothed in the rocreg fit as compared with roccomp. They are different, but not drastically different. The inference on whether the curve areas are the same is similar to example 9. We reject equality at the 0.10 level under rocreg and at the 0.05 level under roccomp.

Each intercept is significantly different from 0 at the 0.05 level and is estimated in a positive direction. Though all but classifier mod2 has 1 in their slope confidence intervals, the high intercepts suggest steep ROC curves and powerful tests.

Also note that the false-positive and true-positive rate points are calculated empirically in the roccomp graph and parametrically in rocreg. In example 9, the false-positive rates calculated by rocreg were calculated empirically, similar to roccomp. But in this example, the rates are calculated based on normal percentiles.

◁

Now we will generate an example to compare rocfit and rocreg under maximum likelihood estimation of a continuous classifier.

▷ Example 14: Maximum likelihood ROC, graphical comparison with rocfit

We generate 500 realizations of a population under threat of disease. One quarter of the population has the disease. A classifier x is measured, which has a control distribution of $N(1,3)$ and a case distribution of $N(1+5,2)$. We will invoke rocreg with the ml option on this generated data. We specify the continuous() option for rocfit and invoke it on the data as well. The continuous() option tells rocfit how many discrete slices to partition the data into before fitting.

For comparison of the two curves, we will use the rocfit postestimation command, rocplot; see [R] **rocfit postestimation**. This command graphs the empirical false-positive and true-positive rates with an overlaid fit of the binormal curve estimated by rocfit. rocplot also supports an addplot() option. We use the saved variables from rocreg in this option to overlay a line plot of the rocreg fit.

```
. clear
. set seed 8675309
. set obs 500
obs was 0, now 500
. generate d = runiform() < .25
. quietly generate double epsilon = 3*invnormal(runiform()) if d == 0
. quietly replace epsilon = 2*invnormal(runiform()) if d == 1
. quietly generate double x = 1 + d*5 + epsilon
```

```
. rocreg d x, probit ml nolog
Parametric ROC estimation
Control standardization: normal
ROC method              : parametric              Link: probit
  Status     : d
  Classifiers: x
  Classifier : x
  Covariate control adjustment model:
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
casecov						
_cons	4.905612	.2411624	20.34	0.000	4.432943	5.378282
casesd						
_cons	2.038278	.1299559	15.68	0.000	1.783569	2.292987
ctrlcov						
_cons	1.010382	.1561482	6.47	0.000	.7043377	1.316427
ctrlsd						
_cons	3.031849	.1104134	27.46	0.000	2.815443	3.248255

```
   Status    : d
   ROC Model :
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
x						
i_cons	2.406743	.193766	12.42	0.000	2.026969	2.786518
s_cons	1.487456	.1092172	13.62	0.000	1.273394	1.701518
auc	.9103292	.012754	71.38	0.000	.8853318	.9353266

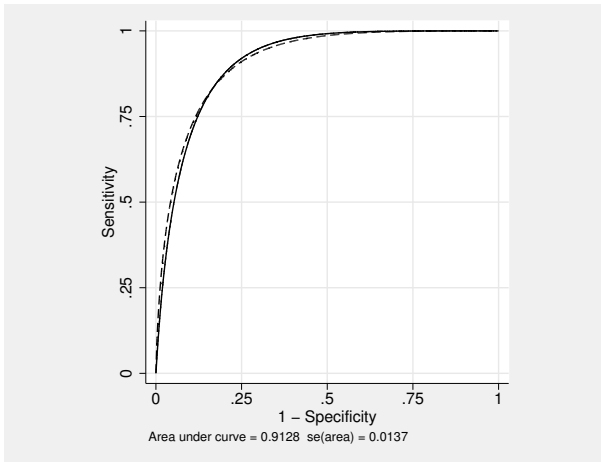
```
. rocfit d x, continuous(10) nolog
Binormal model of d on x                        Number of obs   =       500
Goodness-of-fit chi2(7) =        1.69
Prob > chi2             =      0.9751
Log likelihood          =  -911.91338
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
intercept	2.207250	0.232983	9.47	0.000	1.750611	2.663888
slope (*)	1.281443	0.158767	1.77	0.076	0.970265	1.592620
/cut1	-1.895707	0.130255	-14.55	0.000	-2.151001	-1.640412
/cut2	-1.326900	0.089856	-14.77	0.000	-1.503015	-1.150784
/cut3	-0.723677	0.070929	-10.20	0.000	-0.862695	-0.584660
/cut4	-0.116960	0.064666	-1.81	0.070	-0.243702	0.009782
/cut5	0.442769	0.066505	6.66	0.000	0.312422	0.573116
/cut6	1.065183	0.075744	14.06	0.000	0.916728	1.213637
/cut7	1.689570	0.102495	16.48	0.000	1.488683	1.890457
/cut8	2.495841	0.185197	13.48	0.000	2.132861	2.858821
/cut9	3.417994	0.348485	9.81	0.000	2.734976	4.101012

Index	Indices from binormal fit Estimate	Std. Err.	[95% Conf.	Interval]
ROC area	0.912757	0.013666	0.885972	0.939542
delta(m)	1.722473	0.127716	1.472153	1.972792
d(e)	1.934960	0.125285	1.689405	2.180515
d(a)	1.920402	0.121804	1.681670	2.159135

(*) z test for slope==1

```
. rocplot, plotopts(msymbol(i)) lineopts(lpattern(dash))
>         norefline addplot(line _roc_x _fpr_x, sort(_fpr_x _roc_x)
>         lpattern(solid)) aspectratio(1) legend(off)
```



We find that the curves are close. As before, the `rocfit` estimates are lower for the slope and intercept than under `rocreg`. The AUC estimates are close. Though the slope confidence interval contains 1, a high ROC intercept suggests a steep ROC curve and thus a powerful test.

◁

Saved results

Nonparametric `rocreg` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_strata)`	number of covariate strata
`e(N_clust)`	number of clusters
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`rocreg`
`e(cmdline)`	command as typed
`e(classvars)`	classification variable list
`e(refvar)`	status variable, reference variable
`e(ctrlmodel)`	covariate-adjustment specification
`e(ctrlcov)`	covariate-adjustment variables
`e(pvc)`	percentile value calculation method
`e(title)`	title in estimation output
`e(tiecorrected)`	indicates whether tie correction was used
`e(nobootstrap)`	indicates that bootstrap was performed
`e(bseed)`	seed used in bootstrap, if bootstrap performed
`e(breps)`	number of bootstrap resamples, if bootstrap performed
`e(cc)`	indicates whether case–control groups were used as resampling strata
`e(nobstrata)`	indicates whether resampling should stratify based on control covariates
`e(clustvar)`	name of cluster variable
`e(roc)`	false-positive rates where ROC was estimated
`e(invroc)`	ROC values where false-positive rates were estimated
`e(pauc)`	false-positive rates where pAUC was estimated
`e(auc)`	indicates that AUC was calculated
`e(vce)`	`bootstrap`
`e(properties)`	`b V` (or `b` if bootstrap not performed)

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators
`e(b_bs)`	bootstrap estimates
`e(bias)`	estimated biases
`e(se)`	estimated standard errors
`e(z0)`	median biases
`e(ci_normal)`	normal-approximation confidence intervals
`e(ci_percentile)`	percentile confidence intervals
`e(ci_bc)`	bias-corrected confidence intervals

Functions

`e(sample)`	marks estimation sample

Parametric, bootstrap `rocreg` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_strata)`	number of covariate strata
`e(N_clust)`	number of clusters
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`rocreg`
`e(cmdline)`	command as typed
`e(title)`	title in estimation output
`e(classvars)`	classification variable list
`e(refvar)`	status variable, reference variable
`e(ctrlmodel)`	covariate-adjustment specification
`e(ctrlcov)`	covariate-adjustment variables
`e(pvc)`	percentile value calculation method
`e(title)`	title in estimation output
`e(tiecorrected)`	indicates whether tie correction was used
`e(probit)`	`probit`
`e(roccov)`	ROC covariates
`e(fprpts)`	number of points used as false-positive rate fit points
`e(ctrlfprall)`	indicates whether all observed false-positive rates were used as fit points
`e(nobootstrap)`	indicates that bootstrap was performed
`e(bseed)`	seed used in bootstrap
`e(breps)`	number of bootstrap resamples
`e(cc)`	indicates whether case–control groups were used as resampling strata
`e(nobstrata)`	indicates whether resampling should stratify based on control covariates
`e(clustvar)`	name of cluster variable
`e(vce)`	`bootstrap`
`e(properties)`	`b V` (or `b` if `nobootstrap` is specified)
`e(predict)`	program used to implement `predict`

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators
`e(b_bs)`	bootstrap estimates
`e(reps)`	number of nonmissing results
`e(bias)`	estimated biases
`e(se)`	estimated standard errors
`e(z0)`	median biases
`e(ci_normal)`	normal-approximation confidence intervals
`e(ci_percentile)`	percentile confidence intervals
`e(ci_bc)`	bias-corrected confidence intervals

Functions

`e(sample)`	marks estimation sample

Parametric, maximum likelihood rocreg saves the following in e():

Scalars

e(N)	number of observations
e(N_clust)	number of clusters
e(rank)	rank of e(V)

Macros

e(cmd)	rocreg
e(cmdline)	command as typed
e(classvars)	classification variable list
e(refvar)	status variable
e(ctrlmodel)	linear
e(ctrlcov)	control population covariates
e(roccov)	ROC covariates
e(probit)	probit
e(pvc)	normal
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(vce)	cluster if clustering used
e(vcetype)	robust if multiple classifiers or clustering used
e(ml)	indicates that maximum likelihood estimation was used
e(predict)	program used to implement predict

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

rocreg is implemented as an ado-file.

Assume that we applied a diagnostic test to each of N_0 control and N_1 case subjects. Further assume that the higher the outcome value of the diagnostic test, the higher the risk of the subject being abnormal. Let $y_{1i}, i = 1, 2, \ldots, N_1$, and $y_{0j}, j = 1, 2, \ldots, N_0$, be the values of the diagnostic test for the case and control subjects, respectively. The true status variable D identifies an observation as case $D = 1$ or control $D = 0$. The CDF of the classifier Y is F. Conditional on D, we write the CDF as F_D.

Methods and formulas are presented under the following headings:

ROC statistics
Covariate-adjusted ROC curves
Parametric ROC curves: Estimating equations
Parametric ROC curves: Maximum likelihood

ROC statistics

We obtain these definitions and their estimates from Pepe (2003) and Pepe, Longton, and Janes (2009). The false-positive and true-positive rates at cutoff c are defined as

$$\text{FPR}(y) = P\left(Y \geq y \middle| D = 0\right)$$

$$\text{TPR}(y) = P\left(Y \geq y \middle| D = 1\right)$$

The true-positive rate, or ROC value at false-positive rate u, is given by

$$\text{ROC}(u) = P\left(1 - F_0(Y) \leq u \middle| D = 1\right)$$

When Y is continuous, the false-positive rate can be written as

$$\text{FPR}(y) = 1 - F_0(y)$$

The empirical CDF for the sample $z_1, \ldots, z_n$ is given by

$$\widehat{F}(z) = \sum_{i=1}^{n} \frac{I(z < z_i)}{n}$$

The empirical estimates $\widehat{\text{FPR}}$ and $\widehat{\text{ROC}}$ both use this empirical CDF estimator.

The area under the ROC curve is defined as

$$\text{AUC} = \int_0^1 \text{ROC}(u)\, d_u$$

The partial area under the ROC curve for false-positive rate a is defined as

$$\text{pAUC}(a) = \int_0^a \text{ROC}(u)\, d_u$$

The nonparametric estimate for the AUC is given by

$$\widehat{\text{AUC}} = \sum_{i=1}^{N_1} \frac{1 - \widehat{\text{FPR}}(y_{1i})}{N_1}$$

The nonparametric estimate of pAUC is given by

$$\widehat{\text{pAUC}}(a) = \sum_{i=1}^{N_1} \frac{\max\left\{1 - \widehat{\text{FPR}}(y_{1i}) - (1-a), 0\right\}}{N_1}$$

For discrete classifiers, a correction term is subtracted from the false-positive rate estimate so that the $\widehat{\text{AUC}}$ and $\widehat{\text{pAUC}}$ estimates correspond with a trapezoidal approximation to the area of the ROC curve.

$$\text{FPR}^c(y) = 1 - \widehat{F}_0(y) - \frac{1}{2}\sum_{j=1}^{N_0} \frac{I(y = y_{0j})}{N_0}$$

In the nonparametric estimation of the ROC curve, all inference is performed using the `bootstrap` command (see [R] **bootstrap**). `rocreg` also allows users to calculate the ROC curve and related statistics by assuming a normal control distribution. So these formulas are updated by replacing F_0 by Φ (with adjustment of the marginal mean and variance of the control distribution).

Covariate-adjusted ROC curves

Suppose we observe covariate vector Z in addition to the classifier Y. Let $Z_{1i}, i = 1, 2, \ldots, N_1$, and $Z_{0j}, j = 1, 2, \ldots, N_0$, be the values of the covariates for the case and control subjects, respectively.

The covariate-adjusted ROC curve is defined by Janes and Pepe (2009) as

$$\text{AROC}(t) = E\left\{\text{ROC}\left(t\middle|Z_0\right)\right\}$$

It is calculated by replacing the marginal control CDF estimate, $\widehat{F}_0$, with the conditional control CDF estimate, $\widehat{F}_{0Z}$. If we used a normal control CDF, then we would replace the marginal control mean and variance with the conditional control mean and variance. The formulas of the previous section can be updated for covariate-adjustment by making this substitution of the conditional CDF for the marginal CDF in the false-positive rate calculation.

Because the calculation of the ROC value is now performed based on the conditionally calculated false-positive rate, no further conditioning is made in its calculation under nonparametric estimation.

`rocreg` supports covariate adjustment with stratification and linear regression. Under stratification, separate parameters are estimated for the control distribution at each level of the covariates. Under linear regression, the classifier is regressed on the covariates over the control distribution, and the resulting coefficients serve as parameters for $\widehat{F}_{0Z}$.

Parametric ROC curves: Estimating equations

Under nonparametric estimation of the ROC curve with covariate adjustment, no further conditioning occurs in the ROC curve calculation beyond the use of covariate-adjusted false-positive rates as inputs.

Under parametric estimation of the ROC curve, we can relax this restriction. We model the ROC curve as a cumulative distribution function g (standard normal Φ) invoked with input of a linear polynomial in the corresponding quantile function (here Φ^{-1}) invoked on the false-positive rate u. The constant intercept of the polynomial may depend on covariates; the slope term α (quantile coefficient) may not.

$$\text{ROC}(u) = g\{\mathbf{x}'\boldsymbol{\beta} + \alpha g^{-1}(u)\}$$

Pepe (2003) notes that having a binormal ROC ($g = \Phi$) is equivalent to specifying that some monotone transformation of the data exists to make the case and control classifiers normally distributed. This specification applies to the marginal case and control.

Under weak assumptions about the control distribution of the classifier, we can fit this model by using estimating equations (Alonzo and Pepe 2002). The method can be used without covariate effects in the second stage, assuming a parametric model for the single ROC curve. Using the Alonzo and Pepe (2002) method, the covariate-adjusted ROC curve may be fit parametrically. The marginal ROC curve, involving no covariates in either stage of estimation, can be fit parametrically as well. In addition to the Alonzo and Pepe (2002) explanation, further details are given in Pepe, Longton, and Janes (2009); Janes, Longton, and Pepe (2009); Pepe (2003); and Janes and Pepe (2009).

The algorithm can be described as follows:

1. Estimate the false-positive rates of the classifier `fpr`. These may be computed in any fashion outlined so far: covariate-adjusted, empirically, etc.
2. Determine a set of n_p false-positive rates to use as fitting points $f_1, \ldots, f_{n_p}$. These may be an equispaced grid on $(0, 1)$ or the set of observed false-positive rates from part 1.

3. Expand the case observation portion of the data to include a subobservation for each fitting point. So there are now $N_1(n_p - 1)$ additional observations in the data.
4. Generate a new dummy variable `u`. For subobservation j, $\texttt{u} = I\,(\texttt{fpr} \leq f_j)$.
5. Generate a new variable `quant` containing the quantiles of the false-positive rate fitting points. For subobservation j, $\texttt{quant} = g^{-1}\,(f_j)$.
6. Perform a binary regression (probit, $g = \Phi$) of `fpr` on the covariates `x` and quantile variable `quant`.

The coefficients of part 6 are the coefficients of the ROC model. The coefficients of the covariates coincide naturally with estimates of $\boldsymbol{\beta}$, and the α parameter is estimated by the coefficient on `quant`. Because the method is so general and makes few distributional assumptions, bootstrapping must be performed for inference. If multiple classifiers are to be fit, the algorithm is performed separately for each in each bootstrap, and the bootstrap is used to estimate covariances.

We mentioned earlier that in parametric estimation, the AUC was the only summary parameter that could be estimated initially. This is true when we fit the marginal probit model because there are no covariates in part 6 of the algorithm.

To calculate the AUC statistic under a marginal probit model, we use the formula

$$\text{AUC} = \Phi\left(\frac{\beta_0}{\sqrt{1+\alpha^2}}\right)$$

Alternatively, the AUC for the probit model can be calculated as pAUC(1) in postestimation. Under both models, bootstrapping is performed for inference on the AUC.

Parametric ROC curves: Maximum likelihood

`rocreg` supports another form of parametric ROC estimation: maximum likelihood with a normally distributed classifier. This method assumes that the classifier is a normal linear model on certain covariates, and the covariate effect and variance of the classifier may change between the case and control populations. The model is defined in Pepe (2003, 145).

$$y = \mathbf{z}'\boldsymbol{\beta_0} + D\mathbf{x}'\boldsymbol{\beta_1} + \sigma\,(D)\,\epsilon$$

Our error term, ϵ, is a standard normal random variable. The variable D is our true status variable, being 1 for the case population observations and 0 for the control population observations. The variance function σ is defined as

$$\sigma\,(D) = \sigma_0\,(D = 0) + \sigma_1\,(D = 1)$$

This provides two variance parameters in the model and does not depend on covariate values.

Under this model, the ROC curve is easily derived to be

$$\text{ROC}\,(u) = \Phi\left[\frac{1}{\sigma_1}\left\{\mathbf{x}'\boldsymbol{\beta_1} + \sigma_0\Phi^{-1}\,(u)\right\}\right]$$

We reparameterize the model, creating the parameters $\beta_i = \sigma_1^{-1}\beta_{1i}$ and $\alpha = \sigma_1^{-1}\sigma_0$. We refer to β_0 as the constant intercept, `i_cons`. The parameter α is referred to as the constant slope, `s_cons`.

$$\text{ROC}\,(u) = \Phi\{\mathbf{x}'\boldsymbol{\beta} + \alpha\Phi^{-1}\,(u)\}$$

The original model defining the classifier y leads to the following single observation likelihoods for $D = 0$ and $D = 1$:

$$L(\boldsymbol{\beta_0}, \boldsymbol{\beta_1}, \sigma_1, \sigma_0, \big| D = 0, y, \mathbf{z}, \mathbf{x}) = \frac{1}{\sqrt{2\pi}\sigma_0} \exp \frac{-(y - \mathbf{z}'\boldsymbol{\beta_0})^2}{2\sigma_0^2}$$

$$L(\boldsymbol{\beta_0}, \boldsymbol{\beta_1}, \sigma_1, \sigma_0, \big| D = 1, y, \mathbf{z}, \mathbf{x}) = \frac{1}{\sqrt{2\pi}\sigma_1} \exp \frac{-(y - \mathbf{z}'\boldsymbol{\beta_0} - \mathbf{x}'\boldsymbol{\beta_1})^2}{2\sigma_1^2}$$

These can be combined to yield the observation-level log likelihood:

$$\begin{aligned} \ln L(\boldsymbol{\beta_0}, \boldsymbol{\beta_1}, \sigma_1, \sigma_0, \big| D, y, \mathbf{z}, \mathbf{x}) = & -\frac{\ln 2\pi}{2} \\ & - I(D = 0) \left\{ \ln\sigma_0 + \frac{(y - \mathbf{z}'\boldsymbol{\beta_0})^2}{2\sigma_0^2} \right\} \\ & - I(D = 1) \left\{ \ln\sigma_1 + \frac{(y - \mathbf{z}'\boldsymbol{\beta_0} - \mathbf{x}'\boldsymbol{\beta_1})^2}{2\sigma_1^2} \right\} \end{aligned}$$

When there are multiple classifiers, each classifier is fit separately with maximum likelihood. Then the results are combined by stacking the scores and using the sandwich variance estimator. For more information, see [R] **suest** and the references White (1982); Rogers (1993); and White (1996).

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Also see

[R] **rocreg postestimation** — Postestimation tools for rocreg

[R] **rocregplot** — Plot marginal and covariate-specific ROC curves after rocreg

[R] **rocfit** — Parametric ROC models

[R] **roc** — Receiver operating characteristic (ROC) analysis

Title

rocreg postestimation — Postestimation tools for rocreg

Description

The following commands are of special interest after `rocreg`:

Command	Description
`estat nproc`	nonparametric ROC curve estimation, keeping fit information from `rocreg`
`rocregplot`	plot marginal and covariate-specific ROC curves

For information about `estat nproc`, see below.
For information about `rocregplot`, see [R] **rocregplot**.

The following standard postestimation commands are also available:

Command	Description
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions for parametric ROC curve estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Special-interest postestimation command

The `estat nproc` command allows calculation of all the ROC curve summary statistics for covariate-specific ROC curves, as well as for a nonparametric ROC estimation. Under nonparametric estimation, a single ROC curve is estimated by `rocreg`. Covariates can affect this estimation, but there are no separate covariate-specific ROC curves. Thus the input arguments for `estat nproc` are taken in the command line rather than from the data as variable values.

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic options]
```

statistic	Description
Main	
`at(`*varname*`)`	input variable for statistic
`auc`	total area under the ROC curve; the default
`roc`	ROC values for given false-positive rates in `at()`
`invroc`	false-positive rate for given ROC values in `at()`
`pauc`	partial area under the ROC curve up to each false-positive rate in `at()`
`classvar(`*varname*`)`	statistic for given classifier

options	Description
Options	
`intpts(#)`	points in numeric integration of pAUC calculation
`se(`*newvar*`)`	predict standard errors
`ci(`*stubname*`)`	produce confidence intervals, stored as variables with prefix *stubname* and suffixes `_l` and `_u`
`level(#)`	set confidence level; default is `level(95)`
* `bfile(`*filename*`, ...)`	load dataset containing bootstrap replicates from `rocreg`
* `btype(n | p | bc)`	produce normal-based (`n`), percentile (`p`), or bias-corrected (`bc`) confidence intervals; default is `btype(n)`

* `bfile()` and `btype()` are only allowed with parametric analysis using bootstrap inference.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`at(`*varname*`)` records the variable to be used as input for the above predictions.

`auc` predicts the total area under the ROC curve defined by the covariate values in the data. This is the default statistic.

`roc` predicts the ROC values for false-positive rates stored in *varname* specified in `at()`.

`invroc` predicts the false-positive rates for given ROC values stored in *varname* specified in `at()`.

`pauc` predicts the partial area under the ROC curve up to each false-positive rate stored in *varname* specified in `at()`.

`classvar(`*varname*`)` performs the prediction for the specified classifier.

Options

`intpts(#)` specifies that # points be used in the pAUC calculation.

`se(`*newvar*`)` specifies that standard errors be produced and stored in *newvar*.

`ci(`*stubname*`)` requests that confidence intervals be produced and the lower and upper bounds be stored in *stubname*`_l` and *stubname*`_u`, respectively.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`bfile(`*filename*`, ...)` uses bootstrap replicates of parameters from `rocreg` stored in *filename* to estimate standard errors and confidence intervals of predictions.

`btype(n | p | bc)` specifies whether to produce normal-based (`n`), percentile (`p`), or bias-corrected (`bc`) confidence intervals. The default is `btype(n)`.

Syntax for estat nproc

```
estat nproc [ , estat_nproc_options ]
```

estat_nproc_options	Description
Main	
`auc`	estimate total area under the ROC curve
`roc(`*numlist*`)`	estimate ROC values for given false-positive rates
`invroc(`*numlist*`)`	estimate false-positive rate for given ROC values
`pauc(`*numlist*`)`	estimate partial area under the ROC curve up to each false-positive rate

At least one option must be specified.

Menu

Statistics > Postestimation > Reports and statistics

Options for estat nproc

Main

`auc` estimates the total area under the ROC curve.

`roc(`*numlist*`)` estimates the ROC for each of the false-positive rates in *numlist*. The values in *numlist* must be in the range (0,1).

`invroc(`*numlist*`)` estimates the false-positive rate for each of the ROC values in *numlist*. The values in *numlist* must be in the range (0,1).

`pauc(`*numlist*`)` estimates the partial area under the ROC curve up to each false-positive rate in *numlist*. The values in *numlist* must be in the range (0,1].

Remarks

Remarks are presented under the following headings:

Using predict after rocreg
Using estat nproc

Using predict after rocreg

`predict`, after parametric `rocreg`, predicts the AUC, the ROC value, the false-positive rate (invROC), or the pAUC value. The default is `auc`.

We begin by estimating the area under the ROC curve for each of the three age-specific ROC curves in example 1 of [R] **rocregplot**: 30, 40, and 50 months.

▷ Example 1

In example 6 of [R] **rocreg**, a probit ROC model was fit to audiology test data from Norton et al. (2000). The estimating equations method of Alonzo and Pepe (2002) was used to fit the model. Gender and age were covariates that affected the control distribution of the classifier `y1` (DPOAE 65 at 2 kHz). Age was a ROC covariate for the model, so we fit separate ROC curves at each age.

Following Janes, Longton, and Pepe (2009), we drew the ROC curves for ages 30, 40, and 50 months in example 1 of [R] **rocregplot**. Now we use `predict` to estimate the AUC for the ROC curve at each of those ages.

The bootstrap dataset saved by `rocreg` in example 6 of [R] **rocreg**, `nnhs2y1.dta`, is used in the `bfile()` option.

We will store the AUC prediction in the new variable `predAUC`. We specify the `se()` option with the new variable name `seAUC` to produce an estimate of the prediction's standard error. By specifying the stubname `cin` in `ci()`, we tell `predict` to create normal-based confidence intervals (the default) as new variables `cin_l` and `cin_u`.

```
. use http://www.stata-press.com/data/r12/nnhs
(Norton - neonatal audiology data)
. rocreg d y1, probit ctrlcov(currage male) ctrlmodel(linear) roccov(currage)
> cluster(id) bseed(56930) bsave(nnhs2y1)
  (output omitted)
. set obs 5061
obs was 5058, now 5061
. quietly replace currage = 30 in 5059
. quietly replace currage = 40 in 5060
. quietly replace currage = 50 in 5061
. predict predAUC in 5059/5061, auc se(seAUC) ci(cin) bfile(nnhs2y1)
. list currage predAUC seAUC cin* in 5059/5061
```

	currage	predAUC	seAUC	cin_l	cin_u
5059.	30	.5209999	.0712928	.3812686	.6607312
5060.	40	.6479176	.0286078	.5918474	.7039879
5061.	50	.7601378	.0746157	.6138937	.9063819

As expected, we find the AUC to increase with age.

Essentially, we have a stored bootstrap sample of ROC covariate coefficient estimates in `nnhs2y1.dta`. We calculate the AUC using each set of coefficient estimates, resulting in a sample of AUC estimates. Then the bootstrap standard error and confidence intervals are calculated based on this AUC sample. Further details of the computation of the standard error and percentile confidence intervals can be found in *Methods and formulas* and in [R] **bootstrap**.

We can also produce percentile or bias-corrected confidence intervals by specifying `btype(p)` or `btype(bc)`, which we now demonstrate.

```
. drop *AUC*
. predict predAUC in 5059/5061, auc se(seAUC) ci(cip) bfile(nnhs2y1) btype(p)
. list currage predAUC cip* in 5059/5061
```

	currage	predAUC	cip_l	cip_u
5059.	30	.5209999	.3760555	.6513149
5060.	40	.6479176	.5893397	.7032645
5061.	50	.7601378	.5881404	.8836223

```
. drop *AUC*
. predict predAUC in 5059/5061, auc se(seAUC) ci(cibc) bfile(nnhs2y1) btype(bc)
. list currage predAUC cibc* in 5059/5061
```

	currage	predAUC	cibc_l	cibc_u
5059.	30	.5209999	.3736968	.6500064
5060.	40	.6479176	.588947	.7010052
5061.	50	.7601378	.5812373	.8807758

◁

`predict` can also estimate the ROC value and the false-positive rate (invROC).

▷ Example 2

In example 7 of [R] **rocreg**, we fit the ROC curve for status variable hearing loss (`d`) and classifier negative signal-to-noise ratio `nsnr` with ROC covariates frequency (`xf`), intensity (`xl`), and hearing loss severity (`xd`). The data were obtained from Stover et al. (1996). The model fit was probit with bootstrap resampling. We saved 50 bootstrap replications in the dataset `nsnrf.dta`.

The covariate value combinations `xf = 10.01`, `xl = 5.5`, and `xd = .5`, and `xf = 10.01`, `xl = 6.5`, and `xd = 4` are of interest. In example 3 of [R] **rocregplot**, we estimated the ROC values for false-positive rates 0.2 and 0.7 and the false-positive rate for a ROC value of 0.5 by using `rocregplot`. We will use `predict` to replicate the estimation.

We begin by appending observations with our desired covariate combinations to the data. We also create two new variables: `rocinp`, which contains the ROC values for which we wish to predict the corresponding invROC values, and `invrocinp`, which contains the invROC values corresponding to the ROC values we wish to predict.

```
. clear
. input xf xl xd rocinp invrocinp
           xf         xl         xd     rocinp  invrocinp
  1. 10.01 5.5 .5 .2 .
  2. 10.01 6.5 4  .2 .
  3. 10.01 5.5 .5 .7 .5
  4. 10.01 6.5 4  .7 .5
  5. end
. save newdata
file newdata.dta saved
. use http://www.stata-press.com/data/r12/dp
(Stover - DPOAE test data)
. quietly rocreg d nsnr, ctrlcov(xf xl) roccov(xf xl xd) probit cluster(id)
> nobstrata ctrlfprall bseed(156385) breps(50) ctrlmodel(strata) bsave(nsnrf)
. append using newdata
. list xf xl xd invrocinp rocinp in 1849/1852
```

	xf	xl	xd	invroc~p	rocinp
1849.	10.01	5.5	.5	.	.2
1850.	10.01	6.5	4	.	.2
1851.	10.01	5.5	.5	.5	.7
1852.	10.01	6.5	4	.5	.7

Now we will use `predict` to estimate the ROC value for the false-positive rates stored in `rocinp`. We specify the `roc` option, and we specify `rocinp` in the `at()` option. The other options, `se()` and `ci()`, are used to obtain standard errors and confidence intervals, respectively. The dataset of bootstrap samples, `nsnrf.dta`, is specified in `bfile()`. After prediction, we list the point estimates and standard errors.

```
. predict rocit in 1849/1852, roc at(rocinp) se(seroc) ci(cin) bfile(nsnrf)
. list xf xl xd rocinp rocit seroc if !missing(rocit)
```

	xf	xl	xd	rocinp	rocit	seroc
1849.	10.01	5.5	.5	.2	.7652956	.0735506
1850.	10.01	6.5	4	.2	.9672505	.0227977
1851.	10.01	5.5	.5	.7	.9835816	.0204353
1852.	10.01	6.5	4	.7	.999428	.0011309

These results match example 3 of [R] **rocregplot**. We list the confidence intervals next. These also conform to the `rocregplot` results from example 3 in [R] **rocregplot**. We begin with the confidence intervals for ROC under the covariate values `xf=10.01`, `xl=5.5`, and `xd=.5`.

```
. list xf xl xd rocinp rocit cin* if inlist(_n, 1849, 1851)
```

	xf	xl	xd	rocinp	rocit	cin_l	cin_u
1849.	10.01	5.5	.5	.2	.7652956	.6211391	.9094521
1851.	10.01	5.5	.5	.7	.9835816	.9435292	1.023634

Now we list the ROC confidence intervals under the covariate values `xf=10.01`, `xl=6.5`, and `xd=4`.

```
. list xf xl xd rocinp rocit cin* if inlist(_n, 1850, 1852)
```

	xf	xl	xd	rocinp	rocit	cin_l	cin_u
1850.	10.01	6.5	4	.2	.9672505	.9225678	1.011933
1852.	10.01	6.5	4	.7	.999428	.9972115	1.001644

Now we will predict the false-positive rate for a ROC value by specifying the `invroc` option. We pass the `invrocinp` variable as an argument to the `at()` option. Again we list the point estimates and standard errors first.

```
. drop ci*
. predict invrocit in 1849/1852, invroc at(invrocinp) se(serocinv) ci(cin)
> bfile(nsnrf)
. list xf xl xd invrocinp invrocit serocinv if !missing(invrocit)
```

	xf	xl	xd	invroc~p	invrocit	serocinv
1851.	10.01	5.5	.5	.5	.0615144	.0254042
1852.	10.01	6.5	4	.5	.0043298	.0045938

These also match those of example 3 of [R] **rocregplot**. Listing the confidence intervals shows identical results as well. First we list the confidence intervals under the covariate values `xf=10.01`, `xl=5.5`, and `xd=.5`.

```
. list xf xl xd invrocinp invrocit cin* in 1851
```

	xf	xl	xd	invroc~p	invrocit	cin_l	cin_u
1851.	10.01	5.5	.5	.5	.0615144	.0117231	.1113057

Now we list the confidence intervals for false-positive rate under the covariate values `xf=10.01`, `xl=6.5`, and `xd=4`.

```
. list xf xl xd invrocinp invrocit cin* in 1852
```

	xf	xl	xd	invroc~p	invrocit	cin_l	cin_u
1852.	10.01	6.5	4	.5	.0043298	-.004674	.0133335

◁

The `predict` command can also be used after a maximum-likelihood ROC model is fit.

Example 3

In the previous example, we revisited the estimating equations fit of a probit model with ROC covariates frequency (xf), intensity (xl), and hearing loss severity (xd) to the Stover et al. (1996) audiology study data. A maximum likelihood fit of the same model was performed in example 10 of [R] **rocreg**. In example 2 of [R] **rocregplot**, we used rocregplot to estimate ROC values and false-positive rates for this model under two covariate configurations. We will use predict to obtain the same estimates. We will also estimate the partial area under the ROC curve.

We append the data as in the previous example. This leads to the following four final observations in the data.

```
. use http://www.stata-press.com/data/r12/dp, clear
(Stover - DPOAE test data)
. rocreg d nsnr, probit ctrlcov(xf xl) roccov(xf xl xd) ml cluster(id)
  (output omitted)
. append using newdata
. list xf xl xd invrocinp rocinp in 1849/1852
```

	xf	xl	xd	invroc~p	rocinp
1849.	10.01	5.5	.5	.	.2
1850.	10.01	6.5	4	.	.2
1851.	10.01	5.5	.5	.5	.7
1852.	10.01	6.5	4	.5	.7

Now we predict the ROC value for false-positive rates of 0.2 and 0.7. Under maximum likelihood prediction, only Wald-type confidence intervals are produced. We specify a new variable name for the standard error in the se() option and a stubname for the confidence-interval variables in the ci() option.

```
. predict rocit in 1849/1852, roc at(rocinp) se(seroc) ci(ci)
. list xf xl xd rocinp rocit seroc ci_l ci_u if !missing(rocit), noobs
```

xf	xl	xd	rocinp	rocit	seroc	ci_l	ci_u
10.01	5.5	.5	.2	.7608593	.0510501	.660803	.8609157
10.01	6.5	4	.2	.9499408	.0179824	.914696	.9851856
10.01	5.5	.5	.7	.978951	.0097382	.9598644	.9980376
10.01	6.5	4	.7	.9985001	.0009657	.9966073	1.000393

These results match our estimates in example 2 of [R] **rocregplot**. We also match example 2 of [R] **rocregplot** when we estimate the false-positive rate for a ROC value of 0.5.

```
. drop ci*
. predict invrocit in 1851/1852, invroc at(invrocinp) se(serocinv) ci(ci)
. list xf xl xd invrocinp invrocit serocinv ci_l ci_u if !missing(invrocit), noobs
```

xf	xl	xd	invroc~p	invrocit	serocinv	ci_l	ci_u
10.01	5.5	.5	.5	.0578036	.0198626	.0188736	.0967336
10.01	6.5	4	.5	.0055624	.0032645	-.0008359	.0119607

◁

▷ Example 4

In example 13 of [R] **rocreg**, we fit a maximum-likelihood marginal probit model to each classifier of the fictitious dataset generated from Hanley and McNeil (1983). In example 5 of [R] **rocregplot**, `rocregplot` was used to draw the ROC for the `mod1` and `mod3` classifiers. Estimates of the ROC value and false-positive rate were also obtained with Wald-type confidence intervals.

We return to this example, this time using `predict` to estimate the ROC value and false-positive rate. We will also estimate the pAUC for the false-positive rates of 0.3 and 0.8.

First, we add the input variables to the data. The variable `paucinp` will hold the 0.3 and 0.8 false-positive rates that we will input to pAUC. The variable `invrocinp` holds the ROC value of 0.8 for which we will estimate the false-positive rate. Finally, the variable `rocinp` holds the false-positive rates of 0.15 and 0.75 for which we will estimate the ROC value.

```
. use http://www.stata-press.com/data/r12/ct2, clear
. rocreg status mod1 mod2 mod3, probit ml
  (output omitted)
. quietly generate paucinp = .3 in 111
. quietly replace paucinp = .8 in 112
. quietly generate invrocinp = .8 in 112
. quietly generate rocinp = .15 in 111
. quietly replace rocinp = .75 in 112
```

Then, we estimate the ROC value for false-positive rates 0.15 and 0.75 under classifier `mod1`. The point estimate is stored in `roc1`. Wald confidence intervals and standard errors are also estimated. We find that these results match those of example 5 of [R] **rocregplot**.

```
. predict roc1 in 111/112, classvar(mod1) roc at(rocinp) se(sr1) ci(cir1)
. list rocinp roc1 sr1 cir1* in 111/112
```

	rocinp	roc1	sr1	cir1_l	cir1_u
111.	.15	.7934935	.0801363	.6364293	.9505578
112.	.75	.9931655	.0069689	.9795067	1.006824

Now we perform the same estimation under the classifier `mod3`.

```
. predict roc3 in 111/112, classvar(mod3) roc at(roci) se(sr3) ci(cir3)
. list rocinp roc3 sr3 cir3* in 111/112
```

	rocinp	roc3	sr3	cir3_l	cir3_u
111.	.15	.8888596	.0520118	.7869184	.9908009
112.	.75	.9953942	.0043435	.9868811	1.003907

Next we estimate the false-positive rate for the ROC value of 0.8. These results also match example 5 of [R] **rocregplot**.

```
. predict invroc1 in 112, classvar(mod1) invroc at(invrocinp) se(sir1) ci(ciir1)
. list invrocinp invroc1 sir1 ciir1* in 112
```

	invroc~p	invroc1	sir1	ciir1_l	ciir1_u
112.	.8	.1556435	.069699	.0190361	.292251

```
. predict invroc3 in 112, classvar(mod3) invroc at(invrocinp) se(sir3) ci(ciir3)
. list invrocinp invroc3 sir3 ciir3* in 112
```

	invroc~p	invroc3	sir3	ciir3_l	ciir3_u
112.	.8	.0661719	.045316	-.0226458	.1549896

Finally, we estimate the pAUC for false-positive rates of 0.3 and 0.8. The point estimate is calculated by numeric integration. Wald confidence intervals are obtained with the delta method. Further details are presented in *Methods and formulas*.

```
. predict pauc1 in 111/112, classvar(mod1) pauc at(paucinp) se(sp1) ci(cip1)
. list paucinp pauc1 sp1 cip1* in 111/112
```

	paucinp	pauc1	sp1	cip1_l	cip1_u
111.	.3	.221409	.0240351	.174301	.268517
112.	.8	.7033338	.0334766	.6377209	.7689466

```
. predict pauc3 in 111/112, classvar(mod3) pauc at(paucinp) se(sp3) ci(cip3)
. list paucinp pauc3 sp3 cip3* in 111/112
```

	paucinp	pauc3	sp3	cip3_l	cip3_u
111.	.3	.2540215	.0173474	.2200213	.2880217
112.	.8	.7420408	.0225192	.6979041	.7861776

Using estat nproc

When you initially use `rocreg` to fit a nonparametric ROC curve, you can obtain bootstrap estimates of a ROC value, false-positive rate, area under the ROC curve, and partial area under the ROC curve. The `estat nproc` command allows the user to estimate these parameters after `rocreg` has originally been used.

The seed and resampling settings used by `rocreg` are used by `estat nproc`. So the results for these new statistics are identical to what they would be if they had been initially estimated in the `rocreg` command. These new statistics, together with those previously estimated in `rocreg`, are returned in `r()`.

We demonstrate with an example.

▷ Example 5

In example 3 of [R] **rocreg**, we examined data from a pancreatic cancer study (Wieand et al. 1989). Two continuous classifiers, `y1` (CA 19-9) and `y2` (CA 125), were used for the true status variable `d`. In that example, we estimated various quantities including the false-positive rate for a ROC value of 0.6 and the pAUC for a false-positive rate of 0.5. Here we replicate that estimation with a call to `rocreg` to estimate the former and follow that with a call to `estat nproc` to estimate the latter. For simplicity, we restrict estimation to classifier `y1` (CA 19-9).

We start by executing `rocreg`, estimating the false-positive rate for a ROC value of 0.6. This value is specified in `invroc()`. Case–control resampling is used by specifying the `bootcc` option.

```
. use http://labs.fhcrc.org/pepe/book/data/wiedat2b, clear
(S. Wieand - Pancreatic cancer diagnostic marker data)
. rocreg d y1, invroc(.6) bseed(8378923) bootcc nodots
Bootstrap results
Number of strata   =         2                  Number of obs      =       141
                                                 Replications       =      1000
Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
False-positive rate
   Status    : d
   Classifier: y1
```

invROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.6	0	.0158039	.0267288	-.0523874	.0523874	(N)
				0	.0784314	(P)
				0	.1372549	(BC)

Now we will estimate the pAUC for the false-positive rate of 0.5 using `estat nproc` and the `pauc()` option.

```
. matrix list e(b)
symmetric e(b)[1,1]
          y1:
    invroc_1
y1         0
. estat nproc, pauc(.5)
Bootstrap results
Number of strata   =         2                  Number of obs      =       141
                                                 Replications       =      1000
Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
False-positive rate
   Status    : d
   Classifier: y1
```

invROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.6	0	.0158039	.0267288	-.0523874	.0523874	(N)
				0	.0784314	(P)
				0	.1372549	(BC)

```
Partial area under the ROC curve
   Status    : d
   Classifier: y1
```

pAUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.5	.3932462	-.0000769	.021332	.3514362	.4350562	(N)
				.3492375	.435512	(P)
				.3492375	.435403	(BC)

```
. matrix list r(b)
r(b)[1,2]
           y1:        y1:
     invroc_1     pauc_1
y1          0  .39324619
. matrix list e(b)
symmetric e(b)[1,1]
          y1:
    invroc_1
y1         0
. matrix list r(V)
symmetric r(V)[2,2]
                    y1:        y1:
              invroc_1     pauc_1
y1:invroc_1  .00071443
  y1:pauc_1   -.000326  .00045506
. matrix list e(V)
symmetric e(V)[1,1]
                    y1:
              invroc_1
y1:invroc_1  .00071443
```

◁

The advantages of using `estat nproc` are twofold. First, you can estimate additional parameters of interest without having to respecify the bootstrap settings you did with `rocreg`; instead `estat nproc` uses the bootstrap settings that were stored by `rocreg`. Second, parameters estimated with `estat nproc` are added to those parameters estimated by `rocreg` and returned in the matrices `r(b)` (parameter estimates) and `r(V)` (variance–covariance matrix). Thus you can also obtain correlations between any quantities you wish to estimate.

Saved results

`estat nproc` saves the following in `r()`:

`r(b)`	coefficient vector
`r(V)`	variance–covariance matrix of the estimators
`r(ci_normal)`	normal-approximation confidence intervals
`r(ci_percentile)`	percentile confidence intervals
`r(ci_bc)`	bias-corrected confidence intervals

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Details on computation of the nonparametric ROC curve and the estimation of the parametric ROC curve model coefficients can be found in [R] **rocreg**. Here we describe how to estimate the ROC curve summary statistics for a parametric model. The cumulative distribution function, g, can be the standard normal cumulative distribution function, Φ.

Methods and formulas are presented under the following headings:

Parametric model: Summary parameter definition
Maximum likelihood estimation
Estimating equations estimation

Parametric model: Summary parameter definition

Conditioning on covariates $\mathbf{x}$, we have the following ROC curve model:

$$\text{ROC}(u) = g\{\mathbf{x}'\boldsymbol{\beta} + \alpha g^{-1}(u)\}$$

$\mathbf{x}$ can be constant, and $\boldsymbol{\beta} = \beta_0$, the constant intercept.

We can solve this equation to obtain the false-positive rate value u for a ROC value of r:

$$u = g\left[\{g^{-1}(r) - \mathbf{x}'\boldsymbol{\beta}\}\alpha^{-1}\right]$$

The partial area under the ROC curve for the false-positive rate u is defined by

$$\text{pAUC}(u) = \int_o^u g\{\mathbf{x}'\boldsymbol{\beta} + \alpha g^{-1}(t)\}dt$$

The area under the ROC curve is defined by

$$\text{AUC} = \int_o^1 g\{\mathbf{x}'\boldsymbol{\beta} + \alpha g^{-1}(t)\}dt$$

When g is the standard normal cumulative distribution function Φ, we can express the AUC as

$$\text{AUC} = \Phi\left(\frac{\mathbf{x}'\boldsymbol{\beta}}{\sqrt{1+\alpha^2}}\right)$$

Maximum likelihood estimation

We allow maximum likelihood estimation under probit parametric models, so $g = \Phi$. The ROC value, false-positive rate, and AUC parameters all have closed-form expressions in terms of the covariate values $\mathbf{x}$, coefficient vector $\boldsymbol{\beta}$, and slope parameter α. So to estimate these three types of summary parameters, we use the delta method (Oehlert 1992; Phillips and Park 1988). Particularly, we use the `nlcom` command (see [R] **nlcom**) to implement the delta method.

To estimate the partial area under the ROC curve for false-positive rate u, we use numeric integration. A trapezoidal approximation is used in calculating the integrals. A numeric integral of the $\text{ROC}(t)$ function conditioned on the covariate values $\mathbf{x}$, coefficient vector estimate $\widehat{\boldsymbol{\beta}}$, and slope parameter estimate $\widehat{\alpha}$ is computed over the range $t = [0, u]$. This gives us the point estimate of $\text{pAUC}(u)$.

To calculate the standard error and confidence intervals for the point estimate of $\text{pAUC}(u)$, we again use the delta method. Details on the delta method algorithm can be found in *Methods and formulas* of [R] **nlcom** and the earlier mentioned references.

Under maximum likelihood estimation, the coefficient estimates $\widehat{\boldsymbol{\beta}}$ and slope estimate $\widehat{\alpha}$ are asymptotically normal with variance matrix $\mathbf{V}$. For convenience, we rename the parameter vector $[\boldsymbol{\beta}', \alpha]$ to the k-parameter vector $\boldsymbol{\theta} = [\theta_1, \ldots, \theta_k]$. We will also explicitly refer to the conditioning of the ROC curve by $\boldsymbol{\theta}$ in its mention as $\text{ROC}(t, \boldsymbol{\theta})$.

Under the delta method, the continuous scalar function of the estimate $\widehat{\boldsymbol{\theta}}$, $f(\widehat{\boldsymbol{\theta}})$ has asymptotic mean $f(\boldsymbol{\theta})$ and asymptotic covariance

$$\widehat{\text{Var}}\left\{f(\widehat{\boldsymbol{\theta}})\right\} = \mathbf{f}\mathbf{V}\mathbf{f}'$$

where $\mathbf{f}$ is the $1 \times k$ matrix of derivatives for which

$$\mathbf{f}_{1j} = \frac{\partial f(\boldsymbol{\theta})}{\partial \theta_j} \qquad j = 1, \ldots, k$$

The asymptotic covariance of $f(\widehat{\boldsymbol{\theta}})$ is estimated and then used in conjunction with $f(\widehat{\boldsymbol{\theta}})$ for further inference, including Wald confidence intervals, standard errors, and hypothesis testing.

In the case of $\text{pAUC}(u)$ estimation, our $f(\widehat{\boldsymbol{\theta}})$ is the aforementioned numeric integral of the ROC curve. It estimates $f(\boldsymbol{\theta})$, the true integral of the ROC curve on the $[0, u]$ range. The $\mathbf{V}$ variance matrix is estimated using the likelihood information that `rocreg` calculated, and the estimation is performed by `rocreg` itself.

The partial derivatives of $f(\boldsymbol{\theta})$ can be determined by using Leibnitz's rule (Weisstein 2011):

$$\mathbf{f}_{1j} = \frac{\partial}{\partial \theta_j} \int_0^u \text{ROC}(t, \boldsymbol{\theta}) dt = \int_0^u \frac{\partial}{\partial \theta_j} \text{ROC}(t, \boldsymbol{\theta}) dt \qquad j = 1, \ldots, k$$

When θ_j corresponds with the slope parameter α, we obtain the following partial derivative:

$$\frac{\partial}{\partial \alpha} \text{pAUC}(u) = \int_0^u \phi\{\mathbf{x}'\boldsymbol{\beta} + \alpha\Phi^{-1}(t)\}\Phi^{-1}(t)\, dt$$

The partial derivative of $f(\boldsymbol{\theta})$ [pAUC(u)] for β_0 is the following:

$$\frac{\partial}{\partial \beta_0} \text{pAUC}(u) = \int_0^u \phi\{\mathbf{x}'\boldsymbol{\beta} + \alpha\Phi^{-1}(t)\} dt$$

For a nonintercept coefficient, we obtain the following:

$$\frac{\partial}{\partial \beta_i} \text{pAUC}(u) = \int_0^u x_i \phi\{\mathbf{x}'\boldsymbol{\beta} + \alpha\Phi^{-1}(t)\} dt$$

We can estimate each of these integrals by numeric integration, plugging in the estimates $\widehat{\boldsymbol{\beta}}$ and $\widehat{\alpha}$ for the parameters. This, together with the previously calculated estimate $\widehat{\mathbf{V}}$, provides an estimate of the asymptotic covariance of $f(\widehat{\boldsymbol{\theta}}) = \widehat{\text{pAUC}}(u)$, which allows us to perform further statistical inference on $\text{pAUC}(u)$.

Estimating equations estimation

When we fit a model using the Alonzo and Pepe (2002) estimating equations method, we use the bootstrap to perform inference on the ROC curve summary parameters. Each bootstrap sample provides a sample of the coefficient estimates $\boldsymbol{\beta}$ and the slope estimates α. Using the formulas in *Parametric model: Summary parameter definition* under *Methods and formulas*, we can obtain an estimate of the ROC, false-positive rate, or AUC for each resample. Using numeric integration (with the trapezoidal approximation), we can also estimate the pAUC of the resample.

By making these calculations, we obtain a bootstrap sample of our summary parameter estimate. We then obtain bootstrap standard errors, normal approximation confidence intervals, percentile confidence intervals, and bias-corrected confidence intervals using this bootstrap sample. Further details can be found in [R] **bootstrap**.

References

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Also see

[R] **rocreg** — Receiver operating characteristic (ROC) regression

[R] **rocregplot** — Plot marginal and covariate-specific ROC curves after rocreg

[U] **20 Estimation and postestimation commands**

Title

rocregplot — Plot marginal and covariate-specific ROC curves after rocreg

Syntax

Plot ROC curve after nonparametric analysis

`rocregplot` [, *boot_options* *common_options*]

Plot ROC curve after parametric analysis using bootstrap

`rocregplot` [, *probit_options* *boot_options* *common_options*]

Plot ROC curve after parametric analysis using maximum likelihood

`rocregplot` [, *probit_options* *common_options*]

probit_options	Description
Main	
`at(`*varname*`=#` [*varname*`=#...`]`)` [`at1(`*varname*`=#` [*varname*`=#...`]`)` [`at2(`*varname*`=#` [*varname*`=#...`]`)` [`...`]]]	value of specified covariates/mean of unspecified covariates
* `roc(`*numlist*`)`	show estimated ROC values for given false-positive rates
* `invroc(`*numlist*`)`	show estimated false-positive rates for given ROC values
`level(#)`	set confidence level; default is `level(95)`
Curve	
`line#opts(`*cline_options*`)`	affect rendition of ROC curve #

* Only one of `roc()` or `invroc()` may be specified.

common_options	Description
Main	
`classvars(`*varlist*`)`	restrict plotting of ROC curves to specified classifiers
`norefline`	suppress plotting the reference line
Scatter	
`plot#opts(`*scatter_options*`)`	affect rendition of classifier #s false-positive rate and ROC scatter points; not allowed with `at()`
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

boot_options	Description
Bootstrap	
† `bfile(`*filename*`)`	load dataset containing bootstrap replicates from `rocreg`
`btype(n | p | bc)`	plot normal-based (`n`), percentile (`p`), or bias-corrected (`bc`) confidence intervals; default is `btype(n)`

† `bfile()` is only allowed with parametric analysis using bootstrap inference; in which case this option is required with `roc()` or `invroc()`.

Menu

Statistics > Epidemiology and related > ROC analysis > ROC curves after rocreg

Description

Under parametric estimation, `rocregplot` plots the fitted ROC curves for specified covariate values and classifiers. If `rocreg, probit` or `rocreg, probit ml` were previously used, the false-positive rates (for specified ROC values) and ROC values (for specified false-positive rates) for each curve may also be plotted, along with confidence intervals.

Under nonparametric estimation, `rocregplot` will plot the fitted ROC curves using the `_fpr_*` and `_roc_*` variables produced by `rocreg`. Point estimates and confidence intervals for false-positive rates and ROC values that were computed in `rocreg` may be plotted as well.

probit_options

Main

`at(`*varname*`=# ...)` requests that the covariates specified by *varname* be set to *#*. By default, `rocreg` evaluates the function by setting each covariate to its mean value. This option causes the ROC curve to be evaluated at the value of the covariates listed in `at()` and at the mean of all unlisted covariates.

`at1(`*varname*`=# ...)`, `at2(`*varname*`=# ...)`, ..., `at10(`*varname*`=# ...)` specify that ROC curves (up to 10) be plotted on the same graph. `at1()`, `at2()`, ..., `at10()` work like the `at()` option. They request that the function be evaluated at the value of the covariates specified and at the mean of all unlisted covariates. `at1()` specifies the values of the covariates for the first curve, `at2()` specifies the values of the covariates for the second curve, and so on.

`roc(`*numlist*`)` specifies that estimated ROC values for given false-positive rates be graphed.

`invroc(`*numlist*`)` specifies that estimated false-positive rates for given ROC values be graphed.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**. `level()` may be specified with either `roc()` or `invroc()`.

Curve

`line#opts(`*cline_options*`)` affects the rendition of ROC curve *#*. See [G-3] ***cline_options***.

common_options

Main

`classvars(`*varlist*`)` restricts plotting ROC curves to specified classification variables.

`norefline` suppresses plotting the reference line.

Scatter

`plot#opts(`*scatter_options*`)` affects the rendition of classifier #'s false-positive rate and ROC scatter points. This option applies only to non-ROC covariate estimation graphing. See [G-2] **graph twoway scatter**.

Reference line

`rlopts(`*cline_options*`)` affects rendition of the reference line. See [G-3] ***cline_options***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and options for saving the graph to disk (see [G-3] ***saving_option***).

boot_options

Bootstrap

`bfile(`*filename*`)` uses bootstrap replicates of parameters from `rocreg` stored in *filename* to estimate standard errors and confidence intervals of predictions. `bfile()` must be specified with either `roc()` or `invroc()` if parametric estimation with bootstrapping was used.

`btype(n | p | bc)` indicates the desired type of confidence-interval rendering. `n` draws normal-based, `p` draws percentile, and `bc` draws bias-corrected confidence intervals for specified false-positive rates and ROC values in `roc()` and `invroc()`. The default is `btype(n)`.

Remarks

Remarks are presented under the following headings:

Plotting covariate-specific ROC curves
Plotting marginal ROC curves

Plotting covariate-specific ROC curves

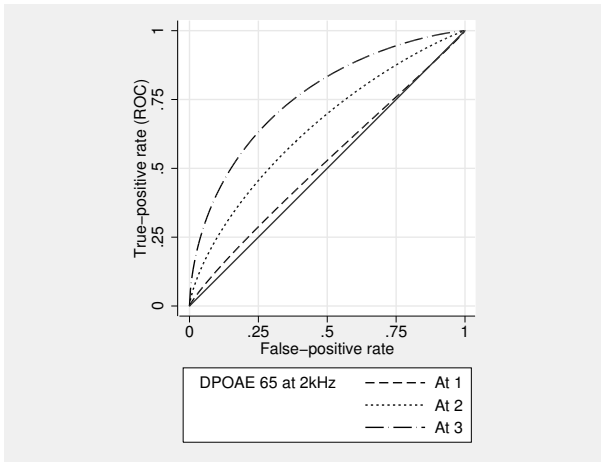
The `rocregplot` command is also demonstrated in [R] **rocreg**. We will further demonstrate its use with several examples. Particularly, we will show how `rocregplot` can draw the ROC curves of covariate models that have been fit using `rocreg`.

Example 1

In example 6 of [R] **rocreg**, we fit a probit ROC model to audiology test data from Norton et al. (2000). The estimating equation method of Alonzo and Pepe (2002) was used to the fit the model. Gender and age were covariates that affected the control distribution of the classifier `y1` (DPOAE 65 at 2 kHz). Age was a ROC covariate for the model, so we fit separate ROC curves at each age.

Following Janes, Longton, and Pepe (2009), we draw the ROC curves for ages 30, 40, and 50 months. The `at1()`, `at2()`, and `at3()` options are used to specify the age covariates.

```
. use http://www.stata-press.com/data/r12/nnhs
(Norton - neonatal audiology data)
. rocreg d y1, probit ctrlcov(currage male) ctrlmodel(linear) roccov(currage)
      cluster(id) bseed(56930) bsave(nnhs2y1, replace)
  (output omitted)
. rocregplot, at1(currage=30) at2(currage=40) at3(currage=50)
```



Here we use the default entries of the legend, which indicate the "at #" within the specified `at*` options and the classifier to which the curve corresponds. ROC curve one corresponds with `currage=30`, two with `currage=40`, and three with `currage=50`. The positive effect of age on the ROC curve is evident. At an age of 30 months (`currage=30`), the ROC curve of `y1` (DPOAE 65 at 2 kHz) is nearly equivalent to that of a noninformative test that gives equal probability to hearing loss. At age 50 months (`currage=50`), corresponding to some of the oldest children in the study, the ROC curve shows that test `y1` (DPOAE 65 at 2 kHz) is considerably more powerful than the noninformative test.

You may create your own legend by specifying the `legend()` option. The default legend is designed for the possibility of multiple covariates. Here we could change the legend entries to `currage` values and gain some extra clarity. However, this may not be feasible when there are many covariates present.

◁

We can also use `rocregplot` after maximum likelihood estimation.

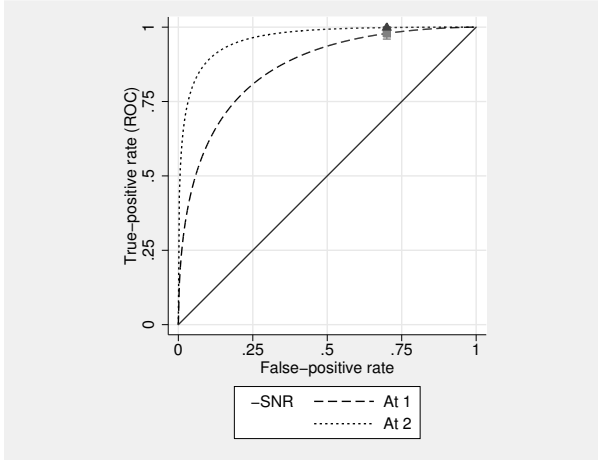
Example 2

We return to the audiology study with frequency (xf), intensity (xl), and hearing loss severity (xd) covariates from Stover et al. (1996) that we examined in example 10 of [R] **rocreg**. Negative signal-to-noise ratio is again used as a classifier. Using maximum likelihood, we fit a probit model to these data with the indicated ROC covariates.

After fitting the model, we wish to compare the ROC curves of two covariate combinations. The first has an intensity value of 5.5 (the lowest intensity, corresponding to 55 decibels) and a frequency of 10.01 (the lowest frequency, corresponding to 1001 hertz). We give the first combination a hearing loss severity value of 0.5 (the lowest). The second covariate combination has the same frequency, but the highest intensity value of 6.5 (65 decibels). We give this second covariate set a higher severity value of 4. We will visually compare the two ROC curves resulting from these two covariate value combinations.

We specify false-positive rates of 0.7 first followed by 0.2 in the `roc()` option to visually compare the size of the ROC curve at large and small false-positive rates. Because maximum likelihood estimation was used to fit the model, a Wald confidence interval is produced for the estimated ROC value and false-positive rate parameters. Further details are found in *Methods and formulas*.

```
. use http://www.stata-press.com/data/r12/dp
(Stover - DPOAE test data)
. rocreg d nsnr, probit ctrlcov(xf xl) roccov(xf xl xd) ml cluster(id)
  (output omitted)
. rocregplot, at1(xf=10.01, xl=5.5, xd=.5) at2(xf=10.01, xl=6.5, xd=4) roc(.7)
ROC curve
   Status    : d
   Classifier: nsnr
Under covariates:
             |       at1
-------------+----------
          xf |     10.01
          xl |       5.5
          xd |        .5
------------------------------------------------------------------------------
         ROC |       Coef.   Std. Err.      [95% Conf. Interval]
-------------+----------------------------------------------------------------
          .7 |    .978951   .0097382       .9598645    .9980376
------------------------------------------------------------------------------
Under covariates:
             |       at2
-------------+----------
          xf |     10.01
          xl |       6.5
          xd |         4
------------------------------------------------------------------------------
         ROC |       Coef.   Std. Err.      [95% Conf. Interval]
-------------+----------------------------------------------------------------
          .7 |   .9985001   .0009657       .9966073    1.000393
------------------------------------------------------------------------------
```



At the higher false-positive rate value of 0.7, we see little difference in the ROC values and note that the confidence intervals nearly overlap. Now we view the same curves with the lower false-positive rate compared.

```
. rocregplot, at1(xf=10.01, xl=5.5, xd=.5) at2(xf=10.01, xl=6.5, xd=4) roc(.2)
ROC curve
   Status    : d
   Classifier: nsnr
Under covariates:
```

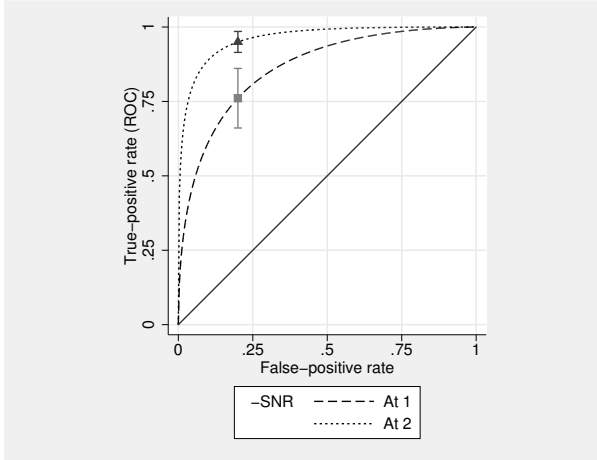
	at1
xf	10.01
xl	5.5
xd	.5

ROC	Coef.	Std. Err.	[95% Conf.	Interval]
.2	.7608593	.0510501	.660803	.8609157

```
Under covariates:
```

	at2
xf	10.01
xl	6.5
xd	4

ROC	Coef.	Std. Err.	[95% Conf.	Interval]
.2	.9499408	.0179824	.914696	.9851856



The lower false-positive rate of 0.2 shows clearly distinguishable ROC values. Now we specify option `invroc(.5)` to view how the false-positive rates vary at a ROC value of 0.5.

```
. rocregplot, at1(xf=10.01, xl=5.5, xd=.5) at2(xf=10.01, xl=6.5, xd=4) invroc(.5)
False-positive rate
   Status    : d
   Classifier: nsnr
Under covariates:
```

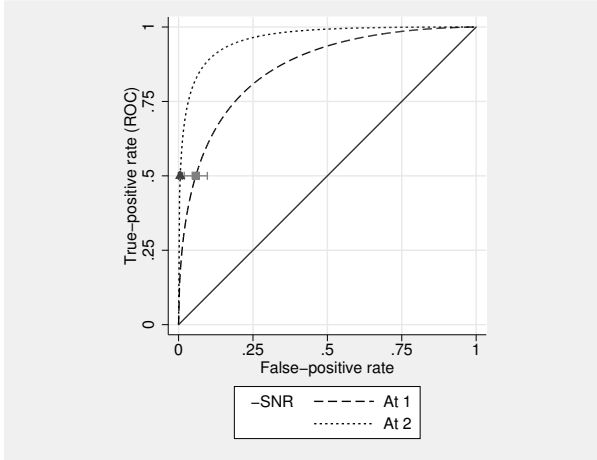
	at1
xf	10.01
xl	5.5
xd	.5

invROC	Coef.	Std. Err.	[95% Conf.	Interval]
.5	.0578036	.0198626	.0188736	.0967336

Under covariates:

	at2
xf	10.01
xl	6.5
xd	4

invROC	Coef.	Std. Err.	[95% Conf.	Interval]
.5	.0055624	.0032645	-.0008359	.0119607



At a ROC value of 0.5, the false-positive rates for both curves are small and close to one another. ◁

❑ Technical note

We can use the `testnl` command to support our visual observations with statistical inference. We use it to perform a Wald test of the null hypothesis that the two ROC curves just rendered are equal at a false-positive rate of 0.7.

```
. testnl normal(_b[i_cons]+10.01*_b[xf]+5.5*_b[xl]
>                + .5*_b[xd]+_b[s_cons]*invnormal(.7)) =
>       normal(_b[i_cons]+10.01*_b[xf]+6.5*_b[xl]
>                + 4*_b[xd]+_b[s_cons]*invnormal(.7))

(1)  normal(_b[i_cons]+10.01*_b[xf]+5.5*_b[xl] +.5*_b[xd]+_b[s_cons]*invnormal(.7))=
     normal(_b[i_cons]+10.01*_b[xf]+6.5*_b[xl] + 4*_b[xd]+_b[s_cons]*invnormal(.7))

           chi2(1) =        4.53
       Prob > chi2 =        0.0332
```

The test is significant at the 0.05 level, and thus we find that the two curves are significantly different. Now we will use `testnl` again to test equality of the false-positive rates for each curve with a ROC value of 0.5. The inverse ROC formula used is derived in *Methods and formulas*.

```
. testnl normal((invnormal(.5)-(_b[i_cons]+10.01*_b[xf]+5.5*_b[xl]+.5*_b[xd]))
>                /_b[s_cons]) =
>       normal((invnormal(.5)-(_b[i_cons]+10.01*_b[xf]+6.5*_b[xl]+4*_b[xd]))
>                /_b[s_cons])

  (1)  normal((invnormal(.5)-(_b[i_cons]+10.01*_b[xf]+5.5*_b[xl]+.5*_b[xd]))
             /_b[s_cons]) =
       normal((invnormal(.5)-(_b[i_cons]+10.01*_b[xf]+6.5*_b[xl]+4*_b[xd]))
             /_b[s_cons])

chi2(1) =        8.01
      Prob > chi2 =        0.0046
```

We again reject the null hypothesis that the two curves are equal at the 0.05 level.

❑

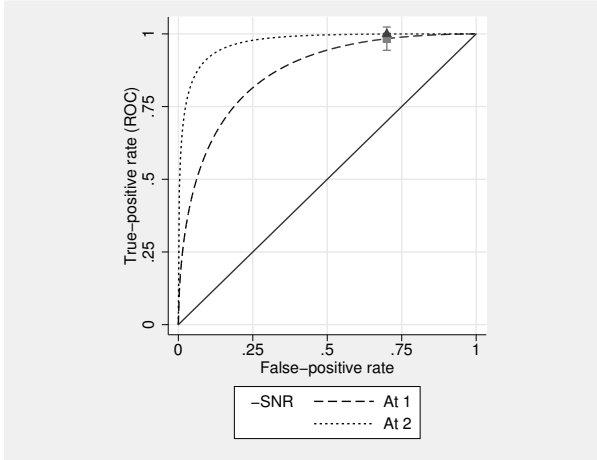
The model of our last example was also fit using the estimating equations method in example 7 of [R] **rocreg**. We will demonstrate `rocregplot` after that model fit as well.

Example 3

In example 2, we used `rocregplot` after a maximum likelihood model fit of the ROC curve for classifier `nsnr` and covariates frequency (`xf`), intensity (`xl`), and hearing loss severity (`xd`). The data were obtained from the audiology study described in Stover et al. (1996). In example 7 of [R] **rocreg**, we fit the model using the estimating equations method of Alonzo and Pepe (2002). Under this method, bootstrap resampling is used to make inferences. We saved 50 bootstrap replications in `nsnrf.dta`, which we re-create below.

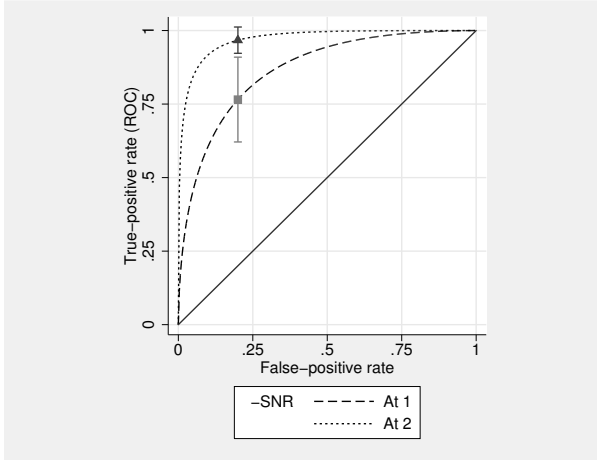
We use `rocregplot` to draw the ROC curves for `nsnr` under the covariate values `xf = 10.01`, `xl = 5.5`, and `xd = .5`, and `xf = 10.01`, `xl = 6.5`, and `xd = 4`. The `at#()` options are used to specify the covariate values. The previous bootstrap results are made available to `rocregplot` with the `bfile()` option. As before, we will specify 0.2 and 0.7 as false-positive rates in the `roc()` option and 0.5 as a ROC value in the `invroc()` option. We do not specify `btype()` and thus our graph will contain normal-based bootstrap confidence bands, the default.

```
. use http://www.stata-press.com/data/r12/dp
(Stover - DPOAE test data)
. rocreg d nsnr, probit ctrlcov(xf xl) roccov(xf xl xd) cluster(id)
> nobstrata ctrlfprall bseed(156385) breps(50) bsave(nsnrf, replace)
  (output omitted)
. rocregplot, at1(xf=10.01, xl=5.5, xd=.5) at2(xf=10.01, xl=6.5, xd=4)
> roc(.7) bfile(nsnrf)
ROC curve
   Status    : d
   Classifier: nsnr
Under covariates:
              |       at1
--------------+----------
           xf |     10.01
           xl |       5.5
           xd |        .5
                                  (Replications based on 208 clusters in id)
------------------------------------------------------------------------------
             |    Observed               Bootstrap
         ROC |       Coef.       Bias    Std. Err.     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          .7 |    .9835816   .0087339    .0204353     .9435292   1.023634  (N)
                                                     .9155462   .9974037  (P)
                                                     .9392258   .9976629 (BC)
------------------------------------------------------------------------------
Under covariates:
              |       at2
--------------+----------
           xf |     10.01
           xl |        6.5
           xd |          4
                                  (Replications based on 208 clusters in id)
------------------------------------------------------------------------------
             |    Observed               Bootstrap
         ROC |       Coef.       Bias    Std. Err.     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          .7 |     .999428   .0006059    .0011309     .9972115   1.001644  (N)
                                                     .9958003   .9999675  (P)
                                                     .9968304   .9999901 (BC)
------------------------------------------------------------------------------
```



As shown in the graph, we find that the ROC values at a false-positive rate of 0.7 are close together, as they were in the maximum likelihood estimation in example 2. We now repeat this process for the lower false-positive rate of 0.2 by using the `roc(.2)` option.

```
. rocregplot, at1(xf=10.01, xl=5.5, xd=.5) at2(xf=10.01, xl=6.5, xd=4)
> roc(.2) bfile(nsnrf)

ROC curve

   Status    : d
   Classifier: nsnr

Under covariates:

             |       at1
-------------+----------
          xf |     10.01
          xl |       5.5
          xd |        .5

                                (Replications based on 208 clusters in id)
------------------------------------------------------------------------------
             |   Observed               Bootstrap
         ROC |      Coef.       Bias    Std. Err.     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          .2 |   .7652956   .0145111    .0735506     .6211391    .9094522  (N)
                                                     .6054495     .878052  (P)
                                                     .6394838    .9033081 (BC)
------------------------------------------------------------------------------

Under covariates:

             |       at2
-------------+----------
          xf |     10.01
          xl |        6.5
          xd |          4

                                (Replications based on 208 clusters in id)
------------------------------------------------------------------------------
             |   Observed               Bootstrap
         ROC |      Coef.       Bias    Std. Err.     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          .2 |   .9672505   .0072429    .0227977     .9225679    1.011933  (N)
                                                     .9025254    .9931714  (P)
                                                     .9235289    .9979637 (BC)
------------------------------------------------------------------------------
```



The ROC values are slightly higher at the false-positive rate of 0.2 than they were in the maximum likelihood estimation in example 2. To see if the false-positive rates differ at a ROC value of 0.5, we specify the `invroc(.5)` option.

```
. rocregplot, at1(xf=10.01, xl=5.5, xd=.5) at2(xf=10.01, xl=6.5, xd=4)
> invroc(.5) bfile(nsnrf)
False-positive rate
   Status    : d
   Classifier: nsnr
Under covariates:
```

	at1
xf	10.01
xl	5.5
xd	.5

(Replications based on 208 clusters in id)

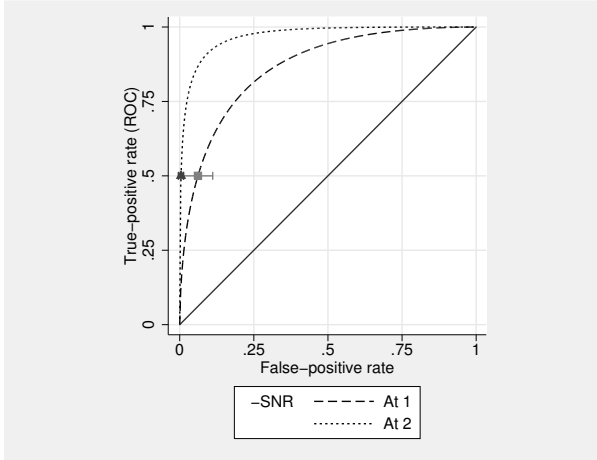
invROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.5	.0615144	-.0063531	.0254042	.0117231	.1113057	(N)
				.0225159	.1265046	(P)
				.0224352	.1265046	(BC)

Under covariates:

	at2
xf	10.01
xl	6.5
xd	4

(Replications based on 208 clusters in id)

invROC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
.5	.0043298	-.0012579	.0045938	-.004674	.0133335	(N)
				.0002773	.0189199	(P)
				.0001292	.0134801	(BC)



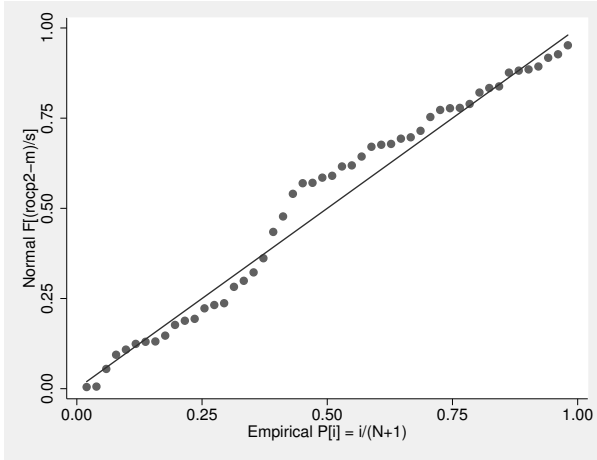
The point estimates of the ROC value and false-positive rate are both computed directly using the point estimates of the ROC coefficients. Calculation of the standard errors and confidence intervals is slightly more complicated. Essentially, we have stored a sample of our ROC covariate coefficient estimates in `nsnrf.dta`. We then calculate the ROC value or false-positive rate estimates using each set of coefficient estimates, resulting in a sample of point estimates. Then the bootstrap standard error and confidence intervals are calculated based on these bootstrap samples. Details of the computation of the standard error and percentile confidence intervals can be found in *Methods and formulas* and in [R] **bootstrap**.

As mentioned in [R] **rocreg**, 50 resamples is a reasonable lower bound for obtaining bootstrap standard errors (Mooney and Duval 1993). However, it may be too low for obtaining percentile and bias-corrected confidence intervals. Normal-based confidence intervals are valid when the bootstrap distribution exhibits normality. See [R] **bootstrap postestimation** for more details.

We can assess the normality of the bootstrap distribution by using a normal probability plot. Stata provides this in the `pnorm` command (see [R] **diagnostic plots**). We will use `nsnrf.dta` to draw a normal probability plot for the ROC estimate corresponding to a false-positive rate of 0.2. We use the covariate values `xf = 10.01`, `xl = 6.5`, and `xd = 4`.

```
. use nsnrf
(bootstrap: rocregnewstat)
. generate double rocp2 = nsnr_b_i_cons + 10.01*nsnr_b_xf + 6.5*nsnr_b_xl +
> 4*nsnr_b_xd+nsnr_b_s_cons*invnormal(.2)
. replace rocp2 = normal(rocp2)
(50 real changes made)
```

```
. pnorm rocp2
```



The closeness of the points to the horizontal line on the normal probability plot shows us that the bootstrap distribution is approximately normal. So it is reasonable to use the normal-based confidence intervals for ROC at a false-positive rate of 0.2 under covariate values `xf = 10.01`, `xl = 6.5`, and `xd = 4`.

◁

Plotting marginal ROC curves

The `rocregplot` command can also be used after fitting models with no covariates. We will demonstrate this with an empirical ROC model fit in [R] **rocreg**.

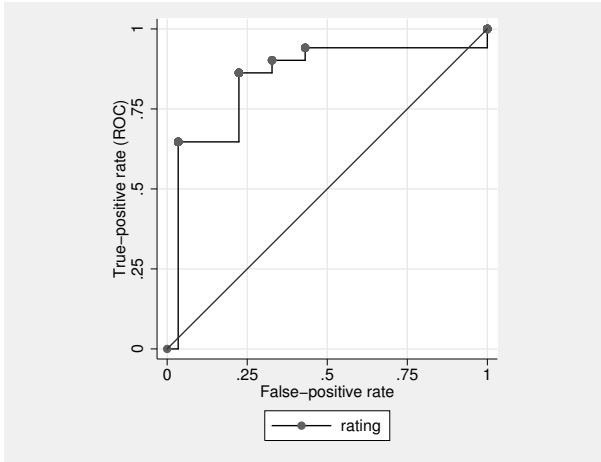
▷ Example 4

We run `rocregplot` after fitting the single-classifier, empirical ROC model shown in example 1 of [R] **rocreg**. There we empirically predicted the ROC curve of the classifier `rating` for the true status variable `disease` from the Hanley and McNeil (1982) data. The `rocreg` command saves variables `_roc_rating` and `_fpr_rating`, which give the ROC values and false-positive rates, respectively, for every value of `rating`. These variables are used by `rocregplot` to render the ROC curve.

```
. use http://www.stata-press.com/data/r12/hanley, clear
. rocreg disease rating, noboot
Nonparametric ROC estimation
Control standardization: empirical
ROC method             : empirical
Area under the ROC curve
   Status    : disease
   Classifier: rating
```

AUC	Observed Coef.	Bias	Bootstrap Std. Err.	[95% Conf.	Interval]	
	.8407708	.	.	.	.	(N)
				.	.	(P)
				.	.	(BC)

```
. rocregplot
```



We end our discussion of `rocregplot` by showing its use after a marginal probit model.

Example 5

In example 13 of [R] **rocreg**, we fit a maximum-likelihood probit model to each classifier of the fictitious dataset generated from Hanley and McNeil (1983).

We use `rocregplot` after the original `rocreg` command to draw the ROC curves for classifiers `mod1` and `mod3`. This is accomplished by specifying the two variables in the `classvars()` option. We will use the `roc()` option to obtain confidence intervals for ROC values at false-positive rates of 0.15 and 0.75. We will specify the `invroc()` option to obtain false-positive rate confidence intervals for a ROC value of 0.8. As mentioned previously, these are Wald confidence intervals.

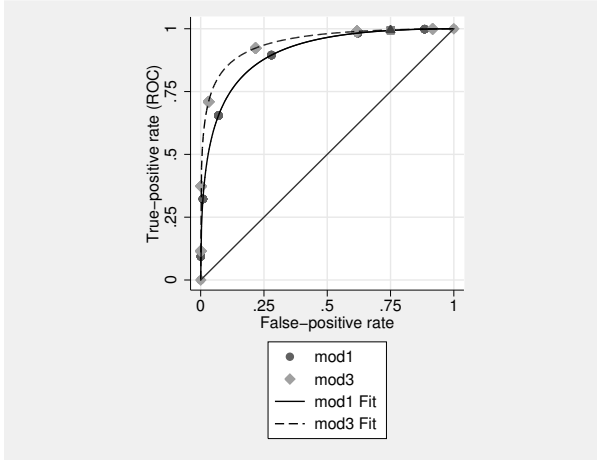
First, we will view results for a false-positive rate of 0.75.

```
. use http://www.stata-press.com/data/r12/ct2, clear
. rocreg status mod1 mod2 mod3, probit ml
  (output omitted)
. rocregplot, classvars(mod1 mod3) roc(.75)
ROC curve
   Status     : status
   Classifier: mod1
```

ROC	Coef.	Std. Err.	[95% Conf.	Interval]
.75	.9931655	.0069689	.9795067	1.006824

```
   Status     : status
   Classifier: mod3
```

ROC	Coef.	Std. Err.	[95% Conf.	Interval]
.75	.9953942	.0043435	.9868811	1.003907



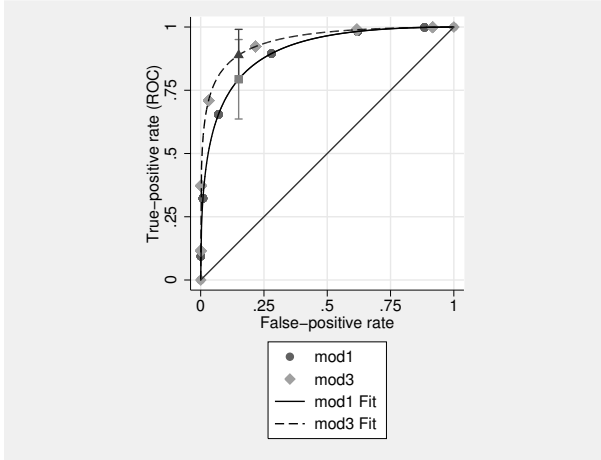
We see that the estimates for each of the two ROC curves are close. Because this is a marginal model, the actual false-positive rate and the true-positive rate for each observation are plotted in the graph. The added point estimates of the ROC value at false-positive rate 0.75 are shown as diamond (`mod3`) and circle (`mod1`) symbols in the upper-right-hand corner of the graph at FPR $= 0.75$. Confidence bands are also plotted at FPR $= 0.75$ but are so narrow that they are barely noticeable. Under both classifiers, the ROC value at 0.75 is very high. Now we will compare these results to those with a lower false-positive rate of 0.15.

```
. rocregplot, classvars(mod1 mod3) roc(.15)
ROC curve
   Status    : status
   Classifier: mod1
```

ROC	Coef.	Std. Err.	[95% Conf.	Interval]
.15	.7934935	.0801363	.6364292	.9505578

```
   Status    : status
   Classifier: mod3
```

ROC	Coef.	Std. Err.	[95% Conf.	Interval]
.15	.8888596	.0520118	.7869184	.9908008



The ROC value for the false-positive rate of 0.15 is more separated in the two classifiers. Here we see that `mod3` has a larger ROC value than `mod1` for this false-positive rate, but the confidence intervals of the estimates overlap.

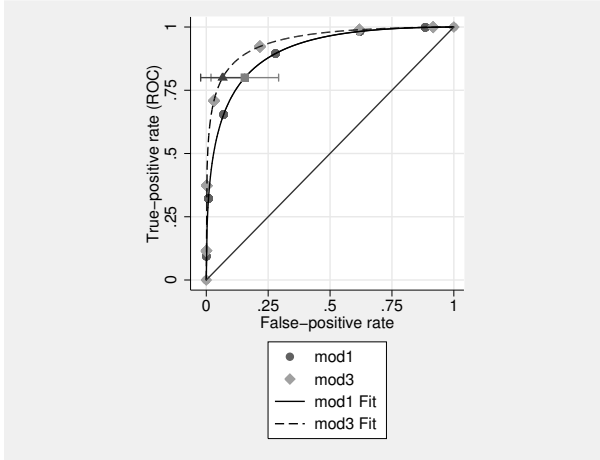
By specifying `invroc(.8)`, we obtain invROC confidence intervals corresponding to a ROC value of 0.8.

```
. rocregplot, classvars(mod1 mod3) invroc(.8)
False-positive rate
   Status    : status
   Classifier: mod1
```

invROC	Coef.	Std. Err.	[95% Conf.	Interval]
.8	.1556435	.069699	.019036	.2922509

```
   Status    : status
   Classifier: mod3
```

invROC	Coef.	Std. Err.	[95% Conf.	Interval]
.8	.0661719	.045316	-.0226458	.1549896



For estimation of the false-positive rate at a ROC value of 0.8, the confidence intervals overlap. Both classifiers require only a small false-positive rate to achieve a ROC value of 0.8.

◁

Methods and formulas

`rocregplot` is implemented as an ado-file.

Details on computation of the nonparametric ROC curve and the estimation of the parametric ROC curve model coefficients can be found in [R] **rocreg**. Here we describe how to estimate the ROC values and false-positive rates of a parametric model. The cumulative distribution function g can be the standard normal cumulative distribution function.

Methods and formulas are presented under the following headings:

Parametric model: Summary parameter definition
Maximum likelihood estimation
Estimating equations estimation

Parametric model: Summary parameter definition

Conditioning on covariates $\mathbf{x}$, we have the following ROC curve model:

$$\text{ROC}\,(u) = g\{\mathbf{x}'\boldsymbol{\beta} + \alpha g^{-1}\,(u)\}$$

$\mathbf{x}$ can be constant, and $\boldsymbol{\beta} = \beta_0$, the constant intercept.

With simple algebra, we can solve this equation to obtain the false-positive rate value u for a ROC value of r:

$$u = g\left[\{g^{-1}\,(r) - \mathbf{x}'\boldsymbol{\beta}\}\alpha^{-1}\right]$$

Maximum likelihood estimation

We allow maximum likelihood estimation under probit parametric models, so $g = \Phi$. The ROC value and false-positive rate parameters all have closed-form expressions in terms of the covariate values $\mathbf{x}$, coefficient vector $\boldsymbol{\beta}$, and slope parameter α. Thus to estimate these two types of summary parameters, we use the delta method (Oehlert 1992; Phillips and Park 1988). Particularly, we use the `nlcom` command (see [R] **nlcom**) to implement the delta method.

Under maximum likelihood estimation, the coefficient estimates $\widehat{\boldsymbol{\beta}}$ and slope estimate $\widehat{\alpha}$ are asymptotically normal with variance matrix $\mathbf{V}$. For convenience, we rename the parameter vector $[\boldsymbol{\beta}', \alpha]$ to the k-parameter vector $\boldsymbol{\theta} = [\theta_1, \ldots, \theta_k]$. We will also explicitly refer to the conditioning of the ROC curve by $\boldsymbol{\theta}$ in its mention as $\text{ROC}(t, \boldsymbol{\theta})$.

Under the delta method, the continuous scalar function of the estimate $\widehat{\boldsymbol{\theta}}$, $f(\widehat{\boldsymbol{\theta}})$ has asymptotic mean $f(\boldsymbol{\theta})$ and asymptotic covariance

$$\widehat{\text{Var}}\left\{f(\widehat{\boldsymbol{\theta}})\right\} = \mathbf{f}\mathbf{V}\mathbf{f}'$$

where $\mathbf{f}$ is the $1 \times k$ matrix of derivatives for which

$$\mathbf{f}_{1j} = \frac{\partial f(\boldsymbol{\theta})}{\partial \theta_j} \qquad j = 1, \ldots, k$$

The asymptotic covariance of $f(\widehat{\boldsymbol{\theta}})$ is estimated and then used in conjunction with $f(\widehat{\boldsymbol{\theta}})$ for further inference, including Wald confidence intervals, standard errors, and hypothesis testing.

Estimating equations estimation

When we fit a model using the Alonzo and Pepe (2002) estimating equations method, we use the bootstrap to perform inference on the ROC curve summary parameters. Each bootstrap sample provides a sample of the coefficient estimates $\boldsymbol{\beta}$ and the slope estimates α. Using the formulas above, we can obtain an estimate of the ROC value or false-positive rate for each resample.

By making these calculations, we obtain a bootstrap sample of our summary parameter estimate. We then obtain bootstrap standard errors, normal approximation confidence intervals, percentile confidence intervals, and bias-corrected confidence intervals using this bootstrap sample. Further details can be found in [R] **bootstrap**.

References

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Bamber, D. 1975. The area above the ordinal dominance graph and the area below the receiver operating characteristic graph. *Journal of Mathematical Psychology* 12: 387–415.

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Hanley, J. A., and B. J. McNeil. 1982. The meaning and use of the area under a receiver operating characteristic (ROC) curve. *Radiology* 143: 29–36.

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Janes, H., G. Longton, and M. S. Pepe. 2009. Accommodating covariates in receiver operating characteristic analysis. *Stata Journal* 9: 17–39.

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Norton, S. J., M. P. Gorga, J. E. Widen, R. C. Folsom, Y. Sininger, B. Cone-Wesson, B. R. Vohr, K. Mascher, and K. Fletcher. 2000. Identification of neonatal hearing impairment: Evaluation of transient evoked otoacoustic emission, distortion product otoacoustic emission, and auditory brain stem response test performance. *Ear and Hearing* 21: 508–528.

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Stover, L., M. P. Gorga, S. T. Neely, and D. Montoya. 1996. Toward optimizing the clinical utility of distortion product otoacoustic emission measurements. *Journal of the Acoustical Society of America* 100: 956–967.

Also see

[R] **rocreg** — Receiver operating characteristic (ROC) regression

[R] **rocreg postestimation** — Postestimation tools for rocreg

[U] **20 Estimation and postestimation commands**

Title

roctab — Nonparametric ROC analysis

Syntax

`roctab` *refvar classvar* [*if*] [*in*] [*weight*] [`,` *options*]

roctab_options	Description
Main	
`lorenz`	report Gini and Pietra indices
`binomial`	calculate exact binomial confidence intervals
`detail`	show details on sensitivity/specificity for each cutpoint
`table`	display the raw data in a $2 \times k$ contingency table
`bamber`	calculate standard errors by using the Bamber method
`hanley`	calculate standard errors by using the Hanley method
`graph`	graph the ROC curve
`norefline`	suppress plotting the 45-degree reference line
`summary`	report the area under the ROC curve
`specificity`	graph sensitivity versus specificity
`level(#)`	set confidence level; default is `level(95)`
Plot	
`plotopts(`*plot_options*`)`	affect rendition of the ROC curve
Reference line	
`rlopts(`*cline_options*`)`	affect rendition of the reference line
Add plots	
`addplot(`*plot*`)`	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

`fweights` are allowed; see [U] **11.1.6 weight**.

plot_options	Description
marker_options	change look of markers (color, size, etc.)
marker_label_options	add marker labels; change look or position
cline_options	change the look of the line

Menu

Statistics > Epidemiology and related > ROC analysis > Nonparametric ROC analysis without covariates

Description

The above command is used to perform receiver operating characteristic (ROC) analyses with rating and discrete classification data.

The two variables *refvar* and *classvar* must be numeric. The reference variable indicates the true state of the observation, such as diseased and nondiseased or normal and abnormal, and must be coded as 0 and 1. The rating or outcome of the diagnostic test or test modality is recorded in *classvar*, which must be at least ordinal, with higher values indicating higher risk.

`roctab` performs nonparametric ROC analyses. By default, `roctab` calculates the area under the ROC curve. Optionally, `roctab` can plot the ROC curve, display the data in tabular form, and produce Lorenz-like plots.

See [R] **rocfit** for a command that fits maximum-likelihood ROC models.

Options

Main

`lorenz` specifies that Gini and Pietra indices be reported. Optionally, `graph` will plot the Lorenz-like curve.

`binomial` specifies that exact binomial confidence intervals be calculated.

`detail` outputs a table displaying the sensitivity, specificity, the percentage of subjects correctly classified, and two likelihood ratios for each possible cutpoint of *classvar*.

`table` outputs a $2 \times k$ contingency table displaying the raw data.

`bamber` specifies that the standard error for the area under the ROC curve be calculated using the method suggested by Bamber (1975). Otherwise, standard errors are obtained as suggested by DeLong, DeLong, and Clarke-Pearson (1988).

`hanley` specifies that the standard error for the area under the ROC curve be calculated using the method suggested by Hanley and McNeil (1982). Otherwise, standard errors are obtained as suggested by DeLong, DeLong, and Clarke-Pearson (1988).

`graph` produces graphical output of the ROC curve. If `lorenz` is specified, graphical output of a Lorenz-like curve will be produced.

`norefline` suppresses plotting the 45-degree reference line from the graphical output of the ROC curve.

`summary` reports the area under the ROC curve, its standard error, and its confidence interval. If `lorenz` is specified, Lorenz indices are reported. This option is needed only when also specifying `graph`.

`specificity` produces a graph of sensitivity versus specificity instead of sensitivity versus (1 − specificity). `specificity` implies `graph`.

`level(#)` specifies the confidence level, as a percentage, for the confidence intervals. The default is `level(95)` or as set by `set level`; see [R] **level**.

Plot

`plotopts(`*plot_options*`)` affects the rendition of the plotted ROC curve—the curve's plotted points connected by lines. The *plot_options* can affect the size and color of markers, whether and how the markers are labeled, and whether and how the points are connected; see [G-3] ***marker_options***, [G-3] ***marker_label_options***, and [G-3] ***cline_options***.

Reference line

`rlopts(`*cline_options*`)` affects the rendition of the reference line; see [G-3] ***cline_options***.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

Remarks are presented under the following headings:

Introduction
Nonparametric ROC curves
Lorenz-like curves

Introduction

The `roctab` command provides nonparametric estimation of the ROC for a given classifier and true-status reference variable. The Lorenz curve functionality of `roctab`, which provides an alternative to standard ROC analysis, is discussed in *Lorenz-like curves*.

See Pepe (2003) for a discussion of ROC analysis. Pepe has posted Stata datasets and programs used to reproduce results presented in the book (http://www.stata.com/bookstore/pepe.html).

Nonparametric ROC curves

The points on the nonparametric ROC curve are generated using each possible outcome of the diagnostic test as a classification cutpoint and computing the corresponding sensitivity and 1−specificity. These points are then connected by straight lines, and the area under the resulting ROC curve is computed using the trapezoidal rule.

▷ Example 1

Hanley and McNeil (1982) presented data from a study in which a reviewer was asked to classify, using a five-point scale, a random sample of 109 tomographic images from patients with neurological problems. The rating scale was as follows: 1 = definitely normal, 2 = probably normal, 3 = questionable, 4 = probably abnormal, and 5 = definitely abnormal. The true disease status was normal for 58 of the patients and abnormal for the remaining 51 patients.

Here we list 9 of the 109 observations:

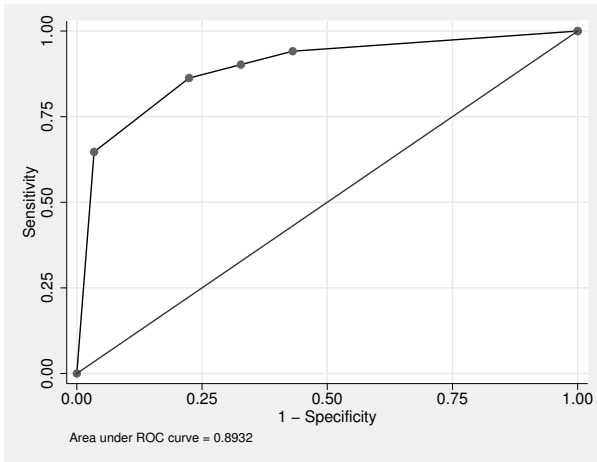
```
. use http://www.stata-press.com/data/r12/hanley
. list disease rating in 1/9
```

	disease	rating
1.	1	5
2.	0	1
3.	1	5
4.	0	4
5.	0	1
6.	0	3
7.	1	5
8.	0	5
9.	0	1

For each observation, `disease` identifies the true disease status of the subject (0 = normal, 1 = abnormal), and `rating` contains the classification value assigned by the reviewer.

We can use `roctab` to calculate and plot the nonparametric ROC curve by specifying both the `summary` and `graph` options. By also specifying the `table` option, we obtain a contingency table summarizing our dataset.

```
. roctab disease rating, table graph summary
```



disease	rating 1	2	3	4	5	Total
0	33	6	6	11	2	58
1	3	2	2	11	33	51
Total	36	8	8	22	35	109

Obs	ROC Area	Std. Err.	−Asymptotic Normal— [95% Conf.	Interval]
109	0.8932	0.0307	0.83295	0.95339

By default, roctab reports the area under the curve, its standard error, and its confidence interval. The graph option can be used to plot the ROC curve.

The ROC curve is plotted by computing the sensitivity and specificity using each value of the rating variable as a possible cutpoint. A point is plotted on the graph for each of the cutpoints. These plotted points are joined by straight lines to form the ROC curve, and the area under the ROC curve is computed using the trapezoidal rule.

We can tabulate the computed sensitivities and specificities for each of the possible cutpoints by specifying detail.

```
. roctab disease rating, detail
Detailed report of sensitivity and specificity
```

Cutpoint	Sensitivity	Specificity	Correctly Classified	LR+	LR-
(>= 1)	100.00%	0.00%	46.79%	1.0000	
(>= 2)	94.12%	56.90%	74.31%	2.1835	0.1034
(>= 3)	90.20%	67.24%	77.98%	2.7534	0.1458
(>= 4)	86.27%	77.59%	81.65%	3.8492	0.1769
(>= 5)	64.71%	96.55%	81.65%	18.7647	0.3655
(> 5)	0.00%	100.00%	53.21%		1.0000

Obs	ROC Area	Std. Err.	—Asymptotic Normal— [95% Conf.	Interval]
109	0.8932	0.0307	0.83295	0.95339

Each cutpoint in the table indicates the ratings used to classify tomographs as being from an abnormal subject. For example, the first cutpoint (>= 1) indicates that all tomographs rated as 1 or greater are classified as coming from abnormal subjects. Because all tomographs have a rating of 1 or greater, all are considered abnormal. Consequently, all abnormal cases are correctly classified (sensitivity = 100%), but none of the normal patients is classified correctly (specificity = 0%). For the second cutpoint (>=2), tomographs with ratings of 1 are classified as normal, and those with ratings of 2 or greater are classified as abnormal. The resulting sensitivity and specificity are 94.12% and 56.90%, respectively. Using this cutpoint, we correctly classified 74.31% of the 109 tomographs. Similar interpretations can be used on the remaining cutpoints. As mentioned, each cutpoint corresponds to a point on the nonparametric ROC curve. The first cutpoint (>=1) corresponds to the point at (1,1), and the last cutpoint (> 5) corresponds to the point at (0,0).

detail also reports two likelihood ratios suggested by Choi (1998): the likelihood ratio for a positive test result (LR+) and the likelihood ratio for a negative test result (LR–). The LR+ is the ratio of the probability of a positive test among the truly positive subjects to the probability of a positive test among the truly negative subjects. The LR– is the ratio of the probability of a negative test among the truly positive subjects to the probability of a negative test among the truly negative subjects. Choi points out that LR+ corresponds to the slope of the line from the origin to the point on the ROC curve determined by the cutpoint. Similarly, LR– corresponds to the slope from the point (1,1) to the point on the ROC curve determined by the cutpoint.

By default, roctab calculates the standard error for the area under the curve by using an algorithm suggested by DeLong, DeLong, and Clarke-Pearson (1988) and asymptotic normal confidence intervals. Optionally, standard errors based on methods suggested by Bamber (1975) or Hanley and McNeil (1982) can be computed by specifying bamber or hanley, respectively, and an exact binomial confidence interval can be obtained by specifying binomial.

```
. roctab disease rating, bamber
                    ROC      Bamber        -Asymptotic Normal--
         Obs       Area     Std. Err.      [95% Conf. Interval]
------------------------------------------------------------------
         109     0.8932       0.0306        0.83317     0.95317
. roctab disease rating, hanley binomial
                    ROC      Hanley        -- Binomial Exact --
         Obs       Area     Std. Err.      [95% Conf. Interval]
------------------------------------------------------------------
         109     0.8932       0.0320        0.81559     0.94180
```

Lorenz-like curves

For applications where it is known that the risk status increases or decreases monotonically with increasing values of the diagnostic test, the ROC curve and associated indices are useful in assessing the overall performance of a diagnostic test. When the risk status does not vary monotonically with increasing values of the diagnostic test, however, the resulting ROC curve can be nonconvex and its indices can be unreliable. For these situations, Lee (1999) proposed an alternative to the ROC analysis based on Lorenz-like curves and the associated Pietra and Gini indices.

Lee (1999) mentions at least three specific situations where results from Lorenz curves are superior to those obtained from ROC curves: 1) a diagnostic test with similar means but very different standard deviations in the abnormal and normal populations, 2) a diagnostic test with bimodal distributions in either the normal or abnormal population, and 3) a diagnostic test distributed symmetrically in the normal population and skewed in the abnormal.

When the risk status increases or decreases monotonically with increasing values of the diagnostic test, the ROC and Lorenz curves yield interchangeable results.

▷ Example 2

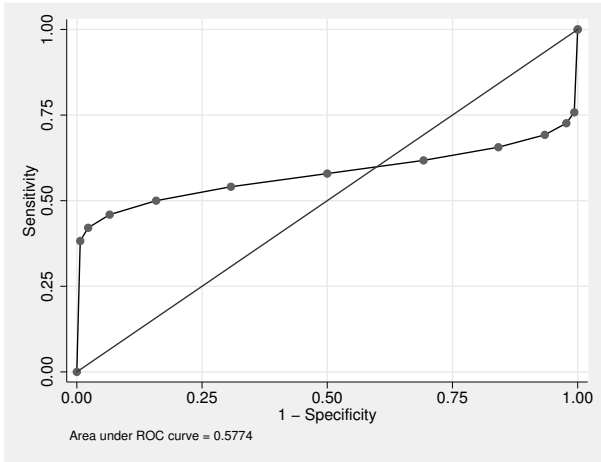
To illustrate the use of the `lorenz` option, we constructed a fictitious dataset that yields results similar to those presented in Table III of Lee (1999). The data assume that a 12-point rating scale was used to classify 442 diseased and 442 healthy subjects. We list a few of the observations.

```
. use http://www.stata-press.com/data/r12/lorenz, clear
. list in 1/7, noobs sep(0)
```

disease	class	pop
0	5	66
1	11	17
0	6	85
0	3	19
0	10	19
0	2	7
1	4	16

The data consist of 24 observations: 12 observations from diseased individuals and 12 from nondiseased individuals. Each observation corresponds to one of the 12 classification values of the rating-scale variable, `class`. The number of subjects represented by each observation is given by the `pop` variable, making this a frequency-weighted dataset. The data were generated assuming a binormal distribution of the latent variable with similar means for the normal and abnormal populations but with the standard deviation for the abnormal population five times greater than that of the normal population.

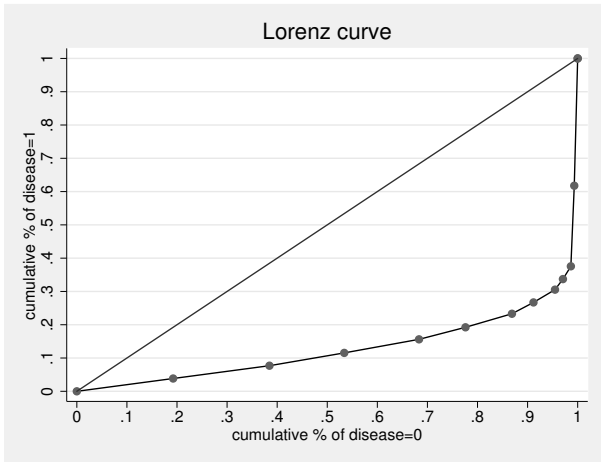
```
. roctab disease class [fweight=pop], graph summary
```



Obs	ROC Area	Std. Err.	−Asymptotic Normal− [95% Conf.	Interval]
884	0.5774	0.0215	0.53517	0.61959

The resulting ROC curve is nonconvex or, as termed by Lee, "wiggly". Lee argues that for this and similar situations, the Lorenz curve and indices are preferred.

```
. roctab disease class [fweight=pop], lorenz graph summary
```




```
Lorenz curve
------------------------------

  Pietra index =   0.6493
  Gini index   =   0.7441
```

Like ROC curves, a more bowed Lorenz curve suggests a better diagnostic test. This bowedness is quantified by the Pietra index, which is geometrically equivalent to twice the largest triangle that

can be inscribed in the area between the curve and the diagonal line, and the Gini index, which is equivalent to twice the area between the Lorenz curve and the diagonal. Lee (1999) provides several additional interpretations for the Pietra and Gini indices.

◁

Saved results

roctab saves the following in r():

Scalars

r(N)	number of observations
r(se)	standard error for the area under the ROC curve
r(lb)	lower bound of CI for the area under the ROC curve
r(ub)	upper bound of CI for the area under the ROC curve
r(area)	area under the ROC curve
r(pietra)	Pietra index
r(gini)	Gini index

Methods and formulas

roctab is implemented as ado-files.

Assume that we applied a diagnostic test to each of N_n normal and N_a abnormal subjects. Further assume that the higher the outcome value of the diagnostic test, the higher the risk of the subject being abnormal. Let $\widehat{\theta}$ be the estimated area under the curve, and let $X_i, i = 1, 2, \ldots, N_a$ and $Y_j, j = 1, 2, \ldots, N_n$ be the values of the diagnostic test for the abnormal and normal subjects, respectively.

The points on the nonparametric ROC curve are generated using each possible outcome of the diagnostic test as a classification cutpoint and computing the corresponding sensitivity and 1−specificity. These points are then connected by straight lines, and the area under the resulting ROC curve is computed using the trapezoidal rule.

The default standard error for the area under the ROC curve is computed using the algorithm described by DeLong, DeLong, and Clarke-Pearson (1988). For each abnormal subject, i, define

$$V_{10}(X_i) = \frac{1}{N_n} \sum_{j=1}^{N_n} \psi(X_i, Y_j)$$

and for each normal subject, j, define

$$V_{01}(Y_j) = \frac{1}{N_a} \sum_{i=1}^{N_a} \psi(X_i, Y_j)$$

where

$$\psi(X, Y) = \begin{cases} 1 & Y < X \\ \frac{1}{2} & Y = X \\ 0 & Y > X \end{cases}$$

Define

$$S_{10} = \frac{1}{N_a - 1} \sum_{i=1}^{N_a} \{V_{10}(X_i) - \widehat{\theta}\}^2$$

and

$$S_{01} = \frac{1}{N_n - 1} \sum_{j=1}^{N_n} \{V_{01}(Y_j) - \widehat{\theta}\}^2$$

The variance of the estimated area under the ROC curve is given by

$$\mathrm{var}(\widehat{\theta}) = \frac{1}{N_a} S_{10} + \frac{1}{N_n} S_{01}$$

The `hanley` standard error for the area under the ROC curve is computed using the algorithm described by Hanley and McNeil (1982). It requires the calculation of two quantities: Q_1 is Pr(two randomly selected abnormal subjects will both have a higher score than a randomly selected normal subject), and Q_2 is Pr(one randomly selected abnormal subject will have a higher score than any two randomly selected normal subjects). The Hanley and McNeil variance of the estimated area under the ROC curve is

$$\mathrm{var}(\widehat{\theta}) = \frac{\widehat{\theta}(1-\widehat{\theta}) + (N_a - 1)(Q_1 - \widehat{\theta}^2) + (N_n - 1)(Q_2 - \widehat{\theta}^2)}{N_a N_n}$$

The `bamber` standard error for the area under the ROC curve is computed using the algorithm described by Bamber (1975). For any two Y values, Y_j and Y_k, and any X_i value, define

$$b_{yyx} = p(Y_j, Y_k < X_i) + p(X_i < Y_j, Y_k) - 2p(Y_j < X_i < Y_k)$$

and similarly, for any two X values, X_i and X_l, and any Y_j value, define

$$b_{xxy} = p(X_i, X_l < Y_j) + p(Y_j < X_i, X_l) - 2p(X_i < Y_j < X_l)$$

Bamber's unbiased estimate of the variance for the area under the ROC curve is

$$\mathrm{var}(\widehat{\theta}) = \frac{1}{4}(N_a-1)(N_n-1)\{p(X \neq Y) + (N_a-1)b_{xxy} + (N_n-1)b_{yyx} - 4(N_a+N_n-1)(\widehat{\theta}-0.5)^2\}$$

Asymptotic confidence intervals are constructed and reported by default, assuming a normal distribution for the area under the ROC curve.

Exact binomial confidence intervals are calculated as described in [R] **ci**, with p equal to the area under the ROC curve.

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Also see

[R] **logistic postestimation** — Postestimation tools for logistic

[R] **roc** — Receiver operating characteristic (ROC) analysis

[R] **roccomp** — Tests of equality of ROC areas

[R] **rocfit** — Parametric ROC models

[R] **rocreg** — Receiver operating characteristic (ROC) regression

Title

rologit — Rank-ordered logistic regression

Syntax

`rologit` *depvar indepvars* [*if*] [*in*] [*weight*] , `group(`*varname*`)` [*options*]

options	Description
Model	
* `group(`*varname*`)`	identifier variable that links the alternatives
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`incomplete(#)`	use # to code unranked alternatives; default is `incomplete(0)`
`reverse`	reverse the preference order
`notestrhs`	keep right-hand-side variables that do not vary within group
`ties(`*spec*`)`	method to handle ties: `exactm`, `breslow`, `efron`, or `none`
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

* `group(`*varname*`)` is required.

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`fweights`, `iweights`, and `pweights` are allowed, except with `ties(efron)`; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Ordinal outcomes > Rank-ordered logistic regression

Description

`rologit` fits the rank-ordered logistic regression model by maximum likelihood (Beggs, Cardell, and Hausman 1981). This model is also known as the Plackett–Luce model (Marden 1995), as the exploded logit model (Punj and Staelin 1978), and as the choice-based method of conjoint analysis (Hair et al. 2010).

rologit expects the data to be in long form, similar to clogit (see [R] **clogit**), in which each of the ranked alternatives forms an observation; all observations related to an individual are linked together by the variable that you specify in the group() option. The distinction from clogit is that *depvar* in rologit records the rankings of the alternatives, whereas for clogit, *depvar* marks only the best alternative by a value not equal to zero. rologit interprets equal scores of *depvar* as ties. The ranking information may be incomplete "at the bottom" (least preferred alternatives). That is, unranked alternatives may be coded as 0 or as a common value that may be specified with the incomplete() option.

If your data record only the unique best alternative, rologit fits the same model as clogit.

Options

Model

group(*varname*) is required, and it specifies the identifier variable (numeric or string) that links the alternatives for an individual, which have been compared and rank ordered with respect to one another.

offset(*varname*); see [R] **estimation options**.

incomplete(*#*) specifies the numeric value used to code alternatives that are not ranked. It is assumed that unranked alternatives are less preferred than the ranked alternatives (that is, the data record the ranking of the most preferred alternatives). It is not assumed that subjects are indifferent between the unranked alternatives. *#* defaults to 0.

reverse specifies that in the preference order, a higher number means a less attractive alternative. The default is that higher values indicate more attractive alternatives. The rank-ordered logit model is not symmetric in the sense that reversing the ordering simply leads to a change in the signs of the coefficients.

notestrhs suppresses the test that the independent variables vary within (at least some of) the groups. Effects of variables that are always constant are not identified. For instance, a rater's gender cannot directly affect his or her rankings; it could affect the rankings only via an interaction with a variable that does vary over alternatives.

ties(*spec*) specifies the method for handling ties (indifference between alternatives) (see [ST] **stcox** for details):

exactm	exact marginal likelihood (default)
breslow	Breslow's method (default if pweights specified)
efron	Efron's method (default if robust VCE)
none	no ties allowed

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If ties(exactm) is specified, *vcetype* may be only oim, bootstrap, or jackknife.

Reporting

level(*#*); see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: iterate(#), trace, [no]log, tolerance(#), ltolerance(#), nrtolerance(#), and nonrtolerance; see [R] **maximize**. These options are seldom used.

The following option is available with rologit but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

The rank-ordered logit model can be applied to analyze how decision makers combine attributes of alternatives into overall evaluations of the attractiveness of these alternatives. The model generalizes a version of McFadden's choice model without alternative-specific covariates, as fit by the clogit command. It uses richer information about the comparison of alternatives, namely, how decision-makers rank the alternatives rather than just specifying the alternative that they like best.

Remarks are presented under the following headings:

Examples
Comparing respondents
Incomplete rankings and ties
Clustered choice data
Comparison of rologit and clogit
On reversals of rankings

Examples

A popular way to study employer preferences for characteristics of employees is the quasi-experimental "vignette method". As an example, we consider the research by de Wolf on the labor market position of social science graduates (de Wolf 2000). This study addresses how the educational portfolio (for example, general skills versus specific knowledge) affects short-term and long-term labor-market opportunities. De Wolf asked 22 human resource managers (the respondents) to rank order the six most suitable candidates of 20 fictitious applicants and to rank order these six candidates for three jobs, namely, 1) researcher, 2) management trainee, and 3) policy adviser. Applicants were described by 10 attributes, including their age, gender, details of their portfolio, and work experience. In this example, we analyze a subset of the data. Also, to simplify the output, we drop, at random, 10 nonselected applicants per case. The resulting dataset includes 29 cases, consisting of 10 applicants each. The data are in long form: observations correspond to alternatives (the applications), and alternatives that figured in one decision task are identified by the variable caseid. We list the observations for caseid==7, in which the respondent considered applicants for a social-science research position.

```
. use http://www.stata-press.com/data/r12/evignet
(Vignet study employer prefs (Inge de Wolf 2000))
. list pref female age grades edufit workexp boardexp if caseid==7, noobs
```

pref	female	age	grades	edufit	workexp	boardexp
0	yes	28	A/B	no	none	no
0	no	25	C/D	yes	one year	no
0	no	25	C/D	yes	none	yes
0	yes	25	C/D	no	internship	yes
1	no	25	C/D	yes	one year	yes
2	no	25	A/B	yes	none	no
3	yes	25	A/B	yes	one year	no
4	yes	25	A/B	yes	none	yes
5	no	25	A/B	yes	internship	no
6	yes	28	A/B	yes	one year	yes

Here six applicants were selected. The rankings are stored in the variable `pref`, where a value of 6 corresponds to "best among the candidates", a value of 5 corresponds to "second-best among the candidates", etc. The applicants with a ranking of 0 were not among the best six candidates for the job. The respondent was not asked to express his preferences among these four applicants, but by the elicitation procedure, it is known that he ranks these four applicants below the six selected applicants. The best candidate was a female, 28 years old, with education fitting the job, with good grades (A/B), with 1 year of work experience, and with experience being a board member of a fraternity, a sports club, etc. The profiles of the other candidates read similarly. Here the respondent completed the task; that is, he selected and rank ordered the six most suitable applicants. Sometimes the respondent performed only part of the task.

```
. list pref female age grades edufit workexp boardexp if caseid==18, noobs
```

pref	female	age	grades	edufit	workexp	boardexp
0	no	25	C/D	yes	none	yes
0	no	25	C/D	no	internship	yes
0	no	28	C/D	no	internship	yes
0	yes	25	A/B	no	one year	no
2	yes	25	A/B	no	none	yes
2	no	25	A/B	no	none	yes
2	no	25	A/B	no	one year	yes
5	no	25	A/B	no	none	yes
5	no	25	A/B	no	none	yes
5	yes	25	A/B	no	none	no

The respondent selected the six best candidates and segmented these six candidates into two groups: one group with the three best candidates, and a second group of three candidates that were "still acceptable". The numbers 2 and 5, indicating these two groups, are arbitrary apart from the implied ranking of the groups. The ties between the candidates in a group indicate that the respondent was not able to rank the candidates within the group.

The purpose of the vignette experiment was to explore and test hypotheses about which of the employees' attributes are valued by employers, how these attributes are weighted depending on the type of job (described by variable `job` in these data), etc. In the psychometric tradition of Thurstone (1927), *value* is assumed to be linear in the attributes, with the coefficients expressing the direction and weight

of the attributes. In addition, it is assumed that *valuation* is to some extent a random procedure, captured by an additive random term. For instance, if value depends only on an applicant's age and gender, we would have

$$\text{value}(\texttt{female}_i, \texttt{age}_i) = \beta_1 \texttt{female}_i + \beta_2 \texttt{age}_i + \epsilon_i$$

where the random residual, ϵ_i, captures all omitted attributes. Thus $\beta_1 > 0$ means that the employer assigns higher value to a woman than to a man. Given this conceptualization of value, it is straightforward to model the decision (selection) among alternatives or the ranking of alternatives: the alternative with the highest value is selected (chosen), or the alternatives are ranked according to their value. To complete the specification of a model of choice and of ranking, we assume that the random residual ϵ_i follows an "extreme value distribution of type I", introduced in this context by Luce (1959). This specific assumption is made mostly for computational convenience.

This model is known by many names. Among others, it is known as the rank-ordered logit model in economics (Beggs, Cardell, and Hausman 1981), as the exploded logit model in marketing research (Punj and Staelin 1978), as the choice-based conjoint analysis model (Hair et al. 2010), and as the Plackett–Luce model (Marden 1995). The model coefficients are estimated using the method of maximum likelihood. The implementation in `rologit` uses an analogy between the rank-ordered logit model and the Cox regression model observed by Allison and Christakis (1994); see *Methods and formulas*. The `rologit` command implements this method for rankings, whereas `clogit` deals with the variant of choices, that is, only the most highly valued alternative is recorded. In the latter case, the model is also known as the Luce–McFadden choice model. In fact, when the data record the most preferred (unique) alternative and no additional ranking information about preferences is available, `rologit` and `clogit` return the same information, though formatted somewhat differently.

```
. rologit pref female age grades edufit workexp boardexp if job==1, group(caseid)
Iteration 0:   log likelihood =  -95.41087
Iteration 1:   log likelihood = -71.180903
Iteration 2:   log likelihood =  -68.47734
Iteration 3:   log likelihood = -68.345918
Iteration 4:   log likelihood = -68.345389
Refining estimates:
Iteration 0:   log likelihood = -68.345389
Rank-ordered logistic regression              Number of obs      =         80
Group variable: caseid                        Number of groups   =          8
No ties in data                               Obs per group: min =         10
                                                             avg =      10.00
                                                             max =         10
                                              LR chi2(6)         =      54.13
Log likelihood = -68.34539                    Prob > chi2        =     0.0000
```

pref	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
female	-.4487287	.3671307	-1.22	0.222	-1.168292	.2708343
age	-.0984926	.0820473	-1.20	0.230	-.2593024	.0623172
grades	3.064534	.6148245	4.98	0.000	1.8595	4.269568
edufit	.7658064	.3602366	2.13	0.034	.0597556	1.471857
workexp	1.386427	.292553	4.74	0.000	.8130341	1.959821
boardexp	.6944377	.3762596	1.85	0.065	-.0430176	1.431893

Focusing only on the variables whose coefficients are significant at the 10% level (we are analyzing 8 respondents only!), the estimated value of an applicant for a job of type 1 (research positions) can be written as

```
value = 3.06*grades + 0.77*edufit + 1.39*workexp + 0.69*boardexp
```

Thus employers prefer applicants for a research position (`job==1`) whose educational portfolio fits the job, who have better grades, who have more relevant work experience, and who have (extracurricular) board experience. They do not seem to care much about the sex and age of applicants, which is comforting.

Given these estimates of the valuation by employers, we consider the probabilities that each of the applications is ranked first. Under the assumption that the ϵ_i are independent and follow an extreme value type I distribution, Luce (1959) showed that the probability, π_i, that alternative i is valued higher than alternatives $2, \ldots, k$ can be written in the multinomial logit form

$$\pi_i = \Pr\{\text{value}_1 > \max(\text{value}_2, \ldots, \text{value}_m)\} = \frac{\exp(\text{value}_i)}{\sum_{j=1}^{k} \exp(\text{value}_i)}$$

The probability of observing a specific ranking can be written as the *product* of such terms, representing a sequential decision interpretation in which the rater first chooses the most preferred alternative, and then the most preferred alternative among the rest, etc.

The probabilities for alternatives to be ranked first are conveniently computed by `predict`.

```
. predict p if e(sample)
(option pr assumed; conditional probability that alternative is ranked first)
(210 missing values generated)
. sort caseid pref p
. list pref p grades edufit workexp boardexp if caseid==7, noobs
```

pref	p	grades	edufit	workexp	boardexp
0	.0027178	C/D	yes	none	yes
0	.0032275	C/D	no	internship	yes
0	.0064231	A/B	no	none	no
0	.0217202	C/D	yes	one year	no
1	.0434964	C/D	yes	one year	yes
2	.0290762	A/B	yes	none	no
3	.2970933	A/B	yes	one year	no
4	.0371747	A/B	yes	none	yes
5	.1163203	A/B	yes	internship	no
6	.4427504	A/B	yes	one year	yes

There clearly is a positive relation between the stated ranking and the predicted probabilities for alternatives to be ranked first, but the association is not perfect. In fact, we would not have expected a perfect association, as the model specifies a (nondegenerate) probability distribution over the possible rankings of the alternatives. These predictions for sets of 10 candidates can also be used to make predictions for subsets of the alternatives. For instance, suppose that only the last three candidates listed in this table would be available. According to parameter estimates of the rank-ordered logit model, the probability that the last of these candidates is selected equals $0.443/(0.037+0.116+0.443) = 0.743$.

Comparing respondents

The `rologit` model assumes that all respondents, HR managers in large public-sector organizations in The Netherlands, use the *same* valuation function; that is, they apply the same decision weights. This is the substantive interpretation of the assumption that the β's are constant between the respondents. To probe this assumption, we could test whether the coefficients vary between different groups of respondents. For a metric characteristic of the HR manager, such as `firmsize`, we can consider a trend-model in the valuation weights,

$$\beta_{ij} = \alpha_{i0} + \alpha_{i1}\texttt{firmsize}_j$$

and we can test that the slopes α_{i1} of `firmsize` are zero.

```
. generate firmsize = employer
. rologit pref edufit grades workexp c.firmsize#c.(edufit grades workexp boardexp)
> if job==1, group(caseid) nolog
Rank-ordered logistic regression              Number of obs      =        80
Group variable: caseid                        Number of groups   =         8
No ties in data                               Obs per group: min =        10
                                                             avg =     10.00
                                                             max =        10
                                              LR chi2(7)         =     57.17
Log likelihood = -66.82346                    Prob > chi2        =    0.0000
```

pref	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
edufit	1.29122	1.13764	1.13	0.256	-.9385127	3.520953
grades	6.439776	2.288056	2.81	0.005	1.955267	10.92428
workexp	1.23342	.8065067	1.53	0.126	-.347304	2.814144
c.firmsize# c.edufit	-.0173333	.0711942	-0.24	0.808	-.1568714	.1222048
c.firmsize# c.grades	-.2099279	.1218251	-1.72	0.085	-.4487008	.028845
c.firmsize# c.workexp	.0097508	.0525081	0.19	0.853	-.0931632	.1126649
c.firmsize# c.boardexp	.0382304	.0227545	1.68	0.093	-.0063676	.0828284

```
. testparm c.firmsize#c.(edufit grades workexp boardexp)
 ( 1)  c.firmsize#c.edufit = 0
 ( 2)  c.firmsize#c.grades = 0
 ( 3)  c.firmsize#c.workexp = 0
 ( 4)  c.firmsize#c.boardexp = 0
           chi2(  4) =    7.14
         Prob > chi2 =    0.1288
```

The Wald test that the slopes of the interacted `firmsize` variables are jointly zero provides no evidence upon which we would reject the null hypothesis; that is, we do not find evidence against the assumption of constant valuation weights of the attributes by firms of different size. We did not enter `firmsize` as a predictor variable. Characteristics of the decision-making agent do not vary between alternatives. Thus an additive effect of these characteristics on the valuation of alternatives does *not* affect the agent's ranking of alternatives and his choice. Consequently the coefficient of `firmsize` is not identified. `rologit` would in fact have diagnosed the problem and dropped `firmsize` from the analysis. Diagnosing this problem can slow the estimation considerably; the test may be suppressed by specifying the `notestrhs` option.

Incomplete rankings and ties

rologit allows incomplete rankings and ties in the rankings as proposed by Allison and Christakis (1994). rologit permits rankings to be incomplete only "at the bottom"; namely, that the ranking of the least attractive alternatives for subjects may not be known—do not confuse this with the situation that a subject is indifferent between these alternatives. This form of incompleteness occurred in the example discussed here, because the respondents were instructed to select and rank only the top six alternatives. It may also be that respondents refused to rank the alternatives that are very unattractive. rologit does not allow other forms of incompleteness, for instance, data in which respondents indicate which of four cars they like best, and which one they like least, but not how they rank the two intermediate cars. Another example of incompleteness that cannot be analyzed with rologit is data in which respondents select the three alternatives they like best but are not requested to express their preferences among the three selected alternatives.

rologit also permits ties in rankings. rologit assumes that if a subject expresses a tie between two or more alternatives, he or she actually holds one particular strict preference ordering, but with all possibilities of a strict ordering consistent with the expressed weak ordering being equally probable. For instance, suppose that a respondent ranks alternative 1 highest. He prefers alternatives 2 and 3 over alternative 4, and he is indifferent between alternatives 2 and 3. We assume that this respondent either has the strict preference ordering $1 > 2 > 3 > 4$ or $1 > 3 > 2 > 4$, with both possibilities being equally likely. From a psychometric perspective, it may actually be more appropriate to also assume that the alternatives 2 and 3 are close; for instance, the difference between the associated valuations (utilities) is less than some threshold or minimally discernible difference. Computationally, however, this is a more demanding model.

Clustered choice data

We have seen that applicants with work experience are in a relatively favorable position. To test whether the effects of work experience vary between the jobs, we can include interactions between the type of job and the attributes of applicants. Such interactions can be obtained using factor variables.

Because some HR managers contributed data for more than one job, we cannot assume that their selection decisions for different jobs are independent. We can account for this by specifying the vce(cluster *clustvar*) option. By treating choice data as incomplete ranking data with only the most preferred alternative marked, rologit may be used to estimate the model parameters for clustered choice data.

```
. rologit pref job##c.(female grades edufit workexp), group(caseid)
> vce(cluster employer) nolog
2.job 3.job omitted because of no within-caseid variance

Rank-ordered logistic regression              Number of obs      =       290
Group variable: caseid                        Number of groups   =        29

Ties handled via the Efron method             Obs per group: min =        10
                                                             avg =     10.00
                                                             max =        10

                                              Wald chi2(12)      =     79.57
Log pseudolikelihood = -296.3855              Prob > chi2        =    0.0000

                              (Std. Err. adjusted for 22 clusters in employer)
```

pref	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
job						
2	0	(omitted)				
3	0	(omitted)				
female	-.2286609	.2519883	-0.91	0.364	-.7225489	.2652272
grades	2.812555	.8517878	3.30	0.001	1.143081	4.482028
edufit	.7027757	.2398396	2.93	0.003	.2326987	1.172853
workexp	1.224453	.3396773	3.60	0.000	.5586978	1.890208
job#c.female						
2	.0293815	.4829166	0.06	0.951	-.9171177	.9758808
3	.1195538	.3688844	0.32	0.746	-.6034463	.8425538
job#c.grades						
2	-2.364247	1.005963	-2.35	0.019	-4.335898	-.3925961
3	-1.88232	.8995277	-2.09	0.036	-3.645362	-.1192782
job#c.edufit						
2	-.267475	.4244964	-0.63	0.529	-1.099473	.5645226
3	-.3182995	.3689972	-0.86	0.388	-1.041521	.4049217
job#c.workexp						
2	-.6870077	.3692946	-1.86	0.063	-1.410812	.0367964
3	-.4656993	.4515712	-1.03	0.302	-1.350763	.4193639

The parameter estimates for the first job type are very similar to those that would have been obtained from an analysis isolated to these data. Differences are due only to an implied change in the method of handling ties. With clustered observations, `rologit` uses Efron's method. If we had specified the `ties(efron)` option with the separate analyses, then the parameter estimates would have been identical to the simultaneous results. Another difference is that `rologit` now reports robust standard errors, adjusted for clustering within respondents. These could have been obtained for the separate analyses, as well by specifying the `vce(robust)` option. In fact, this option would also have forced `rologit` to switch to Efron's method as well.

Given the combined results for the three types of jobs, we can test easily whether the weights for the attributes of applicants vary between the jobs, in other words, whether employers are looking for different qualifications in applicants for different jobs. A Wald test for the equality hypothesis of no difference can be obtained with the `testparm` command:

```
. testparm job#c.(female grades edufit workexp)
 ( 1)  2.job#c.female = 0
 ( 2)  3.job#c.female = 0
 ( 3)  2.job#c.grades = 0
 ( 4)  3.job#c.grades = 0
 ( 5)  2.job#c.edufit = 0
 ( 6)  3.job#c.edufit = 0
 ( 7)  2.job#c.workexp = 0
 ( 8)  3.job#c.workexp = 0
           chi2(  8) =   14.96
         Prob > chi2 =    0.0599
```

We find only mild evidence that employers look for different qualities in candidates according to the job for which they are being considered.

❑ Technical note

Allison (1999) stressed that the comparison between groups of the coefficients of logistic regression is problematic, especially in its latent-variable interpretation. In many common latent-variable models, only the regression coefficients divided by the scale of the latent variable are identified. Thus a comparison of logit regression coefficients between, say, men and women is meaningful only if one is willing to argue that the standard deviation of the latent residual does not differ between the sexes. The rank-ordered logit model is also affected by this problem. While we formulated the model with a scale-free residual, we can actually think of the model for the value of an alternative as being scaled by the standard deviation of the random term, representing other relevant attributes of alternatives. Again comparing attribute weights between jobs is meaningful to the extent that we are willing to defend the proposition that "all omitted attributes" are equally important for different kinds of jobs.

❑

Comparison of rologit and clogit

The rank-ordered logit model also has a sequential interpretation. A subject first chooses the best among the alternatives. Next he or she selects the best alternative among the remaining alternatives, etc. The decisions at each of the subsequent stages are described by a conditional logit model, and a subject is assumed to apply the same decision weights at each stage. Some authors have expressed concern that later choices may well be made more randomly than the first few decisions. A formalization of this idea is a heteroskedastic version of the rank-ordered logit model in which the scale of the random term increases with the number of decisions made (for example, Hausman and Ruud [1987]). This extended model is currently not supported by `rologit`. However, the hypothesis that the same decision weights are applied at the first stage and at later stages can be tested by applying a Hausman test.

First, we fit the rank-ordered logit model on the full ranking data for the first type of job,

```
. rologit pref age female edufit grades workexp boardexp if job==1, group(caseid)
> nolog
Rank-ordered logistic regression                Number of obs      =        80
Group variable: caseid                          Number of groups   =         8
No ties in data                                 Obs per group: min =        10
                                                               avg =     10.00
                                                               max =        10
                                                LR chi2(6)         =     54.13
Log likelihood = -68.34539                      Prob > chi2        =    0.0000
```

pref	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.0984926	.0820473	-1.20	0.230	-.2593024	.0623172
female	-.4487287	.3671307	-1.22	0.222	-1.168292	.2708343
edufit	.7658064	.3602366	2.13	0.034	.0597556	1.471857
grades	3.064534	.6148245	4.98	0.000	1.8595	4.269568
workexp	1.386427	.292553	4.74	0.000	.8130341	1.959821
boardexp	.6944377	.3762596	1.85	0.065	-.0430176	1.431893

and we save the estimates for later use with the `estimates` command.

```
. estimates store Ranking
```

To estimate the decision weights on the basis of the most preferred alternatives only, we create a variable, `best`, that is 1 for the best alternatives, and 0 otherwise. The `by` prefix is useful here.

```
. by caseid (pref), sort: gen best = pref == pref[_N] if job==1
(210 missing values generated)
```

By specifying `(pref)` with `by caseid`, we ensured that the data were sorted in increasing order on `pref` within `caseid`. Hence, the most preferred alternatives are last in the sort order. The expression `pref == pref[_N]` is true (1) for the most preferred alternatives, even if the alternative is not unique, and false (0) otherwise. If the most preferred alternatives were sometimes tied, we could still fit the model for the based-alternatives-only data via `rologit`, but `clogit` would yield different results because it deals with ties in a less appropriate way for continuous valuations. To ascertain whether there are ties in the selected data regarding applicants for research positions, we can combine `by` with `assert`:

```
. by caseid (pref), sort: assert pref[_N-1] != pref[_N] if job==1
```

There are no ties. We can now fit the model on the choice data by using either `clogit` or `rologit`.

```
. rologit best age edufit grades workexp boardexp if job==1, group(caseid) nolog
Rank-ordered logistic regression              Number of obs      =         80
Group variable: caseid                        Number of groups   =          8
No ties in data                               Obs per group: min =         10
                                                             avg =      10.00
                                                             max =         10
                                              LR chi2(5)         =      17.27
Log likelihood = -9.783205                    Prob > chi2        =     0.0040
```

best	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.1048959	.2017068	-0.52	0.603	-.5002339	.2904421
edufit	.4558387	.9336775	0.49	0.625	-1.374136	2.285813
grades	3.443851	1.969002	1.75	0.080	-.4153223	7.303025
workexp	2.545648	1.099513	2.32	0.021	.3906422	4.700655
boardexp	1.765176	1.112763	1.59	0.113	-.4157988	3.946152

```
. estimates store Choice
```

The same results, though with a slightly different formatted header, would have been obtained by using `clogit` on these data.

```
. clogit best age edufit grades workexp boardexp if job==1, group(caseid) nolog
Conditional (fixed-effects) logistic regression   Number of obs    =         80
                                                  LR chi2(5)       =      17.27
                                                  Prob > chi2      =     0.0040
Log likelihood = -9.7832046                       Pseudo R2        =     0.4689
```

best	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	-.1048959	.2017068	-0.52	0.603	-.5002339	.2904421
edufit	.4558387	.9336775	0.49	0.625	-1.374136	2.285813
grades	3.443851	1.969002	1.75	0.080	-.4153223	7.303025
workexp	2.545648	1.099513	2.32	0.021	.3906422	4.700655
boardexp	1.765176	1.112763	1.59	0.113	-.4157988	3.946152

The parameters of the ranking and choice models look different, but the standard errors based on the choice data are much larger. Are we estimating parameters with the ranking data that are different from those with the choice data? A Hausman test compares two estimators of a parameter. One of the estimators should be efficient under the null hypothesis, namely, that choosing the second-best alternative is determined with the same decision weights as the best, etc. In our case, the efficient estimator of the decision weights uses the ranking information. The other estimator should be consistent, even if the null hypothesis is false. In our application, this is the estimator that uses the first-choice data only.

```
. hausman Choice Ranking
```

	Coefficients (b) Choice	(B) Ranking	(b-B) Difference	sqrt(diag(V_b-V_B)) S.E.
age	-.1048959	-.0984926	-.0064033	.1842657
edufit	.4558387	.7658064	-.3099676	.8613846
grades	3.443851	3.064534	.3793169	1.870551
workexp	2.545648	1.386427	1.159221	1.059878
boardexp	1.765176	.6944377	1.070739	1.04722

```
                b = consistent under Ho and Ha; obtained from rologit
     B = inconsistent under Ha, efficient under Ho; obtained from rologit

Test:  Ho:  difference in coefficients not systematic

            chi2(5) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                    =         3.05
          Prob>chi2 =       0.6918
```

We do not find evidence for misspecification. We have to be cautious, though, because Hausman-type tests are often not powerful, and the number of observations in our example is very small, which makes the quality of the method of the null distribution by a chi-squared test rather uncertain.

On reversals of rankings

The rank-ordered logit model has a property that you may find unexpected and even unfortunate. Compare two analyses with the rank-ordered logit model, one in which alternatives are ranked from "most attractive" to "least attractive", the other a reversed analysis in which these alternatives are ranked from "most unattractive" to "least unattractive". By unattractiveness, you probably mean just the opposite of attractiveness, and you expect that the weights of the attributes in predicting "attractiveness" to be minus the weights in predicting "unattractiveness". This is, however, *not* true for the rank-ordered logit model. The assumed distribution of the random residual takes the form $F(\epsilon) = 1 - \exp\{\exp(-\epsilon)\}$. This distribution is right-skewed. Therefore, slightly different models result from adding and subtracting the random residual, corresponding with high-to-low and low-to-high rankings. Thus the estimated coefficients will differ between the two specifications, though usually not in an important way. You may observe the difference by specifying the `reverse` option of `rologit`. Reversing the rank order makes rankings that are incomplete at the bottom become incomplete at the top. Only the first kind of incompleteness is supported by `rologit`. Thus, for this comparison, we exclude the alternatives that are not ranked, omitting the information that ranked alternatives are preferred over excluded ones.

```
. rologit pref grades edufit workexp boardexp if job==1 & pref!=0, group(caseid)
```

(*output omitted*)

```
. estimates store Original
. rologit pref grades edufit workexp boardexp if job==1 & pref!=0, group(caseid)
> reverse
```

(*output omitted*)

```
. estimates store Reversed
```

```
. estimates table Original Reversed, stats(aic bic)
```

Variable	Original	Reversed
grades	2.0032332	-1.0955335
edufit	-.13111006	-.05710681
workexp	1.2805373	-1.2096383
boardexp	.46213212	-.27200317
aic	96.750452	99.665642
bic	104.23526	107.15045

Thus, although the weights of the attributes for reversed rankings are indeed mostly of opposite signs, the magnitudes of the weights and their standard errors differ. Which one is more appropriate? We have no advice to offer here. The specific science of the problem will determine what is appropriate, though we would be surprised indeed if this helps here. Formal testing does not help much either, as the models for the original and reversed rankings are not nested. The model-selection indices, such as the AIC and BIC, however, suggest that you stick to the rank-ordered logit model applied to the original ranking rather than to the reversed ranking.

Saved results

`rologit` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(ll_0)`	log likelihood of the null model ("all rankings are equiprobable")
`e(ll)`	log likelihood
`e(df_m)`	model degrees of freedom
`e(chi2)`	χ^2
`e(p)`	significance
`e(r2_p)`	pseudo-R^2
`e(N_g)`	number of groups
`e(g_min)`	minimum group size
`e(g_avg)`	average group size
`e(g_max)`	maximum group size
`e(code_inc)`	value for incomplete preferences
`e(N_clust)`	number of clusters
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`rologit`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(group)`	name of `group()` variable
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(clustvar)`	name of cluster variable
`e(offset)`	linear offset variable
`e(chi2type)`	`Wald` or `LR`; type of model χ^2 test
`e(reverse)`	`reverse`, if specified
`e(ties)`	`breslow`, `efron`, `exactm`
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(marginsok)`	predictions allowed by `margins`
`e(marginsnotok)`	predictions disallowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators
`e(V_modelbased)`	model-based variance

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`rologit` is implemented as an ado-file.

Allison and Christakis (1994) demonstrate that maximum likelihood estimates for the rank-ordered logit model can be obtained as the maximum partial-likelihood estimates of an appropriately specified Cox regression model for waiting time ([ST] **stcox**). In this analogy, a higher value for an alternative is formally equivalent to a higher hazard rate of failure. `rologit` uses `stcox` to fit the rank-ordered logit model based on such a specification of the data in Cox terms. A higher stated preference is represented by a shorter waiting time until failure. Incomplete rankings are dealt with via censoring. Moreover, decision situations (subjects) are to be treated as strata. Finally, as proposed by Allison and Christakis, ties in rankings are handled by the marginal-likelihood method, specifying that all

strict preference orderings consistent with the stated weak preference ordering are equally likely. The marginal-likelihood estimator is available in `stcox` via the `exactm` option. The methods of the marginal likelihood due to Breslow and Efron are also appropriate for the analysis of rank-ordered logit models. Because in most applications the number of ranked alternatives by one subject will be fairly small (at most, say, 20), the number of ties is small as well, and so you rarely will need to turn to methods to restrict computer time. Because the marginal-likelihood estimator in `stcox` does not support the cluster adjustment or `pweights`, you should use the Efron method in such cases.

This command supports the clustered version of the Huber/White/sandwich estimator of the variance using `vce(robust)` and `vce(cluster` *clustvar*`)`. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*. Specifying `vce(robust)` is equivalent to specifying `vce(cluster` *groupvar*`)`, where *groupvar* is the identifier variable that links the alternatives.

Acknowledgment

The `rologit` command was written by Jeroen Weesie, Department of Sociology, Utrecht University, The Netherlands.

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Also see

[R] **rologit postestimation** — Postestimation tools for rologit

[R] **clogit** — Conditional (fixed-effects) logistic regression

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **nlogit** — Nested logit regression

[R] **slogit** — Stereotype logistic regression

[U] **20 Estimation and postestimation commands**

Title

rologit postestimation — Postestimation tools for rologit

Description

The following postestimation commands are available after `rologit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`	likelihood-ratio test
`margins`[1]	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] The default prediction statistic `pr` cannot be correctly handled by `margins`; however, `margins` can be used after `rologit` with the `predict(xb)` option.

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic* `nooffset`]

statistic	Description
Main	
`pr`	probability that alternatives are ranked first; the default
`xb`	linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if esample() ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability that alternatives are ranked first.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `rologit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

Remarks

See *Comparing respondents* and *Clustered choice data* in [R] **rologit** for examples of the use of `testparm`, an alternative to the `test` command.

See *Comparison of rologit and clogit* and *On reversals of rankings* in [R] **rologit** for examples of the use of `estimates`.

See *Comparison of rologit and clogit* in [R] **rologit** for an example of the use of `hausman`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **rologit** — Rank-ordered logistic regression

[U] **20 Estimation and postestimation commands**

Title

rreg — Robust regression

Syntax

`rreg` *depvar* [*indepvars*] [*if*] [*in*] [, *options*]

options	Description
Model	
`tune(#)`	use # as the biweight tuning constant; default is `tune(7)`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`genwt(`*newvar*`)`	create *newvar* containing the weights assigned to each observation
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Optimization	
optimization_options	control the optimization process; seldom used
`graph`	graph weights during convergence
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`by`, `fracpoly`, `mfp`, `mi estimate`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Other > Robust regression

Description

`rreg` performs one version of robust regression of *depvar* on *indepvars*.

Also see *Robust standard errors* in [R] **regress** for standard regression with robust variance estimates and [R] **qreg** for quantile (including median or least-absolute-residual) regression.

Options

Model

`tune(#)` is the biweight tuning constant. The default is 7, meaning seven times the median absolute deviation (MAD) from the median residual; see *Methods and formulas*. Lower tuning constants downweight outliers rapidly but may lead to unstable estimates (less than 6 is not recommended). Higher tuning constants produce milder downweighting.

Reporting

`level(#)`; see [R] **estimation options**.

`genwt(`*newvar*`)` creates the new variable *newvar* containing the weights assigned to each observation.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Optimization

optimization_options: `iterate(#)`, `tolerance(#)`, `[no]log`. `iterate()` specifies the maximum number of iterations; iterations stop when the maximum change in weights drops below `tolerance()`; and `log`/`nolog` specifies whether to show the iteration log. These options are seldom used.

`graph` allows you to graphically watch the convergence of the iterative technique. The weights obtained from the most recent round of estimation are graphed against the weights obtained from the previous round.

The following option is available with `rreg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

`rreg` first performs an initial screening based on Cook's distance > 1 to eliminate gross outliers before calculating starting values and then performs Huber iterations followed by biweight iterations, as suggested by Li (1985).

▷ Example 1

We wish to examine the relationship between mileage rating, weight, and location of manufacture for the 74 cars in our automobile data. As a point of comparison, we begin by fitting an ordinary regression:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight foreign
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =   69.75
       Model |  1619.2877     2  809.643849            Prob > F      =  0.0000
    Residual |  824.171761    71   11.608053           R-squared     =  0.6627
-------------+------------------------------           Adj R-squared =  0.6532
       Total |  2443.45946    73  33.4720474           Root MSE      =  3.4071

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0065879   .0006371   -10.34   0.000    -.0078583   -.0053175
     foreign |  -1.650029   1.075994    -1.53   0.130      -3.7955    .4954422
       _cons |   41.6797   2.165547    19.25   0.000     37.36172    45.99768
------------------------------------------------------------------------------
```

We now compare this with the results from `rreg`:

```
. rreg mpg weight foreign
   Huber iteration 1:  maximum difference in weights = .80280176
   Huber iteration 2:  maximum difference in weights = .2915438
   Huber iteration 3:  maximum difference in weights = .08911171
   Huber iteration 4:  maximum difference in weights = .02697328
Biweight iteration 5:  maximum difference in weights = .29186818
Biweight iteration 6:  maximum difference in weights = .11988101
Biweight iteration 7:  maximum difference in weights = .03315872
Biweight iteration 8:  maximum difference in weights = .00721325
Robust regression                                     Number of obs =      74
                                                      F(  2,    71) =  168.32
                                                      Prob > F      =  0.0000
```

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0063976	.0003718	-17.21	0.000	-.007139	-.0056562
foreign	-3.182639	.627964	-5.07	0.000	-4.434763	-1.930514
_cons	40.64022	1.263841	32.16	0.000	38.1202	43.16025

Note the large change in the `foreign` coefficient.

◁

❑ Technical note

It would have been better if we had fit the previous robust regression by typing `rreg mpg weight foreign, genwt(w)`. The new variable, `w`, would then contain the estimated weights. Let's pretend that we did this:

```
. rreg mpg weight foreign, genwt(w)
  (output omitted)
. summarize w, detail
                    Robust Regression Weight
-------------------------------------------------------------
      Percentiles      Smallest
 1%           0              0
 5%     .0442957              0
10%     .4674935              0       Obs                  74
25%     .8894815       .0442957       Sum of Wgt.          74

50%     .9690193                      Mean           .8509966
                       Largest       Std. Dev.      .2746451
75%     .9949395       .9996715
90%     .9989245       .9996953       Variance       .0754299
95%     .9996715       .9997343       Skewness      -2.287952
99%     .9998585       .9998585       Kurtosis       6.874605
```

We discover that 3 observations in our data were dropped altogether (they have weight 0). We could further explore our data:

```
. sort w
. list make mpg weight w if w<.467, sep(0)
```

	make	mpg	weight	w
1.	Datsun 210	35	2,020	0
2.	Subaru	35	2,050	0
3.	VW Diesel	41	2,040	0
4.	Plym. Arrow	28	3,260	.04429567
5.	Cad. Seville	21	4,290	.08241943
6.	Toyota Corolla	31	2,200	.10443129
7.	Olds 98	21	4,060	.28141296

Being familiar with the automobile data, we immediately spotted two things: the VW is the only diesel car in our data, and the weight recorded for the Plymouth Arrow is incorrect.

❑

▷ Example 2

If we specify no explanatory variables, `rreg` produces a robust estimate of the mean:

```
. rreg mpg
   Huber iteration 1:  maximum difference in weights = .64471879
   Huber iteration 2:  maximum difference in weights = .05098336
   Huber iteration 3:  maximum difference in weights = .0099887
Biweight iteration 4:  maximum difference in weights = .25197391
Biweight iteration 5:  maximum difference in weights = .00358606
Robust regression                                     Number of obs =      74
                                                      F(  0,    73) =    0.00
                                                      Prob > F      =       .
```

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
_cons	20.68825	.641813	32.23	0.000	19.40912	21.96738

The estimate is given by the coefficient on `_cons`. The mean is 20.69 with an estimated standard error of 0.6418. The 95% confidence interval is $[\,19.4, 22.0\,]$. By comparison, `ci` (see [R] **ci**) gives us the standard calculation:

```
. ci mpg
```

Variable	Obs	Mean	Std. Err.	[95% Conf.	Interval]
mpg	74	21.2973	.6725511	19.9569	22.63769

◁

Saved results

rreg saves the following in e():

Scalars

e(N)	number of observations
e(mss)	model sum of squares
e(df_m)	model degrees of freedom
e(rss)	residual sum of squares
e(df_r)	residual degrees of freedom
e(r2)	R-squared
e(r2_a)	adjusted R-squared
e(F)	F statistic
e(rmse)	root mean squared error
e(rank)	rank of e(V)

Macros

e(cmd)	rreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(genwt)	variable containing the weights
e(title)	title in estimation output
e(model)	ols
e(vce)	ols
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

rreg is implemented as an ado-file.

See Berk (1990), Goodall (1983), and Rousseeuw and Leroy (1987) for a general description of the issues and methods. Hamilton (1991a, 1992) provides a more detailed description of rreg and some Monte Carlo evaluations.

rreg begins by fitting the regression (see [R] **regress**), calculating Cook's D (see [R] **predict** and [R] **regress postestimation**), and excluding any observation for which $D > 1$.

Thereafter rreg works iteratively: it performs a regression, calculates case weights from absolute residuals, and regresses again using those weights. Iterations stop when the maximum change in weights drops below tolerance(). Weights derive from one of two weight functions, Huber weights and biweights. Huber weights (Huber 1964) are used until convergence, and then, from that result, biweights are used until convergence. The biweight was proposed by Beaton and Tukey (1974, 151–152) after the Princeton robustness study (Andrews et al. 1972) had compared various estimators. Both weighting functions are used because Huber weights have problems dealing with severe outliers, whereas biweights sometimes fail to converge or have multiple solutions. The initial Huber weighting should improve the behavior of the biweight estimator.

In Huber weighting, cases with small residuals receive weights of 1; cases with larger residuals receive gradually smaller weights. Let $e_i = y_i - \mathbf{X}_i\mathbf{b}$ represent the ith-case residual. The ith scaled residual $u_i = e_i/s$ is calculated, where $s = M/0.6745$ is the residual scale estimate and

$M = \text{med}(|e_i - \text{med}(e_i)|)$ is the median absolute deviation from the median residual. Huber estimation obtains case weights:

$$w_i = \begin{cases} 1 & \text{if } |u_i| \leq c_h \\ c_h/|u_i| & \text{otherwise} \end{cases}$$

`rreg` defines $c_h = 1.345$, so downweighting begins with cases whose absolute residual exceeds $(1.345/0.6745)M \approx 2M$.

With biweights, all cases with nonzero residuals receive some downweighting, according to the smoothly decreasing biweight function

$$w_i = \begin{cases} \{1 - (u_i/c_b)^2\}^2 & \text{if } |u_i| \leq c_b \\ 0 & \text{otherwise} \end{cases}$$

where $c_b = 4.685 \times$ `tune()`$/7$. Thus when `tune()` $= 7$, cases with absolute residuals of $(4.685/0.6745)M \approx 7M$ or more are assigned 0 weight and thus are effectively dropped. Goodall (1983, 377) suggests using a value between 6 and 9, inclusive, for `tune()` in the biweight case and states that performance is good between 6 and 12, inclusive.

The tuning constants $c_h = 1.345$ and $c_b = 4.685$ (assuming `tune()` is set at the default 7) give `rreg` about 95% of the efficiency of OLS when applied to data with normally distributed errors (Hamilton 1991b). Lower tuning constants downweight outliers more drastically (but give up Gaussian efficiency); higher tuning constants make the estimator more like OLS.

Standard errors are calculated using the pseudovalues approach described in Street, Carroll, and Ruppert (1988).

Acknowledgment

The current version of `rreg` is due to the work of Lawrence Hamilton, Department of Sociology, University of New Hampshire.

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Also see

[R] **rreg postestimation** — Postestimation tools for rreg

[R] **qreg** — Quantile regression

[R] **regress** — Linear regression

[MI] **estimation** — Estimation commands for use with mi estimate

[U] **20 Estimation and postestimation commands**

Title

rreg postestimation — Postestimation tools for rreg

Description

The following postestimation commands are available after `rreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	VCE and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic*]

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`residuals`	residuals
`hat`	diagonal elements of the hat matrix

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`residuals` calculates the residuals.

`hat` calculates the diagonal elements of the hat matrix. You must have run the `rreg` command with the `genwt()` option.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **rreg** — Robust regression

[U] **20 Estimation and postestimation commands**

Title

runtest — Test for random order

Syntax

`runtest` *varname* [*in*] [`,` *options*]

options	Description
`continuity`	continuity correction
`drop`	ignore values equal to the threshold
`split`	randomly split values equal to the threshold as above or below the threshold; default is to count as below
`mean`	use mean as threshold; default is median
`threshold(#)`	assign arbitrary threshold; default is median

Menu

Statistics > Nonparametric analysis > Tests of hypotheses > Test for random order

Description

`runtest` tests whether the observations of *varname* are serially independent—that is, whether they occur in a random order—by counting how many runs there are above and below a threshold. By default, the median is used as the threshold. A small number of runs indicates positive serial correlation; a large number indicates negative serial correlation.

Options

`continuity` specifies a continuity correction that may be helpful in small samples. If there are fewer than 10 observations either above or below the threshold, however, the tables in Swed and Eisenhart (1943) provide more reliable critical values. By default, no continuity correction is used.

`drop` directs `runtest` to ignore any values of *varname* that are equal to the threshold value when counting runs and tabulating observations. By default, `runtest` counts a value as being above the threshold when it is strictly above the threshold and as being below the threshold when it is less than or equal to the threshold.

`split` directs `runtest` to randomly split values of *varname* that are equal to the threshold. In other words, when *varname* is equal to threshold, a "coin" is flipped. If it comes up heads, the value is counted as above the threshold. If it comes up tails, the value is counted as below the threshold.

`mean` directs `runtest` to tabulate runs above and below the mean rather than the median.

`threshold(#)` specifies an arbitrary threshold to use in counting runs. For example, if *varname* has already been coded as a 0/1 variable, the median generally will not be a meaningful separating value.

Remarks

`runtest` performs a nonparametric test of the hypothesis that the observations of *varname* occur in a random order by counting how many runs there are above and below a threshold. If *varname* is positively serially correlated, it will tend to remain above or below its median for several observations in a row; that is, there will be relatively few runs. If, on the other hand, *varname* is negatively serially correlated, observations above the median will tend to be followed by observations below the median and vice versa; that is, there will be relatively many runs.

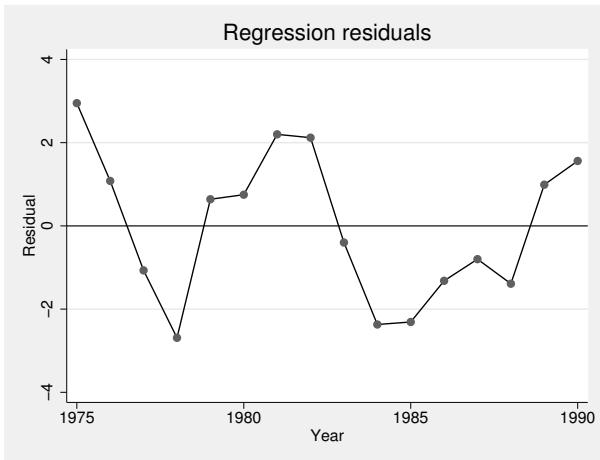
By default, `runtest` uses the median for the threshold, and this is not necessarily the best choice. If `mean` is specified, the mean is used instead of the median. If `threshold(#)` is specified, # is used. Because `runtest` divides the data into two states—above and below the threshold—it is appropriate for data that are already binary; for example, win or lose, live or die, rich or poor, etc. Such variables are often coded as 0 for one state and 1 for the other. Here you should specify `threshold(0)` because, by default, `runtest` separates the observations into those that are greater than the threshold and those that are less than *or equal* to the threshold.

As with most nonparametric procedures, the treatment of ties complicates the test. Observations equal to the threshold value are ties and can be treated in one of three ways. By default, they are treated as if they were below the threshold. If `drop` is specified, they are omitted from the calculation and the total number of observations is adjusted. If `split` is specified, each is randomly assigned to the above- and below-threshold groups. The random assignment is different each time the procedure is run unless you specify the random-number seed; see [R] **set seed**.

▷ Example 1

We can use `runtest` to check regression residuals for serial correlation.

```
. use http://www.stata-press.com/data/r12/run1
. scatter resid year, connect(l) yline(0) title(Regression residuals)
```



The graph gives the impression that these residuals are positively correlated. Excursions above or below zero—the natural threshold for regression residuals—tend to last for several observations. `runtest` can evaluate the statistical significance of this impression.

```
. runtest resid, thresh(0)
 N(resid <= 0) = 8
 N(resid >  0) = 8
           obs = 16
      N(runs) = 5
            z  = -2.07
     Prob>|z| = .04
```

There are five runs in these 16 observations. Using the normal approximation to the true distribution of the number of runs, the five runs in this series are fewer than would be expected if the residuals were serially independent. The p-value is 0.04, indicating a two-sided significant result at the 5% level. If the alternative hypothesis is positive serial correlation, rather than any deviation from randomness, then the one-sided p-value is $0.04/2 = 0.015$. With so few observations, however, the normal approximation may be inaccurate. (Tables compiled by Swed and Eisenhart list five runs as the 5% critical value for a one-sided test.)

`runtest` is a nonparametric test. It ignores the magnitudes of the observations and notes only whether the values are above or below the threshold. We can demonstrate this feature by reducing the information about the regression residuals in this example to a 0/1 variable that indicates only whether a residual is positive or negative.

```
. generate byte sign = resid>0
. runtest sign, thresh(0)
 N(sign <= 0) = 8
 N(sign >  0) = 8
          obs = 16
     N(runs) = 5
           z  = -2.07
    Prob>|z| = .04
```

As expected, `runtest` produces the same answer as before.

◁

❑ Technical note

The run test can also be used to test the null hypothesis that two samples are drawn from the same underlying distribution. The run test is sensitive to differences in the shapes, as well as the locations, of the empirical distributions.

Suppose, for example, that two different additives are added to the oil in 10 different cars during an oil change. The cars are run until a viscosity test determines that another oil change is needed, and the number of miles traveled between oil changes is recorded. The data are

```
. use http://www.stata-press.com/data/r12/additive, clear
. list
```

	additive	miles
1.	1	4024
2.	1	4756
3.	1	7993
4.	1	5025
5.	1	4188
6.	2	3007
7.	2	1988
8.	2	1051
9.	2	4478
10.	2	4232

To test whether the additives generate different distributions of miles between oil changes, we sort the data by `miles` and then use `runtest` to see whether the marker for each additive occurs in random order:

```
. sort miles
. runtest additive, thresh(1)
 N(additive <= 1) = 5
 N(additive >  1) = 5
              obs = 10
         N(runs) = 4
               z  = -1.34
        Prob>|z| = .18
```

Here the additives do not produce statistically different results.

❑

❑ Technical note

A test that is related to the run test is the runs up-and-down test. In the latter test, the data are classified not by whether they lie above or below a threshold but by whether they are steadily increasing or decreasing. Thus an unbroken string of increases in the variable of interest is counted as one run, as is an unbroken string of decreases. According to Madansky (1988), the run test is superior to the runs up-and-down test for detecting trends in the data, but the runs up-and-down test is superior for detecting autocorrelation.

`runtest` can be used to perform a runs up-and-down test. Using the regression residuals from the example above, we can perform a `runtest` on their first differences:

```
. use http://www.stata-press.com/data/r12/run1
. generate resid_D = resid - resid[_n-1]
(1 missing value generated)
. runtest resid_D, thresh(0)
 N(resid_D <= 0) = 7
 N(resid_D >  0) = 8
             obs = 15
        N(runs) = 6
              z  = -1.33
       Prob>|z| = .18
```

Edgington (1961) has compiled a table of the small sample distribution of the runs up-and-down statistic, and this table is reprinted in Madansky (1988). For large samples, the z statistic reported by `runtest` is incorrect for the runs up-and-down test. Let N be the number of observations (15 here), and let r be the number of runs (6). The expected number of runs in the runs up-and-down test is

$$\mu_r = \frac{2N-1}{3}$$

the variance is

$$\sigma_r^2 = \frac{16N-29}{90}$$

and the correct z statistic is

$$\widehat{z} = \frac{r-\mu_r}{\sigma_r}$$

❑

❑ Technical note

`runtest` will tolerate missing values at the beginning or end of a series, as occurred in the technical note above (generating first differences resulted in a missing value for the first observation). `runtest`, however, will issue an error message if there are any missing observations in the interior of the series (in the portion covered by the `in` *range* modifier). To perform the test anyway, simply `drop` the missing observations before using `runtest`.

❑

Saved results

`runtest` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(p)`	p-value of z
`r(N_below)`	number below the threshold	`r(z)`	z statistic
`r(N_above)`	number above the threshold	`r(n_runs)`	number of runs
`r(mean)`	expected number of runs	`r(Var)`	variance of the number of runs

Methods and formulas

`runtest` is implemented as an ado-file.

`runtest` begins by calculating the number of observations below the threshold, n_0; the number of observations above the threshold, n_1; the total number of observations, $N = n_0 + n_1$; and the number of runs, r. These statistics are always reported, so the exact tables of critical values in Swed and Eisenhart (1943) may be consulted if necessary.

The expected number of runs under the null is

$$\mu_r = \frac{2n_0n_1}{N} + 1$$

the variance is

$$\sigma_r^2 = \frac{2n_0n_1\left(2n_0n_1 - N\right)}{N^2\left(N-1\right)}$$

and the normal approximation test statistic is

$$\widehat{z} = \frac{r - \mu_r}{\sigma_r}$$

Acknowledgment

`runtest` was written by Sean Becketti, a past editor of the *Stata Technical Bulletin*.

References

Edgington, E. S. 1961. Probability table for number of runs of signs of first differences in ordered series. *Journal of the American Statistical Association* 56: 156–159.

Madansky, A. 1988. *Prescriptions for Working Statisticians*. New York: Springer.

Swed, F. S., and C. Eisenhart. 1943. Tables for testing randomness of grouping in a sequence of alternatives. *Annals of Mathematical Statistics* 14: 66–87.

Title

sampsi — Sample size and power for means and proportions

Syntax

`sampsi` $\#_1$ $\#_2$ [, *options*]

options	Description
Main	
`onesample`	one-sample test; default is two-sample
`sd1(#)`	standard deviation of sample 1
`sd2(#)`	standard deviation of sample 2
Options	
`alpha(#)`	significance level of test; default is `alpha(0.05)`
`power(#)`	power of test; default is `power(0.90)`
`n1(#)`	size of sample 1
`n2(#)`	size of sample 2
`ratio(#)`	ratio of sample sizes; default is `ratio(1)`
`pre(#)`	number of baseline measurements; default is `pre(0)`
`post(#)`	number of follow-up measurements; default is `post(1)`
`nocontinuity`	do not use continuity correction for two-sample test on proportions
`r0(#)`	correlation between baseline measurements; default is `r0()`=`r1()`
`r1(#)`	correlation between follow-up measurements
`r01(#)`	correlation between baseline and follow-up measurements
`onesided`	one-sided test; default is two-sided
`method(`*method*`)`	analysis method where *method* is `post`, `change`, `ancova`, or `all`; default is `method(all)`

Menu

sampsi

Statistics > Power and sample size > Tests of means and proportions

sampsi with repeated measures

Statistics > Power and sample size > Tests of means with repeated measures

Description

`sampsi` estimates require sample size or power of tests for studies comparing two groups. `sampsi` can be used when comparing means or proportions for simple studies where only one measurement of the outcome is planned and for comparing mean summary statistics for more complex studies where repeated measurements of the outcome on each experimental unit are planned.

If n1(#) or n2(#) is specified, sampsi computes power; otherwise, it computes sample size. For simple studies, if sd1(#) or sd2(#) is specified, sampsi assumes a comparison of means; otherwise, it assumes a comparison of proportions. For repeated measurements, sd1(#) or sd2(#) must be specified. sampsi is an immediate command; all its arguments are numbers; see [U] **19 Immediate commands**.

Options

Main

onesample indicates a one-sample test. The default is two-sample.

sd1(#) and sd2(#) are the standard deviations of population 1 and population 2, respectively. One or both must be specified when doing a comparison of means. When the onesample option is used, sd1(#) is the standard deviation of the single sample (it can be abbreviated as sd(#)). If only one of sd1(#) or sd2(#) is specified, sampsi assumes that sd1() = sd2(). If neither sd1(#) nor sd2(#) is specified, sampsi assumes a test of proportions. For repeated measurements, sd1(#) or sd2(#) must be specified.

Options

alpha(#) is the significance level of the test. The default is alpha(0.05) unless set level has been used to reset the default significance level for confidence intervals. If a set level $\#_{\text{lev}}$ command has been issued, the default value is alpha($1 - \#_{\text{lev}}/100$). See [R] **level**.

power(#) $= 1 - \beta$ is the power of the test. The default is power(0.90).

n1(#) and n2(#) are the sizes of sample 1 and sample 2, respectively. One or both must be specified when computing power. If neither n1(#) nor n2(#) is specified, sampsi computes sample size. When the onesample option is used, n1(#) is the size of the single sample (it can be abbreviated as n(#)). If only one of n1(#) or n2(#) is specified, the unspecified one is computed using the formula ratio = n2()/n1().

ratio(#) is the ratio of sample sizes for two-sample tests: ratio = n2()/n1(). The default is ratio(1).

pre(#) specifies the number of baseline measurements (prerandomization) planned in a repeated-measure study. The default is pre(0).

post(#) specifies the number of follow-up measurements (postrandomization) planned in a repeated-measure study. The default is post(1).

nocontinuity requests power and sample size calculations without the continuity correction for the two-sample test on proportions. If not specified, the continuity correction is used.

r0(#) specifies the correlation between baseline measurements in a repeated-measure study. If r0(#) is not specified, sampsi assumes that r0() = r1().

r1(#) specifies the correlation between follow-up measurements in a repeated-measure study. For a repeated-measure study, either r1(#) or r01(#) must be specified. If r1(#) is not specified, sampsi assumes that r1() = r01().

r01(#) specifies the correlation between baseline and follow-up measurements in a repeated-measure study. For a repeated-measure study, either r01(#) or r1(#) must be specified. If r01(#) is not specified, sampsi assumes that r01() = r1().

onesided indicates a one-sided test. The default is two-sided.

`method(post | change | ancova | all)` specifies the analysis method to be used with repeated measures. `change` and `ancova` can be used only if baseline measurements are planned. The default is `method(all)`, which means to use all three methods. Each method is described in *Methods and formulas*.

Remarks

Remarks are presented under the following headings:

Studies with one measurement of the outcome
Two-sample test of equality of means
One-sample test of mean
Two-sample test of equality of proportions
One-sample test of proportion
Clinical trials with repeated measures

Studies with one measurement of the outcome

For simple studies, where only one measurement of the outcome is planned, `sampsi` computes sample size or power for four types of tests:

1. Two-sample comparison of mean μ_1 of population 1 with mean μ_2 of population 2. The null hypothesis is $\mu_1 = \mu_2$, and normality is assumed. The postulated values of the means are $\mu_1 = \#_1$ and $\mu_2 = \#_2$, and the postulated standard deviations are `sd1(#)` and `sd2(#)`.
2. One-sample comparison of the mean μ of a population with a hypothesized value μ_0. The null hypothesis is $\mu = \mu_0$, and normality is assumed. The first argument, $\#_1$, to `sampsi` is μ_0. The second argument, $\#_2$, is the postulated value of μ, that is, the alternative hypothesis is $\mu = \#_2$. The postulated standard deviation is `sd1(#)`. To get this test, the `onesample` option must be specified.
3. Two-sample comparison of proportion p_1 with proportion p_2. The null hypothesis is $p_1 = p_2$, and the postulated values are $p_1 = \#_1$ and $p_2 = \#_2$.
4. One-sample comparison of a proportion p with a hypothesized value p_0. The null hypothesis is $p = p_0$, where $p_0 = \#_1$. The alternative hypothesis is $p = \#_2$. To get this test, the `onesample` option must be specified.

Examples of these follow.

Two-sample test of equality of means

▷ Example 1

We are doing a study of the relationship of oral contraceptives (OC) and blood pressure (BP) level for women ages 35–39 (Rosner 2006, 331–333). From a pilot study, it was determined that the mean and standard deviation of BP of OC users were 132.86 and 15.34, respectively. The mean and standard deviation of OC nonusers in the pilot study were found to be 127.44 and 18.23. Because it is easier to find OC nonusers than users, we decide that n_2, the size of the sample of OC nonusers, should be twice n_1, the size of the sample of OC users; that is, $r = n_2/n_1 = 2$. To compute the sample sizes for $\alpha = 0.05$ (two-sided) and the power of 0.80, we issue the following command:

```
. sampsi 132.86 127.44, p(0.8) r(2) sd1(15.34) sd2(18.23)
Estimated sample size for two-sample comparison of means
Test Ho: m1 = m2, where m1 is the mean in population 1
                  and m2 is the mean in population 2
Assumptions:
         alpha =   0.0500  (two-sided)
         power =   0.8000
            m1 =   132.86
            m2 =   127.44
           sd1 =    15.34
           sd2 =    18.23
         n2/n1 =     2.00
Estimated required sample sizes:
            n1 =      108
            n2 =      216
```

We now find out that we have only enough money to study 100 subjects from each group. We can compute the power for $n_1 = n_2 = 100$ by typing

```
. sampsi 132.86 127.44, n1(100) sd1(15.34) sd2(18.23)
Estimated power for two-sample comparison of means
Test Ho: m1 = m2, where m1 is the mean in population 1
                  and m2 is the mean in population 2
Assumptions:
         alpha =   0.0500  (two-sided)
            m1 =   132.86
            m2 =   127.44
           sd1 =    15.34
           sd2 =    18.23
sample size n1 =      100
            n2 =      100
         n2/n1 =     1.00
Estimated power:
         power =   0.6236
```

We did not have to specify `n2(#)` or `ratio(#)` because `ratio(1)` is the default.

◁

One-sample test of mean

▷ Example 2

Suppose that we wish to test the effects of a low-fat diet on serum cholesterol levels. We will measure the difference in cholesterol levels for each subject before and after being on the diet. Because there is only one group of subjects, all on the diet, this is a one-sample test, and we must use the `onesample` option with `sampsi`.

Our null hypothesis is that the mean of individual differences in cholesterol level will be zero; that is, $\mu = 0\,\text{mg}/100\,\text{mL}$. If the effect of the diet is as large as a mean difference of $-10\,\text{mg}/100\,\text{mL}$, then we wish to have power of 0.95 for rejecting the null hypothesis. Because we expect a reduction in level, we want to use a one-sided test with $\alpha = 0.025$. From past studies, we estimate that the standard deviation of the difference in cholesterol levels will be about $20\,\text{mg}/100\,\text{mL}$. To compute the required sample size, we type

```
. sampsi 0 -10, sd(20) onesam a(0.025) onesided p(0.95)
Estimated sample size for one-sample comparison of mean
  to hypothesized value
Test Ho: m =      0, where m is the mean in the population
Assumptions:
         alpha =   0.0250  (one-sided)
         power =   0.9500
 alternative m =      -10
            sd =       20
Estimated required sample size:
             n =       52
```

We decide to conduct the study with $n = 60$ subjects, and we wonder what the power will be at a one-sided significance level of $\alpha = 0.01$:

```
. sampsi 0 -10, sd(20) onesam a(0.01) onesided n(60)
Estimated power for one-sample comparison of mean
  to hypothesized value
Test Ho: m =      0, where m is the mean in the population
Assumptions:
         alpha =   0.0100  (one-sided)
 alternative m =      -10
            sd =       20
 sample size n =       60
Estimated power:
         power =   0.9390
```

◁

Two-sample test of equality of proportions

▷ Example 3

We want to conduct a survey on people's opinions of the president's performance. Specifically, we want to determine whether members of the president's party have a different opinion from people with another party affiliation. Using past surveys as a guide, we estimate that only 25% of members of the president's party will say that the president is doing a poor job, whereas 40% of members of other parties will rate the president's performance as poor. We compute the required sample sizes for $\alpha = 0.05$ (two-sided) and the power of 0.90 by typing

```
. sampsi 0.25 0.4
Estimated sample size for two-sample comparison of proportions
Test Ho: p1 = p2, where p1 is the proportion in population 1
                  and p2 is the proportion in population 2
Assumptions:
         alpha =   0.0500  (two-sided)
         power =   0.9000
            p1 =   0.2500
            p2 =   0.4000
         n2/n1 =   1.00
Estimated required sample sizes:
            n1 =      216
            n2 =      216
```

To compute the power for a survey with a sample of $n_1 = 300$ members of the president's party and a sample of $n_2 = 150$ members of other parties, we type

```
. sampsi 0.25 0.4, n1(300) r(0.5)
Estimated power for two-sample comparison of proportions
Test Ho: p1 = p2, where p1 is the proportion in population 1
                  and p2 is the proportion in population 2
Assumptions:
         alpha =   0.0500  (two-sided)
            p1 =   0.2500
            p2 =   0.4000
sample size n1 =      300
            n2 =      150
         n2/n1 =     0.50
Estimated power:
         power =   0.8790
```

◁

One-sample test of proportion

▷ Example 4

Someone claims that females are more likely than males to study French. Our null hypothesis is that the proportion of female French students is 0.5. We wish to compute the sample size that will give us 80% power to reject the null hypothesis if the true proportion of female French students is 0.75:

```
. sampsi 0.5 0.75, power(0.8) onesample
Estimated sample size for one-sample comparison of proportion
  to hypothesized value
Test Ho: p = 0.5000, where p is the proportion in the population
Assumptions:
         alpha =   0.0500  (two-sided)
         power =   0.8000
 alternative p =   0.7500
Estimated required sample size:
             n =       29
```

What is the power if the true proportion of female French students is only 0.6 and the biggest sample of French students we can survey is $n = 200$?

```
. sampsi 0.5 0.6, n(200) onesample
Estimated power for one-sample comparison of proportion
  to hypothesized value
Test Ho: p = 0.5000, where p is the proportion in the population
Assumptions:
         alpha =   0.0500  (two-sided)
 alternative p =   0.6000
 sample size n =      200
Estimated power:
         power =   0.8123
```

◁

❑ Technical note

`r(warning)` is saved only for power calculations for one- and two-sample tests on proportions. If sample sizes are not large enough (Tamhane and Dunlop 2000, 300, 307) for sample proportions to be approximately normally distributed, `r(warning)` is set to 1. Otherwise, a note is displayed in the output, and `r(warning)` is set to 0.

❑

Clinical trials with repeated measures

In randomized controlled trials (RCTs), when comparing a standard treatment with an experimental therapy, it is not unusual for the study design to allow for repeated measurements of the outcome. Typically, one or more measurements are taken at baseline immediately before randomization, and additional measurements are taken at regular intervals during follow-up. Depending on the analysis method planned and the correlations between measurements at different time points, there can be a great increase in efficiency (variance reduction) from such designs over a simple study with only one measurement of the outcome.

Frison and Pocock (1992) discuss three methods used in RCTs to compare two treatments by using a continuous outcome measured at different times on each patient.

Posttreatment means (POST) uses the mean of each patient's follow-up measurements as the summary measurement. It compares the two groups by using a simple t test. This method ignores any baseline measurements.

Mean changes (CHANGE) uses each patient's difference between the mean of the follow-up measurements and the mean of baseline measurements as the summary measurement. It compares the two groups by using a simple t test.

Analysis of covariance (ANCOVA) uses the mean baseline measurement for each patient as a covariate in a linear model for treatment comparisons of follow-up means.

`method()` specifies which of these three analyses is planned to be used. `sampsi` will calculate the decrease in variance of the estimate of treatment effect from the number of measurements at baseline, the number of measurements during follow-up, and the correlations between measurements at different times, and use the calculation to estimate power or sample size, or both.

▷ Example 5

We are designing a clinical trial comparing a new medication for the treatment of angina to a placebo. We are planning on performing an exercise stress test on each patient four times during the study: once at time of treatment randomization and three more times at 4, 6, and 8 weeks after randomization. From each test, we will measure the time in seconds from the beginning of the test until the patient is unable to continue because of angina pain. From a previous pilot study, we estimated the means (`sd#`s) for the new drug and the placebo group to be 498 seconds (20.2) and 485 seconds (19.5), respectively, and an overall correlation at follow-up of 0.7. We will analyze these data by comparing each patient's difference between the mean of posttreatment measurements and the mean of baseline measurements, that is, the change method. To compute the number of subjects needed for allocation to each treatment group for $\alpha = 0.05$ (two-sided) and power of 90%, we issue the following command:

```
. sampsi 498 485, sd1(20.2) sd2(19.5) method(change) pre(1) post(3) r1(.7)

Estimated sample size for two samples with repeated measures

Assumptions:
                                        alpha =   0.0500  (two-sided)
                                        power =   0.9000
                                           m1 =      498
                                           m2 =      485
                                          sd1 =     20.2
                                          sd2 =     19.5
                                        n2/n1 =     1.00
           number of follow-up measurements =        3
 correlation between follow-up measurements =    0.700
            number of baseline measurements =        1
   correlation between baseline & follow-up =    0.700

Method: CHANGE
 relative efficiency =    2.500
    adjustment to sd =    0.632
        adjusted sd1 =   12.776
        adjusted sd2 =   12.333

 Estimated required sample sizes:
                  n1 =       20
                  n2 =       20
```

The output from `sampsi` for repeated measurements includes the specified parameters used to estimate the sample sizes or power, the relative efficiency of the design, and the adjustment to the standard deviation. These last two are the inverse and the square root of the calculated improvement in the variance compared with a similar study where only one measurement is planned.

We see that we need to allocate 20 subjects to each treatment group. Assume that we have funds to enroll only 30 patients into our study. If we randomly assigned 15 patients to each treatment group, what would be the expected power of our study, assuming that all other parameters remain the same?

```
. sampsi 498 485, sd1(20.2) sd2(19.5) meth(change) pre(1) post(3) r1(.7) n1(15)
> n2(15)

Estimated power for two samples with repeated measures

Assumptions:
                                        alpha =   0.0500  (two-sided)
                                           m1 =      498
                                           m2 =      485
                                          sd1 =     20.2
                                          sd2 =     19.5
                                sample size n1 =       15
                                           n2 =       15
                                        n2/n1 =     1.00
           number of follow-up measurements =        3
 correlation between follow-up measurements =    0.700
            number of baseline measurements =        1
   correlation between baseline & follow-up =    0.700

Method: CHANGE
 relative efficiency =    2.500
    adjustment to sd =    0.632
        adjusted sd1 =   12.776
        adjusted sd2 =   12.333

 Estimated power:
              power =    0.809
```

If we enroll 30 patients into our study instead of the recommended 40, the power of the study decreases from 90% to approximately 81%.

◁

Saved results

`sampsi` saves the following in `r()`:

Scalars

`r(N_1)`	sample size n_1
`r(N_2)`	sample size n_2
`r(power)`	power
`r(adj)`	adjustment to the SE
`r(warning)`	0 if assumptions are satisfied and 1 otherwise

Methods and formulas

`sampsi` is implemented as an ado-file.

In the following formulas, α is the significance level, $1-\beta$ is the power, $z_{1-\alpha/2}$ is the $(1-\alpha/2)$ quantile of the normal distribution, and $r = n_2/n_1$ is the ratio of sample sizes. The formulas below are for two-sided tests. The formulas for one-sided tests can be obtained by replacing $z_{1-\alpha/2}$ with $z_{1-\alpha}$.

1. The required sample sizes for a two-sample test of equality of means (assuming normality) are

$$n_1 = \frac{(\sigma_1^2 + \sigma_2^2/r)(z_{1-\alpha/2} + z_{1-\beta})^2}{(\mu_1 - \mu_2)^2}$$

and $n_2 = rn_1$ (Rosner 2006, 332).

2. For a one-sample test of a mean where the null hypothesis is $\mu = \mu_0$ and the alternative hypothesis is $\mu = \mu_{\rm A}$, the required sample size (assuming normality) is

$$n = \left\{ \frac{(z_{1-\alpha/2} + z_{1-\beta})\sigma}{\mu_{\rm A} - \mu_0} \right\}^2$$

(Pagano and Gauvreau 2000, 247–248).

3. The required sample sizes for a two-sample test of equality of proportions (using a normal approximation with a continuity correction) are

$$n_1 = \frac{n'}{4}\left[1 + \left\{1 + \frac{2(r+1)}{n'r\,|\,p_1 - p_2|}\right\}^{1/2}\right]^2$$

$$n_2 = rn_1$$

where

$$n' = \frac{\left[z_{1-\alpha/2}\left\{(r+1)\overline{p}\overline{q}\right\}^{1/2} + z_{1-\beta}\left(rp_1q_1 + p_2q_2\right)^{1/2}\right]^2}{r(p_1 - p_2)^2}$$

and $\overline{p} = (p_1 + rp_2)/(r+1)$ and $\overline{q} = 1 - \overline{p}$ (Fleiss, Levin, and Paik 2003, 76).

Without a continuity correction, the sample sizes are

$$n_1 = n'$$

$$n_2 = rn_1$$

where n' is defined above.

4. For a one-sample test of proportion where the null hypothesis is $p = p_0$ and the alternative hypothesis is $p = p_A$, the required sample size (using a normal approximation) is

$$n = \left[\frac{z_{1-\alpha/2}\{p_0(1-p_0)\}^{1/2} + z_{1-\beta}\{p_A(1-p_A)\}^{1/2}}{p_A - p_0} \right]^2$$

(Pagano and Gauvreau 2000, 332).

5. For repeated measurements, Frison and Pocock (1992) discuss three methods for use in randomized clinical trials to compare two treatments using a continuous outcome measured at different times on each patient. Each uses the average of baseline measurements, $\overline{x}_0$, and follow-up measurements, $\overline{x}_1$:

POST outcome is $\overline{x}_1$, where the analysis is by simple t test.

CHANGE outcome is $\overline{x}_1 - \overline{x}_0$, where the analysis is by simple t test.

ANCOVA outcome is $\overline{x}_1 - \beta\overline{x}_0$, where the β is estimated by analysis of covariance, correcting for the average at baseline.

ANCOVA will always be the most efficient of the three approaches. β is set so that $\beta\overline{x}_0$ accounts for the largest possible variation of $\overline{x}_1$.

For a study with one measurement each at baseline and follow-up, CHANGE will be more efficient than POST, provided that the correlation between measurements at baseline and measurements at follow-up is more than 0.5. POST ignores all baseline measurements, which tends to make it unpopular. CHANGE is the method most commonly used. With more than one baseline measurement, CHANGE and ANCOVA tend to produce similar sample sizes and power.

The improvements in variance of the estimate of treatment effect over a study with only one measurement depend on the number of measurements p at baseline; the number of measurements during follow-up; and the correlations between measurements at baseline $\overline{\rho}_{\text{pre}}$, between measurements at follow-up $\overline{\rho}_{\text{post}}$, and between measurements at baseline and measurements at follow-up $\overline{\rho}_{\text{mix}}$. The improvements in variance for the POST method are given by

$$\frac{1 + (r-1)\overline{\rho}_{\text{post}}}{r}$$

for the CHANGE method by

$$\frac{1 + (r-1)\overline{\rho}_{\text{post}}}{r} + \frac{1 + (p-1)\overline{\rho}_{\text{pre}}}{p} - 2\overline{\rho}_{\text{mix}}$$

and for the ANCOVA method by

$$\frac{1 + (r-1)\overline{\rho}_{\text{post}}}{r} - \frac{\overline{\rho}^2_{\text{mix}} p}{1 + (p-1)\overline{\rho}_{\text{pre}}}$$

Often the three correlations are assumed equal. In data from several trials, Frison and Pocock found that $\overline{\rho}_{\text{pre}}$ and $\overline{\rho}_{\text{post}}$ typically had values around 0.7, whereas $\overline{\rho}_{\text{mix}}$ was nearer 0.5. This finding is consistent with the common finding that measurements closer in time are more strongly correlated.

Power calculations are based on estimates of one variance at all time points.

Acknowledgments

`sampsi` is based on the `sampsiz` command written by Joseph Hilbe of Arizona State University (Hilbe 1993). Paul Seed of Maternal and Fetal Research Unit, St. Thomas' Hospital (Seed 1997, 1998), expanded the command to allow for repeated measurements.

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Also see

[ST] **stpower** — Sample-size, power, and effect-size determination for survival analysis

Title

saved results — Saved results

Syntax

List results from general commands, stored in r()

```
return list [ , all ]
```

List results from estimation commands, stored in e()

```
ereturn list [ , all ]
```

List results from parsing commands, stored in s()

```
sreturn list
```

Description

Results of calculations are saved by many Stata commands so that they can be easily accessed and substituted into later commands.

`return list` lists results stored in `r()`.

`ereturn list` lists results stored in `e()`.

`sreturn list` lists results stored in `s()`.

This entry discusses using saved results. Programmers wishing to save results should see [P] **return** and [P] **ereturn**.

Option

`all` is for use with `return list` and `ereturn list`. `all` specifies that hidden and historical saved results be listed along with the usual saved results. This option is seldom used. See *Using hidden and historical saved results* and *Programming hidden and historical saved results* under *Remarks* of [P] **return** for more information. These sections are written in terms of `return list`, but everything said there applies equally to `ereturn list`.

`all` is not allowed with `sreturn list` because `s()` does not allow hidden or historical results.

Remarks

Stata commands are classified as being

r-class	general commands that save results in `r()`
e-class	estimation commands that save results in `e()`
s-class	parsing commands that save results in `s()`
n-class	commands that do not save in `r()`, `e()`, or `s()`

There is also a c-class, `c()`, containing the values of system parameters and settings, along with certain constants, such as the value of pi; see [P] **creturn**. A program, however, cannot be c-class.

You can look at the *Saved results* section of the manual entry of a command to determine whether it is r-, e-, s-, or n-class, but it is easy enough to guess.

Commands producing statistical results are either r-class or e-class. They are e-class if they present estimation results and r-class otherwise. s-class is a class used by programmers and is primarily used in subprograms performing parsing. n-class commands explicitly state where the result is to go. For instance, `generate` and `replace` are n-class because their syntax is `generate` *varname* `=` ... and `replace` *varname* `=` ....

After executing a command, you can type `return list`, `ereturn list`, or `sreturn list` to see what has been saved.

▷ Example 1

```
. use http://www.stata-press.com/data/r12/auto4
(1978 Automobile Data)
. describe
Contains data from http://www.stata-press.com/data/r12/auto4.dta
  obs:            74                          1978 Automobile Data
 vars:             6                          6 Apr 2011 00:20
 size:         2,072
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
price           int    %8.0gc                 Price
weight          int    %8.0gc                 Weight (lbs.)
mpg             int    %8.0g                  Mileage (mpg)
make            str18  %-18s                  Make and Model
length          int    %8.0g                  Length (in.)
rep78           int    %8.0g                  Repair Record 1978
-------------------------------------------------------------------------------
Sorted by:
. return list
scalars:
            r(changed) =  0
              r(width) =  28
                  r(k) =  6
                  r(N) =  74
```

To view all saved results, including those that are historical or hidden, specify the `all` option.

```
. return list, all
scalars:
            r(changed) =  0
              r(width) =  28
                  r(k) =  6
                  r(N) =  74
Historical; used before Stata 12, may exist only under version control
scalars:
           r(widthmax) =  1048576
              r(k_max) =  2048
              r(N_max) =  2147483647
```

`r(widthmax)`, `r(k_max)`, and `r(N_max)` are historical saved results. They are no longer relevant because Stata dynamically adjusts memory beginning with Stata 12.

◁

❑ Technical note

In the above example, we stated that `r(widthmax)` and `r(N_max)` are no longer relevant. In fact, they are not useful. Stata no longer has a fixed memory size, so the methods used to calculate `r(widthmax)` and `r(N_max)` are no longer appropriate.

❑

▷ Example 2

You can use saved results in expressions.

```
. summarize mpg
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         mpg |         74     21.2973    5.785503         12         41

. return list
scalars:
                  r(N) =  74
              r(sum_w) =  74
               r(mean) =  21.2972972972973
                r(Var) =  33.47204738985561
                 r(sd) =  5.785503209735141
                r(min) =  12
                r(max) =  41
                r(sum) =  1576

. generate double mpgstd = (mpg-r(mean))/r(sd)

. summarize mpgstd
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      mpgstd |         74   -1.64e-16           1  -1.606999    3.40553
```

Be careful to use results stored in `r()` soon because they will be replaced the next time you execute another r-class command. For instance, although `r(mean)` was 21.3 (approximately) after `summarize mpg`, it is −1.64e–16 now because you just ran `summarize` with `mpgstd`.

◁

▷ Example 3

e-class is really no different from r-class, except for where results are stored and that, when an estimation command stores results, it tends to store a lot of them:

```
. regress mpg weight length
  (output omitted)
. ereturn list
scalars:
                  e(N) =  74
               e(df_m) =  2
               e(df_r) =  71
                  e(F) =  69.34050004300227
                 e(r2) =  .6613903979336323
               e(rmse) =  3.413681741382589
                e(mss) =  1616.08062422659
                e(rss) =  827.3788352328695
               e(r2_a) =  .6518520992838754
                 e(ll) =  -194.3267619410807
               e(ll_0) =  -234.3943376482347
               e(rank) =  3
```

```
macros:
             e(cmdline) : "regress mpg weight length"
               e(title) : "Linear regression"
          e(marginsok) : "XB default"
                e(vce) : "ols"
             e(depvar) : "mpg"
                e(cmd) : "regress"
         e(properties) : "b V"
            e(predict) : "regres_p"
              e(model) : "ols"
          e(estat_cmd) : "regress_estat"
matrices:
                  e(b) :  1 x 3
                  e(V) :  3 x 3
functions:
              e(sample)
```

These e-class results will stick around until you run another estimation command. Typing `return list` and `ereturn list` is the easy way to find out what a command stores.

◁

Both r- and e-class results come in four flavors: scalars, macros, matrices, and functions. (s-class results come in only one flavor—macros—and as earlier noted, s-class is used solely by programmers, so ignore it.)

Scalars are just that—numbers by any other name. You can subsequently refer to `r(mean)` or `e(rmse)` in numeric expressions and obtain the result to full precision.

Macros are strings. For instance, `e(depvar)` contains "`mpg`". You can refer to it, too, in subsequent expressions, but really that would be of most use to programmers, who will refer to it using constructs like `"‘e(depvar)’"`. In any case, macros are macros, and you obtain their contents just as you would a local macro, by enclosing their name in single quotes. The name here is the full name, so `‘e(depvar)’` is `mpg`.

Matrices are matrices, and all estimation commands store `e(b)` and `e(V)` containing the coefficient vector and variance–covariance matrix of the estimates (VCE).

Functions are saved by e-class commands only, and the only function existing is `e(sample)`. `e(sample)` evaluates to 1 (meaning true) if the observation was used in the previous estimation and to 0 (meaning false) otherwise.

❑ Technical note

Say that some command set `r(scalar)` and `r(macro)`, the first being stored as a scalar and the second as a macro. In theory, in subsequent use you are supposed to refer to `r(scalar)` and `‘r(macro)’`. In fact, however, you can refer to either one with or without quotes, so you could refer to `‘r(scalar)’` and `r(macro)`. Programmers sometimes do this.

When you refer to `r(scalar)`, you are referring to the full double-precision saved result. Think of `r(scalar)` without quotes as a function returning the value of the saved result `scalar`. When you refer to `r(scalar)` in quotes, Stata understands `‘r(scalar)’` to mean "substitute the printed result of evaluating `r(scalar)`". Pretend that `r(scalar)` equals the number 23. Then `‘r(scalar)’` is `23`, the character `2` followed by `3`.

Referring to `r(scalar)` in quotes is sometimes useful. Say that you want to use the immediate command `ci` with `r(scalar)`. The immediate command `ci` requires its arguments to be numbers—numeric literals in programmer's jargon—and it will not take an expression. Thus you could not type

‘ci r(scalar) ...’. You could, however, type ‘ci ‘r(scalar)’ ...’ because ‘r(scalar)’ is just a numeric literal.

For r(macro), you are supposed to refer to it in quotes: ‘r(macro)’. If, however, you omit the quotes in an expression context, Stata evaluates the macro and then pretends that it is the result of function-returning-string. There are side effects of this, the most important being that the result is trimmed to 80 characters.

Referring to r(macro) without quotes is never a good idea; the feature was included merely for completeness.

You can even refer to r(matrix) in quotes (assume that r(matrix) is a matrix). ‘r(matrix)’ does not result in the matrix being substituted; it returns the word matrix. Programmers sometimes find that useful.

❑

References

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Also see

[P] **ereturn** — Post the estimation results

[P] **return** — Return saved results

[U] **18.8 Accessing results calculated by other programs**

[U] **18.9 Accessing results calculated by estimation commands**

Title

scobit — Skewed logistic regression

Syntax

`scobit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`asis`	retain perfect predictor variables
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`or`	report odds ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Binary outcomes > Skewed logit regression

Description

scobit fits a maximum-likelihood skewed logit model.

See [R] **logistic** for a list of related estimation commands.

Options

Model

noconstant, offset(*varname*), constraints(*constraints*), collinear; see [R] **estimation options**.

asis forces retention of perfect predictor variables and their associated perfectly predicted observations and may produce instabilities in maximization; see [R] **probit**.

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

level(#); see [R] **estimation options**.

or reports the estimated coefficients transformed to odds ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. or may be specified at estimation or when replaying previously estimated results.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with scobit but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Skewed logistic model
Robust standard errors

Skewed logistic model

`scobit` fits maximum likelihood models with dichotomous dependent variables coded as 0/1 (or, more precisely, coded as 0 and not 0).

▷ Example 1

We have data on the make, weight, and mileage rating of 22 foreign and 52 domestic automobiles. We wish to fit a model explaining whether a car is foreign based on its mileage. Here is an overview of our data:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. keep make mpg weight foreign
. describe
Contains data from http://www.stata-press.com/data/r12/auto.dta
  obs:            74                          1978 Automobile Data
 vars:             4                          13 Apr 2011 17:45
 size:         1,702                          (_dta has notes)
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
make            str18  %-18s                  Make and Model
mpg             int    %8.0g                  Mileage (mpg)
weight          int    %8.0gc                 Weight (lbs.)
foreign         byte   %8.0g       origin     Car type
-------------------------------------------------------------------------------
Sorted by:  foreign
     Note:  dataset has changed since last saved
. inspect foreign
foreign:  Car type                              Number of Observations
-----------------------                    ------------------------------
                                                Total   Integers   Nonintegers
|   #                       Negative              -          -          -
|   #                       Zero                 52         52          -
|   #                       Positive             22         22          -
|   #                                          -----      -----      -----
|   #   #                   Total                74         74          -
|   #   #                   Missing               -
+-----------------------                     -----
0                       1                       74
   (2 unique values)
      foreign is labeled and all values are documented in the label.
```

The variable `foreign` takes on two unique values, 0 and 1. The value 0 denotes a domestic car, and 1 denotes a foreign car.

The model that we wish to fit is

$$\Pr(\texttt{foreign} = 1) = F(\beta_0 + \beta_1 \texttt{mpg})$$

where $F(z) = 1 - 1/\{1 + \exp(z)\}^{\alpha}$.

To fit this model, we type

```
. scobit foreign mpg
Fitting logistic model:
Iteration 0:   log likelihood =  -45.03321
Iteration 1:   log likelihood = -39.380959
Iteration 2:   log likelihood = -39.288802
Iteration 3:   log likelihood =  -39.28864
Iteration 4:   log likelihood =  -39.28864
Fitting full model:
Iteration 0:   log likelihood =  -39.28864
Iteration 1:   log likelihood = -39.286393
Iteration 2:   log likelihood = -39.284415
Iteration 3:   log likelihood = -39.284234
Iteration 4:   log likelihood = -39.284197
Iteration 5:   log likelihood = -39.284196
Skewed logistic regression                      Number of obs     =         74
                                                Zero outcomes     =         52
Log likelihood =  -39.2842                      Nonzero outcomes  =         22
------------------------------------------------------------------------------
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         mpg |   .1813879   .2407362     0.75   0.451    -.2904463    .6532222
       _cons |  -4.274883   1.399305    -3.06   0.002    -7.017471   -1.532295
-------------+----------------------------------------------------------------
    /lnalpha |  -.4450405   3.879885    -0.11   0.909    -8.049476    7.159395
-------------+----------------------------------------------------------------
       alpha |   .6407983   2.486224                      .0003193    1286.133
------------------------------------------------------------------------------
Likelihood-ratio test of alpha=1:   chi2(1) =     0.01    Prob > chi2 = 0.9249
Note: likelihood-ratio tests are recommended for inference with scobit models.
```

We find that cars yielding better gas mileage are less likely to be foreign. The likelihood-ratio test at the bottom of the output indicates that the model is not significantly different from a logit model. Therefore, we should use the more parsimonious model.

◁

❑ Technical note

Stata interprets a value of 0 as a negative outcome (failure) and treats all other values (except missing) as positive outcomes (successes). Thus if the dependent variable takes on the values 0 and 1, then 0 is interpreted as failure and 1 as success. If the dependent variable takes on the values 0, 1, and 2, then 0 is still interpreted as failure, but both 1 and 2 are treated as successes.

Formally, when we type `scobit` y x, Stata fits the model

$$\Pr(y_j \neq 0 \mid \mathbf{x}_j) = 1 - 1\Big/\Big\{1 + \exp(\mathbf{x}_j\boldsymbol{\beta})\Big\}^{\alpha}$$

❑

Robust standard errors

If you specify the `vce(robust)` option, `scobit` reports robust standard errors as described in [U] **20.20 Obtaining robust variance estimates**. For the model of `foreign` on `mpg`, the robust calculation increases the standard error of the coefficient on `mpg` by around 25%:

```
. scobit foreign mpg, vce(robust) nolog
Skewed logistic regression                      Number of obs     =         74
                                                Zero outcomes     =         52
Log pseudolikelihood =  -39.2842                Nonzero outcomes  =         22

------------------------------------------------------------------------------
             |               Robust
     foreign |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         mpg |   .1813879   .3028487     0.60   0.549    -.4121847    .7749606
       _cons |  -4.274883   1.335521    -3.20   0.001    -6.892455   -1.657311
-------------+----------------------------------------------------------------
    /lnalpha |  -.4450405    4.71561    -0.09   0.925    -9.687466    8.797385
-------------+----------------------------------------------------------------
       alpha |   .6407983   3.021755                      .0000621    6616.919
------------------------------------------------------------------------------
```

Without `vce(robust)`, the standard error for the coefficient on `mpg` was reported to be 0.241, with a resulting confidence interval of $[-0.29, 0.65]$.

Specifying the `vce(cluster` *clustvar*`)` option relaxes the independence assumption required by the skewed logit estimator to being just independence between clusters. To demonstrate this, we will switch to a different dataset.

▷ Example 2

We are studying the unionization of women in the United States and have a dataset with 26,200 observations on 4,434 women between 1970 and 1988. For our purposes, we will use the variables `age` (the women were 14–26 in 1968 and the data thus span the age range of 16–46), `grade` (years of schooling completed, ranging from 0 to 18), `not_smsa` (28% of the person-time was spent living outside an SMSA—standard metropolitan statistical area), `south` (41% of the person-time was in the South), and `year`. Each of these variables is included in the regression as a covariate along with the interaction between `south` and `year`. This interaction, along with the `south` and `year` variables, is specified in the `scobit` command using factor-variables notation, `south##c.year`. We also have variable `union`. Overall, 22% of the person-time is marked as time under union membership and 44% of these women have belonged to a union.

We fit the following model, ignoring that women are observed an average of 5.9 times each in these data:

```
. use http://www.stata-press.com/data/r12/union, clear
(NLS Women 14-24 in 1968)
. scobit union age grade not_smsa south##c.year, nrtol(1e-3)
  (output omitted)
Skewed logistic regression                      Number of obs     =      26200
                                                Zero outcomes     =      20389
Log likelihood = -13540.61                      Nonzero outcomes  =       5811
```

union	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.0185365	.0043615	4.25	0.000	.0099881	.0270849
grade	.0452803	.0057124	7.93	0.000	.0340842	.0564764
not_smsa	-.1886849	.0317802	-5.94	0.000	-.250973	-.1263968
1.south	-1.422381	.3949298	-3.60	0.000	-2.196429	-.6483327
year	-.0133017	.0049575	-2.68	0.007	-.0230182	-.0035853
south#c.year						
1	.0105663	.0049233	2.15	0.032	.0009168	.0202158
_cons	-10.19247	63.69015	-0.16	0.873	-135.0229	114.6379
/lnalpha	8.972796	63.68825	0.14	0.888	-115.8539	133.7995
alpha	7885.616	502221.1			4.85e-51	1.28e+58

```
Likelihood-ratio test of alpha=1:   chi2(1) =     3.76   Prob > chi2 = 0.0524
Note: likelihood-ratio tests are recommended for inference with scobit models.
```

The reported standard errors in this model are probably meaningless. Women are observed repeatedly, so the observations are not independent. Looking at the coefficients, we find a large southern effect against unionization and a different time trend for the south. The `vce(cluster` *clustvar*`)` option provides a way to fit this model and obtains correct standard errors:

```
. scobit union age grade not_smsa south##c.year, vce(cluster id) nrtol(1e-3)
  (output omitted)
Skewed logistic regression                      Number of obs     =      26200
                                                Zero outcomes     =      20389
Log pseudolikelihood = -13540.61                Nonzero outcomes  =       5811
                                (Std. Err. adjusted for 4434 clusters in idcode)
```

union	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.0185365	.0084867	2.18	0.029	.0019029	.0351701
grade	.0452803	.0125764	3.60	0.000	.0206311	.0699296
not_smsa	-.1886849	.0642035	-2.94	0.003	-.3145214	-.0628484
1.south	-1.422381	.5064916	-2.81	0.005	-2.415086	-.4296756
year	-.0133017	.0090621	-1.47	0.142	-.0310632	.0044597
south#c.year						
1	.0105663	.0063172	1.67	0.094	-.0018152	.0229478
_cons	-10.19247	.9458356	-10.78	0.000	-12.04627	-8.338666
/lnalpha	8.972796	.7483321	11.99	0.000	7.506092	10.4395
alpha	7885.616	5901.06			1819.09	34183.54

`scobit, vce(cluster` *clustvar*`)` is robust to assumptions about within-cluster correlation. That is, it inefficiently sums within cluster for the standard error calculation rather than attempting to exploit what might be assumed about the within-cluster correlation (as do the `xtgee` population-averaged models; see [XT] **xtgee**).

◁

❑ Technical note

The scobit model can be difficult to fit because of the functional form. Often it requires many iterations, or the optimizer prints out warning and informative messages during the optimization. For example, without the `nrtol(1e-3)` option, the model using the `union` dataset will not converge. See [R] **maximize** for details about the optimizer.

❑

❑ Technical note

The main reason for using `scobit` rather that `logit` is that the effects of the regressors on the probability of success are not constrained to be the largest when the probability is 0.5. Rather, the independent variables might show their largest impact when the probability of success is 0.3 or 0.6. This added flexibility results because the scobit function, unlike the logit function, can be skewed and is not constrained to be mirror symmetric about the 0.5 probability of success.

As Nagler (1994) pointed out, the point of maximum impact is constrained under the scobit model to fall within the interval $(0, 1 - e^{(-1)})$ or approximately (0, 0.63). Achen (2002) notes that if we believe the maximum impact to be outside that range, we can instead estimate the "power logit" model by simply reversing the 0s and 1s of our outcome variable and estimating a scobit model on failure, rather than success. We would need to reverse the signs of the coefficients if we wanted to interpret them in terms of impact on success, or we could leave them as they are and interpret them in terms of impact on failure. The important thing to remember is that the scobit model, unlike the logit model, is not invariant to the choice of which result is assigned to success.

❑

Saved results

scobit saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_aux)	number of auxiliary parameters
e(k_dv)	number of dependent variables
e(ll)	log likelihood
e(ll_c)	log likelihood, comparison model
e(N_f)	number of failures (zero outcomes)
e(N_s)	number of successes (nonzero outcomes)
e(alpha)	alpha
e(N_clust)	number of clusters
e(chi2)	χ^2
e(chi2_c)	χ^2 for comparison test
e(p)	significance
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	scobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(footnote)	program used to implement the footnote display
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`scobit` is implemented as an ado-file.

Skewed logit analysis is an alternative to logit that relaxes the assumption that individuals with initial probability of 0.5 are most sensitive to changes in independent variables.

The log-likelihood function for skewed logit is

$$\ln L = \sum_{j \in S} w_j \ln F(\mathbf{x}_j\mathbf{b}) + \sum_{j \notin S} w_j \ln\{1 - F(\mathbf{x}_j\mathbf{b})\}$$

where S is the set of all observations j such that $y_j \neq 0$, $F(z) = 1 - 1/\{1 + \exp(z)\}^{\alpha}$, and w_j denotes the optional weights. $\ln L$ is maximized as described in [R] **maximize**.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`scobit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

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Nagler, J. 1994. Scobit: An alternative estimator to logit and probit. *American Journal of Political Science* 38: 230–255.

Also see

[R] **scobit postestimation** — Postestimation tools for scobit

[R] **cloglog** — Complementary log-log regression

[R] **glm** — Generalized linear models

[R] **logistic** — Logistic regression, reporting odds ratios

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

scobit postestimation — Postestimation tools for scobit

Description

The following postestimation commands are available after `scobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat (svy)`.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` *statistic* `nooffset`]

`predict` [*type*] { *stub*`*` | *newvar*$_{\text{reg}}$ *newvar*$_{\text{lnalpha}}$ } [*if*] [*in*] `, scores`

statistic	Description
Main	
`pr`	probability of a positive outcome; the default
`xb`	$\mathbf{x}_j\mathbf{b}$, linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of a positive outcome.

`xb` calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

`nooffset` is relevant only if you specified `offset(`*varname*`)` for `scobit`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial \ln\alpha$.

Remarks

Once you have fit a model, you can obtain the predicted probabilities by using the `predict` command for both the estimation sample and other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**. Here we will make only a few additional comments.

`predict` without arguments calculates the predicted probability of a positive outcome. With the `xb` option, it calculates the linear combination $\mathbf{x}_j\mathbf{b}$, where $\mathbf{x}_j$ are the independent variables in the jth observation and $\mathbf{b}$ is the estimated parameter vector.

With the `stdp` option, `predict` calculates the standard error of the prediction, which is *not* adjusted for replicated covariate patterns in the data.

▷ Example 1

In example 1 of [R] **scobit**, we fit the model `scobit foreign mpg`. To obtain predicted probabilities, we type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. keep make mpg weight foreign
. scobit foreign mpg
  (output omitted)
. predict p
(option pr assumed; Pr(foreign))
. summarize foreign p
```

Variable	Obs	Mean	Std. Dev.	Min	Max
foreign	74	.2972973	.4601885	0	1
p	74	.2974049	.182352	.0714664	.871624

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **scobit** — Skewed logistic regression

[U] **20 Estimation and postestimation commands**

Title

sdtest — Variance-comparison tests

Syntax

One-sample variance-comparison test

```
sdtest varname == # [ if ] [ in ] [ , level(#) ]
```

Two-sample variance-comparison test

```
sdtest varname1 == varname2 [ if ] [ in ] [ , level(#) ]
```

Two-group variance-comparison test

```
sdtest varname [ if ] [ in ] , by(groupvar) [ level(#) ]
```

Immediate form of one-sample variance-comparison test

```
sdtesti #obs { #mean | . } #sd #val [ , level(#) ]
```

Immediate form of two-sample variance-comparison test

```
sdtesti #obs,1 { #mean,1 | . } #sd,1 #obs,2 { #mean,2 | . } #sd,2 [ , level(#) ]
```

Robust tests for equality of variances

```
robvar varname [ if ] [ in ] , by(groupvar)
```

`by` is allowed with `sdtest` and `robvar`; see [D] **by**.

Menu

one-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > One-sample variance-comparison test

two-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-sample variance-comparison test

two-group

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-group variance-comparison test

immediate command: one-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > One-sample variance-comparison calculator

immediate command: two-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-sample variance-comparison calculator

robvar

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Robust equal-variance test

Description

`sdtest` performs tests on the equality of standard deviations (variances). In the first form, `sdtest` tests that the standard deviation of *varname* is #. In the second form, `sdtest` tests that *varname*$_1$ and *varname*$_2$ have the same standard deviation. In the third form, `sdtest` performs the same test, using the standard deviations of the two groups defined by *groupvar*.

`sdtesti` is the immediate form of `sdtest`; see [U] **19 Immediate commands**.

Both the traditional F test for the homogeneity of variances and Bartlett's generalization of this test to K samples are sensitive to the assumption that the data are drawn from an underlying Gaussian distribution. See, for example, the cautionary results discussed by Markowski and Markowski (1990). Levene (1960) proposed a test statistic for equality of variance that was found to be robust under nonnormality. Then Brown and Forsythe (1974) proposed alternative formulations of Levene's test statistic that use more robust estimators of central tendency in place of the mean. These reformulations were demonstrated to be more robust than Levene's test when dealing with skewed populations.

`robvar` reports Levene's robust test statistic (W_0) for the equality of variances between the groups defined by *groupvar* and the two statistics proposed by Brown and Forsythe that replace the mean in Levene's formula with alternative location estimators. The first alternative (W_{50}) replaces the mean with the median. The second alternative replaces the mean with the 10% trimmed mean (W_{10}).

Options

`level(#)` specifies the confidence level, as a percentage, for confidence intervals of the means. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

`by(`*groupvar*`)` specifies the *groupvar* that defines the groups to be compared. For `sdtest`, there should be two groups, but for `robvar` there may be more than two groups. Do not confuse the `by()` option with the `by` prefix; both may be specified.

Remarks

Remarks are presented under the following headings:

Basic form
Immediate form
Robust test

Basic form

`sdtest` performs two different statistical tests: one testing equality of variances and the other testing that the standard deviation is equal to a known constant. Which test it performs is determined by whether you type a variable name or a number to the right of the equal sign.

▷ Example 1: One-sample test of variance

We have a sample of 74 automobiles. For each automobile, we know the mileage rating. We wish to test whether the overall standard deviation is 5 mpg:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. sdtest mpg == 5
One-sample test of variance
```

Variable	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
mpg	74	21.2973	.6725511	5.785503	19.9569	22.63769

```
    sd = sd(mpg)                                     c = chi2 =  97.7384
Ho: sd = 5                                 degrees of freedom =       73
     Ha: sd < 5                  Ha: sd != 5                 Ha: sd > 5
  Pr(C < c) = 0.9717         2*Pr(C > c) = 0.0565          Pr(C > c) = 0.0283
```

◁

▷ Example 2: Variance ratio test

We are testing the effectiveness of a new fuel additive. We run an experiment on 12 cars, running each without and with the additive. The data can be found in [R] **ttest**. The results for each car are stored in the variables `mpg1` and `mpg2`:

```
. use http://www.stata-press.com/data/r12/fuel
. sdtest mpg1==mpg2
Variance ratio test
```

Variable	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
mpg1	12	21	.7881701	2.730301	19.26525	22.73475
mpg2	12	22.75	.9384465	3.250874	20.68449	24.81551
combined	24	21.875	.6264476	3.068954	20.57909	23.17091

```
    ratio = sd(mpg1) / sd(mpg2)                          f =   0.7054
Ho: ratio = 1                              degrees of freedom =   11, 11
    Ha: ratio < 1               Ha: ratio != 1                 Ha: ratio > 1
  Pr(F < f) = 0.2862         2*Pr(F < f) = 0.5725           Pr(F > f) = 0.7138
```

We cannot reject the hypothesis that the standard deviations are the same.

In [R] **ttest**, we draw an important distinction between paired and unpaired data, which, in this example, means whether there are 12 cars in a before-and-after experiment or 24 different cars. For `sdtest`, on the other hand, there is no distinction. If the data had been unpaired and stored as described in [R] **ttest**, we could have typed `sdtest mpg, by(treated)`, and the results would have been the same.

◁

Immediate form

▷ Example 3: sdtesti

Immediate commands are used not with data, but with reported summary statistics. For instance, to test whether a variable on which we have 75 observations and a reported standard deviation of 6.5 comes from a population with underlying standard deviation 6, we would type

```
. sdtesti 75 . 6.5 6
One-sample test of variance
```

	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf. Interval]
x	75	.	.7505553	6.5	. .

```
    sd = sd(x)                                     c = chi2 =  86.8472
Ho: sd = 6                         degrees of freedom =       74

     Ha: sd < 6                  Ha: sd != 6                 Ha: sd > 6
  Pr(C < c) = 0.8542         2*Pr(C > c) = 0.2916         Pr(C > c) = 0.1458
```

The mean plays no role in the calculation, so it may be omitted.

To test whether the variable comes from a population with the same standard deviation as another for which we have a calculated standard deviation of 7.5 over 65 observations, we would type

```
. sdtesti 75 . 6.5  65 . 7.5
Variance ratio test
```

	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf. Interval]
x	75	.	.7505553	6.5	. .
y	65	.	.9302605	7.5	. .
combined	140	.	.	.	. .

```
    ratio = sd(x) / sd(y)                              f =   0.7511
Ho: ratio = 1                      degrees of freedom =   74, 64

    Ha: ratio < 1               Ha: ratio != 1                 Ha: ratio > 1
  Pr(F < f) = 0.1172         2*Pr(F < f) = 0.2344         Pr(F > f) = 0.8828
```

◁

Robust test

▷ Example 4: robvar

We wish to test whether the standard deviation of the length of stay for patients hospitalized for a given medical procedure differs by gender. Our data consist of observations on the length of hospital stay for 1778 patients: 884 males and 894 females. Length of stay, `lengthstay`, is highly skewed (skewness coefficient = 4.912591) and thus violates Bartlett's normality assumption. Therefore, we use `robvar` to compare the variances.

```
. use http://www.stata-press.com/data/r12/stay
. robvar lengthstay, by(sex)
```

sex	Summary of Length of stay in days Mean	Std. Dev.	Freq.
male	9.0874434	9.7884747	884
female	8.800671	9.1081478	894
Total	8.9432508	9.4509466	1778

```
W0  = .55505315   df(1, 1776)     Pr > F = .45635888
W50 = .42714734   df(1, 1776)     Pr > F = .51347664
W10 = .44577674   df(1, 1776)     Pr > F = .50443411
```

For these data, we cannot reject the null hypothesis that the variances are equal. However, Bartlett's test yields a significance probability of 0.0319 because of the pronounced skewness of the data. ◁

❑ Technical note

`robvar` implements both the conventional Levene's test centered at the mean and a median-centered test. In a simulation study, Conover, Johnson, and Johnson (1981) compare the properties of the two tests and recommend using the median test for asymmetric data, although for small sample sizes the test is somewhat conservative. See Carroll and Schneider (1985) for an explanation of why both mean- and median-centered tests have approximately the same level for symmetric distributions, but for asymmetric distributions the median test is closer to the correct level. ❑

Saved results

`sdtest` and `sdtesti` save the following in `r()`:

Scalars

`r(N)`	number of observations
`r(p_l)`	lower one-sided p-value
`r(p_u)`	upper one-sided p-value
`r(p)`	two-sided p-value
`r(F)`	F statistic
`r(sd)`	standard deviation
`r(sd_1)`	standard deviation for first variable
`r(sd_2)`	standard deviation for second variable
`r(df)`	degrees of freedom
`r(df_1)`	numerator degrees of freedom
`r(df_2)`	denominator degrees of freedom
`r(chi2)`	χ^2

`robvar` saves the following in `r()`:

Scalars

`r(N)`	number of observations
`r(w50)`	Brown and Forsythe's F statistic (median)
`r(p_w50)`	Brown and Forsythe's p-value
`r(w0)`	Levene's F statistic
`r(p_w0)`	Levene's p-value
`r(w10)`	Brown and Forsythe's F statistic (trimmed mean)
`r(p_w10)`	Brown and Forsythe's p-value (trimmed mean)
`r(df_1)`	numerator degrees of freedom
`r(df_2)`	denominator degrees of freedom

Methods and formulas

`sdtest`, `sdtesti`, and `robvar` are implemented as ado-files.

See Armitage et al. (2002, 149–153) or Bland (2000, 171–172) for an introduction and explanation of the calculation of these tests.

The test for $\sigma = \sigma_0$ is given by

$$\chi^2 = \frac{(n-1)s^2}{\sigma_0^2}$$

which is distributed as χ^2 with $n-1$ degrees of freedom.

The test for $\sigma_x^2 = \sigma_y^2$ is given by

$$F = \frac{s_x^2}{s_y^2}$$

which is distributed as F with $n_x - 1$ and $n_y - 1$ degrees of freedom.

`robvar` is also implemented as an ado-file.

Let X_{ij} be the jth observation of X for the ith group. Let $Z_{ij} = |X_{ij} - \overline{X}_i|$, where $\overline{X}_i$ is the mean of X in the ith group. Levene's test statistic is

$$W_0 = \frac{\sum_i n_i(\overline{Z}_i - \overline{Z})^2/(g-1)}{\sum_i \sum_j (Z_{ij} - \overline{Z}_i)^2 / \sum_i (n_i - 1)}$$

where n_i is the number of observations in group i and g is the number of groups. W_{50} is obtained by replacing $\overline{X}_i$ with the ith group median of X_{ij}, whereas W_{10} is obtained by replacing $\overline{X}_i$ with the 10% trimmed mean for group i.

References

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Also see

[R] **ttest** — Mean-comparison tests

Title

search — Search Stata documentation

Syntax

`search` *word* [*word* ...] [`,` *search_options*]

`set searchdefault` {`local`|`net`|`all`} [`,` `permanently`]

`findit` *word* [*word* ...]

search_options	Description
`local`	search using Stata's keyword database; the default
`net`	search across materials available via Stata's `net` command
`all`	search across both the local keyword database and the `net` material
`author`	search by author's name
`entry`	search by entry ID
`exact`	search across both the local keyword database and the `net` materials; prevents matching on abbreviations
`faq`	search the FAQs posted to the Stata website
`historical`	search entries that are of historical interest only
`or`	list an entry if *any* of the words typed after `search` are associated with the entry
`manual`	search the entries in the *Stata Documentation*
`sj`	search the entries in the *Stata Journal* and the STB

Menu

Help > Search...

Description

`search` searches a keyword database and the Internet.

Capitalization of the words following `search` is irrelevant, as is the inclusion or exclusion of special characters such as commas and hyphens.

`set searchdefault` affects the default behavior of the `search` command. `local` is the default.

`findit` is equivalent to `search` *word* [*word* ...]`, all`. `findit` results are displayed in the Viewer. `findit` is the best way to search for information on a topic across all sources, including the online help, the FAQs at the Stata website, the *Stata Journal*, and all Stata-related Internet sources including user-written additions. From `findit`, you can click to go to a source or to install additions.

See [R] **hsearch** for a command that searches help files.

Options for search

`local`, the default (unless changed by `set searchdefault`), specifies that the search be performed using only Stata's keyword database.

`net` specifies that the search be performed across the materials available via Stata's `net` command. Using `search` *word* [*word* ...]`,` `net` is equivalent to typing `net search` *word* [*word* ...] (without options); see [R] **net search**.

`all` specifies that the search be performed across both the local keyword database and the `net` materials.

`author` specifies that the search be performed on the basis of author's name rather than keywords. A search with the `author` option is performed on the local keyword database only.

`entry` specifies that the search be performed on the basis of entry IDs rather than keywords. A search with the `entry` option is performed on the local keyword database only.

`exact` prevents matching on abbreviations. A search with the `exact` option is performed across both the local keyword database and the `net` materials.

`faq` limits the search to the FAQs posted on the Stata website: http://www.stata.com. A search with the `faq` option is performed on the local keyword database only.

`historical` adds to the search entries that are of historical interest only. By default, such entries are not listed. Past entries are classified as historical if they discuss a feature that later became an official part of Stata. Updates to historical entries will always be found, even if `historical` is not specified. A search with the `historical` option is performed on the local keyword database only.

`or` specifies that an entry be listed if any of the words typed after `search` are associated with the entry. The default is to list the entry only if all the words specified are associated with the entry. A search with the `or` option is performed on the local keyword database only.

`manual` limits the search to entries in the *Stata Documentation*; that is, the search is limited to the *User's Guide* and all the reference manuals. A search with the `manual` option is performed on the local keyword database only.

`sj` limits the search to entries in the *Stata Journal* and its predecessor, the *Stata Technical Bulletin*; see [R] **sj**. A search with the `sj` option is performed on the local keyword database only.

Option for set searchdefault

`permanently` specifies that, in addition to making the change right now, the `searchdefault` setting be remembered and become the default setting when you invoke Stata.

Remarks

Remarks are presented under the following headings:

Introduction
Internet searches
Author searches
Entry ID searches
Return codes

Introduction

See [U] **4 Stata's help and search facilities** for a tutorial introduction to `search`. `search` is one of Stata's most useful commands. To understand the advanced features of `search`, you need to know how it works.

`search` has a database—files—containing the titles, etc., of every entry in the *User's Guide*, the *Base Reference Manual*, the *Data-Management Reference Manual*, the *Graphics Reference Manual*, the *Longitudinal-Data/Panel-Data Reference Manual*, the *Multiple-Imputation Reference Manual*, the *Multivariate Statistics Reference Manual*, the *Programming Reference Manual*, the *Structural Equation Modeling Reference Manual*, the *Survey Data Reference Manual*, the *Survival Analysis and Epidemiological Tables Reference Manual*, the *Time-Series Reference Manual*, the *Mata Reference Manual*, undocumented help files, NetCourses, Stata Press books, FAQs posted on the Stata website, selected articles on StataCorp's official blog, selected user-written FAQs and examples, and the articles in the *Stata Journal* and the *Stata Technical Bulletin*. In these files is a list of words, called keywords, associated with each entry.

When you type `search` *xyz*, `search` reads the database and compares the list of keywords with *xyz*. If it finds *xyz* in the list or a keyword that allows an abbreviation of *xyz*, it displays the entry.

When you type `search` *xyz abc*, `search` does the same thing but displays an entry only if it contains both keywords. The order does not matter, so you can `search linear regression` or `search regression linear`.

Obviously, how many entries `search` finds depends on how the search database was constructed. We have included a plethora of keywords under the theory that, for a given request, it is better to list too much rather than risk listing nothing at all. Still, you are in the position of guessing the keywords. Do you look up normality test, normality tests, or tests of normality? Well, normality test would be best, but all would work. In general, use the singular, and strike the unnecessary words. For guidelines for specifying keywords, see [U] **4.6 More on search**.

`set searchdefault` allows you to specify where `search` searches. `set searchdefault local`, the default, restricts `search` to using only Stata's keyword database. `set searchdefault net` restricts `search` to searching only the Internet. `set searchdefault all` indicates that both the keyword database and the Internet are to be searched.

Internet searches

`search` with the `net` option searches the Internet for user-written additions to Stata, including, but not limited to, user-written additions published in the *Stata Journal* (SJ) and the *Stata Technical Bulletin* (STB). `search` *keywords*`, net` performs the same search as the command `net search` (with no options); see [R] **net search**.

```
. search random effect, net
Keyword search
        Keywords:  random effect
          Search:  (1) Web resources from Stata and from other users
Web resources from Stata and other users
(contacting http://www.stata.com)
135 packages found (Stata Journal and STB listed first)
-----------------------------------------------------
st0201 from http://www.stata-journal.com/software/sj10-3
    SJ10-3 st0201.  metaan: Random-effects meta-analysis / metaan:
    Random-effects meta-analysis / by Evangelos Kontopantelis, / National
    Primary Care Research and Development Centre (NPCRDC), / University of
    Manchester, Manchester, UK / David Reeves, / National Primary Care
```

```
st0175 from http://www.stata-journal.com/software/sj9-4
    SJ9-4 st0175.  A menu-driven facility for sample-size... / A menu-driven
    facility for sample-size calculation in / novel multiarm, multistage
    randomized controlled / trials with a time-to-event outcome / by
    Friederike M.-S. Barthel, GlaxoSmithKline / Patrick Royston, UK Medical
sbe24_3 from http://www.stata-journal.com/software/sj9-2
    SJ9-2 sbe24_3.  Update: metan: fixed- and random-effects... / Update:
    metan: fixed- and random-effects meta-analysis / by Ross J. Harris, Roger
    M. Harbord, and Jonathan A. C. Sterne, / Department of Social Medicine,
    University of Bristol / Jonathan J. Deeks, Department of Primary Care
st0156 from http://www.stata-journal.com/software/sj9-1
    SJ9-1 st0156.  Multivariate random-effects meta-analysis / Multivariate
    random-effects meta-analysis / by Ian R. White, MRC Biostatistics Unit, /
    Institute of Public Health, UK / Support:  ian.white@mrc-bsu.cam.ac.uk /
    After installation, type help mvmeta and mvmeta_make
  (output omitted)
(end of search)
```

Author searches

`search` ordinarily compares the words following `search` with the keywords for the entry. If you specify the `author` option, however, it compares the words with the author's name. In the search database, we have filled in author names for all SJ and STB inserts.

For instance, in [R] **kdensity** in this manual you will discover that Isaías H. Salgado-Ugarte wrote the first version of Stata's `kdensity` command and published it in the STB. Assume that you read his original insert and found the discussion useful. You might now wonder what else he has written in the SJ or STB. To find out, you type

```
. search Salgado-Ugarte, author
  (output omitted)
```

Names like Salgado-Ugarte are confusing to many people. `search` does not require you to specify the entire name; what you type is compared with each "word" of the name and, if any part matches, the entry is listed. The hyphen is a special character, and you can omit it. Thus you can obtain the same list by looking up Salgado, Ugarte, or Salgado Ugarte without the hyphen.

Actually, to find all entries written by Salgado-Ugarte, you need to type

```
. search Salgado-Ugarte, author historical
  (output omitted)
```

Prior inserts in the SJ or STB that provide a feature that later was superseded by a built-in feature of Stata are marked as historical in the search database and, by default, are not listed. The `historical` option ensures that all entries are listed.

Entry ID searches

If you specify the `entry` option, `search` compares what you have typed with the entry ID. The entry ID is not the title—it is the reference listed to the left of the title that tells you where to look. For instance, in

```
[R]     regress  . . . . . . . . . . . . . . . . . . . . . . . Linear regression
        (help regress)
```

[R] **regress** is the entry ID. This is a reference, of course, to this manual. In

```
FAQ      . . . . . . . . . . . Analysis of multiple failure-time survival data
         . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . . M. Cleves
         11/99   How do I analyze multiple failure-time data using Stata?
                 http://www.stata.com/support/faqs/stat/stmfail.html
```

"FAQ" is the entry ID. In

```
SJ-7-1  st0118  . . A survey on survey stat.: What is and can be done in Stata
        . . . . . . . . . . . . . . . . . . . . . . F. Kreuter and R. Valliant
        Q1/07  SJ7(1):1--21                                        (no commands)
        discusses survey issues in analyzing complex survey
        data and describes some of Stata's capabilities for
        such analyses
```

"SJ-7-1" is the entry ID.

`search` with the `entry` option searches these entry IDs.

Thus you could generate a table of contents for the *User's Guide* by typing

```
. search [U], entry
  (output omitted)
```

You could generate a table of contents for *Stata Journal*, Volume 1, Issue 1, by typing

```
. search sj-1-1, entry
  (output omitted)
```

To generate a table of contents for the 26th issue of the STB, you would type

```
. search STB-26, entry historical
  (output omitted)
```

The `historical` option here is possibly important. STB-26 was published in July 1995, and perhaps some of its inserts have already been marked historical.

You could obtain a list of all inserts associated with sg53 by typing

```
. search sg53, entry historical
  (output omitted)
```

Again we include the `historical` option in case any of the relevant inserts have been marked historical.

Return codes

In addition to indexing the entries in the *User's Guide* and all the *Reference* manuals, `search` also can be used to search return codes.

To see information on return code 131, type

```
. search rc 131
[P]     error . . . . . . . . . . . . . . . . . . . . . . . . Return code 131
        not possible with test;
        You requested a test of a hypothesis that is nonlinear in the
        variables.  test tests only linear hypotheses.  Use testnl.
```

If you want a list of all Stata return codes, type

```
. search error, entry
  (output omitted)
```

Methods and formulas

`findit` is implemented as an ado-file.

Acknowledgment

`findit` grew from a suggestion by Nicholas J. Cox, Durham University.

Also see

[R] **hsearch** — Search help files

[R] **help** — Display online help

[R] **net search** — Search the Internet for installable packages

[U] **4 Stata's help and search facilities**

Title

serrbar — Graph standard error bar chart

Syntax

`serrbar` *mvar svar xvar* [*if*] [*in*] [, *options*]

options	Description
Main	
`scale(#)`	scale length of graph bars; default is `scale(1)`
Error bars	
rcap_options	affect rendition of capped spikes
Plotted points	
`mvopts(`*scatter_options*`)`	affect rendition of plotted points
Add plots	
`addplot(`*plot*`)`	add other plots to generated graph
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Menu

Statistics > Other > Quality control > Standard error bar chart

Description

`serrbar` graphs *mvar* ± `scale()` × *svar* against *xvar*. Usually, but not necessarily, *mvar* and *svar* will contain means and standard errors or standard deviations of some variable so that a standard error bar chart is produced.

Options

Main

`scale(#)` controls the length of the bars. The upper and lower limits of the bars will be *mvar* + `scale()` × *svar* and *mvar* − `scale()` × *svar*. The default is `scale(1)`.

Error bars

rcap_options affect the rendition of the plotted error bars (the capped spikes). See [G-2] **graph twoway rcap**.

Plotted points

`mvopts(`*scatter_options*`)` affects the rendition of the plotted points (*mvar* versus *xvar*). See [G-2] **graph twoway scatter**.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Remarks

▷ Example 1

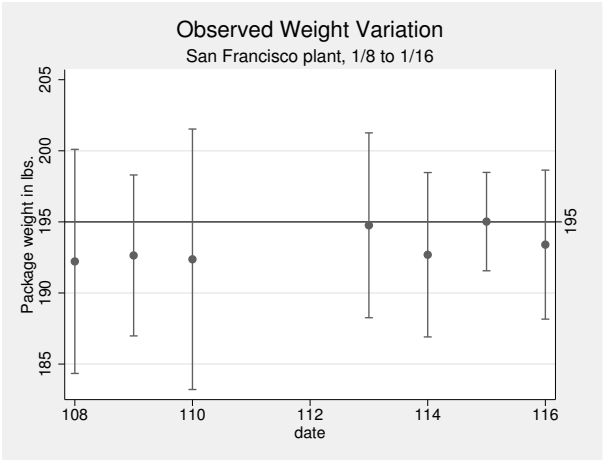
In quality-control applications, the three most commonly used variables with this command are the process mean, process standard deviation, and time. For instance, we have data on the average weights and standard deviations from an assembly line in San Francisco for the period January 8 to January 16. Our data are

```
. use http://www.stata-press.com/data/r12/assembly
. list, sep(0) divider
```

	date	mean	std
1.	108	192.22	3.94
2.	109	192.64	2.83
3.	110	192.37	4.58
4.	113	194.76	3.25
5.	114	192.69	2.89
6.	115	195.02	1.73
7.	116	193.40	2.62

We type `serrbar mean std date, scale(2)` but, after seeing the result, decide to make it fancier:

```
. serrbar mean std date, scale(2) title("Observed Weight Variation")
> sub("San Francisco plant, 1/8 to 1/16") yline(195) yaxis(1 2)
> ylab(195, axis(2)) ytitle("", axis(2))
```



Methods and formulas

`serrbar` is implemented as an ado-file.

Acknowledgment

`serrbar` was written by Nicholas J. Cox of Durham University.

Also see

[R] **qc** — Quality control charts

Title

set — Overview of system parameters

Syntax

`set` [*setcommand* ...]

`set` typed without arguments is equivalent to `query` typed without arguments.

Description

This entry provides a reference to Stata's `set` commands. For many entries, more thorough information is provided elsewhere; see the Reference field in each entry below for the location of this information.

To reset system parameters to factory defaults, see [R] **set_defaults**.

Remarks

`set adosize`
Syntax: `set adosize #` [`, permanently`]
Default: 1,000
Description: sets the maximum amount of memory that automatically loaded do-files may consume. `10` $\leq$ # $\leq$ `10000`.
Reference: [P] **sysdir**

`set autotabgraphs` (Windows only)
Syntax: `set autotabgraphs {on|off}` [`, permanently`]
Default: `off`
Description: determines whether graphs are created as tabs within one window or as separate windows.

`set cformat`
Syntax: `set cformat` [*fmt*] [`, permanently`]
Description: specifies the output format of coefficients, standard errors, and confidence limits in coefficient tables. *fmt* is a numerical format; see [D] **format**.
Reference: [R] **set cformat**

`set checksum`
Syntax: `set checksum {on|off}` [`, permanently`]
Default: `off`
Description: determines whether files should be prevented from being downloaded from the Internet if checksums do not match.
Reference: [D] **checksum**

`set conren` (Unix console only)

Syntax 1: `set conren`
Syntax 2: `set conren clear`
Syntax 3: `set conren` [`sf` | `bf` | `it`] {`result` | [`txt` | `text`] | `input` | `error` | `link` | `hilite`} [*char* [*char*...]]
Syntax 4: `set conren` {`ulon` | `uloff`} [*char* [*char* ...]]
Syntax 5: `set conren reset` [*char* [*char* ...]]
Description: can possibly make the output on your screen appear prettier.
`set conren` displays a list of the currently defined display codes.
`set conren clear` clears all codes.
`set conren` followed by a font type (`bf`, `sf`, or `it`) and display context (`result`, `error`, `link`, or `hilite`) and then followed by a series of space-separated characters sets the code for the specified font type and display context. If the font type is omitted, the code is set to the same specified code for all three font types.
`set conren ulon` and `set conren uloff` set the codes for turning on and off underlining.
`set conren reset` sets the code that will turn off all display and underlining codes.
Reference: [GSU] **conren**

`set copycolor` (Mac and Windows only)

Syntax: `set copycolor` {`automatic`|`asis`|`gs1`|`gs2`|`gs3`} [`, permanently`]
Default: `automatic`
Description: determines how colors are handled when graphs are copied to the Clipboard.
Reference: [G-2] **set printcolor**

`set dockable` (Windows only)

Syntax: `set dockable` {`on`|`off`} [`, permanently`]
Default: `on`
Description: determines whether to enable the use of dockable window characteristics, including the ability to dock or tab a window into another window.

`set dockingguides` (Windows only)

Syntax: `set dockingguides` {`on`|`off`} [`, permanently`]
Default: `on`
Description: determines whether to enable the use of dockable guides when repositioning a dockable window.

`set doublebuffer` (Windows only)

Syntax: `set doublebuffer` {`on`|`off`} [`, permanently`]
Default: `on`
Description: enables or disables double buffering of the Results, Viewer, and Data Editor windows. Double buffering prevents the windows from flickering when redrawn or resized. Users who encounter performance problems such as the Results window outputting very slowly should disable double buffering.

`set dp`
Syntax: `set dp {comma | period} [, permanently]`
Default: `period`
Description: determines whether a period or a comma is to be used as the decimal point.
Reference: [D] **format**

`set emptycells`
Syntax: `set emptycells {keep | drop} [, permanently]`
Default: `keep`
Description: sets what to do with empty cells in interactions.
Reference: [R] **set emptycells**

`set eolchar` (Mac only)
Syntax: `set eolchar {mac | unix} [, permanently]`
Default: `unix`
Description: sets the default end-of-line delimiter for text files created in Stata.

`set fastscroll` (Unix and Windows only)
Syntax: `set fastscroll {on | off} [, permanently]`
Default: `on`
Description: sets the scrolling method for new output in the Results window. Setting `fastscroll` to `on` is faster but can be jumpy. Setting `fastscroll` to `off` is slower but smoother.

`set floatresults` (Windows only)
Syntax: `set floatresults {on | off}`
Default: `off`
Description: determines whether to enable floating window behavior for the Results window. The term "float" in this context means the Results window will always float over the main Stata window; the Results window can never be placed behind the main Stata window. There is no `permanently` option because `permanently` is implied.

`set floatwindows` (Windows only)
Syntax: `set floatwindows {on | off}`
Default: `off`
Description: determines whether to enable floating window behavior for dialog boxes and dockable window. The term "float" in this context means that a window will always float over the main Stata window; these windows cannot be placed behind the main Stata window. There is no `permanently` option because `permanently` is implied.

`set graphics`
Syntax: `set graphics {on | off}`
Default: `on`; default is `off` for console Stata
Description: determines whether graphs are displayed on your monitor.
Reference: [G-2] **set graphics**

set httpproxy
Syntax: set httpproxy {on | off} [, init]
Default: off
Description: turns on/off the use of a proxy server. There is no permanently option because permanently is implied.
Reference: [R] netio

set httpproxyauth
Syntax: set httpproxyauth {on | off}
Default: off
Description: determines whether authorization is required for the proxy server. There is no permanently option because permanently is implied.
Reference: [R] netio

set httpproxyhost
Syntax: set httpproxyhost ["]name["]
Description: sets the name of a host to be used as a proxy server. There is no permanently option because permanently is implied.
Reference: [R] netio

set httpproxyport
Syntax: set httpproxyport #
Default: 8080 if Stata cannot autodetect the proper setting for your computer.
Description: sets the port number for a proxy server. There is no permanently option because permanently is implied.
Reference: [R] netio

set httpproxypw
Syntax: set httpproxypw ["]password["]
Description: sets the appropriate password. There is no permanently option because permanently is implied.
Reference: [R] netio

set httpproxyuser
Syntax: set httpproxyuser ["]name["]
Description: sets the appropriate user ID. There is no permanently option because permanently is implied.
Reference: [R] netio

set include_bitmap (Mac only)
Syntax: set include_bitmap {on | off} [, permanently]
Default: on
Description: sets the output behavior when copying an image to the Clipboard.

`set level`
Syntax: `set level # [, permanently]`
Default: `95`
Description: sets the default significance level for confidence intervals for all commands that report confidence intervals. `10.00` $\leq$ # $\leq$ `99.99`, and # can have at most two digits after the decimal point.
Reference: [R] **level**

`set linegap`
Syntax: `set linegap #`
Default: `1`
Description: sets the space between lines, in pixels, in the Results window. There is no `permanently` option because `permanently` is implied.

`set linesize`
Syntax: `set linesize #`
Default: 1 less than the full width of the screen
Description: sets the line width, in characters, for both the screen and the log file.
Reference: [R] **log**

`set locksplitters` (Windows only)
Syntax: `set locksplitters {on|off} [, permanently]`
Default: `off`
Description: determines whether splitters should be locked so that docked windows cannot be resized.

`set logtype`
Syntax: `set logtype {text|smcl} [, permanently]`
Default: `smcl`
Description: sets the default log filetype.
Reference: [R] **log**

`set lstretch`
Syntax: `set lstretch {on|off} [, permanently]`
Description: specifies whether to automatically widen the coefficient table up to the width of the Results window to accommodate longer variable names.

`set matacache`, `set matafavor`, `set matalibs`, `set matalnum`, `set matamofirst`, `set mataoptimize`, and `set matastrict`; see [M-3] **mata set**.

`set matsize`
Syntax: `set matsize # [, permanently]`
Default: `400` for Stata/MP, Stata/SE, and Stata/IC; `40` for Small Stata
Description: sets the maximum number of variables that can be included in any estimation command. This setting cannot be changed in Small Stata.
`10` $\leq$ # $\leq$ `11000` for Stata/MP and Stata/SE; `10` $\leq$ # $\leq$ `800` for Stata/IC.
Reference: [R] **matsize**

set max_memory
Syntax: set max_memory #[b|k|m|g] [, permanently]
Default: . (all the memory the operating system will supply)
Description: specifies the maximum amount of memory Stata can use to store your data. 2 × segmentsize ≤ # ≤ .
Reference: [D] **memory**

set maxdb
Syntax: set maxdb # [, permanently]
Default: 50
Description: sets the maximum number of dialog boxes whose contents are remembered from one invocation to the next during a session. 5 ≤ # ≤ 1000
Reference: [R] **db**

set maxiter
Syntax: set maxiter # [, permanently]
Default: 16000
Description: sets the default maximum number of iterations for estimation commands. 0 ≤ # ≤ 16000
Reference: [R] **maximize**

set maxvar
Syntax: set maxvar # [, permanently]
Default: 5000 for Stata/MP and Stata/SE, 2048 for Stata/IC, and 99 for Small Stata
Description: sets the maximum number of variables. This can be changed only in Stata/MP and Stata/SE. 2048 ≤ # ≤ 32767
Reference: [D] **memory**

set min_memory
Syntax: set min_memory #[b|k|m|g] [, permanently]
Default: 0
Description: specifies an amount of memory Stata will not fall below. This setting affects efficiency, not the size of datasets you can analyze. 0 ≤ # ≤ max_memory
Reference: [D] **memory**

set more
Syntax: set more {on|off} [, permanently]
Default: on
Description: pauses when —more— is displayed, continuing only when the user presses a key.
Reference: [R] **more**

set niceness
Syntax: set niceness # [, permanently]
Default: 5
Description: affects how soon Stata gives back unused segments to the operating system. 0 ≤ # ≤ 10
Reference: [D] **memory**

`set notifyuser` (Mac only)
Syntax: `set notifyuser {on|off} [, permanently]`
Default: `on`
Description: sets the default Notification Manager behavior in Stata.

`set obs`
Syntax: `set obs #`
Default: current number of observations
Description: changes the number of observations in the current dataset. # must be at least as large as the current number of observations. If there are variables in memory, the values of all new observations are set to *missing*.
Reference: [D] **obs**

`set odbcmgr` (Unix only)
Syntax: `set odbcmgr {iodbc|unixodbc} [, permanently]`
Default: `iodbc`
Description: determines whether iODBC or unixODBC is your ODBC driver manager.
Reference: [D] **odbc**

`set output`
Syntax: `set output {proc|inform|error}`
Default: `proc`
Description: specifies the output to be displayed. `proc` means display all output; `inform` suppresses procedure output but displays informative messages and error messages; `error` suppresses all output except error messages. `set output` is seldom used.
Reference: [P] **quietly**

`set pagesize`
Syntax: `set pagesize #`
Default: 2 less than the physical number of lines on the screen
Description: sets the number of lines between —more— messages.
Reference: [R] **more**

`set pformat`
Syntax: `set pformat [`*fmt*`] [, permanently]`
Description: specifies the output format of p-values in coefficient tables. *fmt* is a numerical format; see [D] **format**.
Reference: [R] **set cformat**

`set pinnable` (Windows only)
Syntax: `set pinnable {on|off} [, permanently]`
Default: `on`
Description: determines whether to enable the use of pinnable window characteristics for certain windows in Stata.

set playsnd (Mac only)
Syntax: set playsnd {on|off} [, permanently]
Default: on
Description: sets the sound behavior for the Notification Manager behavior in Stata.

set printcolor
Syntax: set printcolor {automatic|asis|gs1|gs2|gs3} [, permanently]
Default: automatic
Description: determines how colors are handled when graphs are printed.
Reference: [G-2] **set printcolor**

set processors
Syntax: set processors #
Description: sets the number of processors or cores that Stata/MP will use. The default is the number of processors available on the computer, or the number of processors allowed by Stata/MP's license, whichever is less.

set reventries
Syntax: set reventries # [, permanently]
Default: 5000
Description: sets the number of scrollback lines available in the Review window. $5 \leq \# \leq 32000$.

set revkeyboard (Mac only)
Syntax: set revkeyboard {on|off} [, permanently]
Default: on
Description: sets the keyboard navigation behavior for the Review window. on indicates that you can use the keyboard to navigate and enter items from the Review window into the Command window. off indicates that all keyboard input be directed at the Command window; items can be entered from the Review window only by using the mouse.

set rmsg
Syntax: set rmsg {on|off} [, permanently]
Default: off
Description: indicates whether a return message telling the execution time is to be displayed at the completion of each command.
Reference: [P] **rmsg**

set scheme
Syntax: set scheme *schemename* [, permanently]
Default: s2color
Description: determines the overall look for graphs.
Reference: [G-2] **set scheme**

set scrollbufsize
Syntax: set scrollbufsize #
Default: 200000
Description: sets the scrollback buffer size, in bytes, for the Results window; may be set between 10,000 and 2,000,000.

set searchdefault
Syntax: set searchdefault {local | net | all} [, permanently]
Default: local
Description: sets the default behavior of the search command. set searchdefault local restricts search to use only Stata's keyword database. set searchdefault net restricts search to searching only the Internet. set searchdefault all indicates that both the keyword database and the Internet are to be searched.
Reference: [R] **search**

set seed
Syntax: set seed {# | *code*}
Default: 123456789
Description: specifies initial value of the random-number seed used by the runiform() function.
Reference: [R] **set seed**

set segmentsize
Syntax: set segmentsize #[b | k | m | g] [, permanently]
Default: 32m for 64-bit machines; 16m for 32-bit machines
Description: Stata allocates memory for data in units of segmentsize. This setting changes the amount of memory in a single segment.
1m ≤ # ≤ 32g for 64-bit machines; 1m ≤ # ≤ 1g for 32-bit machines
Reference: [D] **memory**

set sformat
Syntax: set sformat [*fmt*] [, permanently]
Description: specifies the output format of test statistics in coefficient tables.
fmt is a numerical format; see [D] **format**.
Reference: [R] **set cformat**

set showbaselevels
Syntax: set showbaselevels [on | off | all] [, permanently]
Description: specifies whether to display base levels of factor variables and their interactions in coefficient tables.
Reference: [R] **set showbaselevels**

set showemptycells
Syntax: set showemptycells [on | off] [, permanently]
Description: specifies whether to display empty cells in coefficient tables.
Reference: [R] **set showbaselevels**

set showomitted
Syntax: set showomitted [on|off] [, permanently]
Description: specifies whether to display omitted coefficients in coefficient tables.
Reference: [R] set showbaselevels

set smoothfonts (Mac only)
Syntax: set smoothfonts {on|off}
Default: on
Description: determines whether to use font smoothing (antialiased text) in the Results, Viewer, and Data Editor windows.

set timeout1
Syntax: set timeout1 #seconds [, permanently]
Default: 30
Description: sets the number of seconds Stata will wait for a remote host to respond to an initial contact before giving up. In general, users should not modify this value unless instructed to do so by Stata Technical Services.
Reference: [R] netio

set timeout2
Syntax: set timeout2 #seconds [, permanently]
Default: 180
Description: sets the number of seconds Stata will keep trying to get information from a remote host after initial contact before giving up. In general, users should not modify this value unless instructed to do so by Stata Technical Services.
Reference: [R] netio

set trace
Syntax: set trace {on|off}
Default: off
Description: determines whether to trace the execution of programs for debugging.
Reference: [P] trace

set tracedepth
Syntax: set tracedepth #
Default: 32000 (equivalent to ∞)
Description: if trace is set on, traces execution of programs and nested programs up to tracedepth. For example, if tracedepth is 2, the current program and any subroutine called would be traced, but subroutines of subroutines would not be traced.
Reference: [P] trace

set traceexpand
Syntax: set traceexpand {on|off} [, permanently]
Default: on
Description: if trace is set on, shows lines both before and after macro expansion. If traceexpand is set off, only the line before macro expansion is shown.
Reference: [P] trace

set tracehilite
Syntax: set tracehilite "*pattern*" [, word]
Default: ""
Description: highlights *pattern* in the trace output.
Reference: [P] **trace**

set traceindent
Syntax: set traceindent {on|off} [, permanently]
Default: on
Description: if trace is set on, indents displayed lines according to their nesting level. The lines of the main program are not indented. Two spaces of indentation are used for each level of nested subroutine.
Reference: [P] **trace**

set tracenumber
Syntax: set tracenumber {on|off} [, permanently]
Default: off
Description: if trace is set on, shows the nesting level numerically in front of the line. Lines of the main program are preceded by 01, lines of subroutines called by the main program are preceded by 02, etc.
Reference: [P] **trace**

set tracesep
Syntax: set tracesep {on|off} [, permanently]
Default: on
Description: if trace is set on, displays a horizontal separator line that displays the name of the subroutine whenever a subroutine is called or exits.
Reference: [P] **trace**

set type
Syntax: set type {float|double} [, permanently]
Default: float
Description: specifies the default storage type assigned to new variables.
Reference: [D] **generate**

set update_interval (Mac and Windows only)
Syntax: set update_interval #
Default: 7
Description: sets the number of days to elapse before performing the next automatic update query.
Reference: [R] **update**

set update_prompt (Mac and Windows only)
Syntax: set update_prompt {on|off}
Default: on
Description: determines wheter a dialog is to be displayed before performing an automatic update query. There is no permanently option because permanently is implied.
Reference: [R] **update**

set update_query (Mac and Windows only)
Syntax: set update_query {on | off}
Default: on
Description: determines whether update query is to be automatically performed when Stata is launched. There is no permanently option because permanently is implied.
Reference: [R] update

set varabbrev
Syntax: set varabbrev {on | off} [, permanently]
Default: on
Description: indicates whether Stata should allow variable abbreviations.
Reference: [P] varabbrev

set varkeyboard (Mac only)
Syntax: set varkeyboard {on | off} [, permanently]
Default: on
Description: sets the keyboard navigation behavior for the Variables window. on indicates that you can use the keyboard to navigate and enter items from the Variables window into the Command window. off indicates that all keyboard input be directed at the Command window; items can be entered from the Variables window only by using the mouse.

Also see

[R] query — Display system parameters

[R] set_defaults — Reset system parameters to original Stata defaults

[M-3] mata set — Set and display Mata system parameters

Title

set cformat — Format settings for coefficient tables

Syntax

```
set cformat [fmt] [, permanently]

set pformat [fmt] [, permanently]

set sformat [fmt] [, permanently]
```

where *fmt* is a numerical format.

Description

`set cformat` specifies the output format of coefficients, standard errors, and confidence limits in coefficient tables.

`set pformat` specifies the output format of p-values in coefficient tables.

`set sformat` specifies the output format of test statistics in coefficient tables.

Option

`permanently` specifies that, in addition to making the change right now, the setting be remembered and become the default setting when you invoke Stata.

Remarks

The formatting of the numbers in the coefficient table can be controlled by using the `set cformat`, `set pformat`, and `set sformat` commands or by using the `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, and `sformat(%`*fmt*`)` options at the time of estimation or on replay of the estimation command. See [R] **estimation options**.

▷ Example 1

We use auto.dta to illustrate.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg weight displacement
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =   66.79
       Model |  1595.40969     2  797.704846            Prob > F      =  0.0000
    Residual |  848.049768    71  11.9443629            R-squared     =  0.6529
-------------+------------------------------           Adj R-squared =  0.6432
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.4561

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |  -.0065671   .0011662    -5.63   0.000    -.0088925   -.0042417
displacement |   .0052808   .0098696     0.54   0.594    -.0143986    .0249602
       _cons |   40.08452   2.02011     19.84   0.000     36.05654    44.11251
------------------------------------------------------------------------------

. set cformat %9.2f
. regress mpg weight displacement
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =   66.79
       Model |  1595.40969     2  797.704846            Prob > F      =  0.0000
    Residual |  848.049768    71  11.9443629            R-squared     =  0.6529
-------------+------------------------------           Adj R-squared =  0.6432
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.4561

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |      -0.01       0.00    -5.63   0.000       -0.01       -0.00
displacement |       0.01       0.01     0.54   0.594       -0.01        0.02
       _cons |      40.08       2.02     19.84   0.000       36.06       44.11
------------------------------------------------------------------------------

. regress mpg weight displacement, cformat(%9.3f)
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  2,    71) =   66.79
       Model |  1595.40969     2  797.704846            Prob > F      =  0.0000
    Residual |  848.049768    71  11.9443629            R-squared     =  0.6529
-------------+------------------------------           Adj R-squared =  0.6432
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.4561

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      weight |      -0.007       0.001    -5.63   0.000       -0.009       -0.004
displacement |       0.005       0.010     0.54   0.594       -0.014        0.025
       _cons |      40.085       2.020     19.84   0.000       36.057       44.113
------------------------------------------------------------------------------
```

To reset the `cformat` setting to its command-specific default, type

```
. set cformat
. regress mpg weight displacement
```

Source	SS	df	MS	Number of obs =	74
				F(2, 71) =	66.79
Model	1595.40969	2	797.704846	Prob > F =	0.0000
Residual	848.049768	71	11.9443629	R-squared =	0.6529
				Adj R-squared =	0.6432
Total	2443.45946	73	33.4720474	Root MSE =	3.4561

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0065671	.0011662	-5.63	0.000	-.0088925	-.0042417
displacement	.0052808	.0098696	0.54	0.594	-.0143986	.0249602
_cons	40.08452	2.02011	19.84	0.000	36.05654	44.11251

Also see

[R] **estimation options** — Estimation options

[R] **set** — Overview of system parameters

[R] **query** — Display system parameters

[U] **20.8 Formatting the coefficient table**

Title

set_defaults — Reset system parameters to original Stata defaults

Syntax

```
set_defaults { category | _all } [ , permanently ]
```

where *category* is one of memory | output | interface | graphics | efficiency | network | update | trace | mata | other

Description

`set_defaults` resets settings made by `set` to the original default settings that were shipped with Stata.

`set_defaults _all` resets all the categories, whereas `set defaults` *category* resets only the settings for the specified category.

Option

`permanently` specifies that, in addition to making the change right now, the settings be remembered and become the default settings when you invoke Stata.

Remarks

▷ Example 1

To assist us in debugging a new command, we modified some of the `trace` settings. To return them to their original values, we type

```
. set_defaults trace
-> set trace off
-> set tracedepth 32000
-> set traceexpand on
-> set tracesep on
-> set traceindent on
-> set tracenumber off
-> set tracehilite ""
(preferences reset)
```

◁

Methods and formulas

`set_defaults` is implemented as an ado-file.

Also see

[R] **query** — Display system parameters

[R] **set** — Overview of system parameters

[M-3] **mata set** — Set and display Mata system parameters

Title

set emptycells — Set what to do with empty cells in interactions

Syntax

```
set emptycells {keep|drop} [, permanently]
```

Description

`set emptycells` allows you to control how Stata handles interaction terms with empty cells. Stata can keep empty cells or drop them. The default is to keep empty cells.

Option

`permanently` specifies that, in addition to making the change right now, the setting be remembered and become the default setting when you invoke Stata.

Remarks

By default, Stata keeps empty cells so they can be reported in the coefficient table. For example, type

```
. use http://www.stata-press.com/data/r12/auto
. regress mpg rep78#foreign, baselevels
```

and you will see a regression of `mpg` on 10 indicator variables because `rep78` takes on 5 values and `foreign` takes on 2 values in the `auto` dataset. Two of those cells will be reported as empty because the data contain no observations of foreign cars with a `rep78` value of 1 or 2.

Many real datasets contain a large number of empty cells, and this could cause the "matsize too small" error, r(908). In that case, type

```
. set emptycells drop
```

to get Stata to drop empty cells from the list of coefficients. If you commonly fit models with empty cells, you can permanently set Stata to drop empty cells by typing the following:

```
. set emptycells drop, permanently
```

Also see

[R] **set** — Overview of system parameters

Title

set seed — Specify initial value of random-number seed

Syntax

```
set seed #
```

```
set seed statecode
```

where

is any number between 0 and $2^{31} - 1$ (2,147,483,647), and

statecode is a random-number state previously obtained from `creturn` value `c(seed)`.

Description

`set seed #` specifies the initial value of the random-number seed used by the random-number functions, such as `runiform()` and `rnormal()`.

`set seed` *statecode* resets the state of the random-number functions to the value specified, which is a state previously obtained from `creturn` value `c(seed)`.

Remarks

Remarks are presented under the following headings:

Examples
Setting the seed
How to choose a seed
Do not set the seed too often
Preserving and restoring the random-number generator state

Examples

1. Specify initial value of random-number seed

   ```
   . set seed 339487731
   ```

2. Create variable `u` containing uniformly distributed pseudorandom numbers on the interval $[0, 1)$

   ```
   . generate u = runiform()
   ```

3. Create variable `z` containing normally distributed random numbers with mean 0 and standard deviation 1

   ```
   . generate z = rnormal()
   ```

4. Obtain state of pseudorandom-number generator and store it in a local macro named `state`

   ```
   . local state = c(seed)
   ```

5. Restore pseudorandom-number generator state to that previously stored in local macro named `state`

   ```
   . set seed `state'
   ```

Setting the seed

Stata's random-number generation functions, such as `runiform()` and `rnormal()`, do not really produce random numbers. These functions are deterministic algorithms that produce numbers that can pass for random. `runiform()` produces numbers that can pass for independent draws from a rectangular distribution over $[0, 1)$; `rnormal()` produces numbers that can pass for independent draws from $N(0, 1)$. Stata's random-number functions are formally called pseudorandom-number functions.

The sequences these functions produce are determined by the seed, which is just a number and which is set to 123456789 every time Stata is launched. This means that `runiform()` produces the same sequence each time you start Stata. The first time you use `runiform()` after Stata is launched, `runiform()` returns 0.136984078446403146. The second time you use it, `runiform()` returns 0.643220667960122228. The third time you use it, ...

To obtain different sequences, you must specify different seeds using the `set seed` command. You might specify the seed 472195:

```
. set seed 472195
```

If you were now to use `runiform()`, the first call would return 0.247166610788553953, the second call would return 0.593119932804256678, and so on. Whenever you `set seed 472195`, `runiform()` will return those numbers the first two times you use it.

Thus you set the seed to obtain different pseudorandom sequences from the pseudorandom-number functions.

If you record the seed you set, pseudorandom results such as results from a simulation or imputed values from `mi impute` can be reproduced later. Whatever you do after setting the seed, if you set the seed to the same value and repeat what you did, you will obtain the same results.

How to choose a seed

Your best choice for the seed is an element chosen randomly from the set $\{0, 1, \ldots, 2{,}147{,}483{,}647\}$. We recommend that, but that is difficult to achieve because finding easy-to-access, truly random sources is difficult.

One person we know uses digits from the serial numbers from dollar bills he finds in his wallet. Of course, the numbers he obtains are not really random, but they are good enough, and they are probably a good deal more random than the seeds most people choose. Some people use dates and times, although we recommend against that because, over the day, it just gets later and later, and that is a pattern. Others try to make up a random number, figuring if they include enough digits, the result just has to be random. This is a variation on the five-second rule for dropped food, and we admit to using both of these rules.

It does not really matter how you set the seed, as long as there is no obvious pattern in the seeds that you set and as long as you do not set the seed too often during a session.

Nonetheless, here are two methods that we have seen used but you should not use:

1. The first time you set the seed, you set the number 1. The next time, you set 2, and then 3, and so on. Variations on this included setting 1001, 1002, 1003, ..., or setting 1001, 2001, 3001, and so on.

   Do not follow any of these procedures. The seeds you set must not exhibit a pattern.

2. To set the seed, you obtain a pseudorandom number from `runiform()` and then use the digits from that to form the seed.

   This is a bad idea because the pseudorandom-number generator can converge to a cycle. If you obtained the pseudorandom-number generator unrelated to those in Stata, this would work well, but then you would have to find a rule to set the first generator's seed. In any case, the pseudorandom-number generators in Stata are all closely related, and so you must not follow this procedure.

Choosing seeds that do not exhibit a pattern is of great importance. That the seeds satisfy the other properties of randomness is minor by comparison.

Do not set the seed too often

We cannot emphasize this enough: Do not set the seed too often.

To see why this is such a bad idea, consider the limiting case: You set the seed, draw one pseudorandom number, reset the seed, draw again, and so continue. The pseudorandom numbers you obtain will be nothing more than the seeds you run through a mathematical function. The results you obtain will not pass for random unless the seeds you choose pass for random. If you already had such numbers, why are you even bothering to use the pseudorandom-number generator?

The definition of too often is more than once per problem.

If you are running a simulation of 10,000 replications, set the seed at the start of the simulation and do not reset it until the 10,000th replication is finished. The pseudorandom-number generators provided by Stata have long periods. The longer you go between setting the seed, the more random-like are the numbers produced.

It is sometimes useful later to be able to reproduce in isolation any one of the replications, and so you might be tempted to set the seed to a known value for each of the replications. We negatively mentioned setting the seed to 1, 2, . . . , and it is in exactly such situations that we have seen this done. The advantage, however, is that you could reproduce the fifth replication merely by setting the seed to 5 and then repeating whatever it is that is to be replicated. If this is your goal, you do not need to reset the seed. You can record the state of the random-number generator, save the state with your replication results, and then use the recorded states later to reproduce whichever of the replications that you wish. This will be discussed in *Preserving and restoring the random-number generator state*.

There is another reason you might be tempted to set the seed more than once per problem. It sometimes happens that you run a simulation, let's say for 5,000 replications, and then you decide you should have run it for 10,000 replications. Instead of running all 10,000 replications afresh, you decide to save time by running another 5,000 replications and then combining those results with your previous 5,000 results. That is okay. We at StataCorp do this kind of thing. If you do this, it is important that you set the seed especially well, particularly if you repeat this process to add yet another 5,000 replications. It is also important that in each run there be a large enough number of replications, which is say thousands of them.

Even so, do not do this: You want 500,000 replications. To obtain them, you run in batches of 1,000, setting the seed 500 times. Unless you have a truly random source for the seeds, it is unlikely you can produce a patternless sequence of 500 seeds. The fact that you ran 1,000 replications in between choosing the seeds does not mitigate the requirement that there be no pattern to the seeds you set.

In all cases, the best solution is to set the seed only once and then use the method we suggest in the next section.

Preserving and restoring the random-number generator state

In the previous section, we discussed the case in which you might be tempted to set the seed more frequently than otherwise necessary, either to save time or to be able to rerun any one of the replications. In such cases, there is an alternative to setting a new seed: recording the state of the pseudorandom-number generator and then restoring the state later should the need arise.

The state of the random-number generator is a string that looks like this:

```
Xb5804563c43f462544a474abacbdd93d00021fb3
```

You can obtain the state from `c(seed)`:

```
. display c(seed)
Xb5804563c43f462544a474abacbdd93d00021fb3
```

The name `c(seed)` is unfortunate because it suggests that Xb5804563c43f462544a474abacbdd93d00021fb3 is nothing more than a seed such as 1073741823 in a different guise. It is not. A better name for `c(seed)` would have been `c(rng_state)`. The state string specifies an entry point into the sequence produced by the pseudorandom-number generator. Let us explain.

The best way to use a pseudorandom-number generator would be to choose a seed once, draw random numbers until you use up the generator, and then get a new generator and choose a new key. Pseudorandom-number generators have a period, after which they repeat the original sequence. That is what we mean by using up a generator. The period of the pseudorandom-number generator that Stata is currently using is over 2^{123}. Stata uses the KISS generator. It is difficult to imagine that you could ever use up KISS.

The string reported by `c(seed)` reports an encoded form of the information necessary for Stata to reestablish exactly where it is located in the pseudorandom-number generator's sequence.

We are not seriously suggesting you choose only one seed over your entire lifetime, but let's look at how you might do that. Sometime after birth, when you needed your first random number, you would set your seed,

```
. set seed 1073741823
```

On that day, you would draw, say, 10,000 pseudorandom numbers, perhaps to impute some missing values. Being done for the day, you type

```
. display c(seed)
X15b512f3b2143ab434f1c92f4e7058e400023bc3
```

The next day, after launching Stata, you type

```
. set seed X15b512f3b2143ab434f1c92f4e7058e400023bc3
```

When you type `set seed` followed by a state string rather than a number, instead of setting the seed, Stata reestablishes the previous state. Thus the next time you draw a pseudorandom number, Stata will produce the 10,001st result after setting seed 1073741823. Let's assume that you draw 100,000 numbers this day. Done for the day, you display `c(seed)`.

```
. display c(seed)
X5d13d693a72ad0602b093cc4f61e07a500020381
```

On the third day, after setting the seed to the string above, you will be in a position to draw the 110,001st pseudorandom number.

In this way, you would eat your way though the 2^{123} random numbers, but you would be unlikely ever to make it to the end. Assuming you did this every day for 100 years, to arrive at the end of the sequence you would need to consume 2.9e+32 pseudorandom numbers per day.

We do not expect you to set the seed just once in your life, but using the state string makes it easy to set the seed just once for a problem.

When we do simulations at StataCorp, we record `c(seed)` for each replication. Just like everybody else, we record results from replications as observations in datasets; we just happen to have an extra variable in the dataset, namely, a string variable named `state`. That string is filled in observation by observation from the then-current values of `c(seed)`, which is a function and so can be used in any context that a function can be used in Stata.

Anytime we want to reproduce a particular replication, we thus have the information we need to reset the pseudorandom-number generator, and having it in the dataset is convenient because we had to go there anyway to determine which replication we wanted to reproduce.

In addition to recording each of the state strings for each replication, we record the closing value of `c(seed)` as a note, which is easy enough to do:

```
. note: closing state ‘c(seed)’
```

If we want to add more replications later, we have a state string that we can use to continue from where we left off.

Also see

[R] **set** — Overview of system parameters

[D] **functions** — Functions

Title

set showbaselevels — Display settings for coefficient tables

Syntax

```
set showbaselevels [on|off|all] [, permanently]

set showemptycells [on|off] [, permanently]

set showomitted [on|off] [, permanently]
```

Description

`set showbaselevels` specifies whether to display base levels of factor variables and their interactions in coefficient tables. `set showbaselevels on` specifies that base levels be reported for factor variables and for interactions whose bases cannot be inferred from their component factor variables. `set showbaselevels all` specifies that all base levels of factor variables and interactions be reported.

`set showemptycells` specifies whether to display empty cells in coefficient tables.

`set showomitted` specifies whether to display omitted coefficients in coefficient tables.

Option

`permanently` specifies that, in addition to making the change right now, the setting be remembered and become the default setting when you invoke Stata.

Remarks

▷ Example 1

We illustrate these three `set` commands using `cholesterol2.dta`.

```
. use http://www.stata-press.com/data/r12/cholesterol2
(Artificial cholesterol data, empty cells)
. generate x = race
. regress chol race##agegrp x
note: 2.race#2.agegrp identifies no observations in the sample
note: x omitted because of collinearity
```

Source	SS	df	MS	Number of obs =	70
				F(13, 56) =	13.51
Model	15751.6113	13	1211.66241	Prob > F =	0.0000
Residual	5022.71559	56	89.6913498	R-squared =	0.7582
				Adj R-squared =	0.7021
Total	20774.3269	69	301.077201	Root MSE =	9.4706

chol	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
race						
2	12.84185	5.989703	2.14	0.036	.8430383	24.84067
3	-.167627	5.989703	-0.03	0.978	-12.16644	11.83119
agegrp						
2	17.24681	5.989703	2.88	0.006	5.247991	29.24562
3	31.43847	5.989703	5.25	0.000	19.43966	43.43729
4	34.86613	5.989703	5.82	0.000	22.86732	46.86495
5	44.43374	5.989703	7.42	0.000	32.43492	56.43256
race#agegrp						
2 2	0	(empty)				
2 3	-22.83983	8.470719	-2.70	0.009	-39.80872	-5.870939
2 4	-14.67558	8.470719	-1.73	0.089	-31.64447	2.293306
2 5	-10.51115	8.470719	-1.24	0.220	-27.48004	6.457735
3 2	-6.054425	8.470719	-0.71	0.478	-23.02331	10.91446
3 3	-11.48083	8.470719	-1.36	0.181	-28.44971	5.488063
3 4	-.6796112	8.470719	-0.08	0.936	-17.6485	16.28928
3 5	-1.578052	8.470719	-0.19	0.853	-18.54694	15.39084
x	0	(omitted)				
_cons	175.2309	4.235359	41.37	0.000	166.7464	183.7153

```
. set showemptycells off
. set showomitted off
. set showbaselevels all
```

```
. regress chol race##agegrp x
note: 2.race#2.agegrp identifies no observations in the sample
note: x omitted because of collinearity
```

Source	SS	df	MS	Number of obs =	70
				F(13, 56) =	13.51
Model	15751.6113	13	1211.66241	Prob > F =	0.0000
Residual	5022.71559	56	89.6913498	R-squared =	0.7582
				Adj R-squared =	0.7021
Total	20774.3269	69	301.077201	Root MSE =	9.4706

chol	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
race						
1	0	(base)				
2	12.84185	5.989703	2.14	0.036	.8430383	24.84067
3	-.167627	5.989703	-0.03	0.978	-12.16644	11.83119
agegrp						
1	0	(base)				
2	17.24681	5.989703	2.88	0.006	5.247991	29.24562
3	31.43847	5.989703	5.25	0.000	19.43966	43.43729
4	34.86613	5.989703	5.82	0.000	22.86732	46.86495
5	44.43374	5.989703	7.42	0.000	32.43492	56.43256
race#agegrp						
1 1	0	(base)				
1 2	0	(base)				
1 3	0	(base)				
1 4	0	(base)				
1 5	0	(base)				
2 1	0	(base)				
2 3	-22.83983	8.470719	-2.70	0.009	-39.80872	-5.870939
2 4	-14.67558	8.470719	-1.73	0.089	-31.64447	2.293306
2 5	-10.51115	8.470719	-1.24	0.220	-27.48004	6.457735
3 1	0	(base)				
3 2	-6.054425	8.470719	-0.71	0.478	-23.02331	10.91446
3 3	-11.48083	8.470719	-1.36	0.181	-28.44971	5.488063
3 4	-.6796112	8.470719	-0.08	0.936	-17.6485	16.28928
3 5	-1.578052	8.470719	-0.19	0.853	-18.54694	15.39084
_cons	175.2309	4.235359	41.37	0.000	166.7464	183.7153

To restore the display of empty cells, omitted predictors, and baselevels to their command-specific default behavior, type

```
. set showemptycells
. set showomitted
. set showbaselevels
. regress chol race##agegrp x
note: 2.race#2.agegrp identifies no observations in the sample
note: x omitted because of collinearity
```

Source	SS	df	MS	Number of obs =	70
				F(13, 56) =	13.51
Model	15751.6113	13	1211.66241	Prob > F =	0.0000
Residual	5022.71559	56	89.6913498	R-squared =	0.7582
				Adj R-squared =	0.7021
Total	20774.3269	69	301.077201	Root MSE =	9.4706

chol	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
race						
2	12.84185	5.989703	2.14	0.036	.8430383	24.84067
3	-.167627	5.989703	-0.03	0.978	-12.16644	11.83119
agegrp						
2	17.24681	5.989703	2.88	0.006	5.247991	29.24562
3	31.43847	5.989703	5.25	0.000	19.43966	43.43729
4	34.86613	5.989703	5.82	0.000	22.86732	46.86495
5	44.43374	5.989703	7.42	0.000	32.43492	56.43256
race#agegrp						
2 2	0	(empty)				
2 3	-22.83983	8.470719	-2.70	0.009	-39.80872	-5.870939
2 4	-14.67558	8.470719	-1.73	0.089	-31.64447	2.293306
2 5	-10.51115	8.470719	-1.24	0.220	-27.48004	6.457735
3 2	-6.054425	8.470719	-0.71	0.478	-23.02331	10.91446
3 3	-11.48083	8.470719	-1.36	0.181	-28.44971	5.488063
3 4	-.6796112	8.470719	-0.08	0.936	-17.6485	16.28928
3 5	-1.578052	8.470719	-0.19	0.853	-18.54694	15.39084
x	0	(omitted)				
_cons	175.2309	4.235359	41.37	0.000	166.7464	183.7153

Also see

[R] **set** — Overview of system parameters

[R] **query** — Display system parameters

Title

signrank — Equality tests on matched data

Syntax

Wilcoxon matched-pairs signed-ranks test

`signrank` *varname* `=` *exp* [*if*] [*in*]

Sign test of matched pairs

`signtest` *varname* `=` *exp* [*if*] [*in*]

`by` is allowed with `signrank` and `signtest`; see [D] **by**.

Menu

signrank

Statistics > Nonparametric analysis > Tests of hypotheses > Wilcoxon matched-pairs signed-rank test

signtest

Statistics > Nonparametric analysis > Tests of hypotheses > Test equality of matched pairs

Description

`signrank` tests the equality of matched pairs of observations by using the Wilcoxon matched-pairs signed-ranks test (Wilcoxon 1945). The null hypothesis is that both distributions are the same.

`signtest` also tests the equality of matched pairs of observations (Arbuthnott [1710], but better explained by Snedecor and Cochran [1989]) by calculating the differences between *varname* and the expression. The null hypothesis is that the median of the differences is zero; no further assumptions are made about the distributions. This, in turn, is equivalent to the hypothesis that the true proportion of positive (negative) signs is one-half.

For equality tests on unmatched data, see [R] **ranksum**.

Remarks

▷ Example 1: signrank

We are testing the effectiveness of a new fuel additive. We run an experiment with 12 cars. We first run each car without the fuel treatment and measure the mileage. We then add the fuel treatment and repeat the experiment. The results of the experiment are

Without treatment	With treatment	Without treatment	With treatment
20	24	18	17
23	25	24	28
21	21	20	24
25	22	24	27
18	23	23	21
17	18	19	23

We create two variables called `mpg1` and `mpg2`, representing mileage without and with the treatment, respectively. We can test the null hypothesis that the treatment had no effect by typing

```
. use http://www.stata-press.com/data/r12/fuel
. signrank mpg1=mpg2
Wilcoxon signed-rank test
        sign |      obs    sum ranks    expected
-------------+---------------------------------
    positive |        3         13.5        38.5
    negative |        8         63.5        38.5
        zero |        1            1           1
-------------+---------------------------------
         all |       12           78          78
unadjusted variance      162.50
adjustment for ties       -1.62
adjustment for zeros      -0.25
                         ------
adjusted variance        160.62
Ho: mpg1 = mpg2
            z =  -1.973
    Prob > |z| =   0.0485
```

The output indicates that we can reject the null hypothesis at any level above 4.85%. ◁

▷ Example 2: signtest

`signtest` tests that the median of the differences is zero, making no further assumptions, whereas `signrank` assumed that the distributions are equal as well. Using the data above, we type

```
. signtest mpg1=mpg2
Sign test
        sign |    observed    expected
-------------+--------------------------
    positive |           3         5.5
    negative |           8         5.5
        zero |           1           1
-------------+--------------------------
         all |          12          12
One-sided tests:
  Ho: median of mpg1 - mpg2 = 0 vs.
  Ha: median of mpg1 - mpg2 > 0
      Pr(#positive >= 3) =
         Binomial(n = 11, x >= 3, p = 0.5) =  0.9673
  Ho: median of mpg1 - mpg2 = 0 vs.
  Ha: median of mpg1 - mpg2 < 0
      Pr(#negative >= 8) =
         Binomial(n = 11, x >= 8, p = 0.5) =  0.1133
```

```
Two-sided test:
  Ho: median of mpg1 - mpg2 = 0 vs.
  Ha: median of mpg1 - mpg2 != 0
      Pr(#positive >= 8 or #negative >= 8) =
         min(1, 2*Binomial(n = 11, x >= 8, p = 0.5)) =  0.2266
```

The summary table indicates that there were three comparisons for which `mpg1` exceeded `mpg2`, eight comparisons for which `mpg2` exceeded `mpg1`, and one comparison for which they were the same.

The output below the summary table is based on the binomial distribution. The significance of the one-sided test, where the alternative hypothesis is that the median of `mpg2` − `mpg1` is greater than zero, is 0.1133. The significance of the two-sided test, where the alternative hypothesis is simply that the median of the differences is different from zero, is $0.2266 = 2 \times 0.1133$. ◁

Saved results

`signrank` saves the following in `r()`:

Scalars

`r(N_neg)`	number of negative comparisons	`r(sum_neg)`	sum of the negative ranks
`r(N_pos)`	number of positive comparisons	`r(z)`	z statistic
`r(N_tie)`	number of tied comparisons	`r(Var_a)`	adjusted variance
`r(sum_pos)`	sum of the positive ranks		

`signtest` saves the following in `r()`:

Scalars

`r(N_neg)`	number of negative comparisons	`r(p_2)`	two-sided probability
`r(N_pos)`	number of positive comparisons	`r(p_neg)`	one-sided probability of negative comparison
`r(N_tie)`	number of tied comparisons	`r(p_pos)`	one-sided probability of positive comparison

Methods and formulas

`signrank` and `signtest` are implemented as ado-files.

For a practical introduction to these techniques with an emphasis on examples rather than theory, see Bland (2000) or Sprent and Smeeton (2007). For a summary of these tests, see Snedecor and Cochran (1989).

Methods and formulas are presented under the following headings:

signrank
signtest

signrank

Both the sign test and Wilcoxon signed-rank tests test the null hypothesis that the distribution of a random variable $D = \textit{varname} - \textit{exp}$ has median zero. The sign test makes no additional assumptions, but the Wilcoxon signed-rank test makes the additional assumption that the distribution of D is symmetric. If $D = X_1 - X_2$, where X_1 and X_2 have the same distribution, then it follows that the distribution of D is symmetric about zero. Thus the Wilcoxon signed-rank test is often described as a test of the hypothesis that two distributions are the same, that is, $X_1 \sim X_2$.

Let d_j denote the difference for any matched pair of observations,

$$d_j = x_{1j} - x_{2j} = \textit{varname} - \textit{exp}$$

for $j = 1, 2, \ldots, n$.

Rank the absolute values of the differences, $|d_j|$, and assign any tied values the average rank. Consider the signs of d_j, and let

$$r_j = \text{sign}(d_j)\,\text{rank}(|d_j|)$$

be the signed ranks. The test statistic is

$$T_{\text{obs}} = \sum_{j=1}^{n} r_j = (\text{sum of ranks for } + \text{ signs}) - (\text{sum of ranks for } - \text{ signs})$$

The null hypothesis is that the distribution of d_j is symmetric about 0. Hence the likelihood is unchanged if we flip signs on the d_j, and thus the randomization datasets are the 2^n possible sign changes for the d_j. Thus the randomization distribution of our test statistic T can be computed by considering all the 2^n possible values of

$$T = \sum_{j=1}^{n} S_j r_j$$

where the r_j are the observed signed ranks (considered fixed) and S_j is either $+1$ or -1.

With this distribution, the mean and variance of T are given by

$$E(T) = 0 \qquad \text{and} \qquad \text{Var}_{\text{adj}}(T) = \sum_{j=1}^{n} r_j^2$$

The test statistic for the Wilcoxon signed-rank test is often expressed (equivalently) as the sum of the positive signed-ranks, T_+, where

$$E(T_+) = \frac{n(n+1)}{4} \qquad \text{and} \qquad \text{Var}_{\text{adj}}(T_+) = \frac{1}{4}\sum_{j=1}^{n} r_j^2$$

Zeros and ties do not affect the theory above, and the exact variance is still given by the above formula for $\text{Var}_{\text{adj}}(T_+)$. When $d_j = 0$ is observed, d_j will always be zero in each of the randomization datasets (using $\text{sign}(0) = 0$). When there are ties, you can assign averaged ranks for each group of ties and then treat them the same as the other ranks.

The "unadjusted variance" reported by `signrank` is the variance that the randomization distribution would have had if there had been no ties or zeros:

$$\text{Var}_{\text{unadj}}(T_+) = \frac{1}{4}\sum_{j=1}^{n} j^2 = \frac{n(n+1)(2n+1)}{24}$$

The adjustment for zeros is the change in the variance when the ranks for the zeros are signed to make $r_j = 0$,

$$\Delta\text{Var}_{\text{zero adj}}(T_+) = -\frac{1}{4}\sum_{j=1}^{n_0} j^2 = -\frac{n_0(n_0+1)(2n_0+1)}{24}$$

where n_0 is the number of zeros. The adjustment for ties is the change in the variance when the ranks (for nonzero observations) are replaced by averaged ranks:

$$\Delta\mathrm{Var}_{\text{ties adj}}(T_+) = \mathrm{Var}_{\text{adj}}(T_+) - \mathrm{Var}_{\text{unadj}}(T_+) - \Delta\mathrm{Var}_{\text{zero adj}}(T_+)$$

A normal approximation is used to calculate

$$z = \frac{T_+ - E(T_+)}{\sqrt{\mathrm{Var}_{\text{adj}}(T_+)}}$$

signtest

The test statistic for the sign test is the number n_+ of differences

$$d_j = x_{1j} - x_{2j} = \textit{varname} - \textit{exp}$$

greater than zero. Assuming that the probability of a difference being equal to zero is exactly zero, then, under the null hypothesis, $n_+ \sim \text{binomial}(n, p = 1/2)$, where n is the total number of observations.

But what if some differences are zero? This question has a ready answer if you view the test from the perspective of Fisher's Principle of Randomization (Fisher 1935). Fisher's idea (stated in a modern way) was to look at a family of transformations of the observed data such that the a priori likelihood (under the null hypothesis) of the transformed data is the same as the likelihood of the observed data. The distribution of the test statistic is then produced by calculating its value for each of the transformed "randomization" datasets, assuming that each dataset is equally likely.

For the sign test, the "data" are simply the set of signs of the differences. Under the null hypothesis of the sign test, the probability that d_j is less than zero is equal to the probability that d_j is greater than zero. Thus you can transform the observed signs by flipping any number of them, and the set of signs will have the same likelihood. The 2^n possible sign changes form the family of randomization datasets. If you have no zeros, this procedure again leads to $n_+ \sim \text{binomial}(n, p = 1/2)$.

If you do have zeros, changing their signs leaves them as zeros. So, if you observe n_0 zeros, each of the 2^n sign-change datasets will also have n_0 zeros. Hence, the values of n_+ calculated over the sign-change datasets range from 0 to $n - n_0$, and the "randomization" distribution of n_+ is $\text{binomial}(n - n_0, p = 1/2)$.

The work of Arbuthnott (1710) and later eighteenth-century contributions is discussed by Hald (2003, chap. 17).

Frank Wilcoxon (1892–1965) was born in Ireland to American parents. After working in various occupations (including merchant seaman, oil-well pump attendant, and tree surgeon), he settled in chemistry, gaining degrees from Rutgers and Cornell and employment from various companies. Working mainly on the development of fungicides and insecticides, Wilcoxon became interested in statistics in 1925 and made several key contributions to nonparametric methods. After retiring from industry, he taught statistics at Florida State until his death.

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Also see

[R] **ranksum** — Equality tests on unmatched data

[R] **ttest** — Mean-comparison tests

Title

simulate — Monte Carlo simulations

Syntax

`simulate` [*exp_list*] `,` `reps(#)` [*options*] `:` *command*

options	Description
`nodots`	suppress replication dots
`noisily`	display any output from *command*
`trace`	trace *command*
`saving(`*filename*`, ...)`	save results to *filename*
`nolegend`	suppress table legend
`verbose`	display the full table legend
`seed(#)`	set random-number seed to #

All weight types supported by *command* are allowed; see [U] **11.1.6 weight**.

exp_list contains	(*name*: *elist*)
	elist
	eexp
elist contains	*newvar* = (*exp*)
	(*exp*)
eexp is	*specname*
	[*eqno*]*specname*
specname is	_b
	_b[]
	_se
	_se[]
eqno is	##
	name

exp is a standard Stata expression; see [U] **13 Functions and expressions**.

Distinguish between `[]`, which are to be typed, and [], which indicate optional arguments.

Description

`simulate` eases the programming task of performing Monte Carlo–type simulations. Typing

```
. simulate exp_list, reps(#): command
```

runs *command* for # replications and collects the results in *exp_list*.

command defines the command that performs one simulation. Most Stata commands and user-written programs can be used with `simulate`, as long as they follow standard Stata syntax; see [U] **11 Language syntax**. The `by` prefix may not be part of *command*.

exp_list specifies the expression to be calculated from the execution of *command*. If no expressions are given, *exp_list* assumes a default, depending upon whether *command* changes results in `e()` or `r()`. If *command* changes results in `e()`, the default is `_b`. If *command* changes results in `r()` (but not `e()`), the default is all the scalars posted to `r()`. It is an error not to specify an expression in *exp_list* otherwise.

Options

`reps(#)` is required—it specifies the number of replications to be performed.

`nodots` suppresses display of the replication dots. By default, one dot character is displayed for each successful replication. A red 'x' is displayed if *command* returns an error or if one of the values in *exp_list* is missing.

`noisily` requests that any output from *command* be displayed. This option implies the `nodots` option.

`trace` causes a trace of the execution of *command* to be displayed. This option implies the `noisily` option.

`saving(`*filename*`[ , `*suboptions*`])` creates a Stata data file (`.dta` file) consisting of (for each statistic in *exp_list*) a variable containing the simulated values.

`double` specifies that the results for each replication be stored as `doubles`, meaning 8-byte reals. By default, they are stored as `floats`, meaning 4-byte reals.

`every(#)` specifies that results be written to disk every #th replication. `every()` should be specified only in conjunction with `saving()` when *command* takes a long time for each replication. This will allow recovery of partial results should some other software crash your computer. See [P] **postfile**.

`replace` specifies that *filename* be overwritten if it exists.

`nolegend` suppresses display of the table legend. The table legend identifies the rows of the table with the expressions they represent.

`verbose` requests that the full table legend be displayed. By default, coefficients and standard errors are not displayed.

`seed(#)` sets the random-number seed. Specifying this option is equivalent to typing the following command before calling `simulate`:

```
. set seed #
```

Remarks

For an introduction to Monte Carlo methods, see Cameron and Trivedi (2010, chap. 4). White (2010) provides a command for analyzing results of simulation studies.

▷ Example 1

We have a dataset containing means and variances of 100-observation samples from a lognormal distribution (as a first step in evaluating, say, the coverage of a 95%, t-based confidence interval). Then we perform the experiment 1,000 times.

The following command definition will generate 100 independent observations from a lognormal distribution and compute the summary statistics for this sample.

```
program lnsim, rclass
        version 12
        drop _all
        set obs 100
        gen z = exp(rnormal())
        summarize z
        return scalar mean = r(mean)
        return scalar Var  = r(Var)
end
```

We can save 1,000 simulated means and variances from `lnsim` by typing

```
. set seed 1234
. simulate mean=r(mean) var=r(Var), reps(1000) nodots: lnsim
      command:  lnsim
         mean:  r(mean)
          var:  r(Var)
. describe *
              storage  display     value
variable name   type   format      label      variable label
------------------------------------------------------------------------------
mean            float  %9.0g                  r(mean)
var             float  %9.0g                  r(Var)
. summarize
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
        mean |      1000    1.638466     .214371   1.095099   2.887392
         var |      1000     4.63856    6.428406      .8626   175.3746
```

◁

❑ Technical note

Before executing our `lnsim` simulator, we can verify that it works by executing it interactively.

```
. set seed 1234
. lnsim
obs was 0, now 100
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
           z |       100    1.597757    1.734328   .0625807   12.71548
. return list
scalars:
                 r(Var) =  3.007893773683719
                r(mean) =  1.59775722913444
```

❑

▷ Example 2

Consider a more complicated problem. Let's experiment with fitting $y_j = a + bx_j + u_j$ when the true model has $a = 1$, $b = 2$, $u_j = z_j + cx_j$, and when z_j is $N(0, 1)$. We will save the parameter estimates and standard errors and experiment with varying c. x_j will be fixed across experiments but will originally be generated as $N(0, 1)$. We begin by interactively making the true data:

```
. drop _all
. set obs 100
obs was 0, now 100
. set seed 54321
. gen x = rnormal()
. gen true_y = 1+2*x
. save truth
file truth.dta saved
```

Our program is

```
program hetero1
        version 12
        args c
        use truth, clear
        gen y = true_y + (rnormal() + `c'*x)
        regress y x
end
```

Note the use of `` `c' `` in our statement for generating `y`. `c` is a local macro generated from `args c` and thus refers to the first argument supplied to `hetero1`. If we want $c = 3$ for our experiment, we type

```
. simulate _b _se, reps(10000): hetero1 3
```

(*output omitted*)

Our program `hetero1` could, however, be more efficient because it rereads the file `truth` once every replication. It would be better if we could read the data just once. In fact, if we read in the data right before running `simulate`, we really should not have to reread for each subsequent replication. A faster version reads

```
program hetero2
        version 12
        args c
        capture drop y
        gen y = true_y + (rnormal() + `c'*x)
        regress y x
end
```

Requiring that the current dataset has the variables `true_y` and `x` may become inconvenient. Another improvement would be to require that the user supply variable names, such as in

```
program hetero3
        version 12
        args truey x c
        capture drop y
        gen y = `truey' + (rnormal() + `c'*`x')
        regress y x
end
```

Thus we can type

```
. simulate _b _se, reps(10000): hetero3 true_y x 3
```

(*output omitted*)

◁

▷ Example 3

Now let's consider the problem of simulating the ratio of two medians. Suppose that each sample of size n_i comes from a normal population with a mean μ_i and standard deviation σ_i, where $i = 1, 2$. We write the program below and save it as a text file called `myratio.ado` (see [U] **17 Ado-files**). Our program is an `rclass` command that requires six arguments as input, identified by the local macros `n1`, `mu1`, `sigma1`, `n2`, `mu2`, and `sigma2`, which correspond to n_1, μ_1, σ_1, n_2, μ_2, and σ_2, respectively. With these arguments, `myratio` will generate the data for the two samples, use `summarize` to compute the two medians and save the ratio of the medians in `r(ratio)`.

```
program myratio, rclass
        version 12
        args n1 mu1 sigma1 n2 mu2 sigma2
        // generate the data
        drop _all
        local N = `n1'+`n2'
        set obs `N'
        tempvar y
        generate `y' = rnormal()
        replace `y' = cond(_n<=`n1',`mu1'+`y'*`sigma1',`mu2'+`y'*`sigma2')
        // calculate the medians
        tempname m1
        summarize `y' if _n<=`n1', detail
        scalar `m1' = r(p50)
        summarize `y' if _n>`n1', detail
        // save the results
        return scalar ratio = `m1' / r(p50)
end
```

The result of running our simulation is

```
. set seed 19192
. simulate ratio=r(ratio), reps(1000) nodots: myratio 5 3 1 10 3 2
      command:  myratio 5 3 1 10 3 2
        ratio:  r(ratio)
. summarize
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       ratio |       1000     1.08571    .4427828    .3834799   6.742217
```

◁

❑ Technical note

Stata lets us do simulations of simulations and simulations of bootstraps. Stata's `bootstrap` command (see [R] **bootstrap**) works much like `simulate`, except that it feeds the user-written program a bootstrap sample. Say that we want to evaluate the bootstrap estimator of the standard error of the median when applied to lognormally distributed data. We want to perform a simulation, resulting in a dataset of medians and bootstrap estimated standard errors.

As background, `summarize` (see [R] **summarize**) calculates summary statistics, leaving the mean in `r(mean)` and the standard deviation in `r(sd)`. `summarize` with the `detail` option also calculates summary statistics, but more of them, and leaves the median in `r(p50)`.

Thus our plan is to perform simulations by randomly drawing a dataset: we calculate the median of our random sample, we use `bootstrap` to obtain a dataset of medians calculated from bootstrap samples of our random sample, the standard deviation of those medians is our estimate of the standard error, and the summary statistics are saved in the results of `summarize`.

Our simulator is

```
program define bsse, rclass
        version 12
        drop _all
        set obs 100
        gen x = rnormal()
        tempfile bsfile
        bootstrap midp=r(p50), rep(100) saving(‘bsfile’): summarize x, detail
        use ‘bsfile’, clear
        summarize midp
        return scalar mean = r(mean)
        return scalar sd   = r(sd)
end
```

We can obtain final results, running our simulation 1,000 times, by typing

```
. set seed 48901
. simulate med=r(mean) bs_se=r(sd), reps(1000): bsse
      command:  bsse
          med:  r(mean)
        bs_se:  r(sd)
Simulations (1000)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................   50
..................................................  100
..................................................  150
..................................................  200
..................................................  250
..................................................  300
..................................................  350
..................................................  400
..................................................  450
..................................................  500
..................................................  550
..................................................  600
..................................................  650
..................................................  700
..................................................  750
..................................................  800
..................................................  850
..................................................  900
..................................................  950
.................................................. 1000
. summarize
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
         med |      1000   -.0008696    .1210451  -.3132536   .4058724
       bs_se |      1000     .126236     .029646   .0326791   .2596813
```

This is a case where the simulation dots (drawn by default, unless the `nodots` option is specified) will give us an idea of how long this simulation will take to finish as it runs. ❑

Methods and formulas

`simulate` is implemented as an ado-file.

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Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **jackknife** — Jackknife estimation

[R] **permute** — Monte Carlo permutation tests

Title

sj — Stata Journal and STB installation instructions

Description

The *Stata Journal* (SJ) is a quarterly journal containing articles about statistics, data analysis, teaching methods, and effective use of Stata's language. The SJ publishes reviewed papers together with shorter notes and comments, regular columns, tips, book reviews, and other material of interest to researchers applying statistics in a variety of disciplines. You can read all about the *Stata Journal* at http://www.stata-journal.com.

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The predecessor to the *Stata Journal* was the *Stata Technical Bulletin* (STB). The STB was also a printed and electronic journal with corresponding software. PDF copies of all STB journals are available for download for no charge at http://www.stata-press.com/journals/stbj.html. The STB software is available for no charge from our website at http://www.stata.com.

Below are instructions for installing the *Stata Journal* and the *Stata Technical Bulletin* software from our website.

Remarks

Remarks are presented under the following headings:

Installing the Stata Journal software
    Obtaining from the Internet by pointing and clicking
    Obtaining from the Internet via command mode
Installing the STB software
    Obtaining from the Internet by pointing and clicking
    Obtaining from the Internet via command mode

Installing the Stata Journal software

Each issue of the *Stata Journal* is labeled Volume #, Number #. Volume 1 refers to the first year of publication, Volume 2 to the second, and so on. Issues are numbered 1, 2, 3, and 4 within each year. The first issue of the *Journal* was published in the fourth quarter of 2001, and that issue is numbered Volume 1, Number 1. For installation purposes, we refer to this issue as `sj1-1`.

The articles, columns, notes, and comments that make up the *Stata Journal* are assigned a letter-and-number code, called an insert tag, such as st0001, an0034, or ds0011. The letters represent a category: st is the statistics category, an is the announcements category, etc. The numbers are assigned sequentially, so st0001 is the first article in the statistics category.

Sometimes inserts are subsequently updated, either to fix bugs or to add new features. A number such as st0001_1 indicates that this article, column, note, or comment is an update to the original st0001 article. Updates are complete; that is, installing st0001_1 provides all the features of the original article and more.

The *Stata Journal* software may be obtained by pointing and clicking or by using command mode.

The sections below detail how to install an insert. In all cases, pretend that you wish to install insert st0001_1 from sj2-2.

Obtaining from the Internet by pointing and clicking

1. Select **Help > SJ and User-written Programs**.
2. Click on *Stata Journal*.
3. Click on *sj2-2*.
4. Click on *st0001_1*.
5. Click on *(click here to install)*.

Obtaining from the Internet via command mode

Type the following:

```
. net from http://www.stata-journal.com/software
. net cd sj2-2
. net describe st0001_1
. net install st0001_1
```

The above could be shortened to

```
. net from http://www.stata-journal.com/software/sj2-2
. net describe st0001_1
. net install st0001_1
```

Alternatively, you could type

```
. net sj 2-2
. net describe st0001_1
. net install st0001_1
```

but going about it the long way is more entertaining, at least the first time.

Installing the STB software

Each issue of the STB is numbered. STB-1 refers to the first issue (published May 1991), STB-2 refers to the second (published July 1991), and so on.

An issue of the STB consists of inserts—articles—and these are assigned letter-and-number combinations, such as sg84, dm80, sbe26.1, etc. The letters represent a category; for example, sg is the general statistics category and dm the data-management category. The numbers are assigned sequentially, so sbe39 is the 39th insert in the biostatistics and epidemiology series.

Insert sbe39, it turns out, provides a method of accounting for publication bias in meta-analysis; it adds a new command called `metatrim` to Stata. If you installed sbe39, you would have that command and its online help. Insert sbe39 was published in STB-57 (September 2000). Obtaining `metatrim` simply requires going to STB-57 and getting sbe39.

Sometimes inserts were subsequently updated, either to fix bugs or to add new features. sbe39 was updated: the first update is sbe39.1 and the second is sbe39.2. You could install insert sbe39.2, and it would not matter whether you had previously installed sbe39.1. Updates are complete: installing sbe39.2 provides all the features of the original insert and more.

For computer naming purposes, insert sbe39.2 is referred to as `sbe39_2`. When referred to in normal text, however, the insert is still called sbe39.2 because that looks nicer.

Inserts are easily available from the Internet. Inserts may be obtained by pointing and clicking or by using command mode.

The sections below detail how to install an insert. In all cases, pretend that you wish to install insert sbe39.2 from STB-61.

Obtaining from the Internet by pointing and clicking

1. Select **Help > SJ and User-written Programs**.
2. Click on *STB*.
3. Click on *stb61*.
4. Click on *sbe39_2*.
5. Click on *(click here to install)*.

Obtaining from the Internet via command mode

Type the following:

```
. net from http://www.stata.com
. net cd stb
. net cd stb61
. net describe sbe39_2
. net install sbe39_2
```

The above could be shortened to

```
. net from http://www.stata.com/stb/stb61
. net describe sbe39_2
. net install sbe39_2
```

but going about it the long way is more entertaining, at least the first time.

Also see

[R] **search** — Search Stata documentation

[R] **net** — Install and manage user-written additions from the Internet

[R] **net search** — Search the Internet for installable packages

[R] **update** — Update Stata

[U] **3.5 The Stata Journal**

[U] **28 Using the Internet to keep up to date**

[GSM] **19 Updating and extending Stata—Internet functionality**

[GSU] **19 Updating and extending Stata—Internet functionality**

[GSW] **19 Updating and extending Stata—Internet functionality**

Title

sktest — Skewness and kurtosis test for normality

Syntax

`sktest` *varlist* [*if*] [*in*] [*weight*] [`,` `noadjust`]

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Distributional plots and tests > Skewness and kurtosis normality test

Description

For each variable in *varlist*, `sktest` presents a test for normality based on skewness and another based on kurtosis and then combines the two tests into an overall test statistic. `sktest` requires a minimum of 8 observations to make its calculations. See [MV] **mvtest normality** for multivariate tests of normality.

Option

Main

`noadjust` suppresses the empirical adjustment made by Royston (1991c) to the overall χ^2 and its significance level and presents the unaltered test as described by D'Agostino, Belanger, and D'Agostino (1990).

Remarks

Also see [R] **swilk** for the Shapiro–Wilk and Shapiro–Francia tests for normality. Those tests are, in general, preferred for nonaggregated data (Gould and Rogers 1991; Gould 1992; Royston 1991c). Moreover, a normal quantile plot should be used with any test for normality; see [R] **diagnostic plots** for more information.

▷ Example 1

Using our automobile dataset, we will test whether the variables `mpg` and `trunk` are normally distributed:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. sktest mpg trunk
                    Skewness/Kurtosis tests for Normality
                                                       ------- joint ------
    Variable |   Obs   Pr(Skewness)   Pr(Kurtosis)  adj chi2(2)    Prob>chi2
-------------+-------------------------------------------------------------
         mpg |    74        0.0015          0.0804        10.95          0.0042
       trunk |    74        0.9115          0.0445         4.19          0.1228
```

We can reject the hypothesis that mpg is normally distributed, but we cannot reject the hypothesis that trunk is normally distributed, at least at the 12% level. The kurtosis for trunk is 2.19, as can be verified by issuing the command

```
. summarize trunk, detail
```
(*output omitted*)

and the p-value of 0.0445 shown in the table above indicates that it is significantly different from the kurtosis of a normal distribution at the 5% significance level. However, on the basis of skewness alone, we cannot reject the hypothesis that trunk is normally distributed.

◁

❑ Technical note

sktest implements the test as described by D'Agostino, Belanger, and D'Agostino (1990) but with the adjustment made by Royston (1991c). In the above example, if we had specified the noadjust option, the χ^2 values would have been 13.13 for mpg and 4.05 for trunk. With the adjustment, the χ^2 value might show as '.'. This result should be interpreted as an absurdly large number; the data are most certainly not normal.

❑

Saved results

sktest saves the following in r():

Scalars

r(chi2)	χ^2
r(P_skew)	Pr(skewness)
r(P_kurt)	Pr(kurtosis)
r(P_chi2)	Prob > chi2

Matrices

r(N)	matrix of observations
r(Utest)	matrix of test results, one row per variable

Methods and formulas

sktest is implemented as an ado-file.

sktest implements the test described by D'Agostino, Belanger, and D'Agostino (1990) with the empirical correction developed by Royston (1991c).

Let g_1 denote the coefficient of skewness and b_2 denote the coefficient of kurtosis as calculated by summarize, and let n denote the sample size. If weights are specified, then g_1, b_2, and n denote the weighted coefficients of skewness and kurtosis and weighted sample size, respectively. See [R] **summarize** for the formulas for skewness and kurtosis.

To perform the test of skewness, we compute

$$Y = g_1 \left\{ \frac{(n+1)(n+3)}{6(n-2)} \right\}^{1/2}$$

$$\beta_2(g_1) = \frac{3(n^2+27n-70)(n+1)(n+3)}{(n-2)(n+5)(n+7)(n+9)}$$

$$W^2 = -1 + \left[2\left\{\beta_2(g_1) - 1\right\}\right]^{1/2}$$

and

$$\alpha = \left\{2/(W^2-1)\right\}^{1/2}$$

Then the distribution of the test statistic

$$Z_1 = \frac{1}{\sqrt{\ln W}} \ln\left[Y/\alpha + \left\{ (Y/\alpha)^2 + 1 \right\}^{1/2} \right]$$

is approximately standard normal under the null hypothesis that the data are distributed normally.

To perform the test of kurtosis, we compute

$$E(b_2) = \frac{3(n-1)}{n+1}$$

$$\mathrm{var}(b_2) = \frac{24n(n-2)(n-3)}{(n+1)^2(n+3)(n+5)}$$

$$X = \left\{ b_2 - E(b_2) \right\} / \sqrt{\mathrm{var}(b_2)}$$

$$\sqrt{\beta_1(b_2)} = \frac{6(n^2-5n+2)}{(n+7)(n+9)} \left\{ \frac{6(n+3)(n+5)}{n(n-2)(n-3)} \right\}^{1/2}$$

and

$$A = 6 + \frac{8}{\sqrt{\beta_1(b_2)}} \left[\frac{2}{\sqrt{\beta_1(b_2)}} + \left\{ 1 + \frac{4}{\beta_1(b_2)} \right\}^{1/2} \right]$$

Then the distribution of the test statistic

$$Z_2 = \frac{1}{\sqrt{2/(9A)}} \left[\left(1 - \frac{2}{9A} \right) - \left\{ \frac{1-2/A}{1+X\sqrt{2/(A-4)}} \right\}^{1/3} \right]$$

is approximately standard normal under the null hypothesis that the data are distributed normally.

D'Agostino, Balanger, and D'Agostino Jr.'s omnibus test of normality uses the statistic

$$K^2 = Z_1^2 + Z_2^2$$

which has approximately a χ^2 distribution with 2 degrees of freedom under the null of normality.

Royston (1991c) proposed the following adjustment to the test of normality, which `sktest` uses by default. Let $\Phi(x)$ denote the cumulative standard normal distribution function for x, and let $\Phi^{-1}(p)$ denote the inverse cumulative standard normal function [that is, $x = \Phi^{-1}\left\{\Phi(x)\right\}$]. Define the following terms:

$$Z_c = -\Phi^{-1}\left\{\exp\left(-\frac{1}{2}K^2\right)\right\}$$
$$Z_t = 0.55n^{0.2} - 0.21$$
$$a_1 = (-5 + 3.46\ln n)\exp(-1.37\ln n)$$
$$b_1 = 1 + (0.854 - 0.148\ln n)\exp(-0.55\ln n)$$
$$a_2 = a_1 - \{2.13/(1 - 2.37\ln n)\}\, Z_t$$

and

$$b_2 = 2.13/(1 - 2.37\ln n) + b1$$

If $Z_c < -1$ set $Z = Z_c$; else if $Z_c < Z_t$ set $Z = a_1 + b_1 Z_c$; else set $Z = a_2 + b_2 Z_c$. Define $P = 1 - \Phi(Z)$. Then $K^2 = -2\ln P$ is approximately distributed χ^2 with 2 degrees of freedom.

The relative merits of the skewness and kurtosis test versus the Shapiro–Wilk and Shapiro–Francia tests have been a subject of debate. The interested reader is directed to the articles in the *Stata Technical Bulletin*. Our recommendation is to use the Shapiro–Francia test whenever possible, that is, whenever dealing with nonaggregated or ungrouped data (Gould and Rogers 1991; Gould 1992); see [R] **swilk**. If normality is rejected, use `sktest` to determine the source of the problem.

As both D'Agostino, Belanger, and D'Agostino (1990) and Royston (1991d) mention, researchers should also examine the normal quantile plot to determine normality rather than blindly relying on a few test statistics. See the `qnorm` command documented in [R] **diagnostic plots** for more information on normal quantile plots.

`sktest` is similar in spirit to the Jarque–Bera (1987) test of normality. The Jarque–Bera test statistic is also calculated from the sample skewness and kurtosis, though it is based on asymptotic standard errors with no corrections for sample size. In effect, `sktest` offers two adjustments for sample size, that of Royston (1991c) and that of D'Agostino, Belanger, and D'Agostino (1990).

Acknowledgments

`sktest` has benefited greatly by the comments and work of Patrick Royston of the MRC Clinical Trials Unit, London; at this point, the program should be viewed as due as much to Royston as to us, except, of course, for any errors. We are also indebted to Nicholas J. Cox, Durham University, for helpful comments.

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Also see

[R] **diagnostic plots** — Distributional diagnostic plots

[R] **ladder** — Ladder of powers

[R] **lv** — Letter-value displays

[R] **swilk** — Shapiro–Wilk and Shapiro–Francia tests for normality

[MV] **mvtest normality** — Multivariate normality tests

Title

slogit — Stereotype logistic regression

Syntax

`slogit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`dimension(#)`	dimension of the model; default is `dimension(1)`
`baseoutcome(#|lbl)`	set the base outcome to # or *lbl*; default is the last outcome
`constraints(`*numlist*`)`	apply specified linear constraints
`collinear`	keep collinear variables
`nocorner`	do not generate the corner constraints
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`initialize(`*initype*`)`	method of initializing scale parameters; *initype* can be `constant`, `random`, or `svd`; see *Options* for details
`nonormalize`	do not normalize the numeric variables
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Categorical outcomes > Stereotype logistic regression

Description

`slogit` fits maximum-likelihood stereotype logistic regression models as developed by Anderson (1984). Like multinomial logistic and ordered logistic models, stereotype logistic models are for use with categorical dependent variables. In a multinomial logistic model, the categories cannot be ranked, whereas in an ordered logistic model the categories follow a natural ranking scheme. You can view stereotype logistic models as a compromise between those two models. You can use them when you are unsure of the relevance of the ordering, as is often the case when subjects are asked to assess or judge something. You can also use them in place of multinomial logistic models when you suspect that some of the alternatives are similar. Unlike ordered logistic models, stereotype logistic models do not impose the proportional-odds assumption.

Options

Model

`dimension(#)` specifies the dimension of the model, which is the number of equations required to describe the relationship between the dependent variable and the independent variables. The maximum dimension is $\min(m-1, p)$, where m is the number of categories of the dependent variable and p is the number of independent variables in the model. The stereotype model with maximum dimension is a reparameterization of the multinomial logistic model.

`baseoutcome(#|`*lbl*`)` specifies the outcome level whose scale parameters and intercept are constrained to be zero. The base outcome may be specified as a number of a label. By default, `slogit` assumes that the outcome levels are ordered and uses the largest level of the dependent variable as the base outcome.

`constraints(`*numlist*`)`, `collinear`; see [R] **estimation options**.

By default, the linear equality constraints suggested by Anderson (1984), termed the corner constraints, are generated for you. You can add constraints to these as needed, or you can turn off the corner constraints by specifying `nocorner`. These constraints are in addition to the constraints placed on the ϕ parameters corresponding to `baseoutcome(#)`.

`nocorner` specifies that `slogit` not generate the corner constraints. If you specify `nocorner`, you must specify at least `dimension()` $\times$ `dimension()` constraints for the model to be identified.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

If specifying `vce(bootstrap)` or `vce(jackknife)`, you must also specify `baseoutcome()`.

Reporting

`level(#)`; see [R] **estimation options**.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

initialize(constant | random | svd) specifies how initial estimates are computed. The default, initialize(constant), is to set the scale parameters to the constant $\min(1/2, 1/d)$, where d is the dimension specified in dimension().

initialize(random) requests that uniformly distributed random numbers between 0 and 1 be used as initial values for the scale parameters. If you specify this option, you should also use set seed to ensure that you can replicate your results; see [R] **set seed**.

initialize(svd) requests that a singular value decomposition (SVD) be performed on the matrix of regression estimates from mlogit to reduce its rank to the dimension specified in dimension(). slogit uses the reduced-rank components of the SVD as initial estimates for the scale and regression coefficients. For details, see *Methods and formulas*.

nonormalize specifies that the numeric variables not be normalized. Normalization of the numeric variables improves numerical stability but consumes more memory in generating temporary double-precision variables. Variables that are of type byte are not normalized, and if initial estimates are specified using the from() option, normalization of variables is not performed. See *Methods and formulas* for more information.

The following option is available with slogit but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
One-dimensional model
Higher-dimension models

Introduction

Stereotype logistic models are often used when subjects are requested to assess or judge something. For example, consider a survey in which consumers may be asked to rate the quality of a product on a scale from 1 to 5, with 1 indicating poor quality and 5 indicating excellent quality. If the categories are monotonically related to an underlying latent variable, the ordered logistic model is appropriate. However, suppose that consumers assess quality not just along one dimension, but rather weigh two or three latent factors. Stereotype logistic regression allows you to specify multiple equations to capture the effects of those latent variables, which you then parameterize in terms of observable characteristics. Unlike with multinomial logit, the number of equations you specify could be less than $m - 1$, where m is the number of categories of the dependent variable.

Stereotype logistic models are also used when categories may be indistinguishable. Suppose that a consumer must choose among A, B, C, or D. Multinomial logistic modeling assumes that the four choices are distinct in the sense that a consumer choosing one of the goods can distinguish its characteristics from the others. If goods A and B are in fact similar, consumers may be randomly picking between the two. One alternative is to combine the two categories and fit a three-category multinomial logistic model. A more flexible alternative is to use a stereotype logistic model.

In the multinomial logistic model, you estimate $m-1$ parameter vectors $\widetilde{\boldsymbol{\beta}}_k$, $k = 1, \ldots, m-1$, where m is the number of categories of the dependent variable. The stereotype logistic model is a restriction on the multinomial model in the sense that there are d parameter vectors, where d is between one and $\min(m-1, p)$, and p is the number of regressors. The relationship between the stereotype model's coefficients $\boldsymbol{\beta}_j$, $j = 1, \ldots, d$, and the multinomial model's coefficients is $\widetilde{\boldsymbol{\beta}}_k = -\sum_{j=1}^{d} \phi_{jk}\boldsymbol{\beta}_j$. The ϕs are scale parameters to be estimated along with the $\boldsymbol{\beta}_j$s.

Given a row vector of covariates $\mathbf{x}$, let $\eta_k = \theta_k - \sum_{j=1}^{d} \phi_{jk}\mathbf{x}\boldsymbol{\beta}_j$. The probability of observing outcome k is

$$\Pr(Y_i = k) = \begin{cases} \dfrac{\exp(\eta_k)}{1 + \sum_{l=1}^{m-1} \exp(\eta_l)} & k < m \\ \dfrac{1}{1 + \sum_{l=1}^{m-1} \exp(\eta_l)} & k = m \end{cases}$$

This model includes a set of θ parameters so that each equation has an unrestricted constant term. If $d = m-1$, the stereotype model is just a reparameterization of the multinomial logistic model. To identify the ϕs and the $\boldsymbol{\beta}$s, you must place at least d^2 restrictions on the parameters. By default, `slogit` uses the "corner constraints" $\phi_{jj} = 1$ and $\phi_{jk} = 0$ for $j \neq k$, $k \leq d$, and $j \leq d$.

For a discussion of the stereotype logistic model, see Lunt (2005).

One-dimensional model

▷ Example 1

We have 2 years of repair rating data on the make, price, mileage rating, and gear ratio of 104 foreign and 44 domestic automobiles (with 13 missing values on repair rating). We wish to fit a stereotype logistic model to discriminate between the levels of repair rating using mileage, price, gear ratio, and origin of the manufacturer. Here is an overview of our data:

```
. use http://www.stata-press.com/data/r12/auto2yr
(Automobile Models)
. tabulate repair
```

repair	Freq.	Percent	Cum.
Poor	5	3.70	3.70
Fair	19	14.07	17.78
Average	57	42.22	60.00
Good	38	28.15	88.15
Excellent	16	11.85	100.00
Total	135	100.00	

The variable `repair` can take five values, 1, ..., 5, which represent the subjective rating of the car model's repair record as *Poor*, *Fair*, *Average*, *Good*, and *Excellent*.

We wish to fit the one-dimensional stereotype logistic model

$$\eta_k = \theta_k - \phi_k\left(\beta_1\texttt{foreign} + \beta_2\texttt{mpg} + \beta_3\texttt{price} + \beta_4\texttt{gratio}\right)$$

for $k < 5$ and $\eta_5 = 0$. To fit this model, we type

```
. slogit repair foreign mpg price gratio
Iteration 0:   log likelihood = -173.78178  (not concave)
Iteration 1:   log likelihood = -164.77316
Iteration 2:   log likelihood =  -161.7069
Iteration 3:   log likelihood = -159.76138
Iteration 4:   log likelihood = -159.34327
Iteration 5:   log likelihood = -159.25914
Iteration 6:   log likelihood = -159.25691
Iteration 7:   log likelihood = -159.25691
Stereotype logistic regression                  Number of obs   =        135
                                                Wald chi2(4)    =       9.33
Log likelihood = -159.25691                     Prob > chi2     =     0.0535
 ( 1)  [phi1_1]_cons = 1
```

repair	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
foreign	5.947382	2.094126	2.84	0.005	1.84297	10.05179
mpg	.1911968	.08554	2.24	0.025	.0235414	.3588521
price	-.0000576	.0001357	-0.42	0.671	-.0003236	.0002083
gratio	-4.307571	1.884713	-2.29	0.022	-8.00154	-.6136017
/phi1_1	1	(constrained)				
/phi1_2	1.262268	.3530565	3.58	0.000	.5702904	1.954247
/phi1_3	1.17593	.3169397	3.71	0.000	.5547394	1.79712
/phi1_4	.8657195	.2411228	3.59	0.000	.3931275	1.338311
/phi1_5	0	(base outcome)				
/theta1	-6.864749	4.21252	-1.63	0.103	-15.12114	1.391639
/theta2	-7.613977	4.861803	-1.57	0.117	-17.14294	1.914981
/theta3	-5.80655	4.987508	-1.16	0.244	-15.58189	3.968786
/theta4	-3.85724	3.824132	-1.01	0.313	-11.3524	3.637922
/theta5	0	(base outcome)				

```
(repair=Excellent is the base outcome)
```

The coefficient associated with the first scale parameter, ϕ_{11}, is 1, and its standard error and other statistics are missing. This is the corner constraint applied to the one-dimensional model; in the header, this constraint is listed as `[phi1_1]_cons = 1`. Also, the ϕ and θ parameters that are associated with the base outcome are identified. Keep in mind, though, that there are no coefficient estimates for `[phi1_5]_cons` or `[theta5]_cons` in the `ereturn` matrix `e(b)`. The Wald statistic is for a test of the joint significance of the regression coefficients on `foreign`, `mpg`, `price`, and `gratio`.

The one-dimensional stereotype model restricts the multinomial logistic regression coefficients $\widetilde{\boldsymbol{\beta}}_k$, $k = 1, \ldots, m-1$ to be parallel; that is, $\widetilde{\boldsymbol{\beta}}_k = -\phi_k \boldsymbol{\beta}$. As Lunt (2001) discusses, in the one-dimensional stereotype model, one linear combination $\mathbf{x}_i\boldsymbol{\beta}$ best discriminates the outcomes of the dependent variable, and the scale parameters ϕ_k measure the distance between the outcome levels and the linear predictor. If $\phi_1 \geq \phi_2 \geq \cdots \phi_{m-1} \geq \phi_m \equiv 0$, the model suggests that the subjective assessment of the dependent variable is indeed ordered. Here the maximum likelihood estimates of the ϕs are not monotonic, as would be assumed in an ordered logit model.

We test that $\phi_1 = \phi_2$ by typing

```
. test [phi1_2]_cons = [phi1_1]_cons
 ( 1)  - [phi1_1]_cons + [phi1_2]_cons = 0
           chi2(  1) =    0.55
         Prob > chi2 =    0.4576
```

Because the two parameters are not statistically different, we decide to add a constraint to force $\phi_1 = \phi_2$:

```
. constraint 1 [phi1_2]_cons = [phi1_1]_cons
. slogit repair foreign mpg price gratio, constraint(1) nolog
Stereotype logistic regression                  Number of obs   =        135
                                                Wald chi2(4)    =      21.28
Log likelihood = -159.65769                     Prob > chi2     =     0.0003
 ( 1)  [phi1_1]_cons = 1
 ( 2)  - [phi1_1]_cons + [phi1_2]_cons = 0
```

repair	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
foreign	7.166515	1.690177	4.24	0.000	3.853829	10.4792
mpg	.2340043	.0807042	2.90	0.004	.0758271	.3921816
price	-.000041	.0001618	-0.25	0.800	-.0003581	.000276
gratio	-5.218107	1.798717	-2.90	0.004	-8.743528	-1.692686
/phi1_1	1	(constrained)				
/phi1_2	1	(constrained)				
/phi1_3	.9751096	.1286563	7.58	0.000	.7229478	1.227271
/phi1_4	.7209343	.1220353	5.91	0.000	.4817494	.9601191
/phi1_5	0	(base outcome)				
/theta1	-8.293452	4.645182	-1.79	0.074	-17.39784	.8109368
/theta2	-6.958451	4.629292	-1.50	0.133	-16.0317	2.114795
/theta3	-5.620232	4.953981	-1.13	0.257	-15.32986	4.089392
/theta4	-3.745624	3.809189	-0.98	0.325	-11.2115	3.720249
/theta5	0	(base outcome)				

(repair=Excellent is the base outcome)

The ϕ estimates are now monotonically decreasing and the standard errors of the ϕs are small relative to the size of the estimates, so we conclude that, with the exception of outcomes *Poor* and *Fair*, the groups are distinguishable for the one-dimensional model and that the quality assessment can be ordered.

◁

Higher-dimension models

The stereotype logistic model is not limited to ordered categorical dependent variables; you can use it on nominal data to reduce the dimension of the regressions. Recall that a multinomial model fit to a categorical dependent variable with m levels will have $m - 1$ sets of regression coefficients. However, a model with fewer dimensions may fit the data equally well, suggesting that some of the categories are indistinguishable.

▷ Example 2

As discussed in [R] **mlogit**, we have data on the type of health insurance available to 616 psychologically depressed subjects in the United States (Tarlov et al. 1989; Wells et al. 1989). Patients may have either an indemnity (fee-for-service) plan or a prepaid plan, such as an HMO, or may be uninsured. Demographic variables include age, gender, race, and site.

First, we fit the saturated, two-dimensional model that is equivalent to a multinomial logistic model. We choose the base outcome to be 1 (indemnity insurance) because that is the default for `mlogit`.

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)

. slogit insure age male nonwhite i.site, dim(2) base(1)

Iteration 0:   log likelihood = -534.36165
Iteration 1:   log likelihood = -534.36165

Stereotype logistic regression                  Number of obs   =        615
                                                Wald chi2(10)   =      38.17
Log likelihood = -534.36165                     Prob > chi2     =     0.0000

 ( 1)  [phi1_2]_cons = 1
 ( 2)  [phi1_3]_cons = 0
 ( 3)  [phi2_2]_cons = 0
 ( 4)  [phi2_3]_cons = 1
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
dim1						
age	.011745	.0061946	1.90	0.058	-.0003962	.0238862
male	-.5616934	.2027465	-2.77	0.006	-.9590693	-.1643175
nonwhite	-.9747768	.2363213	-4.12	0.000	-1.437958	-.5115955
site						
2	-.1130359	.2101903	-0.54	0.591	-.5250013	.2989296
3	.5879879	.2279351	2.58	0.010	.1412433	1.034733
dim2						
age	.0077961	.0114418	0.68	0.496	-.0146294	.0302217
male	-.4518496	.3674867	-1.23	0.219	-1.17211	.268411
nonwhite	-.2170589	.4256361	-0.51	0.610	-1.05129	.6171725
site						
2	1.211563	.4705127	2.57	0.010	.2893747	2.133751
3	.2078123	.3662926	0.57	0.570	-.510108	.9257327
/phi1_1	0	(base outcome)				
/phi1_2	1	(constrained)				
/phi1_3	0	(omitted)				
/phi2_1	0	(base outcome)				
/phi2_2	0	(omitted)				
/phi2_3	1	(constrained)				
/theta1	0	(base outcome)				
/theta2	.2697127	.3284422	0.82	0.412	-.3740222	.9134476
/theta3	-1.286943	.5923219	-2.17	0.030	-2.447872	-.1260134

(insure=Indemnity is the base outcome)

For comparison, we also fit the model by using `mlogit`:

```
. mlogit insure age male nonwhite i.site, nolog
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(10)     =      42.99
                                                Prob > chi2     =     0.0000
Log likelihood = -534.36165                     Pseudo R2       =     0.0387
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
Indemnity	(base outcome)					
Prepaid						
age	-.011745	.0061946	-1.90	0.058	-.0238862	.0003962
male	.5616934	.2027465	2.77	0.006	.1643175	.9590693
nonwhite	.9747768	.2363213	4.12	0.000	.5115955	1.437958
site						
2	.1130359	.2101903	0.54	0.591	-.2989296	.5250013
3	-.5879879	.2279351	-2.58	0.010	-1.034733	-.1412433
_cons	.2697127	.3284422	0.82	0.412	-.3740222	.9134476
Uninsure						
age	-.0077961	.0114418	-0.68	0.496	-.0302217	.0146294
male	.4518496	.3674867	1.23	0.219	-.268411	1.17211
nonwhite	.2170589	.4256361	0.51	0.610	-.6171725	1.05129
site						
2	-1.211563	.4705127	-2.57	0.010	-2.133751	-.2893747
3	-.2078123	.3662926	-0.57	0.570	-.9257327	.510108
_cons	-1.286943	.5923219	-2.17	0.030	-2.447872	-.1260134

Apart from having opposite signs, the coefficients from the stereotype logistic model are identical to those from the multinomial logit model. Recall the definition of η_k given in the *Remarks*, particularly the minus sign in front of the summation. One other difference in the output is that the constant estimates labeled `/theta` in the `slogit` output are the constants labeled `_cons` in the `mlogit` output.

Next we examine the one-dimensional model.

```
. slogit insure age male nonwhite i.site, dim(1) base(1) nolog
Stereotype logistic regression                  Number of obs   =        615
                                                Wald chi2(5)    =      28.20
Log likelihood = -539.75205                     Prob > chi2     =     0.0000
 ( 1)  [phi1_2]_cons = 1
```

insure	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
age	.0108366	.0061918	1.75	0.080	-.0012992	.0229723
male	-.5032537	.2078171	-2.42	0.015	-.9105678	-.0959396
nonwhite	-.9480351	.2340604	-4.05	0.000	-1.406785	-.489285
site						
2	-.2444316	.2246366	-1.09	0.277	-.6847113	.1958481
3	.556665	.2243799	2.48	0.013	.1168886	.9964415
/phi1_1	0	(base outcome)				
/phi1_2	1	(constrained)				
/phi1_3	.0383539	.4079705	0.09	0.925	-.7612535	.8379613
/theta1	0	(base outcome)				
/theta2	.187542	.3303847	0.57	0.570	-.4600001	.835084
/theta3	-1.860134	.2158898	-8.62	0.000	-2.28327	-1.436997

```
(insure=Indemnity is the base outcome)
```

We have reduced a two-dimensional multinomial model to one dimension, reducing the number of estimated parameters by four and decreasing the model likelihood by ≈ 5.4.

`slogit` does not report a model likelihood-ratio test. The test of $d = 1$ (a one-dimensional model) versus $d = 0$ (the null model) does not have an asymptotic χ^2 distribution because the unconstrained ϕ parameters (`/phi1_3` in the previous example) cannot be identified if $\boldsymbol{\beta} = 0$. More generally, this problem precludes testing any hierarchical model of dimension d versus $d - 1$. Of course, the likelihood-ratio test of a full-dimension model versus $d = 0$ is valid because the full model is just multinomial logistic, and all the ϕ parameters are fixed at 0 or 1.

◁

❑ Technical note

The stereotype model is a special case of the reduced-rank vector generalized linear model discussed by Yee and Hastie (2003). If we define $\eta_{ik} = \theta_k - \sum_{j=1}^{d} \phi_{jk} \mathbf{x}_i \boldsymbol{\beta}_j$, for $k = 1, \ldots, m-1$, we can write the expression in matrix notation as

$$\boldsymbol{\eta}_i = \boldsymbol{\theta} + \boldsymbol{\Phi} \left(\mathbf{x}_i \mathbf{B}\right)'$$

where $\boldsymbol{\Phi}$ is a $(m-1) \times d$ matrix containing the ϕ_{jk} parameters and $\mathbf{B}$ is a $p \times d$ matrix with columns containing the $\boldsymbol{\beta}_j$ parameters, $j = 1, \ldots, d$. The factorization $\boldsymbol{\Phi}\mathbf{B}'$ is not unique because $\boldsymbol{\Phi}\mathbf{B}' = \boldsymbol{\Phi}\mathbf{M}\mathbf{M}^{-1}\mathbf{B}'$ for any nonsingular $d \times d$ matrix $\mathbf{M}$. To avoid this identifiability problem, we choose $\mathbf{M} = \boldsymbol{\Phi}_1^{-1}$, where

$$\boldsymbol{\Phi} = \begin{pmatrix} \boldsymbol{\Phi}_1 \\ \boldsymbol{\Phi}_2 \end{pmatrix}$$

and $\mathbf{\Phi}_1$ is $d \times d$ of rank d so that

$$\mathbf{\Phi M} = \begin{pmatrix} \mathbf{I}_d \\ \mathbf{\Phi}_2\mathbf{\Phi}_1^{-1} \end{pmatrix}$$

and $\mathbf{I}_d$ is a $d \times d$ identity matrix. Thus the corner constraints used by `slogit` are $\phi_{jj} \equiv 1$ and $\phi_{jk} \equiv 0$ for $j \neq k$ and $k, j \leq d$.

❑

Saved results

`slogit` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_indvars)`	number of independent variables
`e(k_out)`	number of outcomes
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(df_m)`	Wald test degrees of freedom
`e(df_0)`	null model degrees of freedom
`e(k_dim)`	model dimension
`e(i_base)`	base outcome index
`e(ll)`	log likelihood
`e(ll_0)`	null model log likelihood
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance
`e(ic)`	number of iterations
`e(rank)`	rank of `e(V)`
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	slogit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(indvars)	independent variables
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(out#)	outcome labels, # = 1,..., e(k_out)
e(chi2type)	Wald; type of model χ^2 test
e(labels)	outcome labels or numeric levels
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins
e(footnote)	program used to implement the footnote display
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(outcomes)	outcome values
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

slogit is implemented as an ado-file.

slogit obtains the maximum likelihood estimates for the stereotype logistic model by using ml; see [R] **ml**. Each set of regression estimates, one set of $\boldsymbol{\beta}_j$s for each dimension, constitutes one ml model equation. The $d \times (m-1)$ ϕs and the $(m-1)$ θs are ml ancillary parameters.

Without loss of generality, let the base outcome level be the mth level of the dependent variable. Define the row vector $\boldsymbol{\phi}_k = (\phi_{1k}, \ldots, \phi_{dk})$ for $k = 1, \ldots, m-1$, and define the $p \times d$ matrix $\mathbf{B} = (\boldsymbol{\beta}_1, \ldots, \boldsymbol{\beta}_d)$. For observation i, the log odds of outcome level k relative to level m, $k = 1, \ldots, m-1$ is the index

$$\ln\left\{\frac{\Pr(Y_i = k)}{\Pr(Y_i = m)}\right\} = \eta_{ik} = \theta_k - \boldsymbol{\phi}_k \left(\mathbf{x}_i \mathbf{B}\right)' = \theta_k - \boldsymbol{\phi}_k \boldsymbol{\nu}_i'$$

The row vector $\boldsymbol{\nu}_i$ can be interpreted as a latent variable reducing the p-dimensional vector of covariates to a more interpretable $d < p$ dimension.

The probability of the ith observation having outcome level k is then

$$\Pr(Y_i = k) = p_{ik} = \begin{cases} \dfrac{e^{\eta_{ik}}}{1 + \sum_{j=1}^{m-1} e^{\eta_{ij}}}, \text{ if } \quad k < m \\ \dfrac{1}{1 + \sum_{j=1}^{m-1} e^{\eta_{ij}}}, \text{ if } \quad k = m \end{cases}$$

from which the log-likelihood function is computed as

$$L = \sum_{i=1}^{n} w_i \sum_{k=1}^{m} I_k(y_i) \ln(p_{ik}) \tag{1}$$

Here w_i is the weight for observation i and

$$I_k(y_i) = \begin{cases} 1, \text{ if observation } y_i \text{ has outcome } k \\ 0, \text{ otherwise} \end{cases}$$

Numeric variables are normalized for numerical stability during optimization where a new double-precision variable $\widetilde{x}_j$ is created from variable x_j, $j = 1, \ldots, p$, such that $\widetilde{x}_j = (x_j - \bar{x}_j)/s_j$. This feature is turned off if you specify `nonormalize`, or if you use the `from()` option for initial estimates. Normalization is not performed on byte variables, including the indicator variables generated by [R] **xi**. The linear equality constraints for regression parameters, if specified, must be scaled also. Assume that a constraint is applied to the regression parameter associated with variable j and dimension i, β_{ji}, and the corresponding element of the constraint matrix (see [P] **makecns**) is divided by s_j.

After convergence, the parameter estimates for variable j and dimension i—$\widetilde{\beta}_{ji}$, say—are transformed back to their original scale, $\beta_{ji} = \widetilde{\beta}_{ji}/s_j$. For the intercepts, you compute

$$\theta_k = \widetilde{\theta}_k + \sum_{i=1}^{d} \phi_{ik} \sum_{j=1}^{p} \frac{\widetilde{\beta}_{ji} \bar{x}_j}{s_j}$$

Initial values are computed using estimates obtained using `mlogit` to fit a multinomial logistic model. Let the $p \times (m-1)$ matrix $\widetilde{\mathbf{B}}$ contain the multinomial logistic regression parameters less the $m-1$ intercepts. Each ϕ is initialized with constant values $\min(1/2, 1/d)$, the `initialize(constant)` option (the default), or, with uniform random numbers, the `initialize(random)` option. Constraints are then applied to the starting values so that the structure of the $(m-1) \times d$ matrix $\mathbf{\Phi}$ is

$$\mathbf{\Phi} = \begin{pmatrix} \boldsymbol{\phi}_1 \\ \boldsymbol{\phi}_2 \\ \vdots \\ \boldsymbol{\phi}_{m-1} \end{pmatrix} = \begin{pmatrix} \mathbf{I}_d \\ \widetilde{\mathbf{\Phi}} \end{pmatrix}$$

where $\mathbf{I}_d$ is a $d \times d$ identity matrix. Assume that only the corner constraints are used, but any constraints you place on the scale parameters are also applied to the initial scale estimates, so the structure of $\mathbf{\Phi}$ will change accordingly. The ϕ parameters are invariant to the scale of the covariates, so initial estimates in $[\,0, 1\,]$ are reasonable. The constraints guarantee that the rank of $\mathbf{\Phi}$ is at least d, so the initial estimates for the stereotype regression parameters are obtained from $\mathbf{B} = \widetilde{\mathbf{B}}\mathbf{\Phi}(\mathbf{\Phi}'\mathbf{\Phi})^{-1}$.

One other approach for initial estimates is provided: `initialize(svd)`. It starts with the `mlogit` estimates and computes $\widetilde{\mathbf{B}}' = \mathbf{UDV}'$, where $\mathbf{U}_{m-1\times p}$ and $\mathbf{V}_{p\times p}$ are orthonormal matrices and $\mathbf{D}_{p\times p}$ is a diagonal matrix containing the singular values of $\widetilde{\mathbf{B}}$. The estimates for $\mathbf{\Phi}$ and $\mathbf{B}$ are the first d columns of $\mathbf{U}$ and $\mathbf{VD}$, respectively (Yee and Hastie 2003).

The score for regression coefficients is

$$\mathbf{u}_i(\boldsymbol{\beta}_j) = \frac{\partial L_{ik}}{\partial \boldsymbol{\beta}_j} = \mathbf{x}_i \left(\sum_{l=1}^{m-1} \phi_{jl} p_{il} - \phi_{jk} \right)$$

the score for the scale parameters is

$$u_i(\phi_{jl}) = \frac{\partial L_{ik}}{\partial \phi_{jl}} = \begin{cases} \mathbf{x}_i\boldsymbol{\beta}_j(p_{ik} - 1), & \text{if } l = k \\ \mathbf{x}_i\boldsymbol{\beta}_j p_{il}, & \text{if } l \neq k \end{cases}$$

for $l = 1, \ldots, m-1$; and the score for the intercepts is

$$u_i(\theta_l) = \frac{\partial L_{ik}}{\partial \theta_l} = \begin{cases} 1 - p_{ik}, & \text{if } l = k \\ -\,p_{il}, & \text{if } l \neq k \end{cases}$$

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`slogit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **slogit postestimation** — Postestimation tools for slogit

[R] **roc** — Receiver operating characteristic (ROC) analysis

[R] **logistic** — Logistic regression, reporting odds ratios

[R] **mlogit** — Multinomial (polytomous) logistic regression

[R] **ologit** — Ordered logistic regression

[R] **oprobit** — Ordered probit regression

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

slogit postestimation — Postestimation tools for slogit

Description

The following postestimation commands are available after `slogit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predicted probabilities, estimated index and its approximate standard error
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

`predict` [*type*] { *stub*`*` | *newvar* | *newvarlist* } [*if*] [*in*] [`,` *statistic* `outcome(`*outcome*`)`]

`predict` [*type*] { *stub*`*` | *newvarlist* } [*if*] [*in*]`, scores`

statistic	Description
Main	
`pr`	probability of one or all of the dependent variable outcomes; the default
`xb`	index for the *k*th outcome
`stdp`	standard error of the index for the *k*th outcome

If you do not specify `outcome()`, `pr` (with one new variable specified), `xb`, and `stdp` assume `outcome(#1)`.

You specify one or k new variables with `pr`, where k is the number of outcomes.

You specify one new variable with `xb` and `stdp`.

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`pr`, the default, calculates the probability of each of the categories of the dependent variable or the probability of the level specified in `outcome(`*outcome*`)`. If you specify the `outcome(`*outcome*`)` option, you need to specify only one new variable; otherwise, you must specify a new variable for each category of the dependent variable.

`xb` calculates the index, $\theta_k - \sum_{j=1}^{d} \phi_{\mathrm{jk}} \mathbf{x}_i \boldsymbol{\beta}_j$, for outcome level $k \neq$ `e(i_base)` and dimension $d =$ `e(k_dim)`. It returns a vector of zeros if $k =$ `e(i_base)`. A synonym for `xb` is `index`. If `outcome()` is not specified, `outcome(#1)` is assumed.

`stdp` calculates the standard error of the index. A synonym for `stdp` is `seindex`. If `outcome()` is not specified, `outcome(#1)` is assumed.

`outcome(`*outcome*`)` specifies the outcome for which the statistic is to be calculated. `equation()` is a synonym for `outcome()`: it does not matter which you use. `outcome()` or `equation()` can be specified using

`#1`, `#2`, ..., where `#1` means the first category of the dependent variable, `#2` means the second category, etc.;

the values of the dependent variable; or

the value labels of the dependent variable if they exist.

`scores` calculates the equation-level score variables. For models with d dimensions and m levels, $d + (d+1)(m-1)$ new variables are created. Assume $j = 1, \ldots, d$ and $k = 1, \ldots, m$ in the following.

The first d new variables will contain $\partial \ln L / \partial(\mathbf{x}\boldsymbol{\beta}_j)$.

The next $d(m-1)$ new variables will contain $\partial \ln L / \partial \phi_{jk}$.

The last $m-1$ new variables will contain $\partial \ln L / \partial \theta_k$.

Remarks

Once you have fit a stereotype logistic model, you can obtain the predicted probabilities by using the `predict` command for both the estimation sample and other samples; see [U] **20 Estimation and postestimation commands** and [R] **predict**.

`predict` without arguments (or with the `pr` option) calculates the predicted probability of each outcome of the dependent variable. You must therefore give a new variable name for each of the outcomes. To compute the estimated probability of one outcome, you use the `outcome(`*outcome*`)` option where *outcome* is the level encoding the outcome. If the dependent variable's levels are labeled, the outcomes can also be identified by the label values (see [D] **label**).

The `xb` option in conjunction with `outcome(`*outcome*`)` specifies that the index be computed for the outcome encoded by level *outcome*. Its approximate standard error is computed if the `stdp` option is specified. Only one of the `pr`, `xb`, or `stdp` options can be specified with a call to `predict`.

▷ Example 1

In example 2 of [R] **slogit**, we fit the one-dimensional stereotype model, where the *depvar* is `insure` with levels $k = 1$ for outcome *Indemnity*, $k = 2$ for *Prepaid*, and $k = 3$ for *Uninsure*. The base outcome for the model is *Indemnity*, so for $k \neq 1$ the vector of indices for the kth level is

$$\boldsymbol{\eta}_k = \theta_k - \phi_k \left(\beta_1 \texttt{age} + \beta_2 \texttt{male} + \beta_3 \texttt{nonwhite} + \beta_4 \texttt{2.site} + \beta_5 \texttt{3.site}\right)$$

We estimate the group probabilities by calling `predict` after `slogit`.

```
. use http://www.stata-press.com/data/r12/sysdsn1
(Health insurance data)
. slogit insure age male nonwhite i.site, dim(1) base(1) nolog
 (output omitted)
. predict pIndemnity pPrepaid pUninsure, p
. list pIndemnity pPrepaid pUninsure insure in 1/10
```

	pIndem~y	pPrepaid	pUnins~e	insure
1.	.5419344	.3754875	.0825782	Indemnity
2.	.4359638	.496328	.0677081	Prepaid
3.	.5111583	.4105107	.0783309	Indemnity
4.	.3941132	.5442234	.0616633	Prepaid
5.	.4655651	.4625064	.0719285	.
6.	.4401779	.4915102	.0683118	Prepaid
7.	.4632122	.4651931	.0715948	Prepaid
8.	.3772302	.5635696	.0592002	.
9.	.4867758	.4383018	.0749225	Uninsure
10.	.5823668	.3295802	.0880531	Prepaid

Observations 5 and 8 are not used to fit the model because `insure` is missing at these points, but `predict` estimates the probabilities for these observations since none of the independent variables is missing. You can use `if e(sample)` in the call to `predict` to use only those observations that are used to fit the model.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

predict

Let level b be the base outcome that is used to fit the stereotype logistic regression model of dimension d. The index for observation i and level $k \neq b$ is $\eta_{ik} = \theta_k - \sum_{j=1}^{d} \phi_{jk} \mathbf{x}_i \boldsymbol{\beta}_j$. This is the log odds of outcome encoded as level k relative to that of b so that we define $\eta_{ib} \equiv 0$. The outcome probabilities for this model are defined as $\Pr(Y_i = k) = e^{\eta_{ik}} / \sum_{j=1}^{m} e^{\eta_{ij}}$. Unlike in `mlogit`, `ologit`, and `oprobit`, the index is no longer a linear function of the parameters. The standard error of index η_{ik} is thus computed using the delta method (see also [R] **predictnl**).

The equation-level score for regression coefficients is

$$\frac{\partial \ln L_{ik}}{\partial \mathbf{x}_i \boldsymbol{\beta}_j} = \left(\sum_{l=1}^{m-1} \phi_{jl} p_{il} - \phi_{jk} \right)$$

the equation-level score for the scale parameters is

$$\frac{\partial \ln L_{ik}}{\partial \phi_{jl}} = \begin{cases} \mathbf{x}_i \boldsymbol{\beta}_j (p_{ik} - 1), & \text{if } l = k \\ \mathbf{x}_i \boldsymbol{\beta}_j p_{il}, & \text{if } l \neq k \end{cases}$$

for $l = 1, \ldots, m-1$; and the equation-level score for the intercepts is

$$\frac{\partial \ln L_{ik}}{\partial \theta_l} = \begin{cases} 1 - p_{ik}, & \text{if } l = k \\ -p_{il}, & \text{if } l \neq k \end{cases}$$

Also see

[R] **slogit** — Stereotype logistic regression

[U] **20 Estimation and postestimation commands**

Title

smooth — Robust nonlinear smoother

Syntax

`smooth` *smoother*[`,` `twice`] *varname* [*if*] [*in*] `,` `generate(`*newvar*`)`

where *smoother* is specified as *Sm*[*Sm*[...]] and *Sm* is one of

{ 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 }[R]
3[R]S[S | R][S | R]...
E
H

Letters may be specified in lowercase if preferred. Examples of *smoother*[`,twice`] include

3RSSH	3RSSH,twice	4253H	4253H,twice	43RSR2H,twice
3rssh	3rssh,twice	4253h	4253h,twice	43rsr2h,twice

Menu

Statistics > Nonparametric analysis > Robust nonlinear smoother

Description

`smooth` applies the specified resistant, nonlinear smoother to *varname* and stores the smoothed series in *newvar*.

Option

`generate(`*newvar*`)` is required; it specifies the name of the new variable that will contain the smoothed values.

Remarks

Smoothing is an exploratory data-analysis technique for making the general shape of a series apparent. In this approach (Tukey 1977), the observed data series is assumed to be the sum of an underlying process that evolves smoothly (the smooth) and of an unsystematic noise component (the rough); that is,

$$\text{data} = \text{smooth} + \text{rough}$$

Smoothed values z_t are obtained by taking medians (or some other location estimate) of each point in the original data y_t and a few of the points around it. The number of points used is called the span of the smoother. Thus a span-3 smoother produces z_t by taking the median of y_{t-1}, y_t, and y_{t+1}. `smooth` provides running median smoothers of spans 1 to 9—indicated by the digit that specifies their span. Median smoothers are resistant to isolated outliers, so they provide robustness to spikes in the data. Because the median is also a nonlinear operator, such smoothers are known as robust (or resistant) nonlinear smoothers.

smooth also provides the Hanning linear, nonrobust smoother, indicated by the letter H. Hanning is a span-3 smoother with binomial weights. Repeated applications of H—HH, HHH, etc.— provide binomial smoothers of span 5, 7, etc. See Cox (1997, 2004) for a graphical application of this fact.

Because one smoother usually cannot adequately separate the smooth from the rough, compound smoothers—multiple smoothers applied in sequence—are used. The smoother 35H, for instance, then smooths the data with a span-3 median smoother, smooths the result with a span-5 median smoother, and finally smooths that result with the Hanning smoother. smooth allows you to specify any number of smoothers in any sequence.

Three refinements can be combined with the running median and Hanning smoothers. First, the endpoints of a smooth can be given special treatment. This is specified by the E operator. Second, smoothing by 3, the span-3 running median, tends to produce flat-topped hills and valleys. The splitting operator, S, "splits" these repeated values, applies the endpoint operator to them, and then "rejoins" the series. Finally, it is sometimes useful to repeat an odd-span median smoother or the splitting operator until the smooth no longer changes. Following a digit or an S with an R specifies this type of repetition.

Even the best smoother may fail to separate the smooth from the rough adequately. To guard against losing any systematic components of the data series, after smoothing, the smoother can be reapplied to the resulting rough, and any recovered signal can be added back to the original smooth. The twice operator specifies this procedure. More generally, an arbitrary smoother can be applied to the rough (using a second smooth command), and the recovered signal can be added back to the smooth. This more general procedure is called reroughing (Tukey 1977).

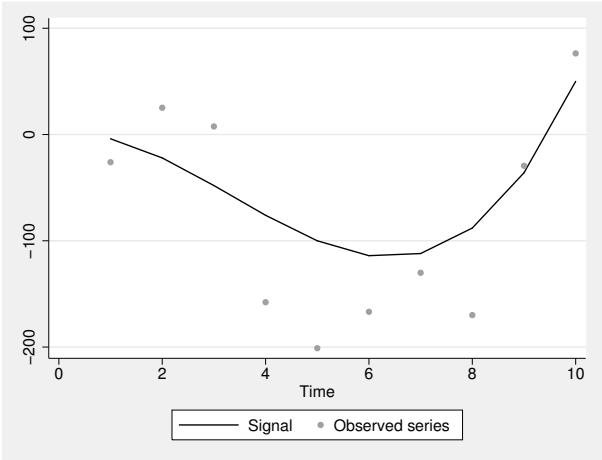
The details of each of the smoothers and operators are explained in *Methods and formulas* below.

▷ Example 1

smooth is designed to recover the general features of a series that has been contaminated with noise. To demonstrate this, we construct a series, add noise to it, and then smooth the noisy version to recover an estimate of the original data. First, we construct and display the data:

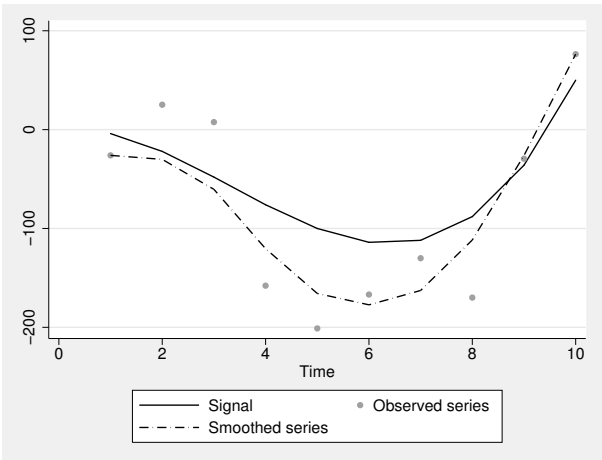
```
. drop _all
. set obs 10
. set seed 123456789
. generate time = _n
. label variable time "Time"
. generate x = _n^3 - 10*_n^2 + 5*_n
. label variable x "Signal"
. generate z = x + 50*rnormal()
. label variable z "Observed series"
```

```
. scatter x z time, c(l .) m(i o) ytitle("")
```



Now we smooth the noisy series, z, assumed to be the only data we would observe:

```
. smooth 4253eh,twice z, gen(sz)
. label variable sz "Smoothed series"
. scatter x z sz time, c(l . l) m(i o i) ytitle("") || scatter sz time,
> c(l . l) m(i o i) ytitle("") clpattern(dash_dot)
```

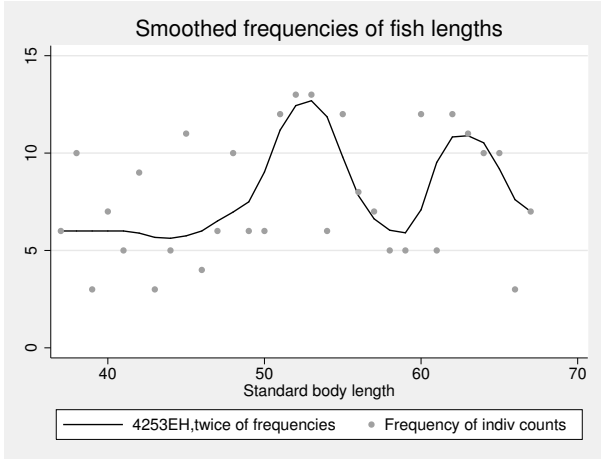


▷ Example 2

Salgado-Ugarte and Curts-García (1993) provide data on the frequencies of observed fish lengths. In this example, the series to be smoothed—the frequencies—is ordered by fish length rather than by time.

```
. use http://www.stata-press.com/data/r12/fishdata, clear
. smooth 4253eh,twice freq, gen(sfreq)
. label var sfreq "4253EH,twice of frequencies"
```

```
. scatter sfreq freq length, c(l .) m(i o)
> title("Smoothed frequencies of fish lengths") ytitle("") xlabel(#4)
```



◁

❑ Technical note

`smooth` allows missing values at the beginning and end of the series, but missing values in the middle are not allowed. Leading and trailing missing values are ignored. If you wish to ignore missing values in the middle of the series, you must `drop` the missing observations before using `smooth`. Doing so, of course, would violate `smooth`'s assumption that observations are equally spaced—each observation represents a year, a quarter, or a month (or a 1-year birth-rate category). In practice, `smooth` produces good results as long as the spaces between adjacent observations do not vary too much.

Smoothing is usually applied to time series, but any variable with a natural order can be smoothed. For example, a smoother might be applied to the birth rate recorded by the age of the mothers (birth rate for 17-year-olds, birth rate for 18-year-olds, and so on).

❑

Methods and formulas

`smooth` is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Running median smoothers of odd span
Running median smoothers of even span
Repeat operator
Endpoint rule
Splitting operator
Hanning smoother
Twicing

Running median smoothers of odd span

The smoother 3 defines

$$z_t = \text{median}(y_{t-1}, y_t, y_{t+1})$$

The smoother 5 defines

$$z_t = \text{median}(y_{t-2}, y_{t-1}, y_t, y_{t+1}, y_{t+2})$$

and so on. The smoother 1 defines $z_t = \text{median}(y_t)$, so it does nothing.

Endpoints are handled by using smoothers of shorter, odd span. Thus for 3,

$$\begin{aligned} z_1 &= y_1 \\ z_2 &= \text{median}(y_1, y_2, y_3) \\ &\vdots \\ z_{N-1} &= \text{median}(y_{N-2}, y_{N-1}, y_N) \\ Z_N &= y_N \end{aligned}$$

For 5,

$$\begin{aligned} z_1 &= y_1 \\ z_2 &= \text{median}(y_1, y_2, y_3) \\ z_3 &= \text{median}(y_1, y_2, y_3, y_4, y_5) \\ z_4 &= \text{median}(y_2, y_3, y_4, y_5, y_6) \\ &\vdots \\ z_{N-2} &= \text{median}(y_{N-4}, y_{N-3}, y_{N-2}, y_{N-1}, y_N) \\ z_{N-1} &= \text{median}(y_{N-2}, y_{N-1}, y_N) \\ Z_N &= y_N \end{aligned}$$

and so on.

Running median smoothers of even span

Define the median() function as returning the linearly interpolated value when given an even number of arguments. Thus the smoother 2 defines

$$z_{t+0.5} = (y_t + y_{t+1})/2$$

The smoother 4 defines $z_{t+0.5}$ as the linearly interpolated median of $(y_{t-1}, y_t, y_{t+1}, y_{t+2})$, and so on. Endpoints are always handled using smoothers of shorter, even span. Thus for 4,

$$
\begin{aligned}
z_{0.5} &= y_1 \\
z_{1.5} &= \text{median}(y_1, y_2) = (y_1 + y_2)/2 \\
z_{2.5} &= \text{median}(y_1, y_2, y_3, y_4) \\
&\vdots \\
z_{N-2.5} &= \text{median}(y_{N-4}, y_{N-3}, y_{N-2}, y_N) \\
z_{N-1.5} &= \text{median}(y_{N-2}, y_{N-1}) \\
z_{N-0.5} &= \text{median}(y_{N-1}, y_N) \\
z_{N+0.5} &= y_N
\end{aligned}
$$

As defined above, an even-span smoother increases the length of the series by 1 observation. However, the series can be recentered on the original observation numbers, and the "extra" observation can be eliminated by smoothing the series again with another even-span smoother. For instance, the smooth of `4` illustrated above could be followed by a smooth of `2` to obtain

$$
\begin{aligned}
z^*_1 &= (z_{0.5} + z_{1.5})/2 \\
z^*_2 &= (z_{1.5} + z_{2.5})/2 \\
z^*_3 &= (z_{2.5} + z_{3.5})/2 \\
&\vdots \\
z^*_{N-2} &= (z_{N-2.5} + z_{N-1.5})/2 \\
z^*_{N-1} &= (z_{N-1.5} + z_{N-0.5})/2 \\
z^*_N &= (z_{N-0.5} + z_{N+0.5})/2
\end{aligned}
$$

`smooth` keeps track of the number of even smoothers applied to the data and expands and shrinks the length of the series accordingly. To ensure that the final smooth has the same number of observations as *varname*, `smooth` requires you to specify an even number of even-span smoothers. However, the pairs of even-span smoothers need not be contiguous; for instance, `4253` and `4523` are both allowed.

Repeat operator

`R` indicates that a smoother is to be repeated until convergence, that is, until repeated applications of the smoother produce the same series. Thus `3` applies the smoother of running medians of span 3. `33` applies the smoother twice. `3R` produces the result of repeating `3` an infinite number of times. `R` should be used only with odd-span smoothers because even-span smoothers are not guaranteed to converge.

The smoother `453R2` applies a span-4 smoother, followed by a span-5 smoother, followed by repeated applications of a span-3 smoother, followed by a span-2 smoother.

Endpoint rule

The endpoint rule E modifies the values z_1 and z_N according to the following formulas:

$$z_1 = \text{median}(3z_2 - 2z_3, z_1, z_2)$$
$$z_N = \text{median}(3z_{N-2} - 2z_{N-1}, z_N, z_{N-1})$$

When the endpoint rule is not applied, endpoints are typically "copied in"; that is, $z_1 = y_1$ and $z_N = y_N$.

Splitting operator

The smoothers 3 and 3R can produce flat-topped hills and valleys. The split operator attempts to eliminate such hills and valleys by splitting the sequence, applying the endpoint rule E, rejoining the series, and then resmoothing by 3R.

The S operator may be applied only after 3, 3R, or S.

We recommend that the S operator be repeated once (SS) or until no further changes take place (SR).

Hanning smoother

H is the Hanning linear smoother:

$$z_t = (y_{t-1} + 2y_t + y_{t+1})/4$$

Endpoints are copied in: $z_1 = y_1$ and $z_N = y_N$. H should be applied only after all nonlinear smoothers.

Twicing

A smoother divides the data into a smooth and a rough:

$$\text{data} = \text{smooth} + \text{rough}$$

If the smoothing is successful, the rough should exhibit no pattern. Twicing refers to applying the smoother to the observed, calculating the rough, and then applying the smoother to the rough. The resulting "smoothed rough" is then added back to the smooth from the first step.

Acknowledgments

smooth was originally written by William Gould (1992)—at which time it was named nlsm—and was inspired by Salgado-Ugarte and Curts-García (1992). Salgado-Ugarte and Curts-García (1993) subsequently reported anomalies in nlsm's treatment of even-span median smoothers. smooth corrects these problems and incorporates other improvements but otherwise is essentially the same as originally published.

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Also see

[R] **lowess** — Lowess smoothing

[R] **lpoly** — Kernel-weighted local polynomial smoothing

[TS] **tssmooth** — Smooth and forecast univariate time-series data

Title

spearman — Spearman's and Kendall's correlations

Syntax

Spearman's rank correlation coefficients

`spearman` [*varlist*] [*if*] [*in*] [, *spearman_options*]

Kendall's rank correlation coefficients

`ktau` [*varlist*] [*if*] [*in*] [, *ktau_options*]

spearman_options	Description
Main	
`stats(`*spearman_list*`)`	list of statistics; select up to three statistics; default is `stats(rho)`
`print(#)`	significance level for displaying coefficients
`star(#)`	significance level for displaying with a star
`bonferroni`	use Bonferroni-adjusted significance level
`sidak`	use Šidák-adjusted significance level
`pw`	calculate all pairwise correlation coefficients by using all available data
`matrix`	display output in matrix form

ktau_options	Description
Main	
`stats(`*ktau_list*`)`	list of statistics; select up to six statistics; default is `stats(taua)`
`print(#)`	significance level for displaying coefficients
`star(#)`	significance level for displaying with a star
`bonferroni`	use Bonferroni-adjusted significance level
`sidak`	use Šidák-adjusted significance level
`pw`	calculate all pairwise correlation coefficients by using all available data
`matrix`	display output in matrix form

`by` is allowed with `spearman` and `ktau`; see [D] **by**.

where the elements of *spearman_list* may be

`rho`	correlation coefficient
`obs`	number of observations
`p`	significance level

and the elements of *ktau_list* may be

`taua`	correlation coefficient τ_a
`taub`	correlation coefficient τ_b
`score`	score
`se`	standard error of score
`obs`	number of observations
`p`	significance level

Menu

spearman

Statistics > Nonparametric analysis > Tests of hypotheses > Spearman's rank correlation

ktau

Statistics > Nonparametric analysis > Tests of hypotheses > Kendall's rank correlation

Description

`spearman` displays Spearman's rank correlation coefficients for all pairs of variables in *varlist* or, if *varlist* is not specified, for all the variables in the dataset.

`ktau` displays Kendall's rank correlation coefficients between the variables in *varlist* or, if *varlist* is not specified, for all the variables in the dataset. `ktau` is intended for use on small- and moderate-sized datasets; it requires considerable computation time for larger datasets.

Options for spearman

Main

`stats(`*spearman_list*`)` specifies the statistics to be displayed in the matrix of output. `stats(rho)` is the default. Up to three statistics may be specified; `stats(rho obs p)` would display the correlation coefficient, number of observations, and significance level. If *varlist* contains only two variables, all statistics are shown in tabular form, and `stats()`, `print()`, and `star()` have no effect unless the `matrix` option is specified.

`print(#)` specifies the significance level of correlation coefficients to be printed. Correlation coefficients with larger significance levels are left blank in the matrix. Typing `spearman, print(.10)` would list only those correlation coefficients that are significant at the 10% level or lower.

`star(#)` specifies the significance level of correlation coefficients to be marked with a star. Typing `spearman, star(.05)` would "star" all correlation coefficients significant at the 5% level or lower.

`bonferroni` makes the Bonferroni adjustment to calculated significance levels. This adjustment affects printed significance levels and the `print()` and `star()` options. Thus `spearman, print(.05) bonferroni` prints coefficients with Bonferroni-adjusted significance levels of 0.05 or less.

`sidak` makes the Šidák adjustment to calculated significance levels. This adjustment affects printed significance levels and the `print()` and `star()` options. Thus `spearman, print(.05) sidak` prints coefficients with Šidák-adjusted significance levels of 0.05 or less.

`pw` specifies that correlations be calculated using pairwise deletion of observations with missing values. By default, `spearman` uses casewise deletion, where observations are ignored if any of the variables in *varlist* are missing.

`matrix` forces `spearman` to display the statistics as a matrix, even if *varlist* contains only two variables. `matrix` is implied if more than two variables are specified.

Options for ktau

Main

`stats(`*ktau_list*`)` specifies the statistics to be displayed in the matrix of output. `stats(taua)` is the default. Up to six statistics may be specified; `stats(taua taub score se obs p)` would display the correlation coefficients τ_a, τ_b, score, standard error of score, number of observations, and significance level. If *varlist* contains only two variables, all statistics are shown in tabular form and `stats()`, `print()`, and `star()` have no effect unless the `matrix` option is specified.

`print(#)` specifies the significance level of correlation coefficients to be printed. Correlation coefficients with larger significance levels are left blank in the matrix. Typing `ktau, print(.10)` would list only those correlation coefficients that are significant at the 10% level or lower.

`star(#)` specifies the significance level of correlation coefficients to be marked with a star. Typing `ktau, star(.05)` would "star" all correlation coefficients significant at the 5% level or lower.

`bonferroni` makes the Bonferroni adjustment to calculated significance levels. This adjustment affects printed significance levels and the `print()` and `star()` options. Thus `ktau, print(.05) bonferroni` prints coefficients with Bonferroni-adjusted significance levels of 0.05 or less.

`sidak` makes the Šidák adjustment to calculated significance levels. This adjustment affects printed significance levels and the `print()` and `star()` options. Thus `ktau, print(.05) sidak` prints coefficients with Šidák-adjusted significance levels of 0.05 or less.

`pw` specifies that correlations be calculated using pairwise deletion of observations with missing values. By default, `ktau` uses casewise deletion, where observations are ignored if any of the variables in *varlist* are missing.

`matrix` forces `ktau` to display the statistics as a matrix, even if *varlist* contains only two variables. `matrix` is implied if more than two variables are specified.

Remarks

▷ Example 1

We wish to calculate the correlation coefficients among marriage rate (`mrgrate`), divorce rate (`divorce_rate`), and median age (`medage`) in state data. We can calculate the standard Pearson correlation coefficients and significance by typing

```
. use http://www.stata-press.com/data/r12/states2
(State data)
. pwcorr mrgrate divorce_rate medage, sig
             |  mrgrate divorc~e   medage
-------------+---------------------------
     mrgrate |   1.0000
             |
             |
divorce_rate |   0.7895   1.0000
             |   0.0000
             |
      medage |   0.0011  -0.1526   1.0000
             |   0.9941   0.2900
             |
```

We can calculate Spearman's rank correlation coefficients by typing

```
. spearman mrgrate divorce_rate medage, stats(rho p)
(obs=50)
```

Key
rho
Sig. level

	mrgrate	divorc~e	medage
mrgrate	1.0000		
divorce_rate	0.6933	1.0000	
	0.0000		
medage	-0.4869	-0.2455	1.0000
	0.0003	0.0857	

The large difference in the results is caused by one observation. Nevada's marriage rate is almost 10 times higher than the state with the next-highest marriage rate. An important feature of the Spearman rank correlation coefficient is its reduced sensitivity to extreme values compared with the Pearson correlation coefficient.

We can calculate Kendall's rank correlations by typing

```
. ktau mrgrate divorce_rate medage, stats(taua taub p)
(obs=50)
```

Key
tau_a
tau_b
Sig. level

	mrgrate	divorc~e	medage
mrgrate	0.9829		
	1.0000		
divorce_rate	0.5110	0.9804	
	0.5206	1.0000	
	0.0000		
medage	-0.3486	-0.1698	0.9845
	-0.3544	-0.1728	1.0000
	0.0004	0.0828	

There are tied values for variables `mrgrate`, `divorce_rate`, and `medage`, so tied ranks are used. As a result, $\tau_a < 1$ on the diagonal (see *Methods and formulas* for the definition of τ_a).

◁

❑ Technical note

According to Conover (1999, 323), "Spearman's ρ tends to be larger than Kendall's τ in absolute value. However, as a test of significance, there is no strong reason to prefer one over the other because both will produce nearly identical results in most cases."

❑

▷ Example 2

We illustrate `spearman` and `ktau` with the auto data, which contains some missing values.

```
.use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. spearman mpg rep78
 Number of obs =      69
Spearman's rho =       0.3098
Test of Ho: mpg and rep78 are independent
    Prob > |t| =       0.0096
```

Because we specified two variables, `spearman` displayed the sample size, correlation, and p-value in tabular form. To obtain just the correlation coefficient displayed in matrix form, we type

```
. spearman mpg rep78, stats(rho) matrix
(obs=69)
```

	mpg	rep78
mpg	1.0000	
rep78	0.3098	1.0000

The `pw` option instructs `spearman` and `ktau` to use all nonmissing observations between a pair of variables when calculating their correlation coefficient. In the output below, some correlations are based on 74 observations, whereas others are based on 69 because 5 observations contain a missing value for `rep78`.

```
. spearman mpg price rep78, pw stats(rho obs p)  star(0.01)
```

Key
rho *Number of obs* *Sig. level*

	mpg	price	rep78
mpg	1.0000 74		
price	-0.5419* 74 0.0000	1.0000 74	
rep78	0.3098* 69 0.0096	0.1028 69 0.4008	1.0000 69

Finally, the bonferroni and sidak options provide adjusted significance levels:

```
. ktau mpg price rep78, stats(taua taub score se p) bonferroni
(obs=69)
```

Key
tau_a
tau_b
score
se of score
Sig. level

	mpg	price	rep78
mpg	0.9471		
	1.0000		
	2222.0000		
	191.8600		
price	-0.3973	1.0000	
	-0.4082	1.0000	
	-932.0000	2346.0000	
	192.4561	193.0682	
	0.0000		
rep78	0.2076	0.0648	0.7136
	0.2525	0.0767	1.0000
	487.0000	152.0000	1674.0000
	181.7024	182.2233	172.2161
	0.0224	1.0000	

◁

Charles Edward Spearman (1863–1945) was a British psychologist who made contributions to correlation, factor analysis, test reliability, and psychometrics. After several years' military service, he obtained a PhD in experimental psychology at Leipzig and became a professor at University College London, where he sustained a long program of work on the interpretation of intelligence tests. Ironically, the rank correlation version bearing his name is not the formula he advocated.

Maurice George Kendall (1907–1983) was a British statistician who contributed to rank correlation, time series, multivariate analysis, among other topics, and wrote many statistical texts. Most notably, perhaps, his advanced survey of the theory of statistics went through several editions, later ones with Alan Stuart; the baton has since passed to others. Kendall was employed in turn as a government and business statistician, as a professor at the London School of Economics, as a consultant, and as director of the World Fertility Survey. He was knighted in 1974.

Saved results

spearman saves the following in r():

Scalars

r(N)	number of observations (last variable pair)
r(rho)	ρ (last variable pair)
r(p)	two-sided p-value (last variable pair)

Matrices

r(Nobs)	number of observations
r(Rho)	ρ
r(P)	two-sided p-value

ktau saves the following in r():

Scalars

r(N)	number of observations (last variable pair)
r(tau_a)	τ_{a} (last variable pair)
r(tau_b)	τ_{b} (last variable pair)
r(score)	Kendall's score (last variable pair)
r(se_score)	se of score (last variable pair)
r(p)	two-sided p-value (last variable pair)

Matrices

r(Nobs)	number of observations
r(Tau_a)	τ_{a}
r(Tau_b)	τ_{b}
r(Score)	Kendall's score
r(Se_Score)	standard error of score
r(P)	two-sided p-value

Methods and formulas

spearman and ktau are implemented as ado-files.

Spearman's (1904) rank correlation is calculated as Pearson's correlation computed on the ranks and average ranks (Conover 1999, 314–315). Ranks are as calculated by egen; see [D] **egen**. The significance is calculated using the approximation

$$p = 2 \times \texttt{ttail}(n-2, |\widehat{\rho}|\sqrt{n-2}/\sqrt{1-\widehat{\rho}^2})$$

For any two pairs of ranks (x_i, y_i) and (x_j, y_j) of one variable pair (*varname*$_1$, *varname*$_2$), $1 \leq i, j \leq n$, where n is the number of observations, define them as concordant if

$$(x_i - x_j)(y_i - y_j) > 0$$

and discordant if this product is less than zero.

Kendall's (1938; also see Kendall and Gibbons [1990] or Bland [2000], 222–225) score S is defined as $C - D$, where C (D) is the number of concordant (discordant) pairs. Let $N = n(n-1)/2$ be the total number of pairs, so τ_{a} is given by

$$\tau_{\mathrm{a}} = S/N$$

and τ_{b} is given by

$$\tau_{\mathrm{b}} = \frac{S}{\sqrt{N-U}\sqrt{N-V}}$$

where

$$U = \sum_{i=1}^{N_1} u_i(u_i - 1)/2$$

$$V = \sum_{j=1}^{N_2} v_j(v_j - 1)/2$$

and where N_1 is the number of sets of tied x values, u_i is the number of tied x values in the ith set, N_2 is the number of sets of tied y values, and v_j is the number of tied y values in the jth set. Under the null hypothesis of independence between *varname*$_1$ and *varname*$_2$, the variance of S is exactly (Kendall and Gibbons 1990, 66)

$$\begin{aligned}\mathrm{Var}(S) =& \frac{1}{18}\left\{n(n-1)(2n+5) - \sum_{i=1}^{N_1} u_i(u_i-1)(2u_i+5) - \sum_{j=1}^{N_2} v_j(v_j-1)(2v_j+5)\right\} \\ &+ \frac{1}{9n(n-1)(n-2)}\left\{\sum_{i=1}^{N_1} u_i(u_i-1)(u_i-2)\right\}\left\{\sum_{j=1}^{N_2} v_j(v_j-1)(v_j-2)\right\} \\ &+ \frac{1}{2n(n-1)}\left\{\sum_{i=1}^{N_1} u_i(u_i-1)\right\}\left\{\sum_{j=1}^{N_2} v_j(v_j-1)\right\}\end{aligned}$$

Using a normal approximation with a continuity correction,

$$z = \frac{|S| - 1}{\sqrt{\mathrm{Var}(S)}}$$

For the hypothesis of independence, the statistics S, τ_{a}, and τ_{b} produce equivalent tests and give the same significance.

For Kendall's τ, the normal approximation is surprisingly accurate for sample sizes as small as 8, at least for calculating p-values under the null hypothesis for continuous variables. (See Kendall and Gibbons [1990, chap. 4], who also present some tables for calculating exact p-values for $n < 10$.) For Spearman's ρ, the normal approximation requires larger samples to be valid.

Let v be the number of variables specified so that $k = v(v-1)/2$ correlation coefficients are to be estimated. If `bonferroni` is specified, the adjusted significance level is $p' = \min(1, kp)$. If `sidak` is specified, $p' = \min\{1, 1-(1-p)^n\}$. See *Methods and formulas* in [R] **oneway** for a more complete description of the logic behind these adjustments.

Early work on rank correlation is surveyed by Kruskal (1958).

Acknowledgment

The original version of `ktau` was written by Sean Becketti, a past editor of the *Stata Technical Bulletin*.

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Also see

[R] **correlate** — Correlations (covariances) of variables or coefficients

[R] **nptrend** — Test for trend across ordered groups

Title

spikeplot — Spike plots and rootograms

Syntax

`spikeplot` *varname* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Main	
`round(#)`	round *varname* to nearest multiple of # (bin width)
`fraction`	make vertical scale the proportion of total values; default is frequencies
`root`	make vertical scale show square roots of frequencies
Plot	
spike_options	affect rendition of plotted spikes
Add plots	
`addplot(`*plot*`)`	add other plots to generated graph
Y axis, X axis, Titles, Legend, Overall, By	
twoway_options	any options documented in [G-3] ***twoway_options***

`fweights`, `aweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.

Menu

Graphics > Distributional graphs > Spike plot and rootogram

Description

`spikeplot` produces a frequency plot for a variable in which the frequencies are depicted as vertical lines from zero. The frequency may be a count, a fraction, or the square root of the count (Tukey's rootogram, circa 1965). The vertical lines may also originate from a baseline other than zero at the user's option.

Options

Main

`round(#)` rounds the values of *varname* to the nearest multiple of #. This action effectively specifies the bin width.

`fraction` specifies that the vertical scale be the proportion of total values (percentage) rather than the count.

`root` specifies that the vertical scale show square roots. This option may not be specified if `fraction` is specified.

Plot

spike_options affect the rendition of the plotted spikes; see [G-2] **graph twoway spike**.

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph. See [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall, By

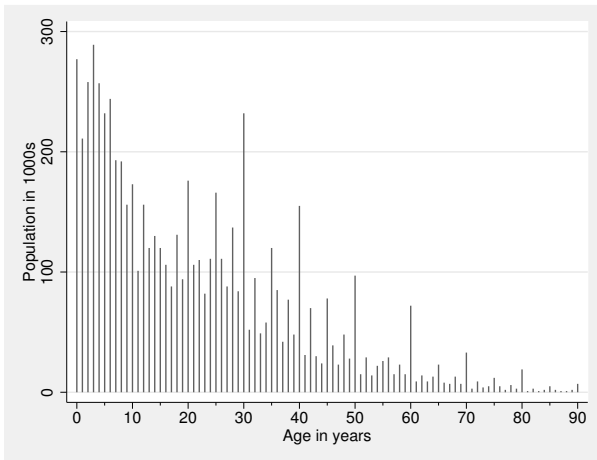
twoway_options are any of the options documented in [G-3] ***twoway_options***. These include options for titling the graph (see [G-3] ***title_options***), options for saving the graph to disk (see [G-3] ***saving_option***), and the `by()` option (see [G-3] ***by_option***).

Remarks

▷ Example 1

Cox and Brady (1997a) present an illustrative example using the age structure of the population of Ghana from the 1960 census (rounded to the nearest 1,000). The dataset has ages from 0 (less than 1 year) to 90. To view the distribution of ages, we would like to use each integer from 0 to 90 as the bins for the dataset.

```
. use http://www.stata-press.com/data/r12/ghanaage
. spikeplot age [fw=pop], ytitle("Population in 1000s") xlab(0(10)90)
> xmtick(5(10)85)
```



The resulting graph shows a "heaping" of ages at the multiples of 5. Also, ages ending in even numbers are more frequent than ages ending in odd numbers (except for 5). This preference for reporting ages is well known in demography and other social sciences.

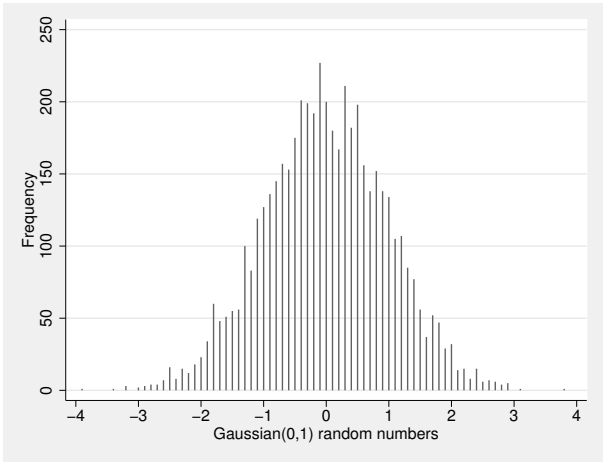
Note also that we used the `ytitle()` option to override the default title of "Frequency" and that we used the `xlab()` and `xmtick()` options with *numlist*s to further customize the resulting graph. See [U] **11.1.8 numlist** for details on specifying *numlist*s.

◁

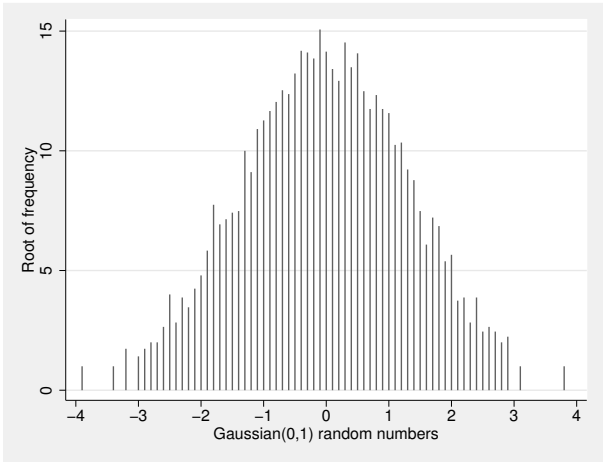
Example 2

The rootogram is a plot of the square-root transformation of the frequency counts. The square root of a normal distribution is a multiple of another normal distribution.

```
. clear
. set seed 1234567
. set obs 5000
obs was 0, now 5000
. generate normal = rnormal()
. label variable normal "Gaussian(0,1) random numbers"
. spikeplot normal, round(.10) xlab(-4(1)4)
```




```
. spikeplot normal, round(.10) xlab(-4(1)4) root
```



Interpreting a histogram in terms of normality is thus similar to interpreting the rootogram for normality.

This example also shows how the `round()` option is used to bin the values for a spike plot of a continuous variable.

▷ Example 3

`spikeplot` can also be used to produce time-series plots. *varname* should be the time variable, and weights should be specified as the values for those times. To get a plot of daily rainfalls, we type

```
. spikeplot day [w=rain] if rain, ytitle("Daily rainfall in mm")
```

The `base()` option of `graph twoway spike` may be used to set a different baseline, such as when we want to show variations relative to an average or to some other measure of level. ◁

Methods and formulas

`spikeplot` is implemented as an ado-file.

Acknowledgments

The original version of `spikeplot` was written by Nicholas J. Cox of Durham University and Anthony R. Brady of the Imperial College School of Medicine (1997a, 1997b).

References

Cox, N. J., and A. R. Brady. 1997a. gr25: Spike plots for histograms, rootograms, and time-series plots. *Stata Technical Bulletin* 36: 8–11. Reprinted in *Stata Technical Bulletin Reprints*, vol. 6, pp. 50–54. College Station, TX: Stata Press.

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Also see

[R] **histogram** — Histograms for continuous and categorical variables

Title

ssc — Install and uninstall packages from SSC

Syntax

Summary of packages most recently added or updated at SSC

```
ssc new [ , saving(filename[ , replace]) type]
```

Summary of most popular packages at SSC

```
ssc hot [ , n(#) author(name) ]
```

Describe a specified package at SSC

```
ssc describe { pkgname | letter } [ , saving(filename[ , replace]) ]
```

Install a specified package from SSC

```
ssc install pkgname [ , all replace]
```

Uninstall from your computer a previously installed package from SSC

```
ssc uninstall pkgname
```

Type a specific file stored at SSC

```
ssc type filename [ , asis]
```

Copy a specific file from SSC to your computer

```
ssc copy filename [ , plus personal replace public binary]
```

where *letter* in `ssc describe` is `a`–`z` or `_`.

Description

`ssc` works with packages (and files) from the Statistical Software Components (SSC) archive, which is often called the Boston College Archive and is provided by http://repec.org.

The SSC has become the premier Stata download site for user-written software on the web. `ssc` provides a convenient interface to the resources available there. For example, on Statalist (see http://www.stata.com/statalist/), users will often write

> The program can be found by typing `ssc install newprogramname`.

Typing that would load everything associated with `newprogramname`, including the help files.

If you are searching for what is available, type `ssc new` and `ssc hot`, and see [R] **search**. `search` searches the SSC and other places, too. `search` provides a GUI interface from which programs can be installed, including the programs at the SSC archive.

You can uninstall particular packages by using `ssc uninstall`. For the packages that you keep, see [R] **adoupdate** for an automated way of keeping those packages up to date.

Command overview

`ssc new` summarizes the packages made available or updated recently. Output is presented in the Stata Viewer, and from there you may click to find out more about individual packages or to install them.

`ssc hot` lists the most popular packages—popular based on a moving average of the number of downloads in the past three months. By default, 10 packages are listed.

`ssc describe` *pkgname* describes, but does not install, the specified package. Use `search` to find packages; see [R] **search**. If you know the package name but do not know the exact spelling, type `ssc describe` followed by one letter, `a`–`z` or `_` (underscore), to list all the packages starting with that letter.

`ssc install` *pkgname* installs the specified package. You do not have to describe a package before installing it. (You may also install a package by using `net install`; see [R] **net**.)

`ssc uninstall` *pkgname* removes the previously installed package from your computer. It does not matter how the package was installed. (`ssc uninstall` is a synonym for `ado uninstall`, so either may be used to installed any package.)

`ssc type` *filename* types a specific file stored at SSC. `ssc cat` is a synonym for `ssc type`, which may appeal to those familiar with Unix.

`ssc copy` *filename* copies a specific file stored at SSC to your computer. By default, the file is copied to the current directory, but you can use options to change this. `ssc copy` is a rarely used alternative to `ssc install ..., all`. `ssc cp` is a synonym for `ssc copy`.

Options for use with ssc new

`saving(`*filename*`[ , replace ])` specifies that the "what's new" summary be saved in *filename*. If *filename* is specified without a suffix, *filename*`.smcl` is assumed. If `saving()` is not specified, `saving(ssc_results.smcl)` is assumed.

`type` specifies that the "what's new" results be displayed in the Results window rather than in the Viewer.

Options for use with ssc hot

`n(#)` specifies the number of packages to list; `n(10)` is the default. Specify `n(.)` to list all packages in order of popularity.

`author(`*name*`)` lists the 10 most popular packages by the specified author. If `n(#)` is also specified, the top # packages are listed.

Option for use with ssc describe

`saving(`*filename*`[ , replace ])` specifies that, in addition to the descriptions being displayed on your screen, it be saved in the specified file.

If *filename* is specified without an extension, `.smcl` will be assumed, and the file will be saved as a SMCL file.

If *filename* is specified with an extension, no default extension is added. If the extension is `.log`, the file will be stored as a text file.

If `replace` is specified, *filename* is replaced if it already exists.

Options for use with ssc install

`all` specifies that any ancillary files associated with the package be downloaded to your current directory, in addition to the program and help files being installed. Ancillary files are files that do not end in `.ado` or `.sthlp` and typically contain datasets or examples of the use of the new command.

You can find out which files are associated with the package by typing `ssc describe` *pkgname* before or after installing. If you install without using the `all` option and then want the ancillary files, you can `ssc install` again.

`replace` specifies that any files being downloaded that already exist on your computer be replaced by the downloaded files. If `replace` is not specified and any files already exist, none of the files from the package is downloaded or installed.

It is better not to specify the `replace` option and wait to see if there is a problem. If there is a problem, it is usually better to uninstall the old package by using `ssc uninstall` or `ado uninstall` (which are, in fact, the same command).

Option for use with ssc type

`asis` affects how files with the suffixes `.smcl` and `.sthlp` are displayed. The default is to interpret SMCL directives the file might contain. `asis` specifies that the file be displayed in raw, uninterpreted form.

Options for use with ssc copy

`plus` specifies that the file be copied to the `PLUS` directory, the directory where user-written additions are installed. Typing `sysdir` will display the identity of the `PLUS` directory on your computer; see [P] **sysdir**.

`personal` specifies that the file be copied to your `PERSONAL` directory as reported by `sysdir`; see [P] **sysdir**.

If neither `plus` nor `personal` is specified, the default is to copy the file to the current directory.

`replace` specifies that, if the file already exists on your computer, the new file replace it.

`public` specifies that the new file be made readable by everyone; otherwise, the file will be created according to the default permission you have set with your operating system.

`binary` specifies that the file being copied is a binary file and that it is to be copied as is. The default is to assume that the file is a text file and change the end-of-line characters to those appropriate for your computer/operating system.

Remarks

Users can add new features to Stata, and some users choose to make new features that they have written available to others via the web. The files that comprise a new feature are called a package, and a package usually consists of one or more ado-files and help files. The `net` command (see [R] **net**) makes it reasonably easy to install and uninstall packages regardless of where they are on the web. One site, the SSC, has become particularly popular as a repository for additions to Stata. Command `ssc` is an easier to use version of `net` designed especially for the SSC.

Many packages are available at the SSC. Packages have names, such as `oaxaca`, `estout`, or `egenmore`. At SSC, capitalization is not significant, so `Oaxaca`, `ESTOUT`, and `EGENmore` are ways of writing the same package names.

When you type

```
. ssc install oaxaca
```

the files associated with the package are downloaded and installed on your computer. Package names usually correspond to the names of the command being added to Stata, so one would expect that installing the package `oaxaca` will add command `oaxaca` to Stata on your computer, and expect that typing `help oaxaca` will provide the documentation. That is the situation here, but that is not always so. Before or after installing a package, type `ssc describe` *pkgname* to obtain the details.

▷ Example 1

`ssc new` summarizes the packages most recently made available or updated. Output is presented in the Viewer, from which you may click on a package name to find out more or install it. For example,

```
. ssc new
(contacting http://repec.org)
  (output omitted)
KHB
 module to decompose total effects into direct and indirect via KHB-method
 Authors: Ulrich Kohler  Kristian Karlson       Req: Stata version 11
 Revised: 2011-05-02
  (output omitted)
TODUMMY
 module to create dummy variables
 Authors: Daniel Klein       Req: Stata version 11
 Revised: 2011-05-07
  (output omitted)
------------------------------------------------------------------------------
 End of recent additions and updates
```

`ssc hot` provides a list of the most popular packages at SSC.

```
. ssc hot
Top 10 packages at SSC
```

Rank	Apr2011 # hits	Package	Author(s)
1	5267.5	outreg2	Roy Wada
2	4226.8	estout	Ben Jann
3	2102.7	psmatch2	Barbara Sianesi, Edwin Leuven
4	2006.2	ivreg2	Mark E Schaffer, Christopher F Baum Steven Stillman
5	1224.0	ranktest	Mark E Schaffer, Frank Kleibergen
6	1126.5	gllamm	Sophia Rabe-Hesketh
7	1067.8	xtabond2	David Roodman
8	928.3	tabout	Ian Watson
9	895.5	xtivreg2	Mark E Schaffer
10	789.3	outreg	John Luke Gallup

```
(Click on package name for description)
```

Use the n(#) option to change the number of packages listed:

```
. ssc hot, n(20)
```

Top 20 packages at SSC

Rank	Apr2011 # hits	Package	Author(s)
1	5267.5	outreg2	Roy Wada
2	4226.8	estout	Ben Jann
3	2102.7	psmatch2	Barbara Sianesi, Edwin Leuven
4	2006.2	ivreg2	Mark E Schaffer, Christopher F Baum, Steven Stillman
5	1224.0	ranktest	Mark E Schaffer, Frank Kleibergen
6	1126.5	gllamm	Sophia Rabe-Hesketh
7	1067.8	xtabond2	David Roodman
8	928.3	tabout	Ian Watson
9	895.5	xtivreg2	Mark E Schaffer
10	789.3	outreg	John Luke Gallup
11	782.8	usespss	Sergiy Radyakin
12	736.5	winsor	Nicholas J. Cox
13	734.0	hprescott	Christopher F Baum
14	571.5	overid	Vince Wiggins, Steven Stillman, Mark E Schaffer, Christopher F Baum
15	565.5	fre	Ben Jann
16	477.0	whitetst	Nicholas J. Cox, Christopher F Baum
17	420.1	spmap	Maurizio Pisati
18	419.5	shp2dta	Kevin Crow
19	416.3	egenmore	Nicholas J. Cox
20	405.2	ice	Patrick Royston

(Click on package name for description)

The author(*name*) option allows you to list the most popular packages by a specific person:

```
. ssc hot, author(baum)
```

Top 10 packages at SSC by author Baum

Rank	Apr2011 # hits	Package	Author(s)
4	2006.2	ivreg2	Mark E Schaffer, Christopher F Baum, Steven Stillman
13	734.0	hprescott	Christopher F Baum
14	571.5	overid	Vince Wiggins, Steven Stillman, Mark E Schaffer, Christopher F Baum
16	477.0	whitetst	Nicholas J. Cox, Christopher F Baum
31	360.5	xttest3	Christopher F Baum
35	342.0	ivendog	Mark E Schaffer, Christopher F Baum, Steven Stillman
44	289.5	xttest2	Christopher F Baum
49	275.0	tsmktim	Christopher F Baum, Vince Wiggins
62	223.8	outtable	Joao Pedro Azevedo, Christopher F Baum
65	217.0	ipshin	Fabian Bornhorst, Christopher F Baum

(Click on package name for description)

ssc describe *pkgname* describes, but does not install, the specified package. You must already know the name of the package. See [R] **search** for assistance in searching for packages. Sometimes you know the package name, but you do not know the exact spelling. Then you can type ssc describe followed by one letter, a–z or _, to list all the packages starting with that letter; even so, using search is better.

```
. ssc describe khb
------------------------------------------------------------------------------
package khb from http://fmwww.bc.edu/repec/bocode/k
------------------------------------------------------------------------------

TITLE
       'KHB': module to decompose total effects into direct and indirect via KHB
> -method
DESCRIPTION/AUTHOR(S)
        decomposes the total effect of a variable into direct and
       indirect effects using the KHB-method developed by Karlson, Holm,
       and Breen (2011). The method is developed for binary and logit
       probit models, but this command also includes other nonlinear
       probability models (ordered and multinomial) and linear
       regression. Contrary to other decomposition methods, the
       KHB-method gives unbiased decompositions, decomposes effects of
       both discrete and continuous variables, and provides analytically
       derived statistical tests for many models of the GLM family.
       KW: decomposition
       KW: effects
       KW: probit
       KW: nonlinear probability model
       Requires: Stata version 11
       Distribution-Date: 20110502
       Author: Ulrich Kohler, WZB
       Support: email kohler@wz-berlin.de
       Author: Kristian Karlson
       Support: email kbk@dpu.dk
INSTALLATION FILES                                  (type net install khb)
       khb.ado
       khb.sthlp
------------------------------------------------------------------------------
(type -ssc install khb- to install)
```

The default setting for the `saving()` option is for the output to be saved with the `.smcl` extension. You could also save the file with a `log` extension, and in this case, the file would be stored as a text file.

```
. ssc describe k, saving(k.index)
  (output omitted)
. ssc describe khb, saving(khb.log)
  (output omitted)
```

`ssc install` *pkgname* installs the specified package. You do not have to describe a package before installing it. There are ways of installing packages other than `ssc install`, such as `net`; see [R] **net**. It does not matter how a package is installed. For instance, a package can be installed using `net` and still be uninstalled using `ssc`.

```
. ssc install khb
checking khb consistency and verifying not already installed...
installing into C:\ado\plus\...
installation complete.
```

`ssc uninstall` *pkgname* removes the specified, previously installed package from your computer. You can uninstall immediately after installation or at any time in the future. (Technical note: `ssc uninstall` is a synonym for `ado uninstall`, so it can uninstall any installed package, not just packages obtained from the SSC.)

```
. ssc uninstall khb
package khb from http://fmwww.bc.edu/repec/bocode/k
      'KHB': module to decompose total effects into direct and indirect via KHB-method
(package uninstalled)
```

`ssc type` *filename* types a specific file stored at the SSC. Although not shown in the syntax diagram, `ssc cat` is a synonym for `ssc type`, which may appeal to those familiar with Unix. To view only the `khb` help file for the `khb` package, you would type

```
Title
    khb Decomposition of total effects into direct and indirect effects using
        the KHB-method
  (output omitted)
```

`ssc copy` *filename* copies a specific file stored at the SSC to your computer. By default, the file is copied to the current directory, but you can use options to change this. `ssc copy` is a rarely used alternative to `ssc install ..., all`. `ssc cp` is a synonym for `ssc copy`.

```
. ssc copy khb.ado
(file khb.ado copied to current directory)
```

◁

For more details on the SSC archive and for information on how to submit your own programs to the SSC, see http://repec.org/bocode/s/sscsubmit.html.

Methods and formulas

`ssc` is implemented as an ado-file.

Acknowledgments

`ssc` is based on `archutil` by Nicholas J. Cox, Durham University, and Christopher Baum, Boston College. The reworking of the original was done with their blessing and their participation.

Christopher Baum maintains the Stata-related files stored at the SSC archive. We thank him for this contribution to the Stata community.

References

Baum, C. F., and N. J. Cox. 1999. ip29: Metadata for user-written contributions to the Stata programming language. *Stata Technical Bulletin* 52: 10–12. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 121–124. College Station, TX: Stata Press.

Cox, N. J., and C. F. Baum. 2000. ip29.1: Metadata for user-written contributions to the Stata programming language. *Stata Technical Bulletin* 54: 21–22. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 124–126. College Station, TX: Stata Press.

Also see

[R] **adoupdate** — Update user-written ado-files

[R] **net** — Install and manage user-written additions from the Internet

[R] **search** — Search Stata documentation

[R] **sj** — Stata Journal and STB installation instructions

[P] **sysdir** — Query and set system directories

Title

stem — Stem-and-leaf displays

Syntax

`stem` *varname* [*if*] [*in*] [, *options*]

options	Description
Main	
`prune`	do not print stems that have no leaves
`round(#)`	round data to this value; default is `round(1)`
`digits(#)`	digits per leaf; default is `digits(1)`
`lines(#)`	number of stems per interval of $10^{\texttt{digits}}$
`width(#)`	stem width; equal to $10^{\texttt{digits}}/\texttt{width}$

`by` is allowed; see [D] **by**.

Menu

Statistics > Summaries, tables, and tests > Distributional plots and tests > Stem-and-leaf display

Description

`stem` displays stem-and-leaf plots.

Options

Main

`prune` prevents printing any stems that have no leaves.

`round(#)` rounds the data to this value and displays the plot in these units. If `round()` is not specified, noninteger data will be rounded automatically.

`digits(#)` sets the number of digits per leaf. The default is 1.

`lines(#)` sets the number of stems per every data interval of $10^{\texttt{digits}}$. The value of `lines()` must divide $10^{\texttt{digits}}$; that is, if `digits(1)` is specified, then `lines()` must divide 10. If `digits(2)` is specified, then `lines()` must divide 100, etc. Only one of `lines()` or `width()` may be specified. If neither is specified, an appropriate value will be set automatically.

`width(#)` sets the width of a stem. `lines()` is equal to $10^{\texttt{digits}}/\texttt{width}$, and this option is merely an alternative way of setting `lines()`. The value of `width()` must divide $10^{\texttt{digits}}$. Only one of `width()` or `lines()` may be specified. If neither is specified, an appropriate value will be set automatically.

Note: If `lines()` or `width()` is not specified, `digits()` may be decreased in some circumstances to make a better-looking plot. If `lines()` or `width()` is set, the user-specified value of `digits()` will not be altered.

Remarks

▷ Example 1

Stem-and-leaf displays are a compact way to present considerable information about a batch of data. For instance, using our automobile data (described in [U] **1.2.2 Example datasets**):

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. stem mpg
Stem-and-leaf plot for mpg (Mileage (mpg))
  1t | 22
  1f | 44444455
  1s | 66667777
  1. | 88888888899999999
  2* | 00011111
  2t | 22222333
  2f | 444455555
  2s | 666
  2. | 8889
  3* | 001
  3t |
  3f | 455
  3s |
  3. |
  4* | 1
```

The stem-and-leaf display provides a way to list our data. The expression to the left of the vertical bar is called the stem; the digits to the right are called the leaves. All the stems that begin with the same digit and the corresponding leaves, written beside each other, reconstruct an observation of the data. Thus, if we look at the four stems that begin with the digit 1 and their corresponding leaves, we see that we have two cars rated at 12 mpg, 6 cars at 14, 2 at 15, and so on. The car with the highest mileage rating in our data is rated at 41 mpg.

The above plot is a five-line plot with `lines()` equal to 5 (five lines per interval of 10) and `width()` equal to 2 (two leaves per stem).

Instead, we could specify `lines(2)`:

```
. stem mpg, lines(2)
Stem-and-leaf plot for mpg (Mileage (mpg))
  1* | 22444444
  1. | 556666777788888888899999999
  2* | 00011111222223334444
  2. | 555556668889
  3* | 0014
  3. | 55
  4* | 1
```

`stem mpg, width(5)` would produce the same plot as above.

The stem-and-leaf display provides a crude histogram of our data, one not so pretty as that produced by `histogram` (see [R] **histogram**), but one that is nonetheless informative.

◁

▷ Example 2

The miles per gallon rating fits easily into a stem-and-leaf display because, in our data, it has two digits. However, `stem` does not require two digits.

```
. stem price, lines(1) digits(3)
Stem-and-leaf plot for price (Price)
   3*** | 291,299,667,748,798,799,829,895,955,984,995
   4*** | 010,060,082,099,172,181,187,195,296,389,424,425,453,482,499, ... (26)
   5*** | 079,104,172,189,222,379,397,705,719,788,798,799,886,899
   6*** | 165,229,295,303,342,486,850
   7*** | 140,827
   8*** | 129,814
   9*** | 690,735
  10*** | 371,372
  11*** | 385,497,995
  12*** | 990
  13*** | 466,594
  14*** | 500
  15*** | 906
```

The `(26)` at the right of the second stem shows that there were 26 leaves on this stem—too many to display on one line.

We can make a more compact stem-and-leaf plot by rounding. To display `stem` in units of 100, we could type

```
. stem price, round(100)
Stem-and-leaf plot for price (Price)
price rounded to nearest multiple of 100
plot in units of 100
   3* | 33778889
   4* | 000011122223444555556677778 99
   5* | 11222447788899
   6* | 2233359
   7* | 18
   8* | 18
   9* | 77
  10* | 44
  11* | 45
  12* | 0
  13* | 056
  14* | 5
  15* | 9
```

`price`, in our data, has four or five digits. `stem` presented the display in terms of units of 100, so a car that cost $3,291 was treated for display purposes as $3,300.

◁

❑ Technical note

Stem-and-leaf diagrams have been used in Japanese railway timetables, as shown in Tufte (1990, 46–47).

❑

Saved results

`stem` saves the following in `r()`:

Scalars

`r(width)`	width of a stem
`r(digits)`	number of digits per leaf; default is 1

Macros

`r(round)`	number specified in `round()`

Methods and formulas

`stem` is implemented as an ado-file.

References

Cox, N. J. 2007. Speaking Stata: Turning over a new leaf. *Stata Journal* 7: 413–433.

Emerson, J. D., and D. C. Hoaglin. 1983. Stem-and-leaf displays. In *Understanding Robust and Exploratory Data Analysis*, ed. D. C. Hoaglin, F. Mosteller, and J. W. Tukey, 7–32. New York: Wiley.

Tufte, E. R. 1990. *Envisioning Information*. Cheshire, CT: Graphics Press.

Tukey, J. W. 1972. Some graphic and semigraphic displays. In *Statistical Papers in Honor of George W. Snedecor*, ed. T. A. Bancroft and S. A. Brown, 293–316. Ames, IA: Iowa State University Press.

——. 1977. *Exploratory Data Analysis*. Reading, MA: Addison–Wesley.

Also see

[R] **histogram** — Histograms for continuous and categorical variables

[R] **lv** — Letter-value displays

Title

stepwise — Stepwise estimation

Syntax

`stepwise` [`,` *options*] `:` *command*

options	Description
Model	
* `pr(#)`	significance level for removal from the model
* `pe(#)`	significance level for addition to the model
Model2	
`forward`	perform forward-stepwise selection
`hierarchical`	perform hierarchical selection
`lockterm1`	keep the first term
`lr`	perform likelihood-ratio test instead of Wald test
Reporting	
display_options	control column formats and line width

* At least one of `pr(#)` or `pe(#)` must be specified.

`by` and `xi` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are allowed if *command* allows them; see [U] **11.1.6 weight**.

All postestimation commands behave as they would after *command* without the `stepwise` prefix; see the postestimation manual entry for *command*.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Other > Stepwise estimation

Description

`stepwise` performs stepwise estimation. Typing

```
. stepwise, pr(#): command
```

performs backward-selection estimation for *command*. The stepwise selection method is determined by the following option combinations:

options	Description
`pr(#)`	backward selection
`pr(#) hierarchical`	backward hierarchical selection
`pr(#) pe(#)`	backward stepwise
`pe(#)`	forward selection
`pe(#) hierarchical`	forward hierarchical selection
`pr(#) pe(#) forward`	forward stepwise

command defines the estimation command to be executed. The following Stata commands are supported by `stepwise`:

`clogit`	`nbreg`	`regress`
`cloglog`	`ologit`	`scobit`
`glm`	`oprobit`	`stcox`
`intreg`	`poisson`	`stcrreg`
`logistic`	`probit`	`streg`
`logit`	`qreg`	`tobit`

`stepwise` expects *command* to have the following form:

command_name [*depvar*] *term* [*term* ...] [*if*] [*in*] [*weight*] [, *command_options*]

where *term* is either *varname* or (*varlist*) (a *varlist* in parentheses indicates that this group of variables is to be included or excluded together). *depvar* is not present when *command_name* is `stcox`, `stcrreg`, or `streg`; otherwise, *depvar* is assumed to be present. For `intreg`, *depvar* is actually two dependent variable names ($depvar_1$ and $depvar_2$).

`sw` is a synonym for `stepwise`.

Options

Model

`pr(#)` specifies the significance level for removal from the model; terms with $p \geq$ `pr()` are eligible for removal.

`pe(#)` specifies the significance level for addition to the model; terms with $p <$ `pe()` are eligible for addition.

Model 2

`forward` specifies the forward-stepwise method and may be specified only when both `pr()` and `pe()` are also specified. Specifying both `pr()` and `pe()` without `forward` results in backward-stepwise selection. Specifying only `pr()` results in backward selection, and specifying only `pe()` results in forward selection.

`hierarchical` specifies hierarchical selection.

`lockterm1` specifies that the first term be included in the model and not be subjected to the selection criteria.

`lr` specifies that the test of term significance be the likelihood-ratio test. The default is the less computationally expensive Wald test; that is, the test is based on the estimated variance–covariance matrix of the estimators.

Reporting

display_options: `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Introduction
Search logic for a step
Full search logic
Examples
Estimation sample considerations
Messages
Programming for stepwise

Introduction

Typing

```
. stepwise, pr(.10): regress y1 x1 x2 d1 d2 d3 x4 x5
```

performs a backward-selection search for the regression model `y1` on `x1`, `x2`, `d1`, `d2`, `d3`, `x4`, and `x5`. In this search, each explanatory variable is said to be a term. Typing

```
. stepwise, pr(.10): regress y1 x1 x2 (d1 d2 d3) (x4 x5)
```

performs a similar backward-selection search, but the variables `d1`, `d2`, and `d3` are treated as one term, as are `x4` and `x5`. That is, `d1`, `d2`, and `d3` may or may not appear in the final model, but they appear or do not appear together.

▷ Example 1

Using the automobile dataset, we fit a backward-selection model of `mpg`:

```
. use http://www.stata-press.com/data/r12/auto
. gen weight2 = weight*weight
. stepwise, pr(.2): regress mpg weight weight2 displ gear turn headroom
> foreign price
                     begin with full model
p = 0.7116 >= 0.2000  removing headroom
p = 0.6138 >= 0.2000  removing displacement
p = 0.3278 >= 0.2000  removing price
```

Source	SS	df	MS	Number of obs =	74
Model	1736.31455	5	347.262911	F(5, 68) =	33.39
Residual	707.144906	68	10.3991898	Prob > F =	0.0000
				R-squared =	0.7106
				Adj R-squared =	0.6893
Total	2443.45946	73	33.4720474	Root MSE =	3.2248

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0158002	.0039169	-4.03	0.000	-.0236162	-.0079842
weight2	1.77e-06	6.20e-07	2.86	0.006	5.37e-07	3.01e-06
foreign	-3.615107	1.260844	-2.87	0.006	-6.131082	-1.099131
gear_ratio	2.011674	1.468831	1.37	0.175	-.9193321	4.94268
turn	-.3087038	.1763099	-1.75	0.084	-.6605248	.0431172
_cons	59.02133	9.3903	6.29	0.000	40.28327	77.75938

This estimation treated each variable as its own term and thus considered each one separately. The engine displacement and gear ratio should really be considered together:

```
. stepwise, pr(.2): regress mpg weight weight2 (displ gear) turn headroom
> foreign price
                     begin with full model
p = 0.7116 >= 0.2000  removing headroom
p = 0.3944 >= 0.2000  removing displacement gear_ratio
p = 0.2798 >= 0.2000  removing price
```

Source	SS	df	MS		
Model	1716.80842	4	429.202105	Number of obs =	74
				F(4, 69) =	40.76
Residual	726.651041	69	10.5311745	Prob > F =	0.0000
				R-squared =	0.7026
				Adj R-squared =	0.6854
Total	2443.45946	73	33.4720474	Root MSE =	3.2452

mpg	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
weight	-.0160341	.0039379	-4.07	0.000	-.0238901	-.0081782
weight2	1.70e-06	6.21e-07	2.73	0.008	4.58e-07	2.94e-06
foreign	-2.758668	1.101772	-2.50	0.015	-4.956643	-.5606925
turn	-.2862724	.176658	-1.62	0.110	-.6386955	.0661508
_cons	65.39216	8.208778	7.97	0.000	49.0161	81.76823

Search logic for a step

Before discussing the complete search logic, consider the logic for a step—the first step—in detail. The other steps follow the same logic. If you type

```
. stepwise, pr(.20): regress y1 x1 x2 (d1 d2 d3) (x4 x5)
```

the logic is

1. Fit the model `y` on `x1 x2 d1 d2 d3 x4 x5`.
2. Consider dropping `x1`.
3. Consider dropping `x2`.
4. Consider dropping `d1 d2 d3`.
5. Consider dropping `x4 x5`.
6. Find the term above that is least significant. If its significance level is ≥ 0.20, remove that term.

If you type

```
. stepwise, pr(.20) hierarchical: regress y1 x1 x2 (d1 d2 d3) (x4 x5)
```

the logic would be different because the `hierarchical` option states that the terms are ordered. The initial logic would become

1. Fit the model `y` on `x1 x2 d1 d2 d3 x4 x5`.
2. Consider dropping `x4 x5`—the last term.
3. If the significance of this last term is ≥ 0.20, remove the term.

The process would then stop or continue. It would stop if `x4 x5` were not dropped, and otherwise, `stepwise` would continue to consider the significance of the next-to-last term, `d1 d2 d3`.

Specifying `pe()` rather than `pr()` switches to forward estimation. If you type

```
. stepwise, pe(.20): regress y1 x1 x2 (d1 d2 d3) (x4 x5)
```

stepwise performs forward-selection search. The logic for the first step is

1. Fit a model of y on nothing (meaning a constant).
2. Consider adding x1.
3. Consider adding x2.
4. Consider adding d1 d2 d3.
5. Consider adding x4 x5.
6. Find the term above that is most significant. If its significance level is < 0.20, add that term.

As with backward estimation, if you specify hierarchical,

```
. stepwise, pe(.20) hierarchical: regress y1 x1 x2 (d1 d2 d3) (x4 x5)
```

the search for the most significant term is restricted to the next term:

1. Fit a model of y on nothing (meaning a constant).
2. Consider adding x1—the first term.
3. If the significance is < 0.20, add the term.

If x1 were added, stepwise would next consider x2; otherwise, the search process would stop.

stepwise can also use a stepwise selection logic that alternates between adding and removing terms. The full logic for all the possibilities is given below.

Full search logic

Option	Logic
`pr()` (backward selection)	Fit the full model on all explanatory variables. While the least-significant term is "insignificant", remove it and reestimate.
`pr() hierarchical` (backward hierarchical selection)	Fit full model on all explanatory variables. While the last term is "insignificant", remove it and reestimate.
`pr() pe()` (backward stepwise)	Fit full model on all explanatory variables. If the least-significant term is "insignificant", remove it and reestimate; otherwise, stop. Do that again: if the least-significant term is "insignificant", remove it and reestimate; otherwise, stop. Repeatedly, if the most-significant excluded term is "significant", add it and reestimate; if the least-significant included term is "insignificant", remove it and reestimate; until neither is possible.
`pe()` (forward selection)	Fit "empty" model. While the most-significant excluded term is "significant", add it and reestimate.
`pe() hierarchical` (forward hierarchical selection)	Fit "empty" model. While the next term is "significant", add it and reestimate.
`pr() pe() forward` (forward stepwise)	Fit "empty" model. If the most-significant excluded term is "significant", add it and reestimate; otherwise, stop. Do that again: if the most-significant excluded term is "significant", add it and reestimate; otherwise, stop. Repeatedly, if the least-significant included term is "insignificant", remove it and reestimate; if the most-significant excluded term is "significant", add it and reestimate; until neither is possible.

Examples

The following two statements are equivalent; both include solely single-variable terms:

```
. stepwise, pr(.2): regress price mpg weight displ
. stepwise, pr(.2): regress price (mpg) (weight) (displ)
```

The following two statements are equivalent; the last term in each is `r1`, ..., `r4`:

```
. stepwise, pr(.2) hierarchical: regress price mpg weight displ (r1-r4)
. stepwise, pr(.2) hierarchical: regress price (mpg) (weight) (displ) (r1-r4)
```

To group variables `weight` and `displ` into one term, type

```
. stepwise, pr(.2) hierarchical: regress price mpg (weight displ) (r1-r4)
```

`stepwise` can be used with commands other than `regress`; for instance,

```
. stepwise, pr(.2): logit outcome (sex weight) treated1 treated2
. stepwise, pr(.2): logistic outcome (sex weight) treated1 treated2
```

Either statement would fit the same model because `logistic` and `logit` both perform logistic regression; they differ only in how they report results; see [R] **logit** and [R] **logistic**.

We use the `lockterm1` option to force the first term to be included in the model. To keep `treated1` and `treated2` in the model no matter what, we type

```
. stepwise, pr(.2) lockterm1: logistic outcome (treated1 treated2) ...
```

After `stepwise` estimation, we can type `stepwise` without arguments to redisplay results,

```
. stepwise
(output from logistic appears)
```

or type the underlying estimation command:

```
. logistic
(output from logistic appears)
```

At estimation time, we can specify options unique to the command being stepped:

```
. stepwise, pr(.2): logit outcome (sex weight) treated1 treated2, or
```

`or` is `logit`'s option to report odds ratios rather than coefficients; see [R] **logit**.

Estimation sample considerations

Whether you use backward or forward estimation, `stepwise` forms an estimation sample by taking observations with nonmissing values of all the variables specified (except for $depvar_1$ and $depvar_2$ for `intreg`). The estimation sample is held constant throughout the stepping. Thus if you type

```
. stepwise, pr(.2) hierarchical: regress amount sk edul sval
```

and variable `sval` is missing in half the data, that half of the data will not be used in the reported model, even if `sval` is not included in the final model.

The function `e(sample)` identifies the sample that was used. `e(sample)` contains 1 for observations used and 0 otherwise. For instance, if you type

```
. stepwise, pr(.2) pe(.10): logistic outcome x1 x2 (x3 x4) (x5 x6 x7)
```

and the final model is outcome on x1, x5, x6, and x7, you could re-create the final regression by typing

```
. logistic outcome x1 x5 x6 x7 if e(sample)
```

You could obtain summary statistics within the estimation sample of the independent variables by typing

```
. summarize x1 x5 x6 x7 if e(sample)
```

If you fit another model, e(sample) will automatically be redefined. Typing

```
. stepwise, lock pr(.2): logistic outcome (x1 x2) (x3 x4) (x5 x6 x7)
```

would automatically drop e(sample) and re-create it.

Messages

note: _____ dropped because of collinearity

Each term is checked for collinearity, and variables within the term are dropped if collinearity is found. For instance, say that you type

```
. stepwise, pr(.2): regress y x1 x2 (r1-r4) (x3 x4)
```

and assume that variables r1 through r4 are mutually exclusive and exhaustive dummy variables—perhaps r1, ..., r4 indicate in which of four regions the subject resides. One of the r1, ..., r4 variables will be automatically dropped to identify the model.

This message should cause you no concern.

Error message: between-term collinearity, variable _____

After removing any within-term collinearity, if stepwise still finds collinearity between terms, it refuses to continue. For instance, assume that you type

```
. stepwise, pr(.2): regress y1 x1 x2 (d1-d8) (r1-r4)
```

Assume that r1, ..., r4 identify in which of four regions the subject resides, and that d1, ..., d8 identify the same sort of information, but more finely. r1, say, amounts to d1 and d2; r2 to d3, d4, and d5; r3 to d6 and d7; and r4 to d8. You can estimate the d* variables or the r* variables, but not both.

It is your responsibility to specify noncollinear terms.

note: _____ dropped because of estimability
note: _____ obs. dropped because of estimability

You probably received this message in fitting a logistic or probit model. Regardless of estimation strategy, stepwise checks that the full model can be fit. The indicated variable had a 0 or infinite standard error.

For logistic, logit, and probit, this message is typically caused by one-way causation. Assume that you type

```
. stepwise, pr(.2): logistic outcome (x1 x2 x3) d1
```

and assume that variable d1 is an indicator (dummy) variable. Further assume that whenever d1 = 1, outcome = 1 in the data. Then the coefficient on d1 is infinite. One (conservative) solution to this problem is to drop the d1 variable and the d1==1 observations. The underlying estimation commands probit, logit, and logistic report the details of the difficulty and solution; stepwise simply accumulates such problems and reports the above summary messages. Thus if you see this message, you could type

```
. logistic outcome x1 x2 x3 d1
```

to see the details. Although you should think carefully about such situations, Stata's solution of dropping the offending variables and observations is, in general, appropriate.

Programming for stepwise

stepwise requires that *command_name* follow standard Stata syntax and allow the if qualifier; see [U] **11 Language syntax**. Furthermore, *command_name* must have sw or swml as a program property; see [P] **program properties**. If *command_name* has swml as a property, *command_name* must save the log-likelihood value in e(ll) and model degrees of freedom in e(df_m).

Saved results

stepwise saves whatever is saved by the underlying estimation command.

Also, stepwise saves stepwise in e(stepwise).

Methods and formulas

stepwise is implemented as an ado-file.

Some statisticians do not recommend stepwise procedures; see Sribney (1998) for a summary.

References

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Also see

[R] **nestreg** — Nested model statistics

Title

suest — Seemingly unrelated estimation

Syntax

`suest` *namelist* [`,` *options*]

where *namelist* is a list of one or more names under which estimation results were saved via `estimates store`; see [R] **estimates store**. Wildcards may be used. `*` and `_all` refer to all stored results. A period (`.`) may be used to refer to the last estimation results, even if they have not (yet) been stored.

options	Description
SE/Robust	
`svy`	survey data estimation
`vce(`*vcetype*`)`	*vcetype* may be `robust` or `cluster` *clustvar*
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`dir`	display a table describing the models
`eform(`*string*`)`	report exponentiated coefficients and label as *string*
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`coeflegend`	display legend instead of statistics

`coeflegend` does not appear in the dialog box.

Menu

Statistics > Postestimation > Tests > Seemingly unrelated estimation

Description

`suest` is a postestimation command; see [U] **20 Estimation and postestimation commands**.

`suest` combines the estimation results—parameter estimates and associated (co)variance matrices—stored under *namelist* into one parameter vector and *simultaneous* (co)variance matrix of the sandwich/robust type. This (co)variance matrix is appropriate even if the estimates were obtained on the same or on overlapping data.

Typical applications of `suest` are tests for intramodel and cross-model hypotheses using `test` or `testnl`, for example, a generalized Hausman specification test. `lincom` and `nlcom` may be used after `suest` to estimate linear combinations and nonlinear functions of coefficients. `suest` may also be used to adjust a standard VCE for clustering or survey design effects.

Different estimators are allowed, for example, a `regress` model and a `probit` model; the only requirement is that `predict` produce equation-level scores with the `score` option after an estimation command. The models may be estimated on different samples, due either to explicit `if` or `in` selection or to missing values. If weights are applied, the same weights (type and values) should be applied to

all models in *namelist*. The estimators should be estimated without `vce(robust)` or `vce(cluster` *clustvar*`)` options. `suest` returns the robust VCE, allows the `vce(cluster` *clustvar*`)` option, and automatically works with results from the `svy` prefix command (only for `vce(linearized)`). See example 7 in [SVY] **svy postestimation** for an example using `suest` with `svy: ologit`.

Because `suest` posts its results like a proper estimation command, its results can be stored via `estimates store`. Moreover, like other estimation commands, `suest` typed without arguments replays the results.

Options

SE/Robust

`svy` specifies that estimation results should be modified to reflect the survey design effects according to the `svyset` specifications, see [SVY] **svyset**.

The `svy` option is implied when `suest` encounters survey estimation results from the `svy` prefix; see [SVY] **svy**. Poststratification is allowed only with survey estimation results from the `svy` prefix.

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification and that allow for intragroup correlation; see [R] ***vce_option***.

The `vce()` option may not be combined with the `svy` option or estimation results from the `svy` prefix.

Reporting

`level(#)` specifies the confidence level, as a percentage, for confidence intervals of the coefficients; see [R] **level**.

`dir` displays a table describing the models in *namelist* just like `estimates dir` *namelist*.

`eform(`*string*`)` displays the coefficient table in exponentiated form: for each coefficient, $\exp(b)$ rather than b is displayed, and standard errors and confidence intervals are transformed. *string* is the table header that will be displayed above the transformed coefficients and must be 11 characters or fewer, for example, `eform("Odds ratio")`.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `suest` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Remarks are presented under the following headings:

Using suest
Remarks on regress
Testing the assumption of the independence of irrelevant alternatives
Testing proportionality
Testing cross-model hypotheses

Using suest

If you plan to use suest, you must take precautions when fitting the original models. These restrictions are relaxed when using svy commands; see [SVY] **svy postestimation**.

1. suest works with estimation commands that allow predict to generate equation-level score variables when supplied with the score (or scores) option. For example, equation-level score variables are generated after running mlogit by typing

```
. predict sc*, scores
```

2. Estimation should take place *without* the vce(robust) or vce(cluster *clustvar*) option. suest always computes the robust estimator of the (co)variance, and suest has a vce(cluster *clustvar*) option.

   The within-model covariance matrices computed by suest are identical to those obtained by specifying a vce(robust) or vce(cluster *clustvar*) option during estimation. suest, however, also estimates the between-model covariances of parameter estimates.

3. Finally, the estimation results to be combined should be stored by estimates store; see [R] **estimates store**.

After estimating and storing a series of estimation results, you are ready to combine the estimation results with suest,

. suest *name1* [*name2* ...] [, vce(cluster *clustvar*)]

and you can subsequently use postestimation commands, such as test, to test hypotheses. Here an important issue is how suest assigns names to the equations. If you specify one model *name*, the original equation names are left unchanged; otherwise, suest constructs new equation names. The coefficients of a single-equation model (such as logit and poisson) that was estimate stored under name *X* are collected under equation *X*. With a multiequation model stored under name *X*, suest prefixes *X*_ to an original equation name *eq*, forming equation name, *X*_*eq*.

❑ Technical note

Earlier we said that standard errors from suest are identical to those obtained by specifying the vce(robust) option with each command individually. Thus if you fit a logistic model using logit with the vce(robust) option, you will get the same standard errors when you type

```
. suest .
```

directly after logit using the same data without the vce(robust) option.

This is not true for multiple estimation results when the estimation samples are not all the same. The standard errors from suest will be slightly smaller than those from individual model fits using the vce(robust) option because suest uses a larger number of observations to estimate the simultaneous (co)variance matrix.

❑

❑ Technical note

In rare circumstances, suest may have to truncate equation names to 32 characters. When equation names are not unique because of truncation, suest numbers the equations within models, using equations named *X*_#.

❑

Remarks on regress

`regress` (see [R] **regress**) does not include its ancillary parameter, the residual variance, in its coefficient vector and (co)variance matrix. Moreover, while the `score` option is allowed with `predict` after `regress`, a score variable is generated for the mean but not for the variance parameter. `suest` contains special code that assigns the equation name `mean` to the coefficients for the mean, adds the equation `lnvar` for the log variance, and computes the appropriate two score variables itself.

Testing the assumption of the independence of irrelevant alternatives

The multinomial logit model and the closely related conditional logit model satisfy a probabilistic version of the assumption of the independence of irrelevant alternatives (IIA), implying that the ratio of the probabilities for two alternatives does not depend on what other alternatives are available. Hausman and McFadden (1984) proposed a test for this assumption that is implemented in the `hausman` command. The standard Hausman test has several limitations. First, the test statistic may be undefined because the estimated VCE does not satisfy the required asymptotic properties of the test. Second, the classic Hausman test applies only to the test of the equality of two estimators. Third, the test requires access to a fully efficient estimator; such an estimator may not be available, for example, if you are analyzing complex survey data. Using `suest` can overcome these three limitations.

▷ Example 1

In our first example, we follow the analysis of the type of health insurance reported in [R] **mlogit** and demonstrate the `hausman` command with the `suest`/`test` combination. We fit the full multinomial logit model for all three alternatives and two restricted multinomial models in which one alternative is excluded. After fitting each of these models, we store the results by using the `store` subcommand of `estimates`. `title()` simply documents the models.

```
. use http://www.stata-press.com/data/r12/sysdsn4
(Health insurance data)

. mlogit insure age male
Iteration 0:   log likelihood = -555.85446
Iteration 1:   log likelihood = -551.32973
Iteration 2:   log likelihood = -551.32802
Iteration 3:   log likelihood = -551.32802
Multinomial logistic regression                 Number of obs   =        615
                                                LR chi2(4)      =       9.05
                                                Prob > chi2     =     0.0598
Log likelihood = -551.32802                     Pseudo R2       =     0.0081

------------------------------------------------------------------------------
      insure |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
Indemnity    |  (base outcome)
-------------+----------------------------------------------------------------
Prepaid      |
         age |  -.0100251   .0060181    -1.67   0.096    -.0218204    .0017702
        male |   .5095747   .1977893     2.58   0.010     .1219147    .8972346
       _cons |   .2633838   .2787575     0.94   0.345    -.2829708    .8097383
-------------+----------------------------------------------------------------
Uninsure     |
         age |  -.0051925   .0113821    -0.46   0.648    -.0275011    .0171161
        male |   .4748547   .3618462     1.31   0.189    -.2343508     1.18406
       _cons |  -1.756843   .5309602    -3.31   0.001    -2.797506   -.7161803
------------------------------------------------------------------------------

. estimates store m1, title(all three insurance forms)
```

```
. quietly mlogit insure age male if insure != "Uninsure":insure
. estimates store m2, title(insure != "Uninsure":insure)
. quietly mlogit insure age male if insure != "Prepaid":insure
. estimates store m3, title(insure != "Prepaid":insure)
```

Having performed the three estimations, we inspect the results. `estimates dir` provides short descriptions of the models that were stored using `estimates store`. Typing `estimates table` lists the coefficients, displaying blanks for a coefficient not contained in a model.

```
. estimates dir
```

name	command	depvar	npar	title
m1	mlogit	insure	9	*all three insurance forms*
m2	mlogit	insure	6	*insure != Uninsure :insure*
m3	mlogit	insure	6	*insure != Prepaid :insure*

```
. estimates table m1 m2 m3, star stats(N ll) keep(Prepaid: Uninsure:)
```

Variable	m1	m2	m3
Prepaid			
age	-.01002511	-.01015205	
male	.50957468**	.51440033**	
_cons	.26338378	.26780432	
Uninsure			
age	-.00519249		-.00410547
male	.47485472		.45910738
_cons	-1.7568431***		-1.8017743***
Statistics			
N	615	570	338
ll	-551.32802	-390.48643	-131.76807

legend: * p<0.05; ** p<0.01; *** p<0.001

Comparing the coefficients between models does not suggest substantial differences. We can formally test that coefficients are the same for the full model `m1` and the restricted models `m2` and `m3` by using the `hausman` command. `hausman` expects the models to be specified in the order "always consistent" first and "efficient under H_0" second.

```
. hausman m2 m1, alleqs constant
```

	Coefficients (b) m2	Coefficients (B) m1	(b-B) Difference	sqrt(diag(V_b-V_B)) S.E.
age	-.0101521	-.0100251	-.0001269	.
male	.5144003	.5095747	.0048256	.0123338
_cons	.2678043	.2633838	.0044205	.

```
                b = consistent under Ho and Ha; obtained from mlogit
    B = inconsistent under Ha, efficient under Ho; obtained from mlogit

Test:  Ho:  difference in coefficients not systematic

              chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                      =        0.08
            Prob>chi2 =      0.9944
            (V_b-V_B is not positive definite)
```

```
. hausman m3 m1, alleqs constant
```

	Coefficients (b) m3	(B) m1	(b-B) Difference	sqrt(diag(V_b-V_B)) S.E.
age	-.0041055	-.0051925	.001087	.0021355
male	.4591074	.4748547	-.0157473	.
_cons	-1.801774	-1.756843	-.0449311	.1333421

```
                b = consistent under Ho and Ha; obtained from mlogit
     B = inconsistent under Ha, efficient under Ho; obtained from mlogit

Test:  Ho:  difference in coefficients not systematic

           chi2(3) = (b-B)'[(V_b-V_B)^(-1)](b-B)
                   =    -0.18    chi2<0 ==> model fitted on these
                                 data fails to meet the asymptotic
                                 assumptions of the Hausman test;
                                 see suest for a generalized test
```

According to the test of `m1` against `m2`, we cannot reject the hypothesis that the coefficients of `m1` and `m2` are the same. The second Hausman test is not well defined—something that happens fairly often. The problem is due to the estimator of the variance `V(b-B)` as `V(b)-V(B)`, which is a feasible estimator only asymptotically. Here it simply is not a proper variance matrix, and the Hausman test becomes undefined.

`suest m1 m2` estimates the simultaneous (co)variance of the coefficients of models `m1` and `m2`. Although `suest` is technically a postestimation command, it acts like an estimation command in that it stores the simultaneous coefficients in `e(b)` and the full (co)variance matrix in `e(V)`. We could have used the `estat vce` command to display the full (co)variance matrix to show that the cross-model covariances were indeed estimated. Typically, we would not have a direct interest in `e(V)`.

```
. suest m1 m2, noomitted
Simultaneous results for m1, m2
                                                  Number of obs   =        615
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
m1_Indemnity						
m1_Prepaid						
age	-.0100251	.0059403	-1.69	0.091	-.0216679	.0016176
male	.5095747	.1988159	2.56	0.010	.1199027	.8992467
_cons	.2633838	.277307	0.95	0.342	-.280128	.8068956
m1_Uninsure						
age	-.0051925	.0109005	-0.48	0.634	-.0265571	.0161721
male	.4748547	.3677326	1.29	0.197	-.2458879	1.195597
_cons	-1.756843	.4971383	-3.53	0.000	-2.731216	-.78247
m2_Indemnity						
m2_Prepaid						
age	-.0101521	.0058988	-1.72	0.085	-.0217135	.0014094
male	.5144003	.1996133	2.58	0.010	.1231654	.9056352
_cons	.2678043	.2744019	0.98	0.329	-.2700134	.8056221

suest created equation names by combining the name under which we stored the results using estimates store with the original equation names. Thus, in the simultaneous estimation result, equation Prepaid originating in model m1 is named m1_Prepaid. According to the McFadden–Hausman specification of a test for IIA, the coefficients of the equations m1_PrePaid and m2_PrePaid should be equal. This equality can be tested easily with the test command. The cons option specifies that the intercept _cons be included in the test.

```
. test [m1_Prepaid = m2_Prepaid], cons
 ( 1)  [m1_Prepaid]age - [m2_Prepaid]age = 0
 ( 2)  [m1_Prepaid]male - [m2_Prepaid]male = 0
 ( 3)  [m1_Prepaid]_cons - [m2_Prepaid]_cons = 0
           chi2(  3) =    0.89
         Prob > chi2 =    0.8266
```

The Hausman test via suest is comparable to that computed by hausman, but they use different estimators of the variance of the difference of the estimates. The hausman command estimates $V(b-B)$ by $V(b)-V(B)$, whereas suest estimates $V(b-B)$ by $V(b)-\mathrm{cov}(b,B)-\mathrm{cov}(B,b)+V(B)$. One advantage of the second estimator is that it is always admissible, so the resulting test is always well defined. This quality is illustrated in the Hausman-type test of IIA comparing models m1 and m3.

```
. suest m1 m3, noomitted
Simultaneous results for m1, m3
                                                Number of obs   =        615
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
m1_Indemnity						
m1_Prepaid						
age	-.0100251	.0059403	-1.69	0.091	-.0216679	.0016176
male	.5095747	.1988159	2.56	0.010	.1199027	.8992467
_cons	.2633838	.277307	0.95	0.342	-.280128	.8068956
m1_Uninsure						
age	-.0051925	.0109005	-0.48	0.634	-.0265571	.0161721
male	.4748547	.3677326	1.29	0.197	-.2458879	1.195597
_cons	-1.756843	.4971383	-3.53	0.000	-2.731216	-.78247
m3_Indemnity						
m3_Uninsure						
age	-.0041055	.0111185	-0.37	0.712	-.0258974	.0176865
male	.4591074	.3601307	1.27	0.202	-.2467357	1.164951
_cons	-1.801774	.5226351	-3.45	0.001	-2.82612	-.7774283

```
. test [m1_Uninsure = m3_Uninsure], cons
 ( 1)  [m1_Uninsure]age - [m3_Uninsure]age = 0
 ( 2)  [m1_Uninsure]male - [m3_Uninsure]male = 0
 ( 3)  [m1_Uninsure]_cons - [m3_Uninsure]_cons = 0
           chi2(  3) =    1.49
         Prob > chi2 =    0.6845
```

Although the classic Hausman test computed by hausman is not defined here, the suest-based test is just fine. We cannot reject the equality of the common coefficients across m1 and m3.

A second advantage of the suest approach is that we can estimate the (co)variance matrix of the multivariate normal distribution of the estimators of the three models m1, m2, and m3 and test that the common coefficients are equal.

```
. suest m*, noomitted
Simultaneous results for m1, m2, m3
                                                  Number of obs   =        615
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
m1_Indemnity						
m1_Prepaid						
age	-.0100251	.0059403	-1.69	0.091	-.0216679	.0016176
male	.5095747	.1988159	2.56	0.010	.1199027	.8992467
_cons	.2633838	.277307	0.95	0.342	-.280128	.8068956
m1_Uninsure						
age	-.0051925	.0109005	-0.48	0.634	-.0265571	.0161721
male	.4748547	.3677326	1.29	0.197	-.2458879	1.195597
_cons	-1.756843	.4971383	-3.53	0.000	-2.731216	-.78247
m2_Indemnity						
m2_Prepaid						
age	-.0101521	.0058988	-1.72	0.085	-.0217135	.0014094
male	.5144003	.1996133	2.58	0.010	.1231654	.9056352
_cons	.2678043	.2744019	0.98	0.329	-.2700134	.8056221
m3_Indemnity						
m3_Uninsure						
age	-.0041055	.0111185	-0.37	0.712	-.0258974	.0176865
male	.4591074	.3601307	1.27	0.202	-.2467357	1.164951
_cons	-1.801774	.5226351	-3.45	0.001	-2.82612	-.7774283

```
. test [m1_Prepaid = m2_Prepaid], cons notest
 ( 1)  [m1_Prepaid]age - [m2_Prepaid]age = 0
 ( 2)  [m1_Prepaid]male - [m2_Prepaid]male = 0
 ( 3)  [m1_Prepaid]_cons - [m2_Prepaid]_cons = 0
. test [m1_Uninsure = m3_Uninsure], cons acc
 ( 1)  [m1_Prepaid]age - [m2_Prepaid]age = 0
 ( 2)  [m1_Prepaid]male - [m2_Prepaid]male = 0
 ( 3)  [m1_Prepaid]_cons - [m2_Prepaid]_cons = 0
 ( 4)  [m1_Uninsure]age - [m3_Uninsure]age = 0
 ( 5)  [m1_Uninsure]male - [m3_Uninsure]male = 0
 ( 6)  [m1_Uninsure]_cons - [m3_Uninsure]_cons = 0
           chi2(  6) =    1.95
         Prob > chi2 =    0.9240
```

Again we do not find evidence against the correct specification of the multinomial logit for type of insurance. The classic Hausman test assumes that one of the estimators (named `B` in `hausman`) is efficient, that is, it has minimal (asymptotic) variance. This assumption ensures that $V(b) - V(B)$ is an admissible, viable estimator for $V(b - B)$. The assumption that we have an efficient estimator is a restrictive one. It is violated, for instance, if our data are clustered. We want to adjust for clustering via a `vce(cluster` *clustvar*`)` option by requesting the cluster-adjusted sandwich estimator of variance. Consequently, in such a case, `hausman` cannot be used. This problem does not exist with the `suest` version of the Hausman test. To illustrate this feature, we suppose that the data are clustered by city—we constructed an imaginary variable `cityid` for this illustration. If we plan to apply `suest`, we would not specify the `vce(cluster` *clustvar*`)` option at the time of estimation.

suest has a vce(cluster *clustvar*) option. Thus we do not need to refit the models; we can call suest and test right away.

```
. suest m1 m2, vce(cluster cityid) noomitted
Simultaneous results for m1, m2
                                                  Number of obs   =        615
                              (Std. Err. adjusted for 260 clusters in cityid)
------------------------------------------------------------------------------
             |               Robust
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
m1_Indemnity |
-------------+----------------------------------------------------------------
m1_Prepaid   |
         age |  -.0100251    .005729    -1.75   0.080    -.0212538    .0012035
        male |   .5095747   .1910496     2.67   0.008     .1351244     .884025
       _cons |   .2633838   .2698797     0.98   0.329    -.2655708    .7923384
-------------+----------------------------------------------------------------
m1_Uninsure  |
         age |  -.0051925   .0104374    -0.50   0.619    -.0256495    .0152645
        male |   .4748547   .3774021     1.26   0.208    -.2648399    1.214549
       _cons |  -1.756843   .4916613    -3.57   0.000    -2.720481   -.7932048
-------------+----------------------------------------------------------------
m2_Indemnity |
-------------+----------------------------------------------------------------
m2_Prepaid   |
         age |  -.0101521   .0057164    -1.78   0.076    -.0213559    .0010518
        male |   .5144003   .1921385     2.68   0.007     .1378158    .8909848
       _cons |   .2678043   .2682193     1.00   0.318    -.2578959    .7935045
------------------------------------------------------------------------------

. test [m1_Prepaid = m2_Prepaid], cons
 ( 1)  [m1_Prepaid]age - [m2_Prepaid]age = 0
 ( 2)  [m1_Prepaid]male - [m2_Prepaid]male = 0
 ( 3)  [m1_Prepaid]_cons - [m2_Prepaid]_cons = 0
           chi2(  3) =    0.79
         Prob > chi2 =    0.8529
```

suest provides some descriptive information about the clustering on cityid. Like any other estimation command, suest informs us that the standard errors are adjusted for clustering. The Hausman-type test obtained from the test command uses a simultaneous (co)variance of m1 and m2 appropriately adjusted for clustering. In this example, we still do not have reason to conclude that the multinomial logit model in this application is misspecified, that is, that IIA is violated.

◁

The multinomial logistic regression model is a special case of the conditional logistic regression model; see [R] **clogit**. Like the multinomial logistic regression model, the conditional logistic regression model also makes the IIA assumption. Consider an example, introduced in [R] **asclogit**, in which the demand for American, Japanese, and European cars is modeled in terms of the number of local dealers of the respective brands and of some individual attributes incorporated in interaction with the nationality of cars. We want to perform a Hausman-type test for IIA comparing the decision between all nationalities with the decision between non-American cars. The following code fragment demonstrates how to conduct a Hausman test for IIA via suest in this case.

```
. clogit choice japan europe maleJap maleEur incJap incEur dealer, group(id)
. estimates store allcars
. clogit choice japan maleJap incJap dealer if car!=1 , group(id)
```

```
. estimates store foreign
. suest allcars foreign
. test [allcars_choice=foreign_choice], common
```

Testing proportionality

The applications of suest that we have discussed so far concern Hausman-type tests for misspecification. To test such a hypothesis, we compared two estimators that have the same probability limit if the hypothesis holds true, but otherwise have different limits. We may also want to compare the coefficients of models (estimators) for other substantive reasons. Although we most often want to test whether coefficients differ between models or estimators, we may occasionally want to test other constraints (see Hausman and Ruud [1987]).

▷ Example 2

In this example, using simulated labor market data for siblings, we consider two dependent variables, income (inc) and whether a person was promoted in the last year (promo). We apply familiar economic arguments regarding human capital, according to which employees have a higher income and a higher probability of being promoted, by having more human capital. Human capital is acquired through formal education (edu) and on-the-job training experience (exp). We study whether income and promotion are "two sides of the same coin", that is, whether they reflect a common latent variable, "human capital". Accordingly, we want to compare the effects of different aspects of human capital on different outcome variables.

We estimate fairly simple labor market equations. The income model is estimated with regress, and the estimation results are stored under the name Inc.

```
. use http://www.stata-press.com/data/r12/income
. regress inc edu exp male
```

Source	SS	df	MS	Number of obs =	277
				F(3, 273) =	42.34
Model	2058.44672	3	686.148908	Prob > F =	0.0000
Residual	4424.05183	273	16.2053181	R-squared =	0.3175
				Adj R-squared =	0.3100
Total	6482.49855	276	23.4873136	Root MSE =	4.0256

inc	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
edu	2.213707	.243247	9.10	0.000	1.734828	2.692585
exp	1.47293	.231044	6.38	0.000	1.018076	1.927785
male	.5381153	.4949466	1.09	0.278	-.436282	1.512513
_cons	1.255497	.3115808	4.03	0.000	.642091	1.868904

```
. est store Inc
```

Being sibling data, the observations are clustered on family of origin, famid. In the estimation of the regression parameters, we did not specify a vce(cluster famid) option to adjust standard errors for clustering on family (famid). Thus the standard errors reported by regress are potentially flawed. This problem will, however, be corrected by specifying a vce(cluster *clustvar*) option with suest.

Next we estimate the promotion equation with probit and again store the results under an appropriate name.

```
. probit promo edu exp male, nolog
Probit regression                                 Number of obs   =        277
                                                  LR chi2(3)      =      49.76
                                                  Prob > chi2     =     0.0000
Log likelihood = -158.43888                       Pseudo R2       =     0.1357
```

promo	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
edu	.4593002	.0898537	5.11	0.000	.2831901	.6354102
exp	.3593023	.0805774	4.46	0.000	.2013735	.5172312
male	.2079983	.1656413	1.26	0.209	-.1166527	.5326494
_cons	-.464622	.1088166	-4.27	0.000	-.6778985	-.2513454

```
. est store Promo
```

The coefficients in the income and promotion equations definitely seem to be different. However, because the scales of the two variables are different, we would not expect the coefficients to be equal. The correct hypothesis here is that the proportionality of the coefficients of the two models, apart from the constant, are equal. This formulation would still reflect that the relative effects of the different aspects of human capital do not differ between the dependent variables. We can obtain a nonlinear Wald test for the hypothesis of proportionality by using the `testnl` command on the combined estimation results of the two estimators. Thus we first have to form the combined estimation results. At this point, we specify the `vce(cluster famid)` option to adjust for the clustering of observations on `famid`.

```
. suest Inc Promo, vce(cluster famid)
Simultaneous results for Inc, Promo
                                                  Number of obs   =        277
                                  (Std. Err. adjusted for 135 clusters in famid)
```

	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
Inc_mean						
edu	2.213707	.2483907	8.91	0.000	1.72687	2.700543
exp	1.47293	.1890583	7.79	0.000	1.102383	1.843478
male	.5381153	.4979227	1.08	0.280	-.4377952	1.514026
_cons	1.255497	.3374977	3.72	0.000	.594014	1.916981
Inc_lnvar						
_cons	2.785339	.079597	34.99	0.000	2.629332	2.941347
Promo_promo						
edu	.4593002	.0886982	5.18	0.000	.2854549	.6331454
exp	.3593023	.079772	4.50	0.000	.2029522	.5156525
male	.2079983	.1691053	1.23	0.219	-.1234419	.5394386
_cons	-.464622	.1042169	-4.46	0.000	-.6688833	-.2603607

The standard errors reported by `suest` are identical to those reported by the respective estimation commands when invoked with the `vce(cluster famid)` option. We are now ready to test for proportionality:

$$H_0 : \frac{\beta^{\text{Income}}_{\text{edu}}}{\beta^{\text{Promotion}}_{\text{edu}}} = \frac{\beta^{\text{Income}}_{\text{exp}}}{\beta^{\text{Promotion}}_{\text{exp}}} = \frac{\beta^{\text{Income}}_{\text{male}}}{\beta^{\text{Promotion}}_{\text{male}}}$$

It is straightforward to translate this into syntax suitable for `testnl`, recalling that the coefficient of variable v in equation eq is denoted by `[`eq`]`v.

```
. testnl [Inc_mean]edu/[Promo_promo]edu =
>        [Inc_mean]exp/[Promo_promo]exp =
>        [Inc_mean]male/[Promo_promo]male
  (1)  [Inc_mean]edu/[Promo_promo]edu = [Inc_mean]exp/[Promo_promo]exp
  (2)  [Inc_mean]edu/[Promo_promo]edu = [Inc_mean]male/[Promo_promo]male
             chi2(2) =        0.61
           Prob > chi2 =        0.7385
```

From the evidence, we fail to reject the hypotheses that the coefficients of the income and promotion equations are proportional. Thus it is not unreasonable to assume that income and promotion can be explained by the same latent variable, "labor market success".

A disadvantage of the nonlinear Wald test is that it is not invariant with respect to representation: a Wald test for a mathematically equivalent formulation of the nonlinear constraint usually leads to a different test result. An equivalent formulation of the proportionality hypothesis is

$$\begin{aligned} H_0\text{:}\quad & \beta^{\text{Income}}_{\text{edu}}\beta^{\text{Promotion}}_{\text{exp}} = \beta^{\text{Promotion}}_{\text{edu}}\beta^{\text{Income}}_{\text{exp}} \quad \text{and} \\ & \beta^{\text{Income}}_{\text{edu}}\beta^{\text{Promotion}}_{\text{male}} = \beta^{\text{Promotion}}_{\text{edu}}\beta^{\text{Income}}_{\text{male}} \end{aligned}$$

This formulation is "more linear" in the coefficients. The asymptotic χ^2 distribution of the nonlinear Wald statistic can be expected to be more accurate for this representation.

```
. testnl ([Inc_mean]edu*[Promo_promo]exp = [Inc_mean]exp*[Promo_promo]edu)
>        ([Inc_mean]edu*[Promo_promo]male = [Inc_mean]male*[Promo_promo]edu)
  (1)  [Inc_mean]edu*[Promo_promo]exp = [Inc_mean]exp*[Promo_promo]edu
  (2)  [Inc_mean]edu*[Promo_promo]male = [Inc_mean]male*[Promo_promo]edu
             chi2(2) =        0.46
           Prob > chi2 =        0.7936
```

Here the two representations lead to similar test statistics and p-values. As before, we fail to reject the hypothesis of proportionality of the coefficients of the two models.

◁

Testing cross-model hypotheses

▷ Example 3

In this example, we demonstrate how some cross-model hypotheses can be tested using the facilities already available in most estimation commands. This demonstration will explain the intricate relationship between the cluster adjustment of the robust estimator of variance and the `suest` command. It will also be made clear that a new facility is required to perform more general cross-model testing.

We want to test whether the effect of x_1 on the binary variable y_1 is the same as the effect of x_2 on the binary y_2; see Clogg, Petkova, and Haritou (1995). In this setting, x_1 may equal x_2, and y_1 may equal y_2. We assume that logistic regression models can be used to model the responses, and for simplicity, we ignore further predictor variables in these models. If the two logit models are fit on independent samples so that the estimators are (stochastically) independent, a Wald test for `_b[x1] = _b[x2]` rejects the null hypothesis if

$$\frac{\widehat{b}(x_1) - \widehat{b}(x_2)}{\left[\widehat{\sigma}^2\left\{\widehat{b}(x_1)\right\} + \widehat{\sigma}^2\left\{\widehat{b}(x_2)\right\}\right]^{1/2}}$$

is larger than the appropriate χ^2_1 threshold. If the models are fit on the *same* sample (or on dependent samples), so that the estimators are stochastically dependent, the above test that ignores the covariance between the estimators is not appropriate.

It is instructive to see how this problem can be tackled by "stacking" data. In the stacked format, we doubled the number of observations. The dependent variable is y_1 in the first half of the data and is y_2 in the second half of the data. The predictor variable z_1 is set to x_1 in the first half of the expanded data and to 0 in the rest. Similarly, z_2 is 0 in the first half and x_2 in the second half. The following diagram illustrates the transformation, in the terminology of the `reshape` command, from wide to long format.

id	y_1	y_2	x_1	x_2
1	y_{11}	y_{21}	x_{11}	x_{21}
2	y_{12}	y_{22}	x_{12}	x_{22}
3	y_{13}	y_{23}	x_{13}	x_{23}

$\Longrightarrow$

id	y	z_1	z_2	model
1	y_{11}	x_{11}	0	1
2	y_{12}	x_{12}	0	1
3	y_{13}	x_{13}	0	1
1	y_{21}	0	x_{21}	2
2	y_{22}	0	x_{22}	2
3	y_{23}	0	x_{23}	2

The observations in the long format data organization are *clustered* on the original subjects and are identified with the identifier `id`. The clustering on `id` has to be accounted for when fitting a simultaneous model. The simplest way to deal with clustering is to use the cluster adjustment of the robust or sandwich estimator; see [P] **_robust**. The data manipulation can be accomplished easily with the `stack` command; see [D] **stack**. Subsequently, we fit a simultaneous logit model and perform a Wald test for the hypothesis that the coefficients of `z1` and `z2` are the same. A full setup to obtain the cross-model Wald test could then be as follows:

```
. generate zero = 0          // a variable that is always 0
. generate one  = 1          // a variable that is always 1
. generate two  = 2          // a variable that is always 2
. stack  id y1 x1 zero one   id y2 zero x2 two, into(id y z1 z2 model)
. generate model2 = (model==2)
. logit y model2 z1 z2, vce(cluster id)
. test _b[z1] = _b[z2]
```

The coefficient of `z1` represents the effect of `x1` on `y1`, and similarly, `z2` for the effect of `x2` on `y2`. The variable `model2` is a dummy for the "second model", which is included to allow the intercept in the second model to differ from that in the first model. The estimates of the coefficient of `z1` and its standard error in the combined model are the same as the estimates of the coefficient of `z1` and its standard error if we fit the model on the unstacked data.

```
. logit y1 x1, vce(robust)
```

The vce(cluster *clustvar*) option specified with the logit command for the stacked data ensures that the covariances of _b[z1] and _b[z2] are indeed estimated. This estimation ensures that the Wald test for the equality of the coefficients is correct. If we had not specified the vce(cluster *clustvar*) option, the (co)variance matrix of the coefficients would have been block-diagonal; that is, the covariances of _b[z1] and _b[z2] would have been 0. Then test would have effectively used the invalid formula for the Wald test for two independent samples.

In this example, the two logit models were fit on the same data. The same setup would apply, without modification, when the two logit models were fit on overlapping data that resulted, for instance, if the y or x variables were missing in some observations.

The suest command allows us to obtain the above Wald test more efficiently by avoiding the data manipulation, obviating the need to fit a model with twice the number of coefficients. The test statistic produced by the above code fragment is *identical* to that obtained via suest on the original (unstacked) data:

```
. logit y1 x1
. estimates store M1
. logit y2 x2
. estimates store M2
. suest M1 M2
. test [M1]x1=[M2]x2
```

The stacking method can be applied not only to the testing of cross-model hypotheses for logit models but also to any estimation command that supports the vce(cluster *clustvar*) option. The stacking approach clearly generalizes to stacking more than two logit or other models, testing more general linear hypotheses, and testing nonlinear cross-model hypotheses (see [R] **testnl**). In all these cases, suest would yield identical statistical results but at smaller costs in terms of data management, computer storage, and computer time.

Is suest nothing but a convenience command? No, there are two disadvantages to the stacking method, both of which are resolved via suest. First, if the models include ancillary parameters (in a regression model, the residual variance; in an ordinal response model, the cutpoints; and in lognormal survival-time regression, the time scale parameter), these parameters are constrained to be equal between the stacked models. In suest, this constraint is relaxed. Second, the stacking method does not generalize to compare different statistical models, such as a probit model and a regression model. As demonstrated in the previous section, suest can deal with this situation.

◁

Saved results

suest saves the following in e():

Scalars

e(N)	number of observations
e(N_clust)	number of clusters
e(rank)	rank of e(V)

Macros

e(cmd)	suest
e(eqnames#)	original names of equations of model #
e(names)	list of model names
e(wtype)	weight type
e(wexp)	weight expression
e(clustvar)	name of cluster variable
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V

Matrices

e(b)	stacked coefficient vector of the models
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

suest is implemented as an ado-file.

The estimation of the simultaneous (co)variance of a series of k estimators is a nonstandard application of the sandwich estimator, as implemented by the command [P] **_robust**. You may want to read this manual entry before reading further.

The starting point is that we have fit k different models on the *same* data—partially overlapping or nonoverlapping data are special cases. We want to derive the *simultaneous* distribution of these k estimators, for instance, to test a cross-estimator hypothesis H_0. As in the framework of Hausman testing, H_0 will often be of the form that different estimators have the same probability limit under some hypothesis, while the estimators have different limits if the hypothesis is violated.

We consider (vector) estimators $\widehat{\boldsymbol{\beta}}_i$ to be defined as "the" solution of the estimation equations $\mathbf{G}_i$,

$$\mathbf{G}_i(\mathbf{b}_i) = \sum_j w_{ij}\mathbf{u}_{ij}(\mathbf{b}_i) = \mathbf{0}, \qquad i = 1, \ldots, k$$

We refer to the $\mathbf{u}_{ij}$ as the "scores". Specifying some weights $w_{ij} = 0$ trivially accommodates for partially overlapping or even disjointed data. Under "suitable regularity conditions" (see White [1982; 1996] for details), the $\widehat{\boldsymbol{\beta}}_i$ are asymptotically normally distributed, with the variance estimated consistently by the sandwich estimator

$$V_i = \mathrm{Var}(\widehat{\boldsymbol{\beta}}_i) = \mathbf{D}_i^{-1} \sum_j w_{ij}\mathbf{u}_{ij}\mathbf{u}_{ij}' \, \mathbf{D}_i^{-1}$$

where $\mathbf{D}_i$ is the Jacobian of $\mathbf{G}_i$ evaluated at $\widehat{\boldsymbol{\beta}}_i$. In the context of maximum likelihood estimation, $\mathbf{D}_i$ can be estimated consistently by (minus) the Hessian of the log likelihood or by the Fisher information matrix. If the model is also well specified, the sandwiched term $(\sum_j w_{ij}\mathbf{u}_{ij}\mathbf{u}_{ij}')$ converges in probability to $\mathbf{D}_i$, so V_i may be consistently estimated by $\mathbf{D}_i^{-1}$.

To derive the simultaneous distribution of the estimators, we consider the "stacked" estimation equation,

$$\mathbf{G}(\widehat{\boldsymbol{\beta}}) = \left\{ \mathbf{G}_1(\widehat{\boldsymbol{\beta}}_1)' \quad \mathbf{G}_1(\widehat{\boldsymbol{\beta}}_2)' \quad \dots \quad \mathbf{G}_k(\widehat{\boldsymbol{\beta}}_k)' \right\}' = \mathbf{0}$$

Under "suitable regularity conditions" (see White [1996] for details), $\widehat{\boldsymbol{\beta}}$ is asymptotically *jointly* normally distributed. The Jacobian and scores of the simultaneous equation are easily expressed in the Jacobian and scores of the separate equations. The Jacobian of $\mathbf{G}$,

$$\mathbf{D}(\widehat{\boldsymbol{\beta}}) = \left. \frac{d\mathbf{G}(\boldsymbol{\beta})}{d\boldsymbol{\beta}} \right|_{\boldsymbol{\beta}=\widehat{\boldsymbol{\beta}}}$$

is block diagonal with blocks $\mathbf{D}_1, \dots, \mathbf{D}_k$. The inverse of $\mathbf{D}(\widehat{\boldsymbol{\beta}})$ is again block diagonal, with the inverses of $\mathbf{D}_i$ on the diagonal. The scores $\mathbf{u}$ of $\mathbf{G}$ are simply obtained as the *concatenated* scores of the separate equations:

$$\mathbf{u}_j = (\mathbf{u}_{1j}' \quad \mathbf{u}_{2j}' \quad \dots \quad \mathbf{u}_{kj}')'$$

Out-of-sample (that is, where $w_{ij} = 0$) values of the score variables are defined as 0 (thus we drop the i subscript from the common weight variable). The sandwich estimator for the asymptotic variance of $\widehat{\boldsymbol{\beta}}$ reads

$$V = \mathrm{Var}(\widehat{\boldsymbol{\beta}}) = \mathbf{D}(\widehat{\boldsymbol{\beta}})^{-1} \left(\sum_j w_j \mathbf{u}_j \mathbf{u}_j' \right) \mathbf{D}(\widehat{\boldsymbol{\beta}})^{-1}$$

Taking a "partitioned" look at this expression, we see that $V(\widehat{\boldsymbol{\beta}}_i)$ is estimated by

$$\mathbf{D}_i^{-1} \left(\sum_j w_j \mathbf{u}_{ij} \mathbf{u}_{ij}' \right) \mathbf{D}_i^{-1}$$

which is, yet again, the familiar sandwich estimator for $\widehat{\boldsymbol{\beta}}_i$ based on the separate estimation equation $\mathbf{G}_i$. Thus considering several estimators simultaneously in this way does not affect the estimators of the asymptotic variances of these estimators. However, as a bonus of stacking, we obtained a sandwich-type estimate of the *covariance* V_{ih} of estimators $\widehat{\boldsymbol{\beta}}_i$ and $\widehat{\boldsymbol{\beta}}_h$,

$$V_{ih} = \mathrm{Cov}(\widehat{\boldsymbol{\beta}}_i, \widehat{\boldsymbol{\beta}}_h) = \mathbf{D}_i^{-1} \left(\sum_j w_j \mathbf{u}_{ij} \mathbf{u}_{ih}' \right) \mathbf{D}_h^{-1}$$

which is also obtained by White (1982).

This estimator for the covariance of estimators is an application of the cluster modification of the sandwich estimator proposed by Rogers (1993). Consider the stacked data format as discussed in the logit example, and assume that Stata would be able to estimate a "stacked model" in which different models apply to different observations, for example, a probit model for the first half, a regression model for the second half, and a one-to-one cluster relation between the first and second half. If there are no common parameters to both models, the score statistics of parameters for the stacked models are zero in the half of the data in which they do not occur. In Rogers' method, we have to sum the score statistics over the observations within a cluster. This step boils down to concatenating the score statistics at the level of the cluster.

We compare the sandwich estimator of the (co)variance V_{12} of two estimators with the estimator of variance $\widetilde{V}_{12}$ applied in the classic Hausman test. Hausman (1978) showed that if $\widehat{\boldsymbol{\beta}}_1$ is consistent under H_0 and $\widehat{\boldsymbol{\beta}}_2$ is efficient under H_0, then asymptotically

$$\mathrm{Cov}(\widehat{\boldsymbol{\beta}}_1, \widehat{\boldsymbol{\beta}}_2) = \mathrm{Var}(\widehat{\boldsymbol{\beta}}_2)$$

and so $\mathrm{var}(\widehat{\boldsymbol{\beta}}_1 - \widehat{\boldsymbol{\beta}}_2)$ is consistently estimated by $V_1 - V_2$.

Acknowledgment

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An earlier version of `suest` was published in the *Stata Technical Bulletin* (1999). The current version of `suest` is not backward compatible with the STB version because of the introduction of new ways to manage estimation results via the `estimates` command.

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Also see

[R] **estimates** — Save and manipulate estimation results

[R] **hausman** — Hausman specification test

[R] **lincom** — Linear combinations of estimators

[R] **nlcom** — Nonlinear combinations of estimators

[R] **test** — Test linear hypotheses after estimation

[R] **testnl** — Test nonlinear hypotheses after estimation

[P] **_robust** — Robust variance estimates

Title

summarize — Summary statistics

Syntax

`summarize` [*varlist*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`detail`	display additional statistics
`meanonly`	suppress the display; calculate only the mean; programmer's option
`format`	use variable's display format
`separator(#)`	draw separator line after every # variables; default is `separator(5)`
display_options	control spacing and base and empty cells

varlist may contain factor variables; see [U] **11.4.3 Factor variables**.
varlist may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`by`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.
`aweights`, `fweights`, and `iweights` are allowed. However, `iweights` may not be used with the `detail` option; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Summary statistics

Description

`summarize` calculates and displays a variety of univariate summary statistics. If no *varlist* is specified, summary statistics are calculated for all the variables in the dataset.

Also see [R] **ci** for calculating the standard error and confidence intervals of the mean.

Options

Main

`detail` produces additional statistics, including skewness, kurtosis, the four smallest and largest values, and various percentiles.

`meanonly`, which is allowed only when `detail` is not specified, suppresses the display of results and calculation of the variance. Ado-file writers will find this useful for fast calls.

`format` requests that the summary statistics be displayed using the display formats associated with the variables rather than the default `g` display format; see [U] **12.5 Formats: Controlling how data are displayed**.

`separator(#)` specifies how often to insert separation lines into the output. The default is `separator(5)`, meaning that a line is drawn after every five variables. `separator(10)` would draw a line after every 10 variables. `separator(0)` suppresses the separation line.

display_options: vsquish, noemptycells, baselevels, allbaselevels; see [R] **estimation options**.

Remarks

summarize can produce two different sets of summary statistics. Without the detail option, the number of nonmissing observations, the mean and standard deviation, and the minimum and maximum values are presented. With detail, the same information is presented along with the variance, skewness, and kurtosis; the four smallest and four largest values; and the 1st, 5th, 10th, 25th, 50th (median), 75th, 90th, 95th, and 99th percentiles.

▷ Example 1: summarize with the separator() option

We have data containing information on various automobiles, among which is the variable mpg, the mileage rating. We can obtain a quick summary of the mpg variable by typing

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. summarize mpg
```

Variable	Obs	Mean	Std. Dev.	Min	Max
mpg	74	21.2973	5.785503	12	41

We see that we have 74 observations. The mean of mpg is 21.3 miles per gallon, and the standard deviation is 5.79. The minimum is 12, and the maximum is 41.

If we had not specified the variable (or variables) we wanted to summarize, we would have obtained summary statistics on all the variables in the dataset:

```
. summarize, separator(4)
```

Variable	Obs	Mean	Std. Dev.	Min	Max
make	0				
price	74	6165.257	2949.496	3291	15906
mpg	74	21.2973	5.785503	12	41
rep78	69	3.405797	.9899323	1	5
headroom	74	2.993243	.8459948	1.5	5
trunk	74	13.75676	4.277404	5	23
weight	74	3019.459	777.1936	1760	4840
length	74	187.9324	22.26634	142	233
turn	74	39.64865	4.399354	31	51
displacement	74	197.2973	91.83722	79	425
gear_ratio	74	3.014865	.4562871	2.19	3.89
foreign	74	.2972973	.4601885	0	1

There are only 69 observations on rep78, so some of the observations are missing. There are no observations on make because it is a string variable.

◁

The idea of the mean is quite old (Plackett 1958), but its extension to a scheme of moment-based measures was not done until the end of the 19th century. Between 1893 and 1905, Pearson discussed and named the standard deviation, skewness, and kurtosis, but he was not the first to use any of these. Thiele (1889), in contrast, had earlier firmly grasped the notion that the m_r provide a systematic basis for discussing distributions. However, even earlier anticipations can also be found. For example, Euler in 1778 used m_2 and m_3 in passing in a treatment of estimation (Hald 1998, 87), but seemingly did not build on that.

Similarly, the idea of the median is quite old. The history of the interquartile range is tangled up with that of the probable error, a long-popular measure. Extending this in various ways to a more general approach based on quantiles (to use a later term) occurred to several people in the nineteenth century. Galton (1875) is a nice example, particularly because he seems so close to the key idea of the quantiles as a function, which took another century to reemerge strongly.

Thorvald Nicolai Thiele (1838–1910) was a Danish scientist who worked in astronomy, mathematics, actuarial science, and statistics. He made many pioneering contributions to statistics, several of which were overlooked until recently. Thiele advocated graphical analysis of residuals checking for trends, symmetry of distributions, and changes of sign, and he even warned against overinterpreting such graphs.

▷ Example 2: summarize with the detail option

The `detail` option provides all the information of a normal `summarize` and more. The format of the output also differs, as shown here:

```
. summarize mpg, detail
                        Mileage (mpg)
-------------------------------------------------------------
      Percentiles      Smallest
 1%           12             12
 5%           14             12
10%           14             14       Obs                  74
25%           18             14       Sum of Wgt.          74
50%           20                      Mean            21.2973
                        Largest       Std. Dev.       5.785503
75%           25             34
90%           29             35       Variance        33.47205
95%           34             35       Skewness        .9487176
99%           41             41       Kurtosis        3.975005
```

As in the previous example, we see that the mean of `mpg` is 21.3 miles per gallon and that the standard deviation is 5.79. We also see the various percentiles. The median of `mpg` (the 50th percentile) is 20 miles per gallon. The 25th percentile is 18, and the 75th percentile is 25.

When we performed `summarize`, we learned that the minimum and maximum were 12 and 41, respectively. We now see that the four smallest values in our dataset are 12, 12, 14, and 14. The four largest values are 34, 35, 35, and 41. The skewness of the distribution is 0.95, and the kurtosis is 3.98. (A normal distribution would have a skewness of 0 and a kurtosis of 3.)

Skewness is a measure of the lack of symmetry of a distribution. If the distribution is symmetric, the coefficient of skewness is 0. If the coefficient is negative, the median is usually greater than the mean and the distribution is said to be skewed left. If the coefficient is positive, the median is usually less than the mean and the distribution is said to be skewed right. *Kurtosis* (from the Greek *kyrtosis*, meaning curvature) is a measure of peakedness of a distribution. The smaller the coefficient of kurtosis, the flatter the distribution. The normal distribution has a coefficient of kurtosis of 3 and provides a convenient benchmark. ◁

Example 3: summarize with the by prefix

`summarize` can usefully be combined with the by *varlist*: prefix. In our dataset, we have a variable, `foreign`, that distinguishes foreign and domestic cars. We can obtain summaries of `mpg` and `weight` within each subgroup by typing

```
. by foreign: summarize mpg weight
```

```
-> foreign = Domestic
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         mpg |         52    19.82692    4.743297        12         34
      weight |         52    3317.115    695.3637      1800       4840

-> foreign = Foreign
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
         mpg |         22    24.77273    6.611187        14         41
      weight |         22    2315.909    433.0035      1760       3420
```

Domestic cars in our dataset average 19.8 miles per gallon, whereas foreign cars average 24.8.

Because by *varlist*: can be combined with `summarize`, it can also be combined with `summarize, detail`:

```
. by foreign: summarize mpg, detail
```

```
-> foreign = Domestic
                          Mileage (mpg)
-------------------------------------------------------------
      Percentiles      Smallest
 1%           12              12
 5%           14              12
10%           14              14       Obs                  52
25%         16.5              14       Sum of Wgt.          52

50%           19                       Mean           19.82692
                        Largest       Std. Dev.      4.743297
75%           22              28
90%           26              29       Variance       22.49887
95%           29              30       Skewness       .7712432
99%           34              34       Kurtosis       3.441459

-> foreign = Foreign
                          Mileage (mpg)
-------------------------------------------------------------
      Percentiles      Smallest
 1%           14              14
 5%           17              17
10%           17              17       Obs                  22
25%           21              18       Sum of Wgt.          22

50%         24.5                       Mean           24.77273
                        Largest       Std. Dev.      6.611187
75%           28              31
90%           35              35       Variance       43.70779
95%           35              35       Skewness        .657329
99%           41              41       Kurtosis        3.10734
```

❑ Technical note

`summarize` respects display formats if we specify the `format` option. When we type `summarize price weight`, we obtain

```
. summarize price weight
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       price |         74    6165.257    2949.496       3291      15906
      weight |         74    3019.459    777.1936       1760       4840
```

The display is accurate but is not as aesthetically pleasing as we may wish, particularly if we plan to use the output directly in published work. By placing formats on the variables, we can control how the table appears:

```
. format price weight %9.2fc
. summarize price weight, format
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       price |         74    6,165.26    2,949.50    3,291.00  15,906.00
      weight |         74    3,019.46      777.19    1,760.00   4,840.00
```

❑

If you specify a weight (see [U] **11.1.6 weight**), each observation is multiplied by the value of the weighting expression before the summary statistics are calculated so that the weighting expression is interpreted as the discrete density of each observation.

▷ Example 4: summarize with factor variables

You can also use `summarize` to obtain summary statistics for factor variables. For example, if you type

```
. summarize i.rep78
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       rep78 |
          2  |         69     .115942    .3225009         0          1
          3  |         69    .4347826    .4993602         0          1
          4  |         69    .2608696    .4423259         0          1
          5  |         69    .1594203    .3687494         0          1
```

you obtain the sample proportions for four of the five levels of the `rep78` variable. For example, 11.6% of the 69 cars with nonmissing values of `rep78` fall into repair category two. When you use factor-variable notation, the base category is suppressed by default. If you type

```
. summarize bn.rep78
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
       rep78 |
          1  |         69    .0289855    .1689948         0          1
          2  |         69     .115942    .3225009         0          1
          3  |         69    .4347826    .4993602         0          1
          4  |         69    .2608696    .4423259         0          1
          5  |         69    .1594203    .3687494         0          1
```

the notation `bn.rep78` indicates that Stata should not suppress the base category so that we see the proportions for all five levels.

We could have used `tabulate oneway rep78` to obtain the sample proportions along with the cumulative proportions. Alternatively, we could have used `proportions rep78` to obtain the sample proportions along with the standard errors of the proportions instead of the standard deviations of the proportions.

◁

▷ Example 5: summarize with weights

We have 1980 census data on each of the 50 states. Included in our variables is `medage`, the median age of the population of each state. If we type `summarize medage`, we obtain unweighted statistics:

```
. use http://www.stata-press.com/data/r12/census
(1980 Census data by state)
. summarize medage
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
      medage |         50       29.54    1.693445       24.2       34.7
```

Also among our variables is `pop`, the population in each state. Typing `summarize medage [w=pop]` produces population-weighted statistics:

```
. summarize medage [w=pop]
(analytic weights assumed)
    Variable |        Obs      Weight        Mean   Std. Dev.       Min        Max
-------------+---------------------------------------------------------------------
      medage |         50   225907472    30.11047     1.66933       24.2       34.7
```

The number listed under `Weight` is the sum of the weighting variable, `pop`, indicating that there are roughly 226 million people in the United States. The `pop`-weighted mean of `medage` is 30.11 (compared with 29.54 for the unweighted statistic), and the weighted standard deviation is 1.67 (compared with 1.69).

◁

▷ Example 6: summarize with weights and the detail option

We can obtain detailed summaries of weighted data as well. When we do this, *all* the statistics are weighted, including the percentiles.

```
. summarize medage [w=pop], detail
(analytic weights assumed)
                          Median age
-------------------------------------------------------------
      Percentiles      Smallest
 1%         27.1           24.2
 5%         27.7           26.1
10%         28.2           27.1       Obs                  50
25%         29.2           27.4       Sum of Wgt.   225907472
50%         29.9                      Mean           30.11047
                       Largest       Std. Dev.       1.66933
75%         30.9             32
90%         32.1           32.1       Variance       2.786661
95%         32.2           32.2       Skewness       .5281972
99%         34.7           34.7       Kurtosis       4.494223
```

◁

❑ Technical note

If you are writing a program and need to access the mean of a variable, the `meanonly` option provides for fast calls. For example, suppose that your program reads as follows:

```
program mean
        summarize '1', meanonly
        display "  mean = " r(mean)
end
```

The result of executing this is

```
. mean price
  mean = 6165.2568
```

❑

Saved results

`summarize` saves the following in `r()`:

Scalars

`r(N)`	number of observations	`r(p50)`	50th percentile (`detail` only)
`r(mean)`	mean	`r(p75)`	75th percentile (`detail` only)
`r(skewness)`	skewness (`detail` only)	`r(p90)`	90th percentile (`detail` only)
`r(min)`	minimum	`r(p95)`	95th percentile (`detail` only)
`r(max)`	maximum	`r(p99)`	99th percentile (`detail` only)
`r(sum_w)`	sum of the weights	`r(Var)`	variance
`r(p1)`	1st percentile (`detail` only)	`r(kurtosis)`	kurtosis (`detail` only)
`r(p5)`	5th percentile (`detail` only)	`r(sum)`	sum of variable
`r(p10)`	10th percentile (`detail` only)	`r(sd)`	standard deviation
`r(p25)`	25th percentile (`detail` only)		

Methods and formulas

Let x denote the variable on which we want to calculate summary statistics, and let x_i, $i = 1, \ldots, n$, denote an individual observation on x. Let v_i be the weight, and if no weight is specified, define $v_i = 1$ for all i.

Define V as the *sum of the weight*:

$$V = \sum_{i=1}^{n} v_i$$

Define w_i to be v_i normalized to sum to n, $w_i = v_i(n/V)$.

The *mean*, $\overline{x}$, is defined as

$$\overline{x} = \frac{1}{n}\sum_{i=1}^{n} w_i x_i$$

The *variance*, s^2, is defined as

$$s^2 = \frac{1}{n-1}\sum_{i=1}^{n} w_i(x_i - \overline{x})^2$$

The *standard deviation*, s, is defined as $\sqrt{s^2}$.

Define m_r as the rth moment about the mean $\overline{x}$:

$$m_r = \frac{1}{n}\sum_{i=1}^{n} w_i(x_i - \overline{x})^r$$

The *coefficient of skewness* is then defined as $m_3 m_2^{-3/2}$. The *coefficient of kurtosis* is defined as $m_4 m_2^{-2}$.

Let $x_{(i)}$ refer to the x in ascending order, and let $w_{(i)}$ refer to the corresponding weights of $x_{(i)}$. The four smallest values are $x_{(1)}$, $x_{(2)}$, $x_{(3)}$, and $x_{(4)}$. The four largest values are $x_{(n)}$, $x_{(n-1)}$, $x_{(n-2)}$, and $x_{(n-3)}$.

To obtain the pth *percentile*, which we will denote as $x_{[p]}$, let $P = np/100$. Let

$$W_{(i)} = \sum_{j=1}^{i} w_{(j)}$$

Find the first index i such that $W_{(i)} > P$. The pth percentile is then

$$x_{[p]} = \begin{cases} \dfrac{x_{(i-1)} + x_{(i)}}{2} & \text{if } W_{(i-1)} = P \\ x_{(i)} & \text{otherwise} \end{cases}$$

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Also see

[R] **ameans** — Arithmetic, geometric, and harmonic means

[R] **centile** — Report centile and confidence interval

[R] **mean** — Estimate means

[R] **proportion** — Estimate proportions

[R] **ratio** — Estimate ratios

[R] **table** — Tables of summary statistics

[R] **tabstat** — Display table of summary statistics

[R] **tabulate, summarize()** — One- and two-way tables of summary statistics

[R] **total** — Estimate totals

[D] **codebook** — Describe data contents

[D] **describe** — Describe data in memory or in file

[D] **inspect** — Display simple summary of data's attributes

[ST] **stsum** — Summarize survival-time data

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtsum** — Summarize xt data

Title

sunflower — Density-distribution sunflower plots

Syntax

`sunflower` *yvar xvar* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Main	
`nograph`	do not show graph
`notable`	do not show summary table; implied when `by()` is specified
marker_options	affect rendition of markers drawn at the plotted points
Bins/Petals	
`binwidth(#)`	width of the hexagonal bins
`binar(#)`	aspect ratio of the hexagonal bins
bin_options	affect rendition of hexagonal bins
`light(#)`	minimum observations for a light sunflower; default is `light(3)`
`dark(#)`	minimum observations for a dark sunflower; default is `dark(13)`
`xcenter(#)`	x-coordinate of the reference bin
`ycenter(#)`	y-coordinate of the reference bin
`petalweight(#)`	observations in a dark sunflower petal
`petallength(#)`	length of sunflower petal as a percentage
petal_options	affect rendition of sunflower petals
`flowersonly`	show petals only; do not render bins
`nosinglepetal`	suppress single petals
Add plots	
`addplot(`*plot*`)`	add other plots to generated graph
Y axis, X axis, Titles, Legend, Overall, By	
twoway_options	any options documented in [G-3] ***twoway_options***

bin_options	Description
[l|d]bstyle(*areastyle*)	overall look of hexagonal bins
[l|d]bcolor(*colorstyle*)	outline and fill color
[l|d]bfcolor(*colorstyle*)	fill color
[l|d]blstyle(*linestyle*)	overall look of outline
[l|d]blcolor(*colorstyle*)	outline color
[l|d]blwidth(*linewidthstyle*)	thickness of outline

petal_options	Description
[l|d]flstyle(*linestyle*)	overall style of sunflower petals
[l|d]flcolor(*colorstyle*)	color of sunflower petals
[l|d]flwidth(*linewidthstyle*)	thickness of sunflower petals

All options are *rightmost*; see [G-4] **concept: repeated options**.
fweights are allowed; see [U] **11.1.6 weight**.

Menu

Graphics > Smoothing and densities > Density-distribution sunflower plot

Description

sunflower draws density-distribution sunflower plots (Plummer and Dupont 2003). These plots are useful for displaying bivariate data whose density is too great for conventional scatterplots to be effective.

A sunflower is several line segments of equal length, called petals, that radiate from a central point. There are two varieties of sunflowers: light and dark. Each petal of a light sunflower represents 1 observation. Each petal of a dark sunflower represents several observations. Dark and light sunflowers represent high- and medium-density regions of the data, and marker symbols represent individual observations in low-density regions.

The plane defined by the variables *yvar* and *xvar* is divided into contiguous hexagonal bins. The number of observations contained within a bin determines how the bin will be represented.

- When there are fewer than light(#) observations in a bin, each point is plotted using the usual marker symbols in a scatterplot.
- Bins with at least light(#) but fewer than dark(#) observations are represented by a light sunflower.
- Bins with at least dark(#) observations are represented by a dark sunflower.

Options

Main

nograph prevents the graph from being generated.

`notable` prevents the summary table from being displayed. This option is implied when the `by()` option is specified.

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

Bins/Petals

`binwidth(#)` specifies the horizontal width of the hexagonal bins in the same units as *xvar*. By default,

$$binwidth = \texttt{max(}\text{rbw, nbw}\texttt{)}$$

where

$$\text{rbw} = \text{range of } xvar/40$$

$$\text{nbw} = \text{range of } xvar/\texttt{max(1,}\text{nb}\texttt{)}$$

and

$$\text{nb} = \texttt{int(min(sqrt(}n\texttt{),10 * log10(}n\texttt{)))}$$

where

$$n = \text{the number of observations in the dataset}$$

`binar(#)` specifies the aspect ratio for the hexagonal bins. The height of the bins is given by

$$binheight = binwidth \times \# \times 2/\sqrt{3}$$

where *binheight* and *binwidth* are specified in the units of *yvar* and *xvar*, respectively. The default is `binar(`*r*`)`, where *r* results in the rendering of regular hexagons.

bin_options affect how the hexagonal bins are rendered.

`lbstyle(`*areastyle*`)` and `dbstyle(`*areastyle*`)` specify the look of the light and dark hexagonal bins, respectively. The options listed below allow you to change each attribute, but `lbstyle()` and `dbstyle()` provide the starting points. See [G-4] ***areastyle*** for a list of available area styles.

`lbcolor(`*colorstyle*`)` and `dbcolor(`*colorstyle*`)` specify one color to be used both to outline the shape and to fill the interior of the light and dark hexagonal bins, respectively. See [G-4] ***colorstyle*** for a list of color choices.

`lbfcolor(`*colorstyle*`)` and `dbfcolor(`*colorstyle*`)` specify the color to be used to fill the interior of the light and dark hexagonal bins, respectively. See [G-4] ***colorstyle*** for a list of color choices.

`lblstyle(`*linestyle*`)` and `dblstyle(`*linestyle*`)` specify the overall style of the line used to outline the area, which includes its pattern (solid, dashed, etc.), thickness, and color. The other options listed below allow you to change the line's attributes, but `lblstyle()` and `dblstyle()` are the starting points. See [G-4] ***linestyle*** for a list of choices.

`lblcolor(`*colorstyle*`)` and `dblcolor(`*colorstyle*`)` specify the color to be used to outline the light and dark hexagonal bins, respectively. See [G-4] ***colorstyle*** for a list of color choices.

`lblwidth(`*linewidthstyle*`)` and `dblwidth(`*linewidthstyle*`)` specify the thickness of the line to be used to outline the light and dark hexagonal bins, respectively. See [G-4] ***linewidthstyle*** for a list of choices.

`light(#)` specifies the minimum number of observations needed for a bin to be represented by a light sunflower. The default is `light(3)`.

`dark(#)` specifies the minimum number of observations needed for a bin to be represented by a dark sunflower. The default is `dark(13)`.

`xcenter(#)` and `ycenter(#)` specify the center of the reference bin. The default values are the median values of *xvar* and *yvar*, respectively. The centers of the other bins are implicitly defined by the location of the reference bin together with the common bin width and height.

`petalweight(#)` specifies the number of observations represented by each petal of a dark sunflower. The default value is chosen so that the maximum number of petals on a dark sunflower is 14.

`petallength(#)` specifies the length of petals in the sunflowers. The value specified is interpreted as a percentage of half the bin width. The default is 100%.

petal_options affect how the sunflower petals are rendered.

`lflstyle(`*linestyle*`)` and `dflstyle(`*linestyle*`)` specify the overall style of the light and dark sunflower petals, respectively.

`lflcolor(`*colorstyle*`)` and `dflcolor(`*colorstyle*`)` specify the color of the light and dark sunflower petals, respectively.

`lflwidth(`*linewidthstyle*`)` and `dflwidth(`*linewidthstyle*`)` specify the width of the light and dark sunflower petals, respectively.

`flowersonly` suppresses rendering of the bins. This option is equivalent to specifying `lbcolor(none)` and `dbcolor(none)`.

`nosinglepetal` suppresses flowers from being drawn in light bins that contain only 1 observation and dark bins that contain as many observations as the petal weight (see the `petalweight()` option).

Add plots

`addplot(`*plot*`)` provides a way to add other plots to the generated graph; see [G-3] ***addplot_option***.

Y axis, X axis, Titles, Legend, Overall, By

twoway_options are any of the options documented in [G-3] ***twoway_options***. These include options for titling the graph (see [G-3] ***title_options***), options for saving the graph to disk (see [G-3] ***saving_option***), and the `by()` option (see [G-3] ***by_option***).

Remarks

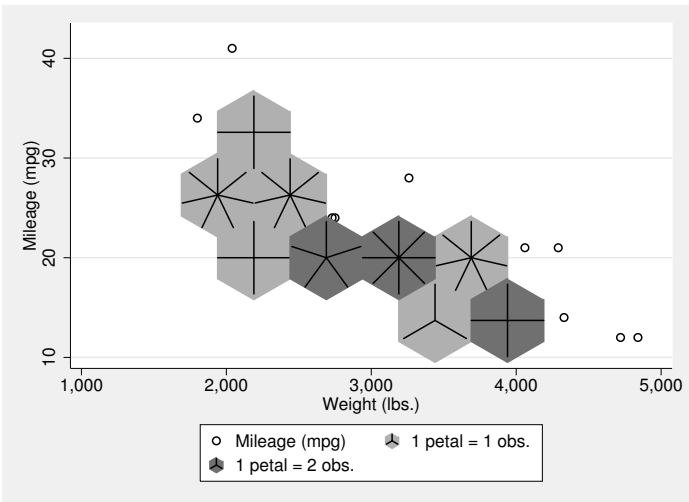
See Dupont (2009, 87–92) for a discussion of sunflower plots and how to create them using Stata.

▷ Example 1

Using the auto dataset, we want to examine the relationship between `weight` and `mpg`. To do that, we type

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. sunflower mpg weight, binwid(500) petalw(2) dark(8)
Bin width          =       500
Bin height         =   8.38703
Bin aspect ratio   =  .0145268
Max obs in a bin   =        15
Light              =         3
Dark               =         8
X-center           =      3190
Y-center           =        20
Petal weight       =         2
```

flower type	petal weight	No. of petals	No. of flowers	estimated obs.	actual obs.
none				10	10
light	1	3	1	3	3
light	1	4	2	8	8
light	1	7	3	21	21
dark	2	4	1	8	8
dark	2	5	1	10	9
dark	2	8	1	16	15
				76	74



The three darkly shaded sunflowers immediately catch our eyes, indicating a group of eight cars that are heavy (nearly 4,000 pounds) and fuel inefficient and two groups of cars that get about 20 miles per gallon and weight in the neighborhood of 3,000 pounds, one with 10 cars and one with 8 cars. The lighter sunflowers with seven petals each indicate groups of seven cars that share similar weight and fuel economy characteristics. To obtain the number of cars in each group, we counted the number of petals in each flower and consulted the graph legend to see how many observations each petal represents.

◁

Methods and formulas

`sunflower` is implemented as an ado-file.

Acknowledgments

We thank William D. Dupont and W. Dale Plummer Jr. (Vanderbilt University), authors of the original `sunflower` command, for their assistance in producing this version.

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Title

sureg — Zellner's seemingly unrelated regression

Syntax

Basic syntax

```
sureg (depvar1 varlist1) (depvar2 varlist2) ... (depvarN varlistN)
    [if] [in] [weight]
```

Full syntax

```
sureg ([eqname1:]depvar1a [depvar1b ...=]varlist1 [, noconstant])
    ([eqname2:]depvar2a [depvar2b ...=]varlist2 [, noconstant])
    ...
    ([eqnameN:]depvarNa [depvarNb ...=]varlistN [, noconstant])
    [if] [in] [weight] [, options]
```

Explicit equation naming (*eqname*`:`) cannot be combined with multiple dependent variables in an equation specification.

options	Description
Model	
`isure`	iterate until estimates converge
`constraints(`*constraints*`)`	apply specified linear constraints
df adj.	
`small`	report small-sample statistics
`dfk`	use small-sample adjustment
`dfk2`	use alternate adjustment
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`corr`	perform Breusch–Pagan test
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Optimization	
optimization_options	control the optimization process; seldom used
`noheader`	suppress header table from above coefficient table
`notable`	suppress coefficient table
`coeflegend`	display legend instead of statistics

varlist$_1$, ..., *varlist*$_N$ may contain factor variables; see [U] **11.4.3 Factor variables**. You must have the same levels of factor variables in all equations that have factor variables.

*depvar*s and the *varlist*s may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `jackknife`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweight`s are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`aweight`s and `fweight`s are allowed; see [U] **11.1.6 weight**.

`noheader`, `notable`, and `coeflegend` do not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Multiple-equation models > Seemingly unrelated regression

Description

`sureg` fits seemingly unrelated regression models (Zellner 1962; Zellner and Huang 1962; Zellner 1963). The acronyms SURE and SUR are often used for the estimator.

Options

Model

`isure` specifies that `sureg` iterate over the estimated disturbance covariance matrix and parameter estimates until the parameter estimates converge. Under seemingly unrelated regression, this iteration converges to the maximum likelihood results. If this option is not specified, `sureg` produces two-step estimates.

`constraints(`*constraints*`)`; see [R] **estimation options**.

df adj.

`small` specifies that small-sample statistics be computed. It shifts the test statistics from chi-squared and z statistics to F statistics and t statistics. Although the standard errors from each equation are computed using the degrees of freedom for the equation, the degrees of freedom for the t statistics are all taken to be those for the first equation.

`dfk` specifies the use of an alternate divisor in computing the covariance matrix for the equation residuals. As an asymptotically justified estimator, `sureg` by default uses the number of sample observations (n) as a divisor. When the `dfk` option is set, a small-sample adjustment is made and the divisor is taken to be $\sqrt{(n-k_i)(n-k_j)}$, where k_i and k_j are the numbers of parameters in equations i and j, respectively.

`dfk2` specifies the use of an alternate divisor in computing the covariance matrix for the equation residuals. When the `dfk2` option is set, the divisor is taken to be the mean of the residual degrees of freedom from the individual equations.

Reporting

`level(#)`; see [R] **estimation options**.

`corr` displays the correlation matrix of the residuals between equations and performs a Breusch–Pagan test for independent equations; that is, the disturbance covariance matrix is diagonal.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Optimization

optimization_options control the iterative process that minimizes the sum of squared errors when isure is specified. These options are seldom used.

iterate(#) specifies the maximum number of iterations. When the number of iterations equals #, the optimizer stops and presents the current results, even if the convergence tolerance has not been reached. The default value of iterate() is the current value of set maxiter (see [R] **maximize**), which is iterate(16000) if maxiter has not been changed.

trace adds to the iteration log a display of the current parameter vector

nolog suppresses the display of the iteration log.

tolerance(#) specifies the tolerance for the coefficient vector. When the relative change in the coefficient vector from one iteration to the next is less than or equal to #, the optimization process is stopped. tolerance(1e-6) is the default.

The following options are available with sureg but are not shown in the dialog box:

noheader suppresses display of the table reporting F statistics, R-squared, and root mean squared error above the coefficient table.

notable suppresses display of the coefficient table.

coeflegend; see [R] **estimation options**.

Remarks

Seemingly unrelated regression models are so called because they appear to be joint estimates from several regression models, each with its own error term. The regressions are related because the (contemporaneous) errors associated with the dependent variables may be correlated. Chapter 5 of Cameron and Trivedi (2010) contains a discussion of the seemingly unrelated regression model and the feasible generalized least-squares estimator underlying it.

▷ Example 1

When we fit models with the same set of right-hand-side variables, the seemingly unrelated regression results (in terms of coefficients and standard errors) are the same as fitting the models separately (using, say, regress). The same is true when the models are nested. Even in such cases, sureg is useful when we want to perform joint tests. For instance, let us assume that we think

$$\texttt{price} = \beta_0 + \beta_1\texttt{foreign} + \beta_2\texttt{length} + u_1$$
$$\texttt{weight} = \gamma_0 + \gamma_1\texttt{foreign} + \gamma_2\texttt{length} + u_2$$

Because the models have the same set of explanatory variables, we could estimate the two equations separately. Yet, we might still choose to estimate them with sureg because we want to perform the joint test $\beta_1 = \gamma_1 = 0$.

We use the small and dfk options to obtain small-sample statistics comparable with regress or mvreg.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. sureg (price foreign length) (weight foreign length), small dfk
Seemingly unrelated regression
```

Equation	Obs	Parms	RMSE	"R-sq"	F-Stat	P
price	74	2	2474.593	0.3154	16.35	0.0000
weight	74	2	250.2515	0.8992	316.54	0.0000

	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
price						
foreign	2801.143	766.117	3.66	0.000	1286.674	4315.611
length	90.21239	15.83368	5.70	0.000	58.91219	121.5126
_cons	-11621.35	3124.436	-3.72	0.000	-17797.77	-5444.93
weight						
foreign	-133.6775	77.47615	-1.73	0.087	-286.8332	19.4782
length	31.44455	1.601234	19.64	0.000	28.27921	34.60989
_cons	-2850.25	315.9691	-9.02	0.000	-3474.861	-2225.639

These two equations have a common set of regressors, and we could have used a shorthand syntax to specify the equations:

```
. sureg (price weight = foreign length), small dfk
```

Here the results presented by `sureg` are the same as if we had estimated the equations separately:

```
. regress price foreign length
  (output omitted)
. regress weight foreign length
  (output omitted)
```

There is, however, a difference. We have allowed u_1 and u_2 to be correlated and have estimated the full variance–covariance matrix of the coefficients. `sureg` has estimated the correlations, but it does not report them unless we specify the `corr` option. We did not remember to specify `corr` when we fit the model, but we can redisplay the results:

```
. sureg, notable noheader corr
Correlation matrix of residuals:
         price  weight
 price  1.0000
weight  0.5840  1.0000
Breusch-Pagan test of independence: chi2(1) =    25.237, Pr = 0.0000
```

The `notable` and `noheader` options prevented `sureg` from redisplaying the header and coefficient tables. We find that, for the same cars, the correlation of the residuals in the `price` and `weight` equations is 0.5840 and that we can reject the hypothesis that this correlation is zero.

We can test that the coefficients on `foreign` are jointly zero in both equations—as we set out to do—by typing `test foreign`; see [R] **test**. When we type a variable without specifying the equation, that variable is tested for zero in all equations in which it appears:

```
. test foreign
 ( 1)  [price]foreign = 0
 ( 2)  [weight]foreign = 0
       F(  2,   142) =   17.99
            Prob > F =    0.0000
```

◁

▷ Example 2

When the models do not have the same set of explanatory variables and are not nested, `sureg` may lead to more efficient estimates than running the models separately as well as allowing joint tests. This time, let us assume that we believe

$$\texttt{price} = \beta_0 + \beta_1\texttt{foreign} + \beta_2\texttt{mpg} + \beta_3\texttt{displ} + u_1$$
$$\texttt{weight} = \gamma_0 + \gamma_1\texttt{foreign} + \gamma_2\texttt{length} + u_2$$

To fit this model, we type

```
. sureg (price foreign mpg displ) (weight foreign length), corr
Seemingly unrelated regression
```

Equation	Obs	Parms	RMSE	"R-sq"	chi2	P
price	74	3	2165.321	0.4537	49.64	0.0000
weight	74	2	245.2916	0.8990	661.84	0.0000

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
price						
foreign	3058.25	685.7357	4.46	0.000	1714.233	4402.267
mpg	-104.9591	58.47209	-1.80	0.073	-219.5623	9.644042
displacement	18.18098	4.286372	4.24	0.000	9.779842	26.58211
_cons	3904.336	1966.521	1.99	0.047	50.0263	7758.645
weight						
foreign	-147.3481	75.44314	-1.95	0.051	-295.2139	.517755
length	30.94905	1.539895	20.10	0.000	27.93091	33.96718
_cons	-2753.064	303.9336	-9.06	0.000	-3348.763	-2157.365

```
Correlation matrix of residuals:

         price  weight
 price  1.0000
weight  0.3285  1.0000

Breusch-Pagan test of independence: chi2(1) =     7.984, Pr = 0.0047
```

In comparison, if we had fit the price model separately,

```
. regress price foreign mpg displ
```

Source	SS	df	MS	Number of obs =	74
				F(3, 70) =	20.13
Model	294104790	3	98034929.9	Prob > F =	0.0000
Residual	340960606	70	4870865.81	R-squared =	0.4631
				Adj R-squared =	0.4401
Total	635065396	73	8699525.97	Root MSE =	2207

price	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
foreign	3545.484	712.7763	4.97	0.000	2123.897	4967.072
mpg	-98.88559	63.17063	-1.57	0.122	-224.8754	27.10426
displacement	22.40416	4.634239	4.83	0.000	13.16146	31.64686
_cons	2796.91	2137.873	1.31	0.195	-1466.943	7060.763

The coefficients are slightly different, but the standard errors are uniformly larger. This would still be true if we specified the dfk option to make a small-sample adjustment to the estimated covariance of the disturbances.

◁

❑ Technical note

Constraints can be applied to SURE models using Stata's standard syntax for constraints. For a general discussion of constraints, see [R] **constraint**; for examples similar to seemingly unrelated regression models, see [R] **reg3**.

❑

Arnold Zellner (1927–2010) was born in New York. He studied physics at Harvard and economics at Berkeley, and then he taught economics at the Universities of Washington and Wisconsin before settling in Chicago in 1966. Among his many major contributions to econometrics and statistics are his work on seemingly unrelated regression, three-stage least squares, and Bayesian econometrics.

Saved results

sureg saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(mss_#)	model sum of squares for equation #
e(df_m#)	model degrees of freedom for equation #
e(rss_#)	residual sum of squares for equation #
e(df_r)	residual degrees of freedom
e(r2_#)	R-squared for equation #
e(F_#)	F statistic for equation # (small only)
e(rmse_#)	root mean squared error for equation #
e(dfk2_adj)	divisor used with VCE when dfk2 specified
e(ll)	log likelihood
e(chi2_#)	χ^2 for equation #
e(p_#)	significance for equation #
e(cons_#)	1 if equation # has a constant, 0 otherwise
e(chi2_bp)	Breusch–Pagan χ^2
e(df_bp)	degrees of freedom for Breusch–Pagan χ^2 test
e(cons_#)	1 when equation # has a constant; 0, otherwise
e(rank)	rank of e(V)
e(ic)	number of iterations

Macros

e(cmd)	sureg
e(cmdline)	command as typed
e(method)	sure or isure
e(depvar)	names of dependent variables
e(exog)	names of exogenous variables
e(eqnames)	names of equations
e(wtype)	weight type
e(wexp)	weight expression
e(corr)	correlation structure
e(small)	small
e(dfk)	alternate divisor (dfk or dfk2 only)
e(properties)	b V
e(predict)	program used to implement predict
e(marginsok)	predictions allowed by margins
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(Sigma)	$\widehat{\mathbf{\Sigma}}$ matrix
e(V)	variance–covariance matrix of the estimators

Functions

e(sample)	marks estimation sample

Methods and formulas

sureg is implemented as an ado-file.

sureg uses the asymptotically efficient, feasible, generalized least-squares algorithm described in Greene (2012, 292–304). The computing formulas are given on page 293–294.

The R-squared reported is the percent of variance explained by the predictors. It may be used for descriptive purposes, but R-squared is not a well-defined concept when GLS is used.

sureg will refuse to compute the estimators if the same equation is named more than once or the covariance matrix of the residuals is singular.

The Breusch and Pagan (1980) χ^2 statistic—a Lagrange multiplier statistic—is given by

$$\lambda = T \sum_{m=1}^{M} \sum_{n=1}^{m-1} r_{mn}^2$$

where r_{mn} is the estimated correlation between the residuals of the M equations and T is the number of observations. It is distributed as χ^2 with $M(M-1)/2$ degrees of freedom.

References

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Zellner, A., and D. S. Huang. 1962. Further properties of efficient estimators for seemingly unrelated regression equations. *International Economic Review* 3: 300–313.

Also see

[R] **sureg postestimation** — Postestimation tools for sureg

[R] **mvreg** — Multivariate regression

[R] **nlsur** — Estimation of nonlinear systems of equations

[R] **reg3** — Three-stage estimation for systems of simultaneous equations

[R] **regress** — Linear regression

[TS] **dfactor** — Dynamic-factor models

Stata Structural Equation Modeling Reference Manual

[U] **20 Estimation and postestimation commands**

Title

sureg postestimation — Postestimation tools for sureg

Description

The following postestimation commands are available after `sureg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`,` `equation(`*eqno*[`,`*eqno*]`)` *statistic*]

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`residuals`	residuals
`difference`	difference between the linear predictions of two equations
`stddp`	standard error of the difference in linear predictions

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`equation(`*eqno*`[ ,`*eqno*`])` specifies to which equation(s) you are referring.

`equation()` is filled in with one *eqno* for the `xb`, `stdp`, and `residuals` options. `equation(#1)` would mean that the calculation is to be made for the first equation, `equation(#2)` would mean the second, and so on. You could also refer to the equations by their names. `equation(income)` would refer to the equation named income and `equation(hours)` to the equation named hours.

If you do not specify `equation()`, the results are the same as if you specified `equation(#1)`.

`difference` and `stddp` refer to between-equation concepts. To use these options, you must specify two equations, for example, `equation(#1,#2)` or `equation(income,hours)`. When two equations must be specified, `equation()` is required.

`xb`, the default, calculates the linear prediction (fitted values)—the prediction of $\mathbf{x}_j\mathbf{b}$ for the specified equation.

`stdp` calculates the standard error of the prediction for the specified equation. It can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`residuals` calculates the residuals.

`difference` calculates the difference between the linear predictions of two equations in the system. With `equation(#1,#2)`, `difference` computes the prediction of `equation(#1)` minus the prediction of `equation(#2)`.

`stddp` is allowed only after you have previously fit a multiple-equation model. The standard error of the difference in linear predictions $(\mathbf{x}_{1j}\mathbf{b} - \mathbf{x}_{2j}\mathbf{b})$ between equations 1 and 2 is calculated.

For more information on using `predict` after multiple-equation estimation commands, see [R] **predict**.

Remarks

For an example of cross-equation testing of parameters using the `test` command, see example 1 in [R] **sureg**.

▷ Example 1

In example 1 of [R] **sureg**, we fit a seemingly unrelated regressions model of `price` and `weight`. Here we obtain the fitted values.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. sureg (price foreign length) (weight foreign length), small dfk
  (output omitted)
. predict phat, equation(price)
(option xb assumed; fitted values)
. predict what, equation(weight)
(option xb assumed; fitted values)
```

```
. summarize price phat weight what
```

Variable	Obs	Mean	Std. Dev.	Min	Max
price	74	6165.257	2949.496	3291	15906
phat	74	6165.257	1656.407	1639.872	9398.138
weight	74	3019.459	777.1936	1760	4840
what	74	3019.459	736.9666	1481.199	4476.331

Just as in single-equation OLS regression, in a SURE model the sample mean of the fitted values for an equation equals the sample mean of the dependent variable.

◁

▷ Example 2

Suppose that for whatever reason we were interested in the difference between the predicted values of `price` and `weight`. `predict` has an option to compute this difference in one step:

```
. predict diff, equation(price, weight) difference
```

`diff` is the same as `phat - what`:

```
. generate mydiff = phat - what
. summarize diff mydiff
```

Variable	Obs	Mean	Std. Dev.	Min	Max
diff	74	3145.797	1233.26	-132.2275	5505.914
mydiff	74	3145.797	1233.26	-132.2275	5505.914

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **sureg** — Zellner's seemingly unrelated regression

[U] **20 Estimation and postestimation commands**

Title

swilk — Shapiro–Wilk and Shapiro–Francia tests for normality

Syntax

Shapiro–Wilk normality test

`swilk` *varlist* [*if*] [*in*] [, *swilk_options*]

Shapiro–Francia normality test

`sfrancia` *varlist* [*if*] [*in*] [, *sfrancia_options*]

swilk_options	Description
Main	
`generate(`*newvar*`)`	create *newvar* containing W test coefficients
`lnnormal`	test for three-parameter lognormality
`noties`	do not use average ranks for tied values

sfrancia_options	Description
Main	
`boxcox`	use the Box–Cox transformation for W'; the default is to use the log transformation
`noties`	do not use average ranks for tied values

`by` is allowed with `swilk` and `sfrancia`; see [D] **by**.

Menu

swilk

Statistics > Summaries, tables, and tests > Distributional plots and tests > Shapiro-Wilk normality test

sfrancia

Statistics > Summaries, tables, and tests > Distributional plots and tests > Shapiro-Francia normality test

Description

`swilk` performs the Shapiro–Wilk W test for normality, and `sfrancia` performs the Shapiro–Francia W' test for normality. `swilk` can be used with $4 \leq n \leq 2000$ observations, and `sfrancia` can be used with $5 \leq n \leq 5000$ observations; see [R] **sktest** for a test allowing more observations. See [MV] **mvtest normality** for multivariate tests of normality.

Options for swilk

Main

`generate(`*newvar*`)` creates new variable *newvar* containing the W test coefficients.

`lnnormal` specifies that the test be for three-parameter lognormality, meaning that $\ln(X-k)$ is tested for normality, where k is calculated from the data as the value that makes the skewness coefficient zero. When simply testing $\ln(X)$ for normality, do not specify this option. See [R] **lnskew0** for estimation of k.

`noties` suppresses use of averaged ranks for tied values when calculating the W test coefficients.

Options for sfrancia

Main

`boxcox` specifies that the Box–Cox transformation of Royston (1983) for calculating W' test coefficients be used instead of the default log transformation (Royston 1993a). Under the Box–Cox transformation, the normal approximation to the sampling distribution of W', used by `sfrancia`, is valid for $5 \leq n \leq 1000$. Under the log transformation, it is valid for $10 \leq n \leq 5000$.

`noties` suppresses use of averaged ranks for tied values when calculating the W' test coefficients.

Remarks

▷ Example 1

Using our automobile dataset, we will test whether the variables `mpg` and `trunk` are normally distributed:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. swilk mpg trunk
                    Shapiro-Wilk W test for normal data
    Variable |   Obs        W           V         z       Prob>z
-------------+--------------------------------------------------
         mpg |    74     0.94821      3.335     2.627     0.00430
       trunk |    74     0.97921      1.339     0.637     0.26215
. sfrancia mpg trunk
                   Shapiro-Francia W' test for normal data
    Variable |   Obs        W'          V'        z       Prob>z
-------------+--------------------------------------------------
         mpg |    74     0.94872      3.650     2.510     0.00604
       trunk |    74     0.98446      1.106     0.195     0.42271
```

We can reject the hypothesis that `mpg` is normally distributed, but we cannot reject that `trunk` is normally distributed.

The values reported under W and W' are the Shapiro–Wilk and Shapiro–Francia test statistics. The tests also report V and V', which are more appealing indexes for departure from normality. The median values of V and V' are 1 for samples from normal populations. Large values indicate nonnormality. The 95% critical values of V (V'), which depend on the sample size, are between 1.2 and 2.4 (2.0 and 2.8); see Royston (1991b). There is no more information in V (V') than in W (W')—one is just the transform of the other.

◁

▷ Example 2

We have data on a variable called `studytime`, which we suspect is distributed lognormally:

```
. use http://www.stata-press.com/data/r12/cancer
(Patient Survival in Drug Trial)
. generate lnstudytime = ln(studytime)
. swilk lnstudytime
                    Shapiro-Wilk W test for normal data
    Variable |   Obs        W           V         z       Prob>z
-------------+--------------------------------------------------
 lnstudytime |    48    0.92731       3.311     2.547     0.00543
```

We can reject the lognormal assumption. We do *not* specify the `lnnormal` option when testing for lognormality. The `lnnormal` option is for three-parameter lognormality.

◁

▷ Example 3

Having discovered that ln(`studytime`) is not distributed normally, we now test that ln(`studytime` $- k$) is normally distributed, where k is chosen so that the resulting skewness is zero. We obtain the estimate for k from `lnskew0`; see [R] **lnskew0**:

```
. lnskew0 lnstudytimek = studytime, level(95)
       Transform |          k     [95% Conf. Interval]       Skewness
-----------------+---------------------------------------------------
  ln(studytim-k) |  -11.01181    -infinity  -.9477328       -.0000173
. swilk lnstudytimek, lnnormal
          Shapiro-Wilk W test for 3-parameter lognormal data
    Variable |   Obs        W           V         z       Prob>z
-------------+--------------------------------------------------
lnstudytimek |    48    0.97064       1.337     1.261     0.10363
```

We cannot reject the hypothesis that ln(`studytime` $+ 11.01181$) is distributed normally. We do specify the `lnnormal` option when using an estimated value of k.

◁

Saved results

`swilk` and `sfrancia` save the following in `r()`:

Scalars

`r(N)`	number of observations	`r(W)`	W or W'
`r(p)`	significance	`r(V)`	V or V'
`r(z)`	z statistic		

Methods and formulas

`swilk` and `sfrancia` are implemented as ado-files.

The Shapiro–Wilk test is based on Shapiro and Wilk (1965) with a new approximation accurate for $4 \leq n \leq 2000$ (Royston 1992). The calculations made by `swilk` are based on Royston (1982, 1992, 1993b).

The Shapiro–Francia test (Shapiro and Francia 1972; Royston 1983; Royston 1993a) is an approximate test that is similar to the Shapiro–Wilk test for very large samples.

Samuel Sanford Shapiro (1930–) earned degrees in statistics and engineering from City College of New York, Columbia, and Rutgers. After employment in the U.S. Army and industry, he joined the faculty at Florida International University in 1972. Shapiro has coauthored various texts in statistics and published several papers on distributional testing and other statistical topics.

Acknowledgment

`swilk` and `sfrancia` were written by Patrick Royston of the MRC Clinical Trials Unit, London.

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Also see

[R] **lnskew0** — Find zero-skewness log or Box–Cox transform

[R] **lv** — Letter-value displays

[R] **sktest** — Skewness and kurtosis test for normality

[MV] **mvtest normality** — Multivariate normality tests

Title

symmetry — Symmetry and marginal homogeneity tests

Syntax

Symmetry and marginal homogeneity tests

`symmetry` *casevar controlvar* [*if*] [*in*] [*weight*] [`,` *options*]

Immediate form of symmetry and marginal homogeneity tests

`symmi` $\#_{11}$ $\#_{12}$ [...] \ $\#_{21}$ $\#_{22}$ [...] [\...] [*if*] [*in*] [`,` *options*]

options	Description
Main	
`notable`	suppress output of contingency table
`contrib`	report contribution of each off-diagonal cell pair
`exact`	perform exact test of table symmetry
`mh`	perform two marginal homogeneity tests
`trend`	perform a test for linear trend in the (log) relative risk (RR)
`cc`	use continuity correction when calculating test for linear trend

`fweights` are allowed; see [U] **11.1.6 weight**.

Menu

symmetry

Statistics > Epidemiology and related > Other > Symmetry and marginal homogeneity test

symmi

Statistics > Epidemiology and related > Other > Symmetry and marginal homogeneity test calculator

Description

`symmetry` performs asymptotic symmetry and marginal homogeneity tests, as well as an exact symmetry test on $K \times K$ tables where there is a 1-to-1 matching of cases and controls (nonindependence). This testing is used to analyze matched-pair case–control data with multiple discrete levels of the exposure (outcome) variable. In genetics, the test is known as the transmission/disequilibrium test (TDT) and is used to test the association between transmitted and nontransmitted parental marker alleles to an affected child (Spieldman, McGinnis, and Ewens 1993). For 2×2 tables, the asymptotic test statistics reduce to the McNemar test statistic, and the exact symmetry test produces an exact McNemar test; see [ST] **epitab**. For many exposure variables, `symmetry` can optionally perform a test for linear trend in the log relative risk.

`symmetry` expects the data to be in the wide format; that is, each observation contains the matched case and control values in variables *casevar* and *controlvar*. Variables can be numeric or string.

`symmi` is the immediate form of `symmetry`. The `symmi` command uses the values specified on the command line; rows are separated by '\', and options are the same as for `symmetry`. See [U] **19 Immediate commands** for a general introduction to immediate commands.

Options

Main

`notable` suppresses the output of the contingency table. By default, `symmetry` displays the $n \times n$ contingency table at the top of the output.

`contrib` reports the contribution of each off-diagonal cell pair to the overall symmetry χ^2.

`exact` performs an exact test of table symmetry. This option is recommended for sparse tables. CAUTION: The exact test requires substantial amounts of time and memory for large tables.

`mh` performs two marginal homogeneity tests that do not require the inversion of the variance–covariance matrix.

By default, `symmetry` produces the Stuart–Maxwell test statistic, which requires the inversion of the nondiagonal variance–covariance matrix, $\mathbf{V}$. When the table is sparse, the matrix may not be of full rank, and then the command substitutes a generalized inverse $\mathbf{V}^*$ for $\mathbf{V}^{-1}$. `mh` calculates optional marginal homogeneity statistics that do not require the inversion of the variance–covariance matrix. These tests may be preferred in certain situations. See *Methods and formulas* and Bickeböller and Clerget-Darpoux (1995) for details on these test statistics.

`trend` performs a test for linear trend in the (log) relative risk (RR). This option is allowed only for numeric exposure (outcome) variables, and its use should be restricted to measurements on the ordinal or the interval scales.

`cc` specifies that the continuity correction be used when calculating the test for linear trend. This correction should be specified only when the levels of the exposure variable are equally spaced.

Remarks

`symmetry` and `symmi` may be used to analyze 1-to-1 matched case–control data with multiple discrete levels of the exposure (outcome) variable.

▷ Example 1

Consider a survey of 344 individuals (BMDP 1990, 267–270) who were asked in October 1986 whether they agreed with President Reagan's handling of foreign affairs. In January 1987, after the Iran-Contra affair became public, these same individuals were surveyed again and asked the same question. We would like to know if public opinion changed over this period.

We first describe the dataset and list a few observations.

```
. use http://www.stata-press.com/data/r12/iran
. describe
Contains data from http://www.stata-press.com/data/r12/iran.dta
  obs:           344
 vars:             2                          29 Jan 2011 02:37
 size:           688
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
before          byte   %8.0g       vlab       Public Opinion before IC
after           byte   %8.0g       vlab       Public Opinion after IC
-------------------------------------------------------------------------------
Sorted by:
```

```
. list in 1/5
```

	before	after
1.	agree	agree
2.	agree	disagree
3.	agree	unsure
4.	disagree	agree
5.	disagree	disagree

Each observation corresponds to one of the 344 individuals. The data are in wide form so that each observation has a before and an after measurement. We now perform the test without options.

```
. symmetry before after
```

Public Opinion before IC	Public Opinion after IC agree	disagree	unsure	Total
agree	47	56	38	141
disagree	28	61	31	120
unsure	26	47	10	83
Total	101	164	79	344

	chi2	df	Prob>chi2
Symmetry (asymptotic)	14.87	3	0.0019
Marginal homogeneity (Stuart-Maxwell)	14.78	2	0.0006

The test first tabulates the data in a $K \times K$ table and then performs Bowker's (1948) test for table symmetry and the Stuart–Maxwell (Stuart 1955; Maxwell 1970) test for marginal homogeneity.

Both the symmetry test and the marginal homogeneity test are highly significant, thus indicating a shift in public opinion.

An exact test of symmetry is provided for use on sparse tables. This test is computationally intensive, so it should not be used on large tables. Because we are working on a fast computer, we will run the symmetry test again and this time include the `exact` option. We will suppress the output of the contingency table by specifying `notable` and include the `contrib` option so that we may further examine the cells responsible for the significant result.

```
. symmetry before after, contrib exact mh notable
```

Cells	Contribution to symmetry chi-squared
n1_2 & n2_1	9.3333
n1_3 & n3_1	2.2500
n2_3 & n3_2	3.2821

	chi2	df	Prob>chi2
Symmetry (asymptotic)	14.87	3	0.0019
Marginal homogeneity (Stuart-Maxwell)	14.78	2	0.0006
Marginal homogeneity (Bickenboller)	13.53	2	0.0012
Marginal homogeneity (no diagonals)	15.25	2	0.0005
Symmetry (exact significance probability)			0.0018

The largest contribution to the symmetry χ^2 is due to cells n_{12} and n_{21}. These correspond to changes between the agree and disagree categories. Of the 344 individuals, 56 (16.3%) changed from the agree to the disagree response, whereas only 28 (8.1%) changed in the opposite direction.

For these data, the results from the exact test are similar to those from the asymptotic test.

◁

▷ Example 2

Breslow and Day (1980, 163) reprinted data from Mack et al. (1976) from a case–control study of the effect of exogenous estrogen on the risk of endometrial cancer. The data consist of 59 elderly women diagnosed with endometrial cancer and 59 disease-free control subjects living in the same community as the cases. Cases and controls were matched on age, marital status, and time living in the community. The data collected included information on the daily dose of conjugated estrogen therapy. Breslow and Day analyzed these data by creating four levels of the dose variable. Here are the data as entered into a Stata dataset:

```
. use http://www.stata-press.com/data/r12/bd163
. list, noobs divider
```

case	control	count
0	0	6
0	0.1-0.299	2
0	0.3-0.625	3
0	0.626+	1
0.1-0.299	0	9
0.1-0.299	0.1-0.299	4
0.1-0.299	0.3-0.625	2
0.1-0.299	0.626+	1
0.3-0.625	0	9
0.3-0.625	0.1-0.299	2
0.3-0.625	0.3-0.625	3
0.3-0.625	0.626+	1
0.626+	0	12
0.626+	0.1-0.299	1
0.626+	0.3-0.625	2
0.626+	0.626+	1

This dataset is in a different format from that of the previous example. Instead of each observation representing one matched pair, each observation represents possibly multiple pairs indicated by the `count` variable. For instance, the first observation corresponds to six matched pairs where neither the case nor the control was on estrogen, the second observation corresponds to two matched pairs where the case was not on estrogen and the control was on 0.1 to 0.299 mg/day, etc.

To use `symmetry` to analyze this dataset, we must specify `fweight` to indicate that in our data there are observations corresponding to more than one matched pair.

```
. symmetry case control [fweight=count]
```

case	control 0	0.1-0.299	0.3-0.625	0.626+	Total
0	6	2	3	1	12
0.1-0.299	9	4	2	1	16
0.3-0.625	9	2	3	1	15
0.626+	12	1	2	1	16
Total	36	9	10	4	59

	chi2	df	Prob>chi2
Symmetry (asymptotic)	17.10	6	0.0089
Marginal homogeneity (Stuart-Maxwell)	16.96	3	0.0007

Both the test of symmetry and the test of marginal homogeneity are highly significant, thus leading us to reject the null hypothesis that there is no effect of exposure to estrogen on the risk of endometrial cancer.

Breslow and Day perform a test for trend assuming that the estrogen exposure levels were equally spaced by recoding the exposure levels as 1, 2, 3, and 4.

We can easily reproduce their results by recoding our data in this way and by specifying the `trend` option. Two new numeric variables were created, `ca` and `co`, corresponding to the variables `case` and `control`, respectively. Below we list some of the data and our results from `symmetry`:

```
. encode case, gen(ca)
. encode control, gen(co)
. label values ca
. label values co
. list in 1/4
```

	case	control	count	ca	co
1.	0	0	6	1	1
2.	0	0.1-0.299	2	1	2
3.	0	0.3-0.625	3	1	3
4.	0	0.626+	1	1	4

```
. symmetry ca co [fw=count], notable trend cc
```

	chi2	df	Prob>chi2
Symmetry (asymptotic)	17.10	6	0.0089
Marginal homogeneity (Stuart-Maxwell)	16.96	3	0.0007
Linear trend in the (log) RR	14.43	1	0.0001

We requested the continuity correction by specifying `cc`. Doing so is appropriate because our coded exposure levels are equally spaced.

The test for trend was highly significant, indicating an increased risk of endometrial cancer with increased dosage of conjugated estrogen.

You must be cautious: the way in which you code the exposure variable affects the linear trend statistic. If instead of coding the levels as 1, 2, 3, and 4, we had instead used 0, 0.2, 0.46, and 0.7

(roughly the midpoint in the range of each level), we would have obtained a χ^2 statistic of 11.19 for these data.

◁

Saved results

`symmetry` saves the following in `r()`:

Scalars

`r(N_pair)`	number of matched pairs
`r(chi2)`	asymptotic symmetry χ^2
`r(df)`	asymptotic symmetry degrees of freedom
`r(p)`	asymptotic symmetry p-value
`r(chi2_sm)`	MH (Stuart–Maxwell) χ^2
`r(df_sm)`	MH (Stuart–Maxwell) degrees of freedom
`r(p_sm)`	MH (Stuart–Maxwell) p-value
`r(chi2_b)`	MH (Bickenböller) χ^2
`r(df_b)`	MH (Bickenböller) degrees of freedom
`r(p_b)`	MH (Bickenböller) p-value
`r(chi2_nd)`	MH (no diagonals) χ^2
`r(df_nd)`	MH (no diagonals) degrees of freedom
`r(p_nd)`	MH (no diagonals) p-value
`r(chi2_t)`	χ^2 for linear trend
`r(p_trend)`	p-value for linear trend
`r(p_exact)`	exact symmetry p-value

Methods and formulas

`symmetry` and `symmi` are implemented as ado-files.

Methods and formulas are presented under the following headings:

Asymptotic tests
Exact symmetry test

Asymptotic tests

Consider a square table with K exposure categories, that is, K rows and K columns. Let n_{ij} be the count corresponding to row i and column j of the table, $N_{ij} = n_{ij} + n_{ji}$, for $i, j = 1, 2, \ldots, K$, and $n_{i.}$, and let $n_{.j}$ be the marginal totals for row i and column j, respectively. Asymptotic tests for symmetry and marginal homogeneity for this $K \times K$ table are calculated as follows:

The null hypothesis of complete symmetry $p_{ij} = p_{ji}$, $i \neq j$, is tested by calculating the test statistic (Bowker 1948)

$$T_{\mathrm{cs}} = \sum_{i<j} \frac{(n_{ij} - n_{ji})^2}{n_{ij} + n_{ji}}$$

which is asymptotically distributed as χ^2 with $K(K-1)/2 - R$ degrees of freedom, where R is the number of off-diagonal cells with $N_{ij} = 0$.

The null hypothesis of marginal homogeneity, $p_{i.} = p_{.i}$, is tested by calculating the Stuart–Maxwell test statistic (Stuart 1955; Maxwell 1970),

$$T_{\mathrm{sm}} = \mathbf{d}' \mathbf{V}^{-1} \mathbf{d}$$

where $\mathbf{d}$ is a column vector with elements equal to the differences $d_i = n_{i.} - n_{.i}$ for $i = 1, 2, \ldots, K$, and $\mathbf{V}$ is the variance–covariance matrix with elements

$$v_{ii} = n_{i.} + n_{.i} - 2n_{ii}$$
$$v_{ij} = -(n_{ij} + n_{ji}), \quad i \neq j$$

T_{sm} is asymptotically χ^2 with $K-1$ degrees of freedom.

This test statistic properly accounts for the dependence between the table's rows and columns. When the matrix $\mathbf{V}$ is not of full rank, a generalized inverse $\mathbf{V}^*$ is substituted for $\mathbf{V}^{-1}$.

The Bickeböller and Clerget-Darpoux (1995) marginal homogeneity test statistic is calculated by

$$T_{\text{mh}} = \sum_i \frac{(n_{i.} - n_{.i})^2}{n_{i.} + n_{.i}}$$

This statistic is asymptotically distributed, under the assumption of marginal independence, as χ^2 with $K-1$ degrees of freedom.

The marginal homogeneity (no diagonals) test statistic T^0_{mh} is calculated in the same way as T_{mh}, except that the diagonal elements do not enter into the calculation of the marginal totals. Unlike the previous test statistic, T^0_{mh} reduces to a McNemar test statistic for 2×2 tables. The test statistic $\{(K-1)/2\}T^0_{\text{mh}}$ is asymptotically distributed as χ^2 with $K-1$ degrees of freedom (Cleves, Olson, and Jacobs 1997; Spieldman and Ewens 1996).

Breslow and Day's test statistic for linear trend in the (log) of RR is

$$\frac{\left\{\sum_{i<j}(n_{ij} - n_{ji})(X_j - X_i) - cc\right\}^2}{\sum_{i<j}(n_{ij} + n_{ji})(X_j - X_i)^2}$$

where the X_j are the doses associated with the various levels of exposure and cc is the continuity correction; it is asymptotically distributed as χ^2 with 1 degree of freedom.

The continuity correction option is applicable only when the levels of the exposure variable are equally spaced.

Exact symmetry test

The exact test is based on a permutation algorithm applied to the null distribution. The distribution of the off-diagonal elements n_{ij}, $i \neq j$, conditional on the sum of the complementary off-diagonal cells, $N_{ij} = n_{ij} + n_{ji}$, can be written as the product of $K(K-1)/2$ binomial random variables,

$$P(\mathbf{n}) = \prod_{i<j} \binom{N_{ij}}{n_{ij}} {\pi_{ij}}^{n_{ij}} (1 - \pi_{ij})^{n_{ij}}$$

where $\mathbf{n}$ is a vector with elements n_{ij} and $\pi_{ij} = E(n_{ij}/N_{ij}|N_{ij})$. Under the null hypothesis of complete symmetry, $\pi_{ij} = \pi_{ji} = 1/2$, and thus the permutation distribution is given by

$$P_0(\mathbf{n}) = \prod_{i<j} \binom{N_{ij}}{n_{ij}} \left(\frac{1}{2}\right)^{N_{ij}}$$

The exact significance test is performed by evaluating

$$P_{\text{cs}} = \sum_{n \in p} P_0(\mathbf{n})$$

where $p = \{n : P_0(\mathbf{n}) < P_0(\mathbf{n}^*)\}$ and $\mathbf{n}^*$ is the observed contingency table data vector. The algorithm evaluates p_{cs} exactly. For information about permutation tests, see Good (2005, 2006).

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Also see

[ST] **epitab** — Tables for epidemiologists

Title

table — Tables of summary statistics

Syntax

`table` *rowvar* [*colvar* [*supercolvar*]] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`contents(`*clist*`)`	contents of table cells; select up to five statistics; default is `contents(freq)`
`by(`*superrowvarlist*`)`	superrow variables
Options	
`cellwidth(#)`	cell width
`csepwidth(#)`	column-separation width
`stubwidth(#)`	stub width
`scsepwidth(#)`	supercolumn-separation width
`center`	center-align table cells; default is right-align
`left`	left-align table cells; default is right-align
`cw`	perform casewise deletion
`row`	add row totals
`col`	add column totals
`scol`	add supercolumn totals
`concise`	suppress rows with all missing entries
`missing`	show missing statistics with period
`replace`	replace current data with table statistics
`name(`*string*`)`	name new variables with prefix *string*
`format(%`*fmt*`)`	display format for numbers in cells; default is `format(%9.0g)`

`by` is allowed; see [D] **by**.

`fweights`, `aweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`pweights` may not be used with `sd`, `semean`, `sebinomial`, or `sepoisson`. `iweights` may not be used with `semean`, `sebinomial`, or `sepoisson`. `aweights` may not be used with `sebinomial` or `sepoisson`.

where the elements of *clist* may be

`freq`	frequency	`n` *varname*	same as `count`
`mean` *varname*	mean of *varname*	`max` *varname*	maximum
`sd` *varname*	standard deviation	`min` *varname*	minimum
`semean` *varname*	standard error of the mean (`sd/sqrt(n)`)	`median` *varname*	median
		`p1` *varname*	1st percentile
`sebinomial` *varname*	standard error of the mean, binomial distribution (`sqrt(p(1-p)/n)`)	`p2` *varname*	2nd percentile
		`...`	3rd–49th percentiles
`sepoisson` *varname*	standard error of the mean, Poisson distribution (`sqrt(mean)`)	`p50` *varname*	50th percentile (`median`)
		`...`	51st–97th percentiles
`sum` *varname*	sum	`p98` *varname*	98th percentile
`rawsum` *varname*	sums ignoring optionally specified weight	`p99` *varname*	99th percentile
`count` *varname*	count of nonmissing observations	`iqr` *varname*	interquartile range

Rows, columns, supercolumns, and superrows are thus defined as

row 1	.
row 2	.

	supercol 1		supercol 2	
	col 1	col 2	col 1	col 2
row 1	.	.	.	.
row 2	.	.	.	.

	col 1	col 2
row 1	.	.
row 2	.	.

	supercol 1		supercol 2	
	col 1	col 2	col 1	col 2
superrow 1:				
row 1	.	.	.	.
row 2	.	.	.	.
superrow 2:				
row 1	.	.	.	.
row 2	.	.	.	.

Menu

Statistics > Summaries, tables, and tests > Tables > Table of summary statistics (table)

Description

`table` calculates and displays tables of statistics.

Options

Main

`contents(`*clist*`)` specifies the contents of the table's cells; if not specified, `contents(freq)` is used by default. `contents(freq)` produces a table of frequencies. `contents(mean mpg)` produces a table of the means of variable `mpg`. `contents(freq mean mpg sd mpg)` produces a table of frequencies together with the mean and standard deviation of variable `mpg`. Up to five statistics may be specified.

`by(`*superrowvarlist*`)` specifies that numeric or string variables be treated as superrows. Up to four variables may be specified in *superrowvarlist*. The `by()` option may be specified with the `by` prefix.

Options

`cellwidth(#)` specifies the width of the cell in units of digit widths; 10 means the space occupied by 10 digits, which is `0123456789`. The default `cellwidth()` is not a fixed number, but a number chosen by `table` to spread the table out while presenting a reasonable number of columns across the page.

`csepwidth(#)` specifies the separation between columns in units of digit widths. The default is not a fixed number, but a number chosen by `table` according to what it thinks looks best.

`stubwidth(#)` specifies the width, in units of digit widths, to be allocated to the left stub of the table. The default is not a fixed number, but a number chosen by `table` according to what it thinks looks best.

`scsepwidth(#)` specifies the separation between supercolumns in units of digit widths. The default is not a fixed number, but a number chosen by `table` to present the results best.

`center` specifies that results be centered in the table's cells. The default is to right-align results. For centering to work well, you typically need to specify a display format as well. `center format(%9.2f)` is popular.

`left` specifies that column labels be left-aligned. The default is to right-align column labels to distinguish them from supercolumn labels, which are left-aligned.

`cw` specifies casewise deletion. If `cw` is not specified, all observations possible are used to calculate each of the specified statistics. `cw` is relevant only when you request a table containing statistics on multiple variables. For instance, `contents(mean mpg mean weight)` would produce a table reporting the means of variables `mpg` and `weight`. Consider an observation in which `mpg` is known but `weight` is missing. By default, that observation will be used in the calculation of the mean of `mpg`. If you specify `cw`, the observation will be excluded in the calculation of the means of both `mpg` and `weight`.

`row` specifies that a row be added to the table reflecting the total across the rows.

`col` specifies that a column be added to the table reflecting the total across columns.

`scol` specifies that a supercolumn be added to the table reflecting the total across supercolumns.

`concise` specifies that rows with all missing entries not be displayed.

`missing` specifies that missing statistics be shown in the table as periods (Stata's missing-value indicator). The default is that missing entries be left blank.

`replace` specifies that the data in memory be replaced with data containing 1 observation per cell (row, column, supercolumn, and superrow) and with variables containing the statistics designated in `contents()`.

This option is rarely specified. If you do not specify this option, the data in memory remain unchanged.

If you do specify this option, the first statistic will be named `table1`, the second `table2`, and so on. For instance, if `contents(mean mpg sd mpg)` was specified, the means of `mpg` would be in variable `table1` and the standard deviations in `table2`.

`name(`*string*`)` is relevant only if you specify `replace`. `name()` allows changing the default stub name that `replace` uses to name the new variables associated with the statistics. If you specify `name(stat)`, the first statistic will be placed in variable `stat1`, the second in `stat2`, and so on.

`format(%`*fmt*`)` specifies the display format for presenting numbers in the table's cells. `format(%9.0g)` is the default; `format(%9.2f)` and `format(%9.2fc)` are popular alternatives. The width of the format you specify does not matter, except that `%`*fmt* must be valid. The width of the cells is chosen by `table` to present the results best. The `cellwidth()` option allows you to override `table`'s choice.

Limits

Up to four variables may be specified in the `by()`, so with the three row, column, and supercolumn variables, seven-way tables may be displayed.

Up to five statistics may be displayed in each cell of the table.

The sum of the number of rows, columns, supercolumns, and superrows is called the number of margins. A table may contain up to 3,000 margins. Thus a one-way table may contain 3,000 rows. A two-way table could contain 2,998 rows and two columns, 2,997 rows and three columns, . . ., 1,500 rows and 1,500 columns, . . ., two rows and 2,998 columns. A three-way table is similarly limited by the sum of the number of rows, columns, and supercolumns. A $r \times c \times d$ table is feasible if $r + c + d \leq 3{,}000$. The limit is set in terms of the sum of the rows, columns, supercolumns, and superrows, and not, as you might expect, in terms of their product.

Remarks

Remarks are presented under the following headings:

One-way tables
Two-way tables
Three-way tables
Four-way and higher-dimensional tables

One-way tables

▷ Example 1

From the automobile dataset, here is a simple one-way table:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. table rep78, contents(mean mpg)
```

Repair Record 1978	mean(mpg)
1	21
2	19.125
3	19.4333
4	21.6667
5	27.3636

We are not limited to including only one statistic:

```
. table rep78, c(n mpg  mean mpg  sd mpg  median mpg)
```

Repair Record 1978	N(mpg)	mean(mpg)	sd(mpg)	med(mpg)
1	2	21	4.24264	21
2	8	19.125	3.758324	18
3	30	19.4333	4.141325	19
4	18	21.6667	4.93487	22.5
5	11	27.3636	8.732385	30

We abbreviated `contents()` as `c()`. The `format()` option will allow us to better format the numbers in the table:

```
. table rep78, c(n mpg  mean mpg  sd mpg  median mpg) format(%9.2f)
```

Repair Record 1978	N(mpg)	mean(mpg)	sd(mpg)	med(mpg)
1	2	21.00	4.24	21.00
2	8	19.12	3.76	18.00
3	30	19.43	4.14	19.00
4	18	21.67	4.93	22.50
5	11	27.36	8.73	30.00

The `center` option will center the results under the headings:

```
. table rep78, c(n mpg  mean mpg  sd mpg  median mpg) format(%9.2f) center
```

Repair Record 1978	N(mpg)	mean(mpg)	sd(mpg)	med(mpg)
1	2	21.00	4.24	21.00
2	8	19.12	3.76	18.00
3	30	19.43	4.14	19.00
4	18	21.67	4.93	22.50
5	11	27.36	8.73	30.00

◁

Two-way tables

▷ Example 2

In example 1, when we typed '`table rep78, ...`', we obtained a one-way table. If we were to type '`table rep78 foreign, ...`', we would obtain a two-way table:

```
. table rep78 foreign, c(mean mpg)
```

Repair Record 1978	Car type	
	Domestic	Foreign
1	21	
2	19.125	
3	19	23.3333
4	18.4444	24.8889
5	32	26.3333

Note the missing cells. Certain combinations of repair record and car type do not exist in our dataset.

As with one-way tables, we can specify a display format for the cells and center the numbers within the cells if we wish.

```
. table rep78 foreign, c(mean mpg) format(%9.2f) center
```

Repair Record 1978	Car type	
	Domestic	Foreign
1	21.00	
2	19.12	
3	19.00	23.33
4	18.44	24.89
5	32.00	26.33

We can obtain row totals by specifying the `row` option and obtain column totals by specifying the `col` option. We specify both below:

```
. table rep78 foreign, c(mean mpg) format(%9.2f) center row col
```

Repair Record 1978	Car type		
	Domestic	Foreign	Total
1	21.00		21.00
2	19.12		19.12
3	19.00	23.33	19.43
4	18.44	24.89	21.67
5	32.00	26.33	27.36
Total	19.54	25.29	21.29

`table` can display multiple statistics within cells, but once we move beyond one-way tables, the table becomes busy:

```
. table foreign rep78, c(mean mpg  n mpg) format(%9.2f) center
```

	Repair Record 1978				
Car type	1	2	3	4	5
Domestic	21.00	19.12	19.00	18.44	32.00
	2	8	27	9	2
Foreign			23.33	24.89	26.33
			3	9	9

This two-way table with two statistics per cell works well here. That was, in part, helped along by our interchanging the rows and columns. We turned the table around by typing `table foreign rep78` rather than `table rep78 foreign`.

Another way to display two-way tables is to specify a row and superrow rather than a row and column. We do that below and display three statistics per cell:

```
. table foreign, by(rep78) c(mean mpg  sd mpg  n mpg) format(%9.2f) center
```

Repair Record 1978 and Car type	mean(mpg)	sd(mpg)	N(mpg)
1			
Domestic	21.00	4.24	2
Foreign			
2			
Domestic	19.12	3.76	8
Foreign			
3			
Domestic	19.00	4.09	27
Foreign	23.33	2.52	3
4			
Domestic	18.44	4.59	9
Foreign	24.89	2.71	9
5			
Domestic	32.00	2.83	2
Foreign	26.33	9.37	9

◁

Three-way tables

▷ Example 3

We have data on the prevalence of byssinosis, a form of pneumoconiosis to which workers exposed to cotton dust are susceptible. The dataset is on 5,419 workers in a large cotton mill. We know whether each worker smokes, his or her race, and the dustiness of the work area. The categorical variables are

`smokes`	Smoker or nonsmoker in the last five years.
`race`	White or other.
`workplace`	1 (most dusty), 2 (less dusty), 3 (least dusty).

Moreover, this dataset includes a frequency-weight variable `pop`. Here is a three-way table showing the fraction of workers with byssinosis:

```
. use http://www.stata-press.com/data/r12/byssin
(Byssinosis incidence)
. table workplace smokes race [fw=pop], c(mean prob)
```

Dustiness of workplace	Race and Smokes			
	other		white	
	no	yes	no	yes
least	.0107527	.0101523	.0081549	.0162774
less	.02	.0081633	.0136612	.0143149
most	.0820896	.1679105	.0833333	.2295082

This table would look better if we showed the fraction to four digits:

```
. table workplace smokes race [fw=pop], c(mean prob) format(%9.4f)
```

Dustiness of workplace	Race and Smokes: other, no	other, yes	white, no	white, yes
least	0.0108	0.0102	0.0082	0.0163
less	0.0200	0.0082	0.0137	0.0143
most	0.0821	0.1679	0.0833	0.2295

In this table, the rows are the dustiness of the workplace, the columns are whether the worker smokes, and the supercolumns are the worker's race.

Now we request that the table include the supercolumn totals by specifying the `sctotal` option, which we can abbreviate as `sc`:

```
. table workplace smokes race [fw=pop], c(mean prob) format(%9.4f) sc
```

Dustiness of workplace	Race and Smokes: other, no	other, yes	white, no	white, yes	Total, no	Total, yes
least	0.0108	0.0102	0.0082	0.0163	0.0090	0.0145
less	0.0200	0.0082	0.0137	0.0143	0.0159	0.0123
most	0.0821	0.1679	0.0833	0.2295	0.0826	0.1929

The supercolumn total is the total over `race` and is divided into its columns based on `smokes`. Here is the table with the column rather than the supercolumn totals:

```
. table workplace smokes race [fw=pop], c(mean prob) format(%9.4f) col
```

Dustiness of workplace	Race and Smokes: other, no	other, yes	other, Total	white, no	white, yes	white, Total
least	0.0108	0.0102	0.0104	0.0082	0.0163	0.0129
less	0.0200	0.0082	0.0135	0.0137	0.0143	0.0140
most	0.0821	0.1679	0.1393	0.0833	0.2295	0.1835

Here is the table with both column and supercolumn totals:

```
. table workplace smokes race [fw=pop], c(mean prob) format(%9.4f) sc col
```

Dustiness of workplace	Race and Smokes: other, no	other, yes	other, Total	white, no	white, yes	white, Total	Total, no	Total, yes	Total, Total
least	0.0108	0.0102	0.0104	0.0082	0.0163	0.0129	0.0090	0.0145	0.0122
less	0.0200	0.0082	0.0135	0.0137	0.0143	0.0140	0.0159	0.0123	0.0138
most	0.0821	0.1679	0.1393	0.0833	0.2295	0.1835	0.0826	0.1929	0.1570

`table` is struggling to keep this table from becoming too wide—notice how it divided the words in the title in the top-left stub. Here, if the table had more columns, or, if we demanded more digits, `table` would be forced to segment the table and present it in pieces, which it would do:

```
. table workplace smokes race [fw=pop], c(mean prob) format(%9.6f) sc col
```

Dustiness of workplace	Race and Smokes: other no	other yes	other Total	white no	white yes	white Total
least	0.010753	0.010152	0.010417	0.008155	0.016277	0.012949
less	0.020000	0.008163	0.013483	0.013661	0.014315	0.014035
most	0.082090	0.167910	0.139303	0.083333	0.229508	0.183521

Dustiness of workplace	Race and Smokes: Total no	Total yes	Total Total
least	0.008990	0.014471	0.012174
less	0.015901	0.012262	0.013846
most	0.082569	0.192905	0.156951

Here three digits is probably enough, so here is the table including all the row, column, and supercolumn totals:

```
. table workplace smokes race [fw=pop], c(mean prob) format(%9.3f)
> sc col row
```

Dustiness of workplace	Race and Smokes: other no	other yes	other Total	white no	white yes	white Total	Total no	Total yes	Total Total
least	0.011	0.010	0.010	0.008	0.016	0.013	0.009	0.014	0.012
less	0.020	0.008	0.013	0.014	0.014	0.014	0.016	0.012	0.014
most	0.082	0.168	0.139	0.083	0.230	0.184	0.083	0.193	0.157
Total	0.025	0.048	0.038	0.014	0.035	0.026	0.018	0.039	0.030

We can show multiple statistics:

```
. table workplace smokes race [fw=pop], c(mean prob  n prob) format(%9.3f)
> sc col row
```

Dustiness of workplace	Race and Smokes: other no	other yes	other Total	white no	white yes	white Total	Total no	Total yes	Total Total
least	0.011	0.010	0.010	0.008	0.016	0.013	0.009	0.014	0.012
	465	591	1,056	981	1,413	2,394	1,446	2,004	3,450
less	0.020	0.008	0.013	0.014	0.014	0.014	0.016	0.012	0.014
	200	245	445	366	489	855	566	734	1,300
most	0.082	0.168	0.139	0.083	0.230	0.184	0.083	0.193	0.157
	134	268	402	84	183	267	218	451	669
Total	0.025	0.048	0.038	0.014	0.035	0.026	0.018	0.039	0.030
	799	1,104	1,903	1,431	2,085	3,516	2,230	3,189	5,419

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Four-way and higher-dimensional tables

▷ Example 4

Let's pretend that our byssinosis dataset also recorded each worker's sex (it does not, and we have made up this extra information). We obtain a four-way table just as we would a three-way table, but we specify the fourth variable as a superrow by including it in the `by()` option:

```
. use http://www.stata-press.com/data/r12/byssin1
(Byssinosis incidence)
. table workplace smokes race [fw=pop], by(sex) c(mean prob) format(%9.3f)
> sc col row
```

Sex and Dustiness of workplace	Race and Smokes: other — no	other — yes	other — Total	white — no	white — yes	white — Total	Total — no	Total — yes	Total — Total
Female									
least	0.006	0.009	0.008	0.009	0.021	0.016	0.009	0.018	0.014
less	0.020	0.008	0.010	0.015	0.015	0.015	0.016	0.012	0.014
most	0.057	0.154	0.141				0.057	0.154	0.141
Total	0.017	0.051	0.043	0.011	0.020	0.016	0.012	0.032	0.024
Male									
least	0.013	0.011	0.012	0.006	0.007	0.006	0.009	0.008	0.009
less	0.020	0.000	0.019	0.000	0.013	0.011	0.016	0.013	0.014
most	0.091	0.244	0.136	0.083	0.230	0.184	0.087	0.232	0.167
Total	0.029	0.041	0.033	0.020	0.056	0.043	0.025	0.052	0.039

If our dataset also included work group and we wanted a five-way table, we could include both the sex and work-group variables in the `by()` option. You may include up to four variables in `by()`, and so produce up to 7-way tables.

◁

Methods and formulas

`table` is implemented as an ado-file. The contents of cells are calculated by `collapse` and are displayed by `tabdisp`; see [D] **collapse** and [P] **tabdisp**.

Also see

[R] **summarize** — Summary statistics

[R] **tabstat** — Display table of summary statistics

[R] **tabulate oneway** — One-way tables of frequencies

[R] **tabulate twoway** — Two-way tables of frequencies

[D] **collapse** — Make dataset of summary statistics

[P] **tabdisp** — Display tables

Title

tabstat — Display table of summary statistics

Syntax

`tabstat` *varlist* [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Main	
`by(`*varname*`)`	group statistics by variable
`statistics(`*statname*`[...])`	report specified statistics
Options	
`labelwidth(#)`	width for `by()` variable labels; default is `labelwidth(16)`
`varwidth(#)`	variable width; default is `varwidth(12)`
`columns(variables)`	display variables in table columns; the default
`columns(statistics)`	display statistics in table columns
`format[(%`*fmt*`)]`	display format for statistics; default format is `%9.0g`
`casewise`	perform casewise deletion of observations
`nototal`	do not report overall statistics; use with `by()`
`missing`	report statistics for missing values of `by()` variable
`noseparator`	do not use separator line between `by()` categories
`longstub`	make left table stub wider
`save`	save summary statistics in `r()`

`by` is allowed; see [D] **by**.

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Tables > Table of summary statistics (tabstat)

Description

`tabstat` displays summary statistics for a series of numeric variables in one table, possibly broken down on (conditioned by) another variable.

Without the `by()` option, `tabstat` is a useful alternative to `summarize` (see [R] **summarize**) because it allows you to specify the list of statistics to be displayed.

With the `by()` option, `tabstat` resembles `tabulate` used with its `summarize()` option in that both report statistics of *varlist* for the different values of *varname*. `tabstat` allows more flexibility in terms of the statistics presented and the format of the table.

`tabstat` is sensitive to the `linesize` (see `set linesize` in [R] **log**); it widens the table if possible and wraps if necessary.

Options

Main

`by(`*varname*`)` specifies that the statistics be displayed separately for each unique value of *varname*; *varname* may be numeric or string. For instance, `tabstat height` would present the overall mean of height. `tabstat height, by(sex)` would present the mean height of males, and of females, and the overall mean height. Do not confuse the `by()` option with the `by` prefix (see [D] **by**); both may be specified.

`statistics(`*statname* [...]`)` specifies the statistics to be displayed; the default is equivalent to specifying `statistics(mean)`. (`stats()` is a synonym for `statistics()`.) Multiple statistics may be specified and are separated by white space, such as `statistics(mean sd)`. Available statistics are

statname	Definition	*statname*	Definition
`mean`	mean	`p1`	1st percentile
`count`	count of nonmissing observations	`p5`	5th percentile
`n`	same as `count`	`p10`	10th percentile
`sum`	sum	`p25`	25th percentile
`max`	maximum	`median`	median (same as `p50`)
`min`	minimum	`p50`	50th percentile (same as `median`)
`range`	range = `max` − `min`	`p75`	75th percentile
`sd`	standard deviation	`p90`	90th percentile
`variance`	variance	`p95`	95th percentile
`cv`	coefficient of variation (`sd/mean`)	`p99`	99th percentile
`semean`	standard error of mean ($\texttt{sd}/\sqrt{\texttt{n}}$)	`iqr`	interquartile range = `p75` − `p25`
`skewness`	skewness	`q`	equivalent to specifying `p25 p50 p75`
`kurtosis`	kurtosis		

Options

`labelwidth(#)` specifies the maximum width to be used within the stub to display the labels of the `by()` variable. The default is `labelwidth(16)`. $8 \leq \# \leq 32$.

`varwidth(#)` specifies the maximum width to be used within the stub to display the names of the variables. The default is `varwidth(12)`. `varwidth()` is effective only with `columns(statistics)`. Setting `varwidth()` implies `longstub`. $8 \leq \# \leq 16$.

`columns(variables | statistics)` specifies whether to display variables or statistics in the columns of the table. `columns(variables)` is the default when more than one variable is specified.

`format` and `format(%`*fmt*`)` specify how the statistics are to be formatted. The default is to use a `%9.0g` format.

`format` specifies that each variable's statistics be formatted with the variable's display format; see [D] **format**.

`format(%`*fmt*`)` specifies the format to be used for all statistics. The maximum width of the specified format should not exceed nine characters.

`casewise` specifies casewise deletion of observations. Statistics are to be computed for the sample that is not missing for any of the variables in *varlist*. The default is to use all the nonmissing values for each variable.

`nototal` is for use with `by()`; it specifies that the overall statistics not be reported.

missing specifies that missing values of the by() variable be treated just like any other value and that statistics should be displayed for them. The default is not to report the statistics for the by()== *missing* group. If the by() variable is a string variable, by()="" is considered to mean missing.

noseparator specifies that a separator line between the by() categories not be displayed.

longstub specifies that the left stub of the table be made wider so that it can include names of the statistics or variables in addition to the categories of by(*varname*). The default is to describe the statistics or variables in a header. longstub is ignored if by(*varname*) is not specified.

save specifies that the summary statistics be returned in r(). The overall (unconditional) statistics are returned in matrix r(StatTotal) (rows are statistics, columns are variables). The conditional statistics are returned in the matrices r(Stat1), r(Stat2), ..., and the names of the corresponding variables are returned in the macros r(name1), r(name2), ...

Remarks

This command is probably most easily understood by going through a series of examples.

▷ Example 1

We have data on the price, weight, mileage rating, and repair record of 22 foreign and 52 domestic 1978 automobiles. We want to summarize these variables for the different origins of the automobiles.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. tabstat price weight mpg rep78, by(foreign)
Summary statistics: mean
  by categories of: foreign (Car type)
 foreign |     price    weight       mpg     rep78
---------+--------------------------------------------
Domestic |  6072.423  3317.115  19.82692  3.020833
 Foreign |  6384.682  2315.909  24.77273  4.285714
---------+--------------------------------------------
   Total |  6165.257  3019.459   21.2973  3.405797
------------------------------------------------------
```

More summary statistics can be requested via the statistics() option. The group totals can be suppressed with the nototal option.

```
. tabstat price weight mpg rep78, by(foreign) stat(mean sd min max) nototal
Summary statistics: mean, sd, min, max
  by categories of: foreign (Car type)
 foreign |     price    weight       mpg     rep78
---------+--------------------------------------------
Domestic |  6072.423  3317.115  19.82692  3.020833
         |  3097.104  695.3637  4.743297   .837666
         |      3291      1800        12         1
         |     15906      4840        34         5
---------+--------------------------------------------
 Foreign |  6384.682  2315.909  24.77273  4.285714
         |  2621.915  433.0035  6.611187  .7171372
         |      3748      1760        14         3
         |     12990      3420        41         5
------------------------------------------------------
```

Although the header of the table describes the statistics running vertically in the "cells", the table may become hard to read, especially with many variables or statistics. The `longstub` option specifies that a column be added describing the contents of the cells. The `format` option can be issued to specify that `tabstat` display the statistics by using the display format of the variables rather than the overall default `%9.0g`.

```
. tabstat price weight mpg rep78, by(foreign) stat(mean sd min max) long format
```

foreign	stats	price	weight	mpg	rep78
Domestic	mean	6,072.4	3,317.1	19.8269	3.02083
	sd	3,097.1	695.364	4.7433	.837666
	min	3,291	1,800	12	1
	max	15,906	4,840	34	5
Foreign	mean	6,384.7	2,315.9	24.7727	4.28571
	sd	2,621.9	433.003	6.61119	.717137
	min	3,748	1,760	14	3
	max	12,990	3,420	41	5
Total	mean	6,165.3	3,019.5	21.2973	3.4058
	sd	2,949.5	777.194	5.7855	.989932
	min	3,291	1,760	12	1
	max	15,906	4,840	41	5

We can specify a layout of the table in which the statistics run horizontally and the variables run vertically by specifying the `col(statistics)` option.

```
. tabstat price weight mpg rep78, by(foreign) stat(min mean max) col(stat) long
```

foreign	variable	min	mean	max
Domestic	price	3291	6072.423	15906
	weight	1800	3317.115	4840
	mpg	12	19.82692	34
	rep78	1	3.020833	5
Foreign	price	3748	6384.682	12990
	weight	1760	2315.909	3420
	mpg	14	24.77273	41
	rep78	3	4.285714	5
Total	price	3291	6165.257	15906
	weight	1760	3019.459	4840
	mpg	12	21.2973	41
	rep78	1	3.405797	5

Finally, `tabstat` can also be used to enhance `summarize` so we can specify the statistics to be displayed. For instance, we can display the number of observations, the mean, the coefficient of variation, and the 25%, 50%, and 75% quantiles for a list of variables.

```
. tabstat price weight mpg rep78, stat(n mean cv q) col(stat)
```

variable	N	mean	cv	p25	p50	p75
price	74	6165.257	.478406	4195	5006.5	6342
weight	74	3019.459	.2573949	2240	3190	3600
mpg	74	21.2973	.2716543	18	20	25
rep78	69	3.405797	.290661	3	3	4

Because we did not specify the by() option, these statistics were not displayed for the subgroups of the data formed by the categories of the by() variable. ◁

Methods and formulas

tabstat is implemented as an ado-file.

Acknowledgments

The tabstat command was written by Jeroen Weesie and Vincent Buskens of Utrecht University in The Netherlands.

Also see

[R] **summarize** — Summary statistics

[R] **table** — Tables of summary statistics

[R] **tabulate, summarize()** — One- and two-way tables of summary statistics

[D] **collapse** — Make dataset of summary statistics

Title

tabulate oneway — One-way tables of frequencies

Syntax

One-way tables

`tabulate` *varname* [*if*] [*in*] [*weight*] [, *tabulate1_options*]

One-way table for each variable—a convenience tool

`tab1` *varlist* [*if*] [*in*] [*weight*] [, *tab1_options*]

tabulate1_options	Description
Main	
`subpop(`*varname*`)`	exclude observations for which *varname* = 0
`missing`	treat missing values like other values
`nofreq`	do not display frequencies
`nolabel`	display numeric codes rather than value labels
`plot`	produce a bar chart of the relative frequencies
`sort`	display the table in descending order of frequency
Advanced	
`generate(`*stubname*`)`	create indicator variables for *stubname*
`matcell(`*matname*`)`	save frequencies in *matname*; programmer's option
`matrow(`*matname*`)`	save unique values of *varname* in *matname*; programmer's option

tab1_options	Description
Main	
`subpop(`*varname*`)`	exclude observations for which *varname* = 0
`missing`	treat missing values like other values
`nofreq`	do not display frequencies
`nolabel`	display numeric codes rather than value labels
`plot`	produce a bar chart of the relative frequencies
`sort`	display the table in descending order of frequency

`by` is allowed with `tabulate` and `tab1`; see [D] **by**.

`fweights`, `aweights`, and `iweights` are allowed by `tabulate`. `fweights` are allowed by `tab1`. See [U] **11.1.6 weight**.

Menu

tabulate oneway

Statistics > Summaries, tables, and tests > Tables > One-way tables

tabulate ..., generate()

Data > Create or change data > Other variable-creation commands > Create indicator variables

tab1

Statistics > Summaries, tables, and tests > Tables > Multiple one-way tables

Description

`tabulate` produces one-way tables of frequency counts.

For information about two-way tables of frequency counts along with various measures of association, including the common Pearson χ^2, the likelihood-ratio χ^2, Cramér's V, Fisher's exact test, Goodman and Kruskal's gamma, and Kendall's τ_b, see [R] **tabulate twoway**.

`tab1` produces a one-way tabulation for each variable specified in *varlist*.

Also see [R] **table** and [R] **tabstat** if you want one-, two-, or n-way tables of frequencies and a wide variety of summary statistics. See [R] **tabulate, summarize()** for a description of `tabulate` with the `summarize()` option; it produces tables (breakdowns) of means and standard deviations. `table` is better than `tabulate, summarize()`, but `tabulate, summarize()` is faster. See [ST] **epitab** for 2×2 tables with statistics of interest to epidemiologists.

Options

Main

`subpop(`*varname*`)` excludes observations for which *varname* $= 0$ in tabulating frequencies. The mathematical results of `tabulate ..., subpop(myvar)` are the same as `tabulate ... if myvar !=0`, but the table may be presented differently. The identities of the rows and columns will be determined from all the data, including the `myvar` $= 0$ group, so there may be entries in the table with frequency 0.

Consider tabulating `answer`, a variable that takes on values 1, 2, and 3, but consider tabulating it just for the `male==1` subpopulation. Assume that `answer` is never 2 in this group. `tabulate answer if male==1` produces a table with two rows: one for answer 1 and one for answer 3. There will be no row for answer 2 because answer 2 was never observed. `tabulate answer, subpop(male)` produces a table with three rows. The row for answer 2 will be shown as having 0 frequency.

`missing` requests that missing values be treated like other values in calculations of counts, percentages, and other statistics.

`nofreq` suppresses the printing of the frequencies.

`nolabel` causes the numeric codes to be displayed rather than the value labels.

`plot` produces a bar chart of the relative frequencies in a one-way table. (Also see [R] **histogram**.)

`sort` puts the table in descending order of frequency (and ascending order of the variable within equal values of frequency).

Advanced

`generate(`*stubname*`)` creates a set of indicator variables (*stubname*`1`, *stubname*`2`, ...) reflecting the observed values of the tabulated variable. The `generate()` option may not be used with the `by` prefix.

`matcell(`*matname*`)` saves the reported frequencies in *matname*. This option is for use by programmers.

`matrow(`*matname*`)` saves the numeric values of the $r \times 1$ row stub in *matname*. This option is for use by programmers. `matrow()` may not be specified if the row variable is a string.

Limits

One-way tables may have a maximum of 12,000 rows (Stata/MP and Stata/SE), 3,000 rows (Stata/IC), or 500 rows (Small Stata).

Remarks

Remarks are presented under the following headings:

tabulate
tab1

For each value of a specified variable, `tabulate` reports the number of observations with that value. The number of times a value occurs is called its *frequency*.

tabulate

▷ Example 1

We have data summarizing the speed limit and the accident rate per million vehicle miles along various Minnesota highways in 1973. The variable containing the speed limit is called `spdlimit`. If we `summarize` the variable, we obtain its mean and standard deviation:

```
. use http://www.stata-press.com/data/r12/hiway
(Minnesota Highway Data, 1973)
. summarize spdlimit
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
    spdlimit |         39          55    5.848977        40         70
```

The average speed limit is 55 miles per hour. We can learn more about this variable by tabulating it:

```
. tabulate spdlimit
Speed limit |      Freq.     Percent        Cum.
------------+-----------------------------------
         40 |          1        2.56        2.56
         45 |          3        7.69       10.26
         50 |          7       17.95       28.21
         55 |         15       38.46       66.67
         60 |         11       28.21       94.87
         65 |          1        2.56       97.44
         70 |          1        2.56      100.00
------------+-----------------------------------
      Total |         39      100.00
```

We see that one highway has a speed limit of 40 miles per hour, three have speed limits of 45, 7 of 50, and so on. The column labeled `Percent` shows the percentage of highways in the dataset that have the indicated speed limit. For instance, 38.46% of highways in our dataset have a speed limit of 55 miles per hour. The final column shows the cumulative percentage. We see that 66.67% of highways in our dataset have a speed limit of 55 miles per hour or less.

◁

▷ Example 2

The `plot` option places a sideways histogram alongside the table:

```
. tabulate spdlimit, plot
```

Speed limit	Freq.	
40	1	*
45	3	***
50	7	*******
55	15	***************
60	11	**********
65	1	*
70	1	*
Total	39	

Of course, `graph` can produce better-looking histograms; see [R] **histogram**.

◁

▷ Example 3

`tabulate` labels tables using *variable* and *value labels* if they exist. To demonstrate how this works, let's add a new variable to our dataset that categorizes `spdlimit` into three categories. We will call this new variable `spdcat`:

```
. generate spdcat=recode(spdlimit,50,60,70)
```

The `recode()` function divides `spdlimit` into 50 miles per hour or below, 51–60, and above 60; see [D] **functions**. We specified the breakpoints in the arguments `(spdlimit,50,60,70)`. The first argument is the variable to be recoded. The second argument is the first breakpoint, the third argument is the second breakpoint, and so on. We can specify as many breakpoints as we wish.

`recode()` used our arguments not only as the breakpoints but also to label the results. If `spdlimit` is less than or equal to 50, `spdcat` is set to 50; if `spdlimit` is between 51 and 60, `spdcat` is 60; otherwise, `spdcat` is arbitrarily set to 70. (See [U] **25 Working with categorical data and factor variables**.)

Because we just created the variable `spdcat`, it is not yet labeled. When we make a table using this variable, `tabulate` uses the variable's name to label it:

```
. tabulate spdcat
```

spdcat	Freq.	Percent	Cum.
50	11	28.21	28.21
60	26	66.67	94.87
70	2	5.13	100.00
Total	39	100.00	

Even through the table is not well labeled, `recode()`'s coding scheme provides us with clues as to the table's meaning. The first line of the table corresponds to 50 miles per hour and below, the next to 51 through 60 miles per hour, and the last to above 60 miles per hour.

We can improve this table by labeling the values and variables:

```
. label define scat 50 "40 to 50" 60 "55 to 60" 70 "Above 60"
. label values spdcat scat
. label variable spdcat "Speed Limit Category"
```

We define a *value label* called `scat` that attaches labels to the numbers 50, 60, and 70 using the `label define` command; see [U] **12.6.3 Value labels**. We label the value 50 as '`40 to 50`', because we looked back at our original tabulation in the first example and saw that the speed limit was never less than 40. Similarly, we could have labeled the last category '`65 to 70`' because the speed limit is never greater than 70 miles per hour.

Next we requested that Stata label the values of the new variable `spdcat` using the value label `scat`. Finally, we labeled our variable `Speed Limit Category`. We are now ready to `tabulate` the result:

```
. tabulate spdcat
```

Speed Limit Category	Freq.	Percent	Cum.
40 to 50	11	28.21	28.21
55 to 60	26	66.67	94.87
Above 60	2	5.13	100.00
Total	39	100.00	

◁

▷ Example 4

If we have missing values in our dataset, `tabulate` ignores them unless we explicitly indicate otherwise. We have no missing data in our example, so let's add some:

```
. replace spdcat=. in 39
(1 real change made, 1 to missing)
```

We changed the first observation on `spdcat` to *missing*. Let's now `tabulate` the result:

```
. tabulate spdcat
```

Speed Limit Category	Freq.	Percent	Cum.
40 to 50	11	28.95	28.95
55 to 60	26	68.42	97.37
Above 60	1	2.63	100.00
Total	38	100.00	

Comparing this output with that in the previous example, we see that the total frequency count is now one less than it was—38 rather than 39. Also, the '`Above 60`' category now has only one observation where it used to have two, so we evidently changed a road with a high speed limit.

We want `tabulate` to treat missing values just as it treats numbers, so we specify the `missing` option:

```
. tabulate spdcat, missing
```

Speed Limit Category	Freq.	Percent	Cum.
40 to 50	11	28.21	28.21
55 to 60	26	66.67	94.87
Above 60	1	2.56	97.44
.	1	2.56	100.00
Total	39	100.00	

We now see our missing value—the last category, labeled '.', shows a frequency count of 1. The table sum is once again 39.

Let's put our dataset back as it was originally:

```
. replace spdcat=70 in 39
(1 real change made)
```

◁

❑ Technical note

`tabulate` also can automatically create indicator variables from categorical variables. We will briefly review that capability here, but see [U] **25 Working with categorical data and factor variables** for a complete description. Let's begin by describing our highway dataset:

```
. describe
Contains data from http://www.stata-press.com/data/r12/hiway.dta
  obs:            39                          Minnesota Highway Data, 1973
 vars:             2                          16 Nov 2010 12:39
 size:           351
```

variable name	storage type	display format	value label	variable label
spdlimit	byte	%8.0g		Speed limit
rate	float	%9.0g	rcat	Accident rate per million vehicle miles
spdcat	float	%9.0g	scat	Speed Limit Category

```
Sorted by:
     Note:  dataset has changed since last saved
```

Our dataset contains three variables. We will type `tabulate spdcat, generate(spd)`, `describe` our data, and then explain what happened.

```
. tabulate spdcat, generate(spd)
```

Speed Limit Category	Freq.	Percent	Cum.
40 to 50	11	28.21	28.21
55 to 60	26	66.67	94.87
Above 60	2	5.13	100.00
Total	39	100.00	

```
. describe
Contains data from http://www.stata-press.com/data/r12/hiway.dta
  obs:            39                          Minnesota Highway Data, 1973
 vars:             6                          16 Nov 2010 12:39
 size:           468
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
spdlimit        byte   %8.0g                  Speed limit
rate            float  %9.0g       rcat       Accident rate per million
                                                vehicle miles
spdcat          float  %9.0g       scat       Speed Limit Category
spd1            byte   %8.0g                  spdcat==40 to 50
spd2            byte   %8.0g                  spdcat==55 to 60
spd3            byte   %8.0g                  spdcat==Above 60
-------------------------------------------------------------------------------
Sorted by:
     Note:  dataset has changed since last saved
```

When we typed `tabulate` with the `generate()` option, Stata responded by producing a one-way frequency table, so it appeared that the option did nothing. Yet when we `describe` our dataset, we find that we now have *six* variables instead of the original three. The new variables are named `spd1`, `spd2`, and `spd3`.

When we specify the `generate()` option, we are telling Stata to not only produce the table but also create a set of indicator variables that correspond to that table. Stata adds a numeric suffix to the name we specify in the parentheses. `spd1` refers to the first line of the table, `spd2` to the second line, and so on. Also Stata labels the variables so that we know what they mean. `spd1` is an indicator variable that is *true* (takes on the value 1) when `spdcat` is between 40 and 50; otherwise, it is zero. (There is an exception: if `spdcat` is missing, so are the `spd1`, `spd2`, and `spd3` variables. This did not happen in our dataset.)

We want to prove our claim. Because we have not yet introduced two-way tabulations, we will use the `summarize` statement:

```
. summarize spdlimit if spd1==1
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
    spdlimit |        11    47.72727    3.437758        40         50

. summarize spdlimit if spd2==1
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
    spdlimit |        26    57.11538    2.519157        55         60

. summarize spdlimit if spd3==1
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
    spdlimit |         2        67.5    3.535534        65         70
```

Notice the indicated minimum and maximum in each of the tables above. When we restrict the sample to `spd1`, `spdlimit` is between 40 and 50; when we restrict the sample to `spd2`, `spdlimit` is between 55 and 60; when we restrict the sample to `spd3`, `spdlimit` is between 65 and 70.

Thus `tabulate` provides an easy way to create indicator (sometimes called dummy) variables. For an overview of indicator and categorical variables, see [U] **25 Working with categorical data and factor variables**.

❑

tab1

tab1 is a convenience tool. Typing

```
. tab1 myvar thisvar thatvar, plot
```

is equivalent to typing

```
. tabulate myvar, plot
. tabulate thisvar, plot
. tabulate thatvar, plot
```

Saved results

tabulate and tab1 save the following in r():

Scalars

r(N)	number of observations	r(r)	number of rows

Methods and formulas

tab1 is implemented as an ado-file.

References

Cox, N. J. 2009. Speaking Stata: I. J. Good and quasi-Bayes smoothing of categorical frequencies. *Stata Journal* 9: 306–314.

Harrison, D. A. 2006. Stata tip 34: Tabulation by listing. *Stata Journal* 6: 425–427.

Also see

[R] **table** — Tables of summary statistics

[R] **tabstat** — Display table of summary statistics

[R] **tabulate twoway** — Two-way tables of frequencies

[R] **tabulate, summarize()** — One- and two-way tables of summary statistics

[D] **collapse** — Make dataset of summary statistics

[ST] **epitab** — Tables for epidemiologists

[SVY] **svy: tabulate oneway** — One-way tables for survey data

[SVY] **svy: tabulate twoway** — Two-way tables for survey data

[XT] **xttab** — Tabulate xt data

[U] **12.6.3 Value labels**

[U] **25 Working with categorical data and factor variables**

Title

tabulate twoway — Two-way tables of frequencies

Syntax

Two-way tables

`tabulate` *varname*$_1$ *varname*$_2$ [*if*] [*in*] [*weight*] [, *options*]

Two-way tables for all possible combinations—a convenience tool

`tab2` *varlist* [*if*] [*in*] [*weight*] [, *options*]

Immediate form of two-way tabulations

`tabi` #$_{11}$ #$_{12}$ [...] \ #$_{21}$ #$_{22}$ [...] [\ ...] [, *options*]

options	Description
Main	
`chi2`	report Pearson's χ^2
`exact`[`(#)`]	report Fisher's exact test
`gamma`	report Goodman and Kruskal's gamma
`lrchi2`	report likelihood-ratio χ^2
`taub`	report Kendall's τ_b
`V`	report Cramér's V
`cchi2`	report Pearson's χ^2 in each cell
`column`	report relative frequency within its column of each cell
`row`	report relative frequency within its row of each cell
`clrchi2`	report likelihood-ratio χ^2 in each cell
`cell`	report the relative frequency of each cell
`expected`	report expected frequency in each cell
`nofreq`	do not display frequencies
`missing`	treat missing values like other values
`wrap`	do not wrap wide tables
[`no`]`key`	report/suppress cell contents key
`nolabel`	display numeric codes rather than value labels
`nolog`	do not display enumeration log for Fisher's exact test
* `firstonly`	show only tables that include the first variable in *varlist*
Advanced	
`matcell(`*matname*`)`	save frequencies in *matname*; programmer's option
`matrow(`*matname*`)`	save unique values of *varname*$_1$ in *matname*; programmer's option
`matcol(`*matname*`)`	save unique values of *varname*$_2$ in *matname*; programmer's option
‡ `replace`	replace current data with given cell frequencies
`all`	equivalent to specifying `chi2 lrchi2 V gamma taub`

*firstonly is available only for tab2.

‡replace is available only for tabi.

by is allowed with tabulate and tab2; see [D] by.

fweights, aweights, and iweights are allowed by tabulate. fweights are allowed by tab2. See [U] 11.1.6 weight.

all does not appear in the dialog box.

Menu

tabulate

Statistics > Summaries, tables, and tests > Tables > Two-way tables with measures of association

tab2

Statistics > Summaries, tables, and tests > Tables > All possible two-way tabulations

tabi

Statistics > Summaries, tables, and tests > Tables > Table calculator

Description

tabulate produces two-way tables of frequency counts, along with various measures of association, including the common Pearson's χ^2, the likelihood-ratio χ^2, Cramér's V, Fisher's exact test, Goodman and Kruskal's gamma, and Kendall's τ_b.

Line size is respected. That is, if you resize the Results window before running tabulate, the resulting two-way tabulation will take advantage of the available horizontal space. Stata for Unix(console) users can instead use the set linesize command to take advantage of this feature.

tab2 produces all possible two-way tabulations of the variables specified in *varlist*.

tabi displays the $r \times c$ table, using the values specified; rows are separated by '\'. If no options are specified, it is as if exact were specified for 2×2 tables and chi2 were specified otherwise. See [U] 19 Immediate commands for a general description of immediate commands. See *Tables with immediate data* below for examples using tabi.

See [R] tabulate oneway if you want one-way tables of frequencies. See [R] table and [R] tabstat if you want one-, two-, or n-way tables of frequencies and a wide variety of summary statistics. See [R] tabulate, summarize() for a description of tabulate with the summarize() option; it produces tables (breakdowns) of means and standard deviations. table is better than tabulate, summarize(), but tabulate, summarize() is faster. See [ST] epitab for 2×2 tables with statistics of interest to epidemiologists.

Options

Main

chi2 calculates and displays Pearson's χ^2 for the hypothesis that the rows and columns in a two-way table are independent. chi2 may not be specified if aweights or iweights are specified.

`exact`[`(#)`] displays the significance calculated by Fisher's exact test and may be applied to $r \times c$ as well as to 2×2 tables. For 2×2 tables, both one- and two-sided probabilities are displayed. For $r \times c$ tables, one-sided probabilities are displayed. The optional positive integer # is a multiplier on the amount of memory that the command is permitted to consume. The default is 1. This option should not be necessary for reasonable $r \times c$ tables. If the command terminates with error 910, try `exact(2)`. The maximum row or column dimension allowed when computing Fisher's exact test is the maximum row or column dimension for `tabulate` (see `help limits`).

`gamma` displays Goodman and Kruskal's gamma along with its asymptotic standard error. `gamma` is appropriate only when both variables are ordinal. `gamma` may not be specified if `aweights` or `iweights` are specified.

`lrchi2` displays the likelihood-ratio χ^2 statistic. `lrchi2` may not be specified if `aweights` or `iweights` are specified.

`taub` displays Kendall's τ_b along with its asymptotic standard error. `taub` is appropriate only when both variables are ordinal. `taub` may not be specified if `aweights` or `iweights` are specified.

`V` (note capitalization) displays Cramér's V. `V` may not be specified if `aweights` or `iweights` are specified.

`cchi2` displays each cell's contribution to Pearson's chi-squared in a two-way table.

`column` displays the relative frequency of each cell within its column in a two-way table.

`row` displays the relative frequency of each cell within its row in a two-way table.

`clrchi2` displays each cell's contribution to the likelihood-ratio chi-squared in a two-way table.

`cell` displays the relative frequency of each cell in a two-way table.

`expected` displays the expected frequency of each cell in a two-way table.

`nofreq` suppresses the printing of the frequencies.

`missing` requests that missing values be treated like other values in calculations of counts, percentages, and other statistics.

`wrap` requests that Stata take no action on wide, two-way tables to make them readable. Unless `wrap` is specified, wide tables are broken into pieces to enhance readability.

[`no`]`key` suppresses or forces the display of a key above two-way tables. The default is to display the key if more than one cell statistic is requested, and otherwise to omit it. `key` forces the display of the key. `nokey` suppresses its display.

`nolabel` causes the numeric codes to be displayed rather than the value labels.

`nolog` suppresses the display of the log for Fisher's exact test. Using Fisher's exact test requires counting all tables that have a probability exceeding that of the observed table given the observed row and column totals. The log counts down each stage of the network computations, starting from the number of columns and counting down to 1, displaying the number of nodes in the network at each stage. A log is not displayed for 2×2 tables.

`firstonly`, available only with `tab2`, restricts the output to only those tables that include the first variable in *varlist*. Use this option to interact one variable with a set of others.

Advanced

`matcell(`*matname*`)` saves the reported frequencies in *matname*. This option is for use by programmers.

`matrow(`*matname*`)` saves the numeric values of the $r \times 1$ row stub in *matname*. This option is for use by programmers. `matrow()` may not be specified if the row variable is a string.

`matcol(`*matname*`)` saves the numeric values of the $1 \times c$ column stub in *matname*. This option is for use by programmers. `matcol()` may not be specified if the column variable is a string.

`replace` indicates that the immediate data specified as arguments to the `tabi` command be left as the current data in place of whatever data were there.

The following option is available with `tabulate` but is not shown in the dialog box:

`all` is equivalent to specifying `chi2 lrchi2 V gamma taub`. Note the omission of `exact`. When `all` is specified, `no` may be placed in front of the other options. `all noV` requests all association measures except Cramér's V (and Fisher's exact). `all exact` requests all association measures, including Fisher's exact test. `all` may not be specified if `aweights` or `iweights` are specified.

Limits

Two-way tables may have a maximum of 1,200 rows and 80 columns (Stata/MP and Stata/SE), 300 rows and 20 columns (Stata/IC), or 160 rows and 20 columns (Small Stata). If larger tables are needed, see [R] **table**.

Remarks

Remarks are presented under the following headings:

tabulate
Measures of association
N-way tables
Weighted data
Tables with immediate data
tab2

For each value of a specified variable (or a set of values for a pair of variables), `tabulate` reports the number of observations with that value. The number of times a value occurs is called its *frequency*.

tabulate

▷ Example 1

`tabulate` will make two-way tables if we specify two variables following the word `tabulate`. In our highway dataset, we have a variable called `rate` that divides the accident rate into three categories: below 4, 4–7, and above 7 per million vehicle miles. Let's make a table of the speed limit category and the accident-rate category:

```
. use http://www.stata-press.com/data/r12/hiway2
(Minnesota Highway Data, 1973)
. tabulate spdcat rate
```

Speed Limit Category	Accident rate per million vehicle miles			
	Below 4	4-7	Above 7	Total
40 to 50	3	5	3	11
55 to 60	19	6	1	26
Above 60	2	0	0	2
Total	24	11	4	39

The table indicates that three stretches of highway have an accident rate below 4 and a speed limit of 40 to 50 miles per hour. The table also shows the row and column sums (called the *marginals*). The number of highways with a speed limit of 40 to 50 miles per hour is 11, which is the same result we obtained in our previous one-way tabulations.

Stata can present this basic table in several ways—16, to be precise—and we will show just a few below. It might be easier to read the table if we included the row percentages. For instance, of 11 highways in the lowest speed limit category, three are also in the lowest accident-rate category. Three-elevenths amounts to some 27.3%. We can ask Stata to fill in this information for us by using the `row` option:

```
. tabulate spdcat rate, row
```

Key
frequency *row percentage*

Speed Limit Category	Accident rate per million vehicle miles			
	Below 4	4-7	Above 7	Total
40 to 50	3	5	3	11
	27.27	45.45	27.27	100.00
55 to 60	19	6	1	26
	73.08	23.08	3.85	100.00
Above 60	2	0	0	2
	100.00	0.00	0.00	100.00
Total	24	11	4	39
	61.54	28.21	10.26	100.00

The number listed below each frequency is the percentage of cases that each cell represents out of its row. That is easy to remember because we see 100% listed in the "`Total`" column. The bottom row is also informative. We see that 61.54% of all the highways in our dataset fall into the lowest accident-rate category, that 28.21% are in the middle category, and that 10.26% are in the highest.

`tabulate` can calculate column percentages and cell percentages, as well. It does so when we specify the `column` or `cell` options, respectively. We can even specify them together. Below is a table that includes everything:

```
. tabulate spdcat rate, row column cell
```

Key
frequency *row percentage* *column percentage* *cell percentage*

Speed Limit Category	Accident rate per million vehicle miles: Below 4	4-7	Above 7	Total
40 to 50	3	5	3	11
	27.27	45.45	27.27	100.00
	12.50	45.45	75.00	28.21
	7.69	12.82	7.69	28.21
55 to 60	19	6	1	26
	73.08	23.08	3.85	100.00
	79.17	54.55	25.00	66.67
	48.72	15.38	2.56	66.67
Above 60	2	0	0	2
	100.00	0.00	0.00	100.00
	8.33	0.00	0.00	5.13
	5.13	0.00	0.00	5.13
Total	24	11	4	39
	61.54	28.21	10.26	100.00
	100.00	100.00	100.00	100.00
	61.54	28.21	10.26	100.00

The number at the top of each cell is the frequency count. The second number is the row percentage—they sum to 100% going across the table. The third number is the column percentage—they sum to 100% going down the table. The bottom number is the cell percentage—they sum to 100% going down all the columns and across all the rows. For instance, highways with a speed limit above 60 miles per hour and in the lowest accident rate category account for 100% of highways with a speed limit above 60 miles per hour; 8.33% of highways in the lowest accident-rate category; and 5.13% of all our data.

A fourth option, `nofreq`, tells Stata not to print the frequency counts. To construct a table consisting of only row percentages, we type

```
. tabulate spdcat rate, row nofreq
```

Speed Limit Category	Accident rate per million vehicle miles: Below 4	4-7	Above 7	Total
40 to 50	27.27	45.45	27.27	100.00
55 to 60	73.08	23.08	3.85	100.00
Above 60	100.00	0.00	0.00	100.00
Total	61.54	28.21	10.26	100.00

◁

Measures of association

▷ Example 2

`tabulate` will calculate the Pearson χ^2 test for the independence of the rows and columns if we specify the `chi2` option. Suppose that we have 1980 census data on 956 cities in the United States and wish to compare the age distribution across regions of the country. Assume that `agecat` is the median age in each city and that `region` denotes the region of the country in which the city is located.

```
. use http://www.stata-press.com/data/r12/citytemp2
(City Temperature Data)
. tabulate region agecat, chi2
```

Census Region	agecat 19-29	30-34	35+	Total
NE	46	83	37	166
N Cntrl	162	92	30	284
South	139	68	43	250
West	160	73	23	256
Total	507	316	133	956

Pearson chi2(6) = 61.2877 Pr = 0.000

We obtain the standard two-way table and, at the bottom, a summary of the χ^2 test. Stata informs us that the χ^2 associated with this table has 6 degrees of freedom and is 61.29. The observed differences are significant.

The table is, perhaps, easier to understand if we suppress the frequencies and print just the row percentages:

```
. tabulate region agecat, row nofreq chi2
```

Census Region	agecat 19-29	30-34	35+	Total
NE	27.71	50.00	22.29	100.00
N Cntrl	57.04	32.39	10.56	100.00
South	55.60	27.20	17.20	100.00
West	62.50	28.52	8.98	100.00
Total	53.03	33.05	13.91	100.00

Pearson chi2(6) = 61.2877 Pr = 0.000

◁

▷ Example 3

We have data on dose level and outcome for a set of patients and wish to evaluate the association between the two variables. We can obtain all the association measures by specifying the `all` and `exact` options:

```
. use http://www.stata-press.com/data/r12/dose
. tabulate dose function, all exact
Enumerating sample-space combinations:
stage 3:  enumerations = 1
stage 2:  enumerations = 9
stage 1:  enumerations = 0
```

Dosage	Function < 1 hr	1 to 4	4+	Total
1/day	20	10	2	32
2/day	16	12	4	32
3/day	10	16	6	32
Total	46	38	12	96

```
          Pearson chi2(4) =   6.7780   Pr = 0.148
 likelihood-ratio chi2(4) =   6.9844   Pr = 0.137
               Cramer's V =   0.1879
                    gamma =   0.3689  ASE = 0.129
          Kendall's tau-b =   0.2378  ASE = 0.086
           Fisher's exact =                 0.145
```

We find evidence of association but not enough to be truly convincing.

If we had not also specified the `exact` option, we would not have obtained Fisher's exact test. Stata can calculate this statistic both for 2×2 tables and for $r \times c$. For 2×2 tables, the calculation is almost instant. On more general tables, however, the calculation can take longer.

We carefully constructed our example so that `all` would be meaningful. Kendall's τ_b and Goodman and Kruskal's gamma are relevant only when both dimensions of the table can be ordered, say, from low to high or from worst to best. The other statistics, however, are always applicable.

◁

❑ Technical note

Be careful when attempting to compute the p-value for Fisher's exact test because the number of tables that contribute to the p-value can be extremely large and a solution may not be feasible. The errors that are indicative of this situation are errors 910, exceeded memory limitations, and 1401, integer overflow due to large row-margin frequencies. If execution terminates because of memory limitations, use `exact(2)` to permit the algorithm to consume twice the memory, `exact(3)` for three times the memory, etc. The default memory usage should be sufficient for reasonable tables.

❑

N-way tables

If you need more than two-way tables, your best alternative to is use `table`, not `tabulate`; see [R] **table**.

The technical note below shows you how to use `tabulate` to create a sequence of two-way tables that together form, in effect, a three-way table, but using `table` is easy and produces prettier results:

```
. use http://www.stata-press.com/data/r12/birthcat
(City data)
. table birthcat region agecat, c(freq)
```

	agecat and Census Region							
	19-29				30-34			
birthcat	NE	N Cntrl	South	West	NE	N Cntrl	South	West
29-136	11	23	11	11	34	27	10	8
137-195	31	97	65	46	48	58	45	42
196-529	4	38	59	91	1	3	12	21

	agecat and Census Region			
	35+			
birthcat	NE	N Cntrl	South	West
29-136	34	26	27	18
137-195	3	4	7	4
196-529			4	

❑ Technical note

We can make n-way tables by combining the by *varlist*: prefix with `tabulate`. Continuing with the dataset of 956 cities, say that we want to make a table of age category by birth-rate category by region of the country. The birth-rate category variable is named `birthcat` in our dataset. To make separate tables for each age category, we would type

```
. by agecat, sort: tabulate birthcat region
```

```
-> agecat = 19-29
```

	Census Region				
birthcat	NE	N Cntrl	South	West	Total
29-136	11	23	11	11	56
137-195	31	97	65	46	239
196-529	4	38	59	91	192
Total	46	158	135	148	487

```
-> agecat = 30-34
```

	Census Region				
birthcat	NE	N Cntrl	South	West	Total
29-136	34	27	10	8	79
137-195	48	58	45	42	193
196-529	1	3	12	21	37
Total	83	88	67	71	309

```
-> agecat = 35+
```

birthcat	Census Region NE	N Cntrl	South	West	Total
29-136	34	26	27	18	105
137-195	3	4	7	4	18
196-529	0	0	4	0	4
Total	37	30	38	22	127

❑

Weighted data

▷ Example 4

`tabulate` can process weighted as well as unweighted data. As with all Stata commands, we indicate the weight by specifying the [*weight*] modifier; see [U] **11.1.6 weight**.

Continuing with our dataset of 956 cities, we also have a variable called `pop`, the population of each city. We can make a table of region by age category, weighted by population, by typing

```
. tabulate region agecat [freq=pop]
```

Census Region	agecat 19-29	30-34	35+	Total
NE	4,721,387	10,421,387	5,323,610	20,466,384
N Cntrl	16,901,550	8,964,756	4,015,593	29,881,899
South	13,894,254	7,686,531	4,141,863	25,722,648
West	16,698,276	7,755,255	2,375,118	26,828,649
Total	52,215,467	34,827,929	15,856,184	102899580

If we specify the `cell`, `column`, or `row` options, they will also be appropriately weighted. Below we repeat the table, suppressing the counts and substituting row percentages:

```
. tabulate region agecat [freq=pop], nofreq row
```

Census Region	agecat 19-29	30-34	35+	Total
NE	23.07	50.92	26.01	100.00
N Cntrl	56.56	30.00	13.44	100.00
South	54.02	29.88	16.10	100.00
West	62.24	28.91	8.85	100.00
Total	50.74	33.85	15.41	100.00

◁

Tables with immediate data

▷ Example 5

`tabi` ignores the dataset in memory and uses as the table the values that we specify on the command line:

```
. tabi 30 18 \ 38 14
```

row	col 1	2	Total
1	30	18	48
2	38	14	52
Total	68	32	100

```
          Fisher's exact =                 0.289
  1-sided Fisher's exact =                 0.179
```

We may specify any of the options of `tabulate` and are not limited to 2×2 tables:

```
. tabi 30 18 38 \ 13 7 22, chi2 exact
Enumerating sample-space combinations:
stage 3:  enumerations = 1
stage 2:  enumerations = 3
stage 1:  enumerations = 0
```

row	col 1	2	3	Total
1	30	18	38	86
2	13	7	22	42
Total	43	25	60	128

```
       Pearson chi2(2) =   0.7967   Pr = 0.671
        Fisher's exact =                 0.707
. tabi 30 13 \ 18 7 \ 38 22, all exact col
```

Key
frequency *column percentage*

```
Enumerating sample-space combinations:
stage 3:  enumerations = 1
stage 2:  enumerations = 3
stage 1:  enumerations = 0
```

row	col 1	2	Total
1	30	13	43
	34.88	30.95	33.59
2	18	7	25
	20.93	16.67	19.53
3	38	22	60
	44.19	52.38	46.88
Total	86	42	128
	100.00	100.00	100.00

```
          Pearson chi2(2) =   0.7967   Pr = 0.671
 likelihood-ratio chi2(2) =   0.7985   Pr = 0.671
               Cramer's V =   0.0789
                    gamma =   0.1204  ASE = 0.160
          Kendall's tau-b =   0.0630  ASE = 0.084
           Fisher's exact =                 0.707
```

For 2 × 2 tables, both one- and two-sided Fisher's exact probabilities are displayed; this is true of both `tabulate` and `tabi`. See *Cumulative incidence data* and *Case–control data* in [ST] **epitab** for more discussion on the relationship between one- and two-sided probabilities.

◁

❑ Technical note

`tabi`, as with all immediate commands, leaves any data in memory undisturbed. With the `replace` option, however, the data in memory are replaced by the data from the table:

```
. tabi 30 18 \ 38 14, replace
           |        col
       row |         1          2 |     Total
-----------+----------------------+----------
         1 |        30         18 |        48
         2 |        38         14 |        52
-----------+----------------------+----------
     Total |        68         32 |       100

          Fisher's exact =                 0.289
  1-sided Fisher's exact =                 0.179
. list

     +-----------------+
     | row   col   pop |
     |-----------------|
  1. |   1     1    30 |
  2. |   1     2    18 |
  3. |   2     1    38 |
  4. |   2     2    14 |
     +-----------------+
```

With this dataset, you could re-create the above table by typing

```
. tabulate row col [freq=pop], exact
           |        col
       row |         1          2 |     Total
-----------+----------------------+----------
         1 |        30         18 |        48
         2 |        38         14 |        52
-----------+----------------------+----------
     Total |        68         32 |       100

          Fisher's exact =                 0.289
  1-sided Fisher's exact =                 0.179
```

❑

tab2

tab2 is a convenience tool. Typing

```
. tab2 myvar thisvar thatvar, chi2
```

is equivalent to typing

```
. tabulate myvar thisvar, chi2
. tabulate myvar thatvar, chi2
. tabulate thisvar thatvar, chi2
```

Saved results

tabulate, tab2, and tabi save the following in r():

Scalars

r(N)	number of observations	r(p_exact)	Fisher's exact p
r(r)	number of rows	r(chi2_lr)	likelihood-ratio χ^2
r(c)	number of columns	r(p_lr)	significance of likelihood-ratio χ^2
r(chi2)	Pearson's χ^2	r(CramersV)	Cramér's V
r(p)	significance of Pearson's χ^2	r(ase_gam)	ASE of gamma
r(gamma)	gamma	r(ase_taub)	ASE of τ_{b}
r(p1_exact)	one-sided Fisher's exact p	r(taub)	τ_{b}

r(p1_exact) is defined only for 2×2 tables. Also, the matrow(), matcol(), and matcell() options allow you to obtain the row values, column values, and frequencies, respectively.

Methods and formulas

tab2 and tabi are implemented as ado-files.

Let n_{ij}, $i = 1, \ldots, I$ and $j = 1, \ldots, J$, be the number of observations in the ith row and jth column. If the data are not weighted, n_{ij} is just a count. If the data are weighted, n_{ij} is the sum of the weights of all data corresponding to the (i, j) cell.

Define the row and column marginals as

$$n_{i\cdot} = \sum_{j=1}^{J} n_{ij} \qquad\qquad n_{\cdot j} = \sum_{i=1}^{I} n_{ij}$$

and let $n = \sum_i \sum_j n_{ij}$ be the overall sum. Also, define the concordance and discordance as

$$A_{ij} = \sum_{k>i}\sum_{l>j} n_{kl} + \sum_{k<i}\sum_{l<j} n_{kl} \qquad\qquad D_{ij} = \sum_{k>i}\sum_{l<j} n_{kl} + \sum_{k<i}\sum_{l>j} n_{kl}$$

along with twice the number of concordances $P = \sum_i \sum_j n_{ij} A_{ij}$ and twice the number of discordances $Q = \sum_i \sum_j n_{ij} D_{ij}$.

The Pearson χ^2 statistic with $(I-1)(J-1)$ degrees of freedom (so called because it is based on Pearson (1900); see Conover [1999, 240] and Fienberg [1980, 9]) is defined as

$$X^2 = \sum_i \sum_j \frac{(n_{ij} - m_{ij})^2}{m_{ij}}$$

where $m_{ij} = n_{i\cdot} n_{\cdot j} / n$.

The likelihood-ratio χ^2 statistic with $(I-1)(J-1)$ degrees of freedom (Fienberg 1980, 40) is defined as

$$G^2 = 2\sum_i \sum_j n_{ij} \ln(n_{ij}/m_{ij})$$

Cramér's V (Cramér 1946) is a measure of association designed so that the attainable upper bound is 1. For 2×2 tables, $-1 \leq V \leq 1$, and otherwise, $0 \leq V \leq 1$.

$$V = \begin{cases} (n_{11}n_{22} - n_{12}n_{21})/(n_{1\cdot}n_{2\cdot}n_{\cdot 1}n_{\cdot 2})^{1/2} & \text{for } 2 \times 2 \\ \left\{(X^2/n)/\min(I-1, J-1)\right\}^{1/2} & \text{otherwise} \end{cases}$$

Gamma (Goodman and Kruskal 1954, 1959, 1963, 1972; also see Agresti [2010,186–188]) ignores tied pairs and is based only on the number of concordant and discordant pairs of observations, $-1 \leq \gamma \leq 1$,

$$\gamma = (P-Q)/(P+Q)$$

with asymptotic variance

$$16\sum_i \sum_j n_{ij}(QA_{ij} - PD_{ij})^2/(P+Q)^4$$

Kendall's τ_b (Kendall 1945; also see Agresti 2010, 188–189), $-1 \leq \tau_b \leq 1$, is similar to gamma, except that it uses a correction for ties,

$$\tau_b = (P-Q)/(w_r w_c)^{1/2}$$

with asymptotic variance

$$\frac{\sum_i \sum_j n_{ij}(2w_r w_c d_{ij} + \tau_b v_{ij})^2 - n^3 \tau_b^2 (w_r + w_c)^2}{(w_r w_c)^4}$$

where

$$\begin{aligned} w_r &= n^2 - \sum_i n_{i\cdot}^2 \\ w_c &= n^2 - \sum_j n_{\cdot j}^2 \\ d_{ij} &= A_{ij} - D_{ij} \\ v_{ij} &= n_{i\cdot} w_c + n_{\cdot j} w_r \end{aligned}$$

Fisher's exact test (Fisher 1935; Finney 1948; see Zelterman and Louis [1992, 293–301] for the 2×2 case) yields the probability of observing a table that gives at least as much evidence of association as the one actually observed under the assumption of no association. Holding row and column marginals fixed, the hypergeometric probability P of every possible table A is computed, and the

$$P = \sum_{T \in A} \Pr(T)$$

where A is the set of all tables with the same marginals as the observed table, T^*, such that $\Pr(T) \leq \Pr(T^*)$. For 2×2 tables, the one-sided probability is calculated by further restricting A to tables in the same tail as T^*. The first algorithm extending this calculation to $r \times c$ tables was Pagano and Halvorsen (1981); the one implemented here is the FEXACT algorithm by Mehta and Patel (1986). This is a search-tree clipping method originally published by Mehta and Patel (1983) with further refinements by Joe (1988) and Clarkson, Fan, and Joe (1993). Fisher's exact test is a permutation test. For more information on permutation tests, see Good (2005 and 2006) and Pesarin (2001).

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Also see

[R] **table** — Tables of summary statistics

[R] **tabstat** — Display table of summary statistics

[R] **tabulate oneway** — One-way tables of frequencies

[R] **tabulate, summarize()** — One- and two-way tables of summary statistics

[D] **collapse** — Make dataset of summary statistics

[ST] **epitab** — Tables for epidemiologists

[SVY] **svy: tabulate oneway** — One-way tables for survey data

[SVY] **svy: tabulate twoway** — Two-way tables for survey data

[XT] **xttab** — Tabulate xt data

[U] **12.6.3 Value labels**

[U] **25 Working with categorical data and factor variables**

Title

tabulate, summarize() — One- and two-way tables of summary statistics

Syntax

`tabulate` *varname*$_1$ [*varname*$_2$] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`summarize(`*varname*$_3$`)`	report summary statistics for *varname*$_3$
[`no`]`means`	include or suppress means
[`no`]`standard`	include or suppress standard deviations
[`no`]`freq`	include or suppress frequencies
[`no`]`obs`	include or suppress number of observations
`nolabel`	show numeric codes, not labels
`wrap`	do not break wide tables
`missing`	treat missing values of *varname*$_1$ and *varname*$_2$ as categories

`by` is allowed; see [D] **by**.

`aweights` and `fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Tables > One/two-way table of summary statistics

Description

`tabulate, summarize()` produces one- and two-way tables (breakdowns) of means and standard deviations. See [R] **tabulate oneway** and [R] **tabulate twoway** for one- and two-way frequency tables. See [R] **table** for a more flexible command that produces one-, two-, and n-way tables of frequencies and a wide variety of summary statistics. `table` is better, but `tabulate, summarize()` is faster. Also see [R] **tabstat** for yet another alternative.

Options

Main

`summarize(`*varname*$_3$`)` identifies the name of the variable for which summary statistics are to be reported. If you do not specify this option, a table of frequencies is produced; see [R] **tabulate oneway** and [R] **tabulate twoway**. The description here concerns `tabulate` when this option is specified.

[no]means includes or suppresses only the means from the table.

The summarize() table normally includes the mean, standard deviation, frequency, and, if the data are weighted, number of observations. Individual elements of the table may be included or suppressed by the [no]means, [no]standard, [no]freq, and [no]obs options. For example, typing

```
. tabulate category, summarize(myvar) means standard
```

produces a summary table by category containing only the means and standard deviations of myvar. You could also achieve the same result by typing

```
. tabulate category, summarize(myvar) nofreq
```

[no]standard includes or suppresses only the standard deviations from the table; see [no]means option above.

[no]freq includes or suppresses only the frequencies from the table; see [no]means option above.

[no]obs includes or suppresses only the reported number of observations from the table. If the data are not weighted, the number of observations is identical to the frequency, and by default only the frequency is reported. If the data are weighted, the frequency refers to the sum of the weights. See [no]means option above.

nolabel causes the numeric codes to be displayed rather than the label values.

wrap requests that no action be taken on wide tables to make them readable. Unless wrap is specified, wide tables are broken into pieces to enhance readability.

missing requests that missing values of *varname*$_1$ and *varname*$_2$ be treated as categories rather than as observations to be omitted from the analysis.

Remarks

tabulate with the summarize() option produces one- and two-way tables of summary statistics. When combined with the by prefix, it can produce n-way tables as well.

Remarks are presented under the following headings:

One-way tables
Two-way tables

One-way tables

▷ Example 1

We have data on 74 automobiles. Included in our dataset are the variables foreign, which marks domestic and foreign cars, and mpg, the car's mileage rating. Typing tabulate foreign displays a breakdown of the number of observations we have by the values of the foreign variable.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. tabulate foreign
   Car type |      Freq.     Percent        Cum.
------------+-----------------------------------
   Domestic |         52       70.27       70.27
    Foreign |         22       29.73      100.00
------------+-----------------------------------
      Total |         74      100.00
```

We discover that we have 52 domestic cars and 22 foreign cars in our dataset. If we add the `summarize(`*varname*`)` option, however, `tabulate` produces a table of summary statistics for *varname*:

```
. tabulate foreign, summarize(mpg)
```

Car type	Summary of Mileage (mpg) Mean	Std. Dev.	Freq.
Domestic	19.826923	4.7432972	52
Foreign	24.772727	6.6111869	22
Total	21.297297	5.7855032	74

We also discover that the average gas mileage for domestic cars is about 20 mpg and the average foreign is almost 25 mpg. Overall, the average is 21 mpg in our dataset.

◁

❑ Technical note

We might now wonder if the difference in gas mileage between foreign and domestic cars is statistically significant. We can use the `oneway` command to find out; see [R] **oneway**. To obtain an analysis-of-variance table of `mpg` on `foreign`, we type

```
. oneway mpg foreign
```

Source	Analysis of Variance SS	df	MS	F	Prob > F
Between groups	378.153515	1	378.153515	13.18	0.0005
Within groups	2065.30594	72	28.6848048		
Total	2443.45946	73	33.4720474		

```
Bartlett's test for equal variances:  chi2(1) =   3.4818  Prob>chi2 = 0.062
```

The F statistic is 13.18, and the difference between foreign and domestic cars' mileage ratings is significant at the 0.05% level.

There are several ways that we could have statistically compared mileage ratings—see, for instance, [R] **anova**, [R] **oneway**, [R] **regress**, and [R] **ttest**—but `oneway` seemed the most convenient.

❑

Two-way tables

▷ Example 2

`tabulate, summarize` can be used to obtain two-way as well as one-way breakdowns. For instance, we obtained summary statistics on `mpg` decomposed by `foreign` by typing `tabulate foreign, summarize(mpg)`. We can specify up to two variables before the comma:

```
. generate wgtcat = autocode(weight,4,1760,4840)
. tabulate wgtcat foreign, summarize(mpg)
        Means, Standard Deviations and Frequencies of Mileage (mpg)
```

wgtcat	Car type Domestic	Foreign	Total
2530	28.285714	27.0625	27.434783
	3.0937725	5.9829619	5.2295149
	7	16	23
3300	21.75	19.6	21.238095
	2.4083189	3.4351128	2.7550819
	16	5	21
4070	17.26087	14	17.125
	1.8639497	0	1.9406969
	23	1	24
4840	14.666667	.	14.666667
	3.32666	.	3.32666
	6	0	6
Total	19.826923	24.772727	21.297297
	4.7432972	6.6111869	5.7855032
	52	22	74

In addition to the means, standard deviations, and frequencies for each weight–mileage cell, also reported are the summary statistics by weight, by mileage, and overall. For instance, the last row of the table reveals that the average mileage of domestic cars is 19.83 and that of foreign cars is 24.77—domestic cars yield poorer mileage than foreign cars. But we now see that domestic cars yield better gas mileage within weight class—the reason domestic cars yield poorer gas mileage is because they are, on average, heavier.

◁

▷ Example 3

If we do not specify the statistics to be included in a table, `tabulate` reports the mean, standard deviation, and frequency. We can specify the statistics that we want to see using the `means`, `standard`, and `freq` options:

```
. tabulate wgtcat foreign, summarize(mpg) means
                        Means of Mileage (mpg)
```

wgtcat	Car type Domestic	Foreign	Total
2530	28.285714	27.0625	27.434783
3300	21.75	19.6	21.238095
4070	17.26087	14	17.125
4840	14.666667	.	14.666667
Total	19.826923	24.772727	21.297297

When we specify one or more of the `means`, `standard`, and `freq` options, only those statistics are displayed. Thus we could obtain a table containing just the means and standard deviations by typing `means standard` after the `summarize(mpg)` option. We can also suppress selected statistics by placing `no` in front of the option name. Another way of obtaining only the means and standard deviations is to add the `nofreq` option:

```
. tabulate wgtcat foreign, summarize(mpg) nofreq
```

Means and Standard Deviations of Mileage (mpg)

wgtcat	Car type Domestic	Foreign	Total
2530	28.285714 3.0937725	27.0625 5.9829619	27.434783 5.2295149
3300	21.75 2.4083189	19.6 3.4351128	21.238095 2.7550819
4070	17.26087 1.8639497	14 0	17.125 1.9406969
4840	14.666667 3.32666	. .	14.666667 3.32666
Total	19.826923 4.7432972	24.772727 6.6111869	21.297297 5.7855032

Also see

[R] **table** — Tables of summary statistics

[R] **tabstat** — Display table of summary statistics

[R] **tabulate oneway** — One-way tables of frequencies

[R] **tabulate twoway** — Two-way tables of frequencies

[D] **collapse** — Make dataset of summary statistics

[SVY] **svy: tabulate oneway** — One-way tables for survey data

[SVY] **svy: tabulate twoway** — Two-way tables for survey data

[U] **12.6 Dataset, variable, and value labels**

[U] **25 Working with categorical data and factor variables**

Title

test — Test linear hypotheses after estimation

Syntax

Basic syntax

`test` *coeflist* (*Syntax 1*)

`test` *exp*`=`*exp*`[=...]` (*Syntax 2*)

`test [`*eqno*`]` `[:` *coeflist*`]` (*Syntax 3*)

`test [`*eqno*`=`*eqno*`[=...]]` `[:` *coeflist*`]` (*Syntax 4*)

`testparm` *varlist* `[, equal equation(`*eqno*`)]`

Full syntax

`test (`*spec*`)` `[(`*spec*`) ...]` `[,` *test_options*`]`

test_options	Description
Options	
`mtest[(`*opt*`)]`	test each condition separately
`coef`	report estimated constrained coefficients
`accumulate`	test hypothesis jointly with previously tested hypotheses
`notest`	suppress the output
`common`	test only variables common to all the equations
`constant`	include the constant in coefficients to be tested
`nosvyadjust`	compute unadjusted Wald tests for survey results
`minimum`	perform test with the constant, drop terms until the test becomes nonsingular, and test without the constant on the remaining terms; highly technical
`matvlc(`*matname*`)`	save the variance–covariance matrix; programmer's option

coeflist and *varlist* may contain factor variables and time-series operators; see [U] **11.4.3 Factor variables** and [U] **11.4.4 Time-series varlists**.

`matvlc(`*matname*`)` does not appear in the dialog box.

Syntax 1 tests that coefficients are 0.

Syntax 2 tests that linear expressions are equal.

Syntax 3 tests that coefficients in *eqno* are 0.

Syntax 4 tests equality of coefficients between equations.

spec is one of

coeflist
exp=*exp* [=*exp*]
[*eqno*] [: *coeflist*]
[*eqno*$_1$=*eqno*$_2$ [=...]] [: *coeflist*]

coeflist is

coef [*coef* ...]
[*eqno*]*coef* [[*eqno*]*coef*...]
[*eqno*] _b[*coef*] [[*eqno*] _b[*coef*]...]

exp is a linear expression containing

coef
_b[*coef*]
_b[*eqno*:*coef*]
[*eqno*]*coef*
[*eqno*] _b[*coef*]

eqno is

##
name

coef identifies a coefficient in the model. *coef* is typically a variable name, a level indicator, an interaction indicator, or an interaction involving continuous variables. Level indicators identify one level of a factor variable and interaction indicators identify one combination of levels of an interaction; see [U] **11.4.3 Factor variables**. *coef* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

Although not shown in the syntax diagram, parentheses around *spec* are required only with multiple specifications. Also, the diagram does not show that `test` may be called without arguments to redisplay the results from the last `test`.

`anova` and `manova` (see [R] **anova** and [MV] **manova**) allow the `test` syntax above plus more (see [R] **anova postestimation** for `test` after `anova`; see [MV] **manova postestimation** for `test` after `manova`).

Menu

test

Statistics > Postestimation > Tests > Test linear hypotheses

testparm

Statistics > Postestimation > Tests > Test parameters

Description

`test` performs Wald tests of simple and composite linear hypotheses about the parameters of the most recently fit model.

`test` supports `svy` estimators (see [SVY] **svy estimation**), carrying out an adjusted Wald test by default in such cases. `test` can be used with `svy` estimation results, see [SVY] **svy postestimation**.

`testparm` provides a useful alternative to `test` that permits *varlist* rather than a list of coefficients (which is often nothing more than a list of variables), allowing the use of standard Stata notation, including '`-`' and '`*`', which are given the *exp*ression interpretation by `test`.

`test` and `testparm` perform Wald tests. For likelihood-ratio tests, see [R] **lrtest**. For Wald-type tests of nonlinear hypotheses, see [R] **testnl**. To display estimates for one-dimensional linear or nonlinear expressions of coefficients, see [R] **lincom** and [R] **nlcom**.

See [R] **anova postestimation** for additional `test` syntax allowed after `anova`.

See [MV] **manova postestimation** for additional `test` syntax allowed after `manova`.

Options for testparm

`equal` tests that the variables appearing in *varlist*, which also appear in the previously fit model, are equal to each other rather than jointly equal to zero.

`equation(`*eqno*`)` is relevant only for multiple-equation models, such as `mvreg`, `mlogit`, and `heckman`. It specifies the equation for which the all-zero or all-equal hypothesis is tested. `equation(#1)` specifies that the test be conducted regarding the first equation `#1`. `equation(price)` specifies that the test concern the equation named `price`.

Options for test

Options

`mtest`$\left[\right.$`(`*opt*`)`$\left.\right]$ specifies that tests be performed for each condition separately. *opt* specifies the method for adjusting p-values for multiple testing. Valid values for *opt* are

`bonferroni`	Bonferroni's method
`holm`	Holm's method
`sidak`	Šidák's method
`noadjust`	no adjustment is to be made

Specifying `mtest` without an argument is equivalent to `mtest(noadjust)`.

`coef` specifies that the constrained coefficients be displayed.

`accumulate` allows a hypothesis to be tested jointly with the previously tested hypotheses.

`notest` suppresses the output. This option is useful when you are interested only in the joint test of several hypotheses, specified in a subsequent call of `test, accumulate`.

`common` specifies that when you use the [*eqno*$_1$`=`*eqno*$_2$$\left[\right.$`=`...$\left.\right]$`]` form of *spec*, the variables common to the equations *eqno*$_1$, *eqno*$_2$, etc., be tested. The default action is to complain if the equations have variables not in common.

`constant` specifies that `_cons` be included in the list of coefficients to be tested when using the [*eqno*$_1$`=`*eqno*$_2$$\left[\right.$`=`...$\left.\right]$`]` or [*eqno*] forms of *spec*. The default is not to include `_cons`.

`nosvyadjust` is for use with `svy` estimation commands; see [SVY] **svy estimation**. It specifies that the Wald test be carried out without the default adjustment for the design degrees of freedom. That is, the test is carried out as $W/k \sim F(k,d)$ rather than as $(d-k+1)W/(kd) \sim F(k,d-k+1)$, where k = the dimension of the test and d = the total number of sampled PSUs minus the total number of strata.

`minimum` is a highly technical option. It first performs the test with the constant added. If this test is singular, coefficients are dropped until the test becomes nonsingular. Then the test without the constant is performed with the remaining terms.

The following option is available with `test` but is not shown in the dialog box:

`matvlc(`*matname*`)`, a programmer's option, saves the variance–covariance matrix of the linear combinations involved in the suite of tests. For the test of the linear constraints $Lb = c$, *matname* contains $L\mathbf{V}L'$, where $\mathbf{V}$ is the estimated variance–covariance matrix of b.

Remarks

Remarks are presented under the following headings:

Introductory examples
Special syntaxes after multiple-equation estimation
Constrained coefficients
Multiple testing

Introductory examples

`test` performs F or χ^2 tests of linear restrictions applied to the most recently fit model (for example, `regress` or `svy: regress` in the linear regression case; `logit`, `stcox`, `svy: logit`, ... in the single-equation maximum-likelihood case; and `mlogit`, `mvreg`, `streg`, ... in the multiple-equation maximum-likelihood case). `test` may be used after *any* estimation command, although for maximum likelihood techniques, `test` produces a Wald test that depends only on the estimate of the covariance matrix—you may prefer to use the more computationally expensive likelihood-ratio test; see [U] **20 Estimation and postestimation commands** and [R] **lrtest**.

There are several variations on the syntax for `test`. The second syntax,

`test` *exp*=*exp*[`=`...]

is allowed after any form of estimation. After fitting a model of *depvar* on `x1`, `x2`, and `x3`, typing `test x1+x2=x3` tests the restriction that the coefficients on `x1` and `x2` sum to the coefficient on `x3`. The expressions can be arbitrarily complicated; for instance, typing `test x1+2*(x2+x3)=x2+3*x3` is the same as typing `test x1+x2=x3`.

As a convenient shorthand, `test` also allows you to specify equality for multiple expressions; for example, `test x1+x2 = x3+x4 = x5+x6` tests that the three specified pairwise sums of coefficients are equal.

`test` understands that when you type `x1`, you are referring to the coefficient on `x1`. You could also more explicitly type `test _b[x1]+_b[x2]=_b[x3]`; or you could `test _coef[x1]+_coef[x2]=_coef[x3]`, or `test [#1]x1+[#1]x2=[#1]x3`, or many other things because there is more than one way to refer to an estimated coefficient; see [U] **13.5 Accessing coefficients and standard errors**. The shorthand involves less typing. On the other hand, you must be more explicit after estimation of multiple-equation models because there may be more than one coefficient associated

with an independent variable. You might type, for instance, `test [#2]x1+[#2]x2=[#2]x3` to test the constraint in equation 2 or, more readably, `test [ford]x1+[ford]x2=[ford]x3`, meaning that Stata will test the constraint on the equation corresponding to `ford`, which might be equation 2. `ford` would be an equation name after, say, `sureg`, or, after `mlogit`, `ford` would be one of the outcomes. For `mlogit`, you could also type `test [2]x1+[2]x2=[2]x3`—note the lack of the `#`—meaning not equation 2, but the equation corresponding to the numeric outcome 2. You can even test constraints across equations: `test [ford]x1+[ford]x2=[buick]x3`.

The syntax

`test` *coeflist*

is available after all estimation commands and is a convenient way to test that multiple coefficients are zero following estimation. A *coeflist* can simply be a list of variable names,

`test` *varname* [*varname* ...]

and it is most often specified that way. After you have fit a model of `depvar` on `x1`, `x2`, and `x3`, typing `test x1 x3` tests that the coefficients on `x1` and `x3` are jointly zero. After multiple-equation estimation, this would test that the coefficients on `x1` and `x3` are zero in all equations that contain them. You can also be more explicit and type, for instance, `test [ford]x1 [ford]x3` to test that the coefficients on `x1` and `x3` are zero in the equation for `ford`.

In the multiple-equation case, there are more alternatives. You could also test that the coefficients on `x1` and `x3` are zero in the equation for `ford` by typing `test [ford]: x1 x3`. You could test that all coefficients except the coefficient on the constant are zero in the equation for `ford` by typing `test [ford]`. You could test that the coefficients on `x1` and `x3` in the equation for `ford` are equal to the corresponding coefficients in the equation corresponding to `buick` by typing `test[ford=buick]: x1 x3`. You could test that all the corresponding coefficients except the constant in three equations are equal by typing `test [ford=buick=volvo]`.

`testparm` is much like the first syntax of `test`. Its usefulness will be demonstrated below.

The examples below use `regress`, but what is said applies equally after any single-equation estimation command (such as `logistic`). It also applies after multiple-equation estimation commands as long as references to coefficients are qualified with an equation name or number in square brackets placed before them. The convenient syntaxes for dealing with tests of many coefficients in multiple-equation models are demonstrated in *Special syntaxes after multiple-equation estimation* below.

▷ Example 1

We have 1980 census data on the 50 states recording the birth rate in each state (`brate`), the median age (`medage`), and the region of the country in which each state is located.

The `region` variable is 1 if the state is in the Northeast, 2 if the state is in the North Central, 3 if the state is in the South, and 4 if the state is in the West. We estimate the following regression:

```
. use http://www.stata-press.com/data/r12/census3
(1980 Census data by state)
. regress brate medage c.medage#c.medage i.region
      Source |       SS       df       MS              Number of obs =      50
-------------+------------------------------           F(  5,    44) =  100.63
       Model |  38803.4208     5  7760.68416            Prob > F      =  0.0000
    Residual |  3393.39921    44  77.1227094            R-squared     =  0.9196
-------------+------------------------------           Adj R-squared =  0.9104
       Total |   42196.82    49  861.159592            Root MSE      =   8.782

------------------------------------------------------------------------------
       brate |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      medage |  -109.0958   13.52452    -8.07   0.000    -136.3527   -81.83892
             |
  c.medage#  |
  c.medage |   1.635209   .2290536     7.14   0.000     1.173582    2.096836
             |
      region |
          2  |   15.00283   4.252067     3.53   0.001     6.433353    23.57231
          3  |   7.366445   3.953335     1.86   0.069    -.6009775    15.33387
          4  |   21.39679   4.650601     4.60   0.000     12.02412    30.76946
             |
       _cons |   1947.611   199.8405     9.75   0.000     1544.859    2350.363
------------------------------------------------------------------------------
```

`test` can now be used to perform a variety of statistical tests. Specify the `coeflegend` option with your estimation command to see a legend of the coefficients and how to specify them; see [R] **estimation options**. We can test the hypothesis that the coefficient on `3.region` is zero by typing

```
. test 3.region=0
 ( 1)  3.region = 0
       F(  1,    44) =    3.47
            Prob > F =    0.0691
```

The F statistic with 1 numerator and 44 denominator degrees of freedom is 3.47. The significance level of the test is 6.91%—we can reject the hypothesis at the 10% level but not at the 5% level.

This result from `test` is identical to one presented in the output from `regress`, which indicates that the t statistic on the `3.region` coefficient is 1.863 and that its significance level is 0.069. The t statistic presented in the output can be used to test the hypothesis that the corresponding coefficient is zero, although it states the test in slightly different terms. The F distribution with 1 numerator degree of freedom is, however, identical to the t^2 distribution. We note that $1.863^2 \approx 3.47$ and that the significance levels in each test agree, although one extra digit is presented by the `test` command.

◁

❑ Technical note

After all estimation commands, including those that use the maximum likelihood method, the test that one variable is zero is identical to that reported by the command's output. The tests are performed in the same way—using the estimated covariance matrix—and are known as Wald tests. If the estimation command reports significance levels and confidence intervals using z rather than t statistics, `test` reports results using the χ^2 rather than the F statistic.

❑

▷ Example 2

If that were all `test` could do, it would be useless. We can use `test`, however, to perform other tests. For instance, we can `test` the hypothesis that the coefficient on `2.region` is 21 by typing

```
. test 2.region=21
 ( 1)  2.region = 21
       F(  1,    44) =    1.99
            Prob > F =    0.1654
```

We find that we cannot reject that hypothesis, or at least we cannot reject it at any significance level below 16.5%.

◁

▷ Example 3

The previous test is useful, but we could almost as easily perform it by hand using the results presented in the regression output if we were well read on our statistics. We could type

```
. display Ftail(1,44,((_coef[2.region]-21)/4.252068)^2)
.16544873
```

So, now let's `test` something a bit more difficult: whether the coefficient on `2.region` is the same as the coefficient on `4.region`:

```
. test 2.region=4.region
 ( 1)  2.region - 4.region = 0
       F(  1,    44) =    2.84
            Prob > F =    0.0989
```

We find that we cannot reject the equality hypothesis at the 5% level, but we can at the 10% level.

◁

▷ Example 4

When we tested the equality of the `2.region` and `4.region` coefficients, Stata rearranged our algebra. When Stata displayed its interpretation of the specified test, it indicated that we were testing whether `2.region` *minus* `4.region` is zero. The rearrangement is innocuous and, in fact, allows Stata to perform much more complicated algebra, for instance,

```
. test 2*(2.region-3*(3.region-4.region))=3.region+2.region+6*(4.region-3.region)
 ( 1)  2.region - 3.region = 0
       F(  1,    44) =    5.06
            Prob > F =    0.0295
```

Although we requested what appeared to be a lengthy hypothesis, once Stata simplified the algebra, it realized that all we wanted to do was test whether the coefficient on `2.region` is the same as the coefficient on `3.region`.

◁

❑ Technical note

Stata's ability to simplify and test complex hypotheses is limited to *linear* hypotheses. If you attempt to `test` a nonlinear hypothesis, you will be told that it is not possible:

```
. test 2.region/3.region=2.region+3.region
not possible with test
r(131);
```

To test a nonlinear hypothesis, see [R] **testnl**.

❑

▷ Example 5

The real power of `test` is demonstrated when we test *joint* hypotheses. Perhaps we wish to test whether the region variables, taken as a whole, are significant by testing whether the coefficients on `2.region`, `3.region`, and `4.region` are simultaneously zero. `test` allows us to specify multiple conditions to be tested, each embedded within parentheses.

```
. test (2.region=0) (3.region=0) (4.region=0)
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

`test` displays the set of conditions and reports an F statistic of 8.85. `test` also reports the degrees of freedom of the test to be 3, the "dimension" of the hypothesis, and the residual degrees of freedom, 44. The significance level of the test is close to 0, so we can strongly reject the hypothesis of no difference between the regions.

An alternative method to specify simultaneous hypotheses uses the convenient shorthand of conditions with multiple equality operators.

```
. test 2.region=3.region=4.region=0
 ( 1)  2.region - 3.region = 0
 ( 2)  2.region - 4.region = 0
 ( 3)  2.region = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

◁

❑ Technical note

Another method to test simultaneous hypotheses is to specify a `test` for each constraint and `accumulate` it with the previous constraints:

```
. test 2.region=0
 ( 1)  2.region = 0
       F(  1,    44) =   12.45
            Prob > F =    0.0010
. test 3.region=0, accumulate
 ( 1)  2.region = 0
 ( 2)  3.region = 0
       F(  2,    44) =    6.42
            Prob > F =    0.0036
. test 4.region=0, accumulate
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

We tested the hypothesis that the coefficient on `2.region` was zero by typing `test 2.region=0`. We then tested whether the coefficient on `3.region` was also zero by typing `test 3.region=0, accumulate`. The `accumulate` option told Stata that this was not the start of a new test but a continuation of a previous one. Stata responded by showing us the two equations and reporting an F statistic of 6.42. The significance level associated with those two coefficients being zero is 0.36%.

When we added the last constraint `test 4.region=0, accumulate`, we discovered that the three region variables are significant. If all we wanted was the overall significance and we did not want to bother seeing the interim results, we could have used the `notest` option:

```
. test 2.region=0, notest
 ( 1)  2.region = 0
. test 3.region=0, accumulate notest
 ( 1)  2.region = 0
 ( 2)  3.region = 0
. test 4.region=0, accumulate
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

❑

▷ Example 6

Because tests that coefficients are zero are so common in applied statistics, the `test` command has a more convenient syntax to accommodate this case:

```
. test 2.region 3.region 4.region
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

◁

▷ Example 7

We will now show how to use `testparm`. In its first syntax, `test` accepts a list of variable names but not a *varlist*.

```
. test i(2/4).region
i not found
r(111);
```

In the varlist, `i(2/4).region` means all the level variables from `2.region` through `4.region`, yet we received an error. `test` does not actually understand varlists, but `testparm` does. In fact, it understands only varlists.

```
. testparm i(2/4).region
 ( 1)  2.region = 0
 ( 2)  3.region = 0
 ( 3)  4.region = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

Another way to test all the `region` variables is to type `testparm i.region`.

That `testparm` accepts varlists has other advantages that do not involve factor variables. Suppose that we have a dataset that has dummy variables `reg2`, `reg3`, and `reg4`, rather than the categorical variable `region`.

```
. use http://www.stata-press.com/data/r12/census4
(birth rate, median age)
. regress brate medage c.medage#c.medage reg2 reg3 reg4
  (output omitted)
. test reg2-reg4
- not found
r(111);
```

In a varlist, `reg2-reg4` means variables `reg2` and `reg4` and all the variables between, yet we received an error. `test` is confused because the `-` has two meanings: it means subtraction in an expression and "through" in a *varlist*. Similarly, '`*`' means "any set of characters" in a *varlist* and multiplication in an expression. `testparm` avoids this confusion—it allows only a *varlist*.

```
. testparm reg2-reg4
 ( 1)  reg2 = 0
 ( 2)  reg3 = 0
 ( 3)  reg4 = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

`testparm` has another advantage. We have five variables in our dataset that start with the characters `reg`: `region`, `reg1`, `reg2`, `reg3`, and `reg4`. `reg*` thus means those five variables:

```
. describe reg*
              storage  display     value
variable name   type   format      label      variable label
------------------------------------------------------------------------------
region          int    %8.0g       region     Census Region
reg1            byte   %9.0g                  region==NE
reg2            byte   %9.0g                  region==N Cntrl
reg3            byte   %9.0g                  region==South
reg4            byte   %9.0g                  region==West
```

We cannot type `test reg*` because, in an expression, '`*`' means multiplication, but here is what would happen if we attempted to test all the variables that begin with `reg`:

```
. test region reg1 reg2 reg3 reg4
region not found
r(111);
```

The variable `region` was not included in our model, so it was not found. However, with `testparm`,

```
. testparm reg*
 ( 1)  reg2 = 0
 ( 2)  reg3 = 0
 ( 3)  reg4 = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

That is, `testparm` took `reg*` to mean all variables that start with `reg` that were in our model.

◁

❑ Technical note

Actually, `reg*` means what it always does—all variables in our dataset that begin with `reg`—in this case, `region reg1 reg2 reg3 reg4`. `testparm` just ignores any variables you specify that are not in the model.

❑

▷ Example 8

We just used `test` (`testparm`, actually, but it does not matter) to test the hypothesis that `reg2`, `reg3`, and `reg4` are jointly zero. We can review the results of our last test by typing `test` without arguments:

```
. test
 ( 1)  reg2 = 0
 ( 2)  reg3 = 0
 ( 3)  reg4 = 0
       F(  3,    44) =    8.85
            Prob > F =    0.0001
```

◁

❑ Technical note

`test` does not care how we build joint hypotheses; we may freely mix different forms of syntax. (We can even start with `testparm`, but we cannot use it thereafter because it does not have an `accumulate` option.)

Say that we type `test reg2 reg3 reg4` to test that the coefficients on our region dummies are jointly zero. We could then add a fourth constraint, say, that `medage` = 100, by typing `test medage=100, accumulate`. Or, if we had introduced the `medage` constraint first (our first `test` command had been `test medage=100`), we could then add the region dummy test by typing `test reg2 reg3 reg4, accumulate` or `test (reg2=0) (reg3=0) (reg4=0), accumulate`.

Remember that all previous tests are cleared when we do not specify the `accumulate` option. No matter what tests we performed in the past, if we type `test medage c.medage#c.medage`, omitting the `accumulate` option, we would test that `medage` and `c.medage#c.medage` are jointly zero.

❑

▷ Example 9

Let's return to our `census3.dta` dataset and test the hypothesis that all the included regions have the *same* coefficient—that the Northeast is significantly different from the rest of the nation:

```
. use http://www.stata-press.com/data/r12/census3
(1980 Census data by state)
. regress brate medage c.medage#c.medage i.region
  (output omitted)
. test 2.region=3.region=4.region
 ( 1)  2.region - 3.region = 0
 ( 2)  2.region - 4.region = 0
       F(  2,    44) =    8.23
            Prob > F =    0.0009
```

We find that they are not all the same. The syntax `2.region=3.region=4.region` with multiple `=` operators is just a convenient shorthand for typing that the first expression equals the second expression and that the first expression equals the third expression,

```
. test (2.region=3.region) (2.region=4.region)
```

We performed the test for equality of the three regions by imposing two constraints: region 2 has the same coefficient as region 3, and region 2 has the same coefficient as region 4. Alternatively, we could have tested that the coefficients on regions 2 and 3 are the same and that the coefficients on regions 3 and 4 are the same. We would obtain the same results in either case.

To test for equality of the three regions, we might, likely by mistake, type equality constraints for *all* pairs of regions:

```
. test (2.region=3.region) (2.region=4.region) (3.region=4.region)
 ( 1)  2.region - 3.region = 0
 ( 2)  2.region - 4.region = 0
 ( 3)  3.region - 4.region = 0
       Constraint 3 dropped
       F(  2,    44) =    8.23
            Prob > F =    0.0009
```

Equality of regions 2 and 3 and of regions 2 and 4, however, implies equality of regions 3 and 4. `test` recognized that the last constraint is implied by the other constraints and hence dropped it.

◁

❑ Technical note

Generally, Stata uses `=` for assignment, as in `gen` *newvar* `=` *exp*, and `==` as the operator for testing equality in expressions. For your convenience, `test` allows both `=` and `==` to be used.

❑

▷ Example 10

The test for the equality of the regions is also possible with the `testparm` command. When we include the `equal` option, `testparm` tests that the coefficients of all the variables specified are equal:

```
. testparm i(2/4).region, equal
 ( 1) - 2.region + 3.region = 0
 ( 2) - 2.region + 4.region = 0
       F(  2,    44) =    8.23
            Prob > F =    0.0009
```

We can also obtain the equality test by accumulating single equality tests.

```
. test 2.region=3.region, notest
 ( 1)  2.region - 3.region = 0
. test 2.region=4.region, accum
 ( 1)  2.region - 3.region = 0
 ( 2)  2.region - 4.region = 0
       F(  2,    44) =    8.23
            Prob > F =    0.0009
```

◁

❑ Technical note

If we specify a set of inconsistent constraints, `test` will tell us by dropping the constraint or constraints that led to the inconsistency. For instance, let's `test` that the coefficients on region 2 and region 4 are the same, add the test that the coefficient on region 2 is 20, and finally add the test that the coefficient on region 4 is 21:

```
. test (2.region=4.region) (2.region=20) (4.region=21)
 ( 1)  2.region - 4.region = 0
 ( 2)  2.region = 20
 ( 3)  4.region = 21
       Constraint 2 dropped
       F(  2,    44) =    1.82
            Prob > F =    0.1737
```

`test` informed us that it was dropping constraint 2. All three equations cannot be simultaneously true, so `test` drops whatever it takes to get back to something that makes sense.

❑

Special syntaxes after multiple-equation estimation

Everything said above about tests after single-equation estimation applies to tests after multiple-equation estimation, as long as you remember to specify the equation name. To demonstrate, let's estimate a seemingly unrelated regression by using `sureg`; see [R] **sureg**.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. sureg (price foreign mpg displ) (weight foreign length)
Seemingly unrelated regression
```

Equation	Obs	Parms	RMSE	"R-sq"	chi2	P
price	74	3	2165.321	0.4537	49.64	0.0000
weight	74	2	245.2916	0.8990	661.84	0.0000

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
price						
foreign	3058.25	685.7357	4.46	0.000	1714.233	4402.267
mpg	-104.9591	58.47209	-1.80	0.073	-219.5623	9.644042
displacement	18.18098	4.286372	4.24	0.000	9.779842	26.58211
_cons	3904.336	1966.521	1.99	0.047	50.0263	7758.645
weight						
foreign	-147.3481	75.44314	-1.95	0.051	-295.2139	.517755
length	30.94905	1.539895	20.10	0.000	27.93091	33.96718
_cons	-2753.064	303.9336	-9.06	0.000	-3348.763	-2157.365

To test the significance of `foreign` in the `price` equation, we could type

```
. test [price]foreign
 ( 1)  [price]foreign = 0
           chi2(  1) =   19.89
         Prob > chi2 =    0.0000
```

which is the same result reported by `sureg`: $4.460^2 \approx 19.89$. To test `foreign` in both equations, we could type

```
. test [price]foreign [weight]foreign
 ( 1)  [price]foreign = 0
 ( 2)  [weight]foreign = 0
           chi2(  2) =   31.61
         Prob > chi2 =    0.0000
```

or

```
. test foreign
 ( 1)  [price]foreign = 0
 ( 2)  [weight]foreign = 0
           chi2(  2) =   31.61
         Prob > chi2 =    0.0000
```

This last syntax—typing the variable name by itself—tests the coefficients in all equations in which they appear. The variable `length` appears in only the `weight` equation, so typing

```
. test length
 ( 1)  [weight]length = 0
           chi2(  1) =  403.94
         Prob > chi2 =    0.0000
```

yields the same result as typing `test [weight]length`. We may also specify a linear expression rather than a list of coefficients:

```
. test mpg=displ
 ( 1)  [price]mpg - [price]displ = 0
           chi2(  1) =    4.85
         Prob > chi2 =    0.0277
```

or

```
. test [price]mpg = [price]displ
 ( 1)  [price]mpg - [price]displ = 0
           chi2(  1) =    4.85
         Prob > chi2 =    0.0277
```

A variation on this syntax can be used to test cross-equation constraints:

```
. test [price]foreign = [weight]foreign
 ( 1)  [price]foreign - [weight]foreign = 0
           chi2(  1) =   23.07
         Prob > chi2 =    0.0000
```

Typing an equation name in square brackets by itself tests all the coefficients except the intercept in that equation:

```
. test [price]
 ( 1)  [price]foreign = 0
 ( 2)  [price]mpg = 0
 ( 3)  [price]displacement = 0
           chi2(  3) =   49.64
         Prob > chi2 =    0.0000
```

Typing an equation name in square brackets, a colon, and a list of variable names tests those variables in the specified equation:

```
. test [price]: foreign displ
 ( 1)  [price]foreign = 0
 ( 2)  [price]displacement = 0
           chi2(  2) =   25.19
         Prob > chi2 =    0.0000
```

`test [`*eqname*$_1$`=`*eqname*$_2$`]` tests that all the coefficients in the two equations are equal. We cannot use that syntax here because there are different variables in the model:

```
. test [price=weight]
variables differ between equations
(to test equality of coefficients in common, specify option -common-)
r(111);
```

The `common` option specifies a test of the equality coefficients common to the equations `price` and `weight`,

```
. test [price=weight], common
 ( 1)  [price]foreign - [weight]foreign = 0
           chi2(  1) =   23.07
         Prob > chi2 =    0.0000
```

By default, `test` does not include the constant, the coefficient of the constant variable `_cons`, in the test. The `cons` option specifies that the constant be included.

```
. test [price=weight], common cons
 ( 1)  [price]foreign - [weight]foreign = 0
 ( 2)  [price]_cons - [weight]_cons = 0
           chi2(  2) =   51.23
         Prob > chi2 =  0.0000
```

We can also use a modification of this syntax with the model if we also type a colon and the names of the variables we want to test:

```
. test [price=weight]: foreign
 ( 1)  [price]foreign - [weight]foreign = 0
           chi2(  1) =   23.07
         Prob > chi2 =    0.0000
```

We have only one variable in common between the two equations, but if there had been more, we could have listed them.

Finally, a simultaneous test of multiple constraints may be specified just as after single-equation estimation.

```
. test ([price]: foreign) ([weight]: foreign)
 ( 1)  [price]foreign = 0
 ( 2)  [weight]foreign = 0
           chi2(  2) =   31.61
         Prob > chi2 =  0.0000
```

`test` can also test for equality of coefficients across more than two equations. For instance, `test [eq1=eq2=eq3]` specifies a test that the coefficients in the three equations `eq1`, `eq2`, and `eq3` are equal. This requires that the same variables be included in the three equations. If some variables are entered only in some of the equations, you can type `test [eq1=eq2=eq3], common` to test that the coefficients of the variables common to all three equations are equal. Alternatively, you can explicitly list the variables for which equality of coefficients across the equations is to be tested. For instance, `test [eq1=eq2=eq3]: time money` tests that the coefficients of the variables `time` and `money` do not differ between the equations.

❑ Technical note

`test [eq1=eq2=eq3], common` tests the equality of the coefficients common to all equations, but it does *not* test the equality of all common coefficients. Consider the case where

`eq1`	contains the variables `var1 var2 var3`
`eq2`	contains the variables `var1 var2 var4`
`eq3`	contains the variables `var1 var3 var4`

Obviously, only `var1` is common to all three equations. Thus `test [eq1=eq2=eq3], common` tests that the coefficients of `var1` do not vary across the equations, so it is equivalent to `test [eq1=eq2=eq3]: var1`. To perform a test of the coefficients of variables common to two equations, you could explicitly list the constraints to be tested,

```
. test ([eq1=eq2=eq3]:var1) ([eq1=eq2]:var2) ([eq1=eq3]:var3) ([eq2=eq3]:var4)
```

or use `test` with the `accumulate` option, and maybe also with the `notest` option, to form the appropriate joint hypothesis:

```
. test [eq1=eq2], common notest
. test [eq1=eq3], common accumulate notest
. test [eq2=eq3], common accumulate
```

❑

Constrained coefficients

If the test indicates that the data do not allow you to conclude that the constraints are not satisfied, you may want to inspect the constrained coefficients. The `coef` option specified that the constrained results, estimated by GLS, are shown.

```
. test [price=weight], common coef
 ( 1)  [price]foreign - [weight]foreign = 0
           chi2(  1) =   23.07
         Prob > chi2 =    0.0000

Constrained coefficients
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
price						
foreign	-216.4015	74.06083	-2.92	0.003	-361.558	-71.2449
mpg	-121.5717	58.36972	-2.08	0.037	-235.9742	-7.169116
displacement	7.632566	3.681114	2.07	0.038	.4177148	14.84742
_cons	7312.856	1834.034	3.99	0.000	3718.215	10907.5
weight						
foreign	-216.4015	74.06083	-2.92	0.003	-361.558	-71.2449
length	30.34875	1.534815	19.77	0.000	27.34057	33.35693
_cons	-2619.719	302.6632	-8.66	0.000	-3212.928	-2026.51

The constrained coefficient of `foreign` is -216.40 with standard error 74.06 in equations `price` and `weight`. The other coefficients and their standard errors are affected by imposing the equality constraint of the two coefficients of `foreign` because the unconstrained estimates of these two coefficients were correlated with the estimates of the other coefficients.

❑ Technical note

The two-step constrained coefficients b_c displayed by `test, coef` are asymptotically equivalent to the one-stage constrained estimates that are computed by specifying the constraints during estimation using the `constraint()` option of estimation commands (Gourieroux and Monfort 1995, chap. 10). Generally, one-step constrained estimates have better small-sample properties. For inspection and interpretation, however, two-step constrained estimates are a convenient alternative. Moreover, some estimation commands (for example, `stcox`, many `xt` estimators) do not have a `constraint()` option.

❑

Multiple testing

When performing the test of a joint hypothesis, you might want to inspect the underlying 1-degree-of-freedom hypotheses. Which constraint "is to blame"? `test` displays the univariate as well as the simultaneous test if the `mtest` option is specified. For example,

```
. test [price=weight], common cons mtest
 ( 1)  [price]foreign - [weight]foreign = 0
 ( 2)  [price]_cons - [weight]_cons = 0

------------------------------------------------------------------------------
             |        chi2     df       p
-------------+----------------------------------------------------------------
         (1) |       23.07      1     0.0000 #
         (2) |       11.17      1     0.0008 #
-------------+----------------------------------------------------------------
         all |       51.23      2     0.0000
------------------------------------------------------------------------------
                                  # unadjusted p-values
```

Both coefficients seem to contribute to the highly significant result. The 1-degree-of-freedom test shown here is identical to those if `test` had been invoked to test just this simple hypotheses. There is, of course, a real risk in inspecting these simple hypotheses. Especially in high-dimensional hypotheses, you may easily find one hypothesis that happens to be significant. Multiple testing procedures are designed to provide some safeguard against this risk. p-values of the univariate hypotheses are modified so that the probability of falsely rejecting one of the null hypotheses is bounded. `test` provides the methods based on Bonferroni, Šidák, and Holm.

```
. test [price=weight], common cons mtest(b)
 ( 1)  [price]foreign - [weight]foreign = 0
 ( 2)  [price]_cons - [weight]_cons = 0

------------------------------------------------------------------------------
             |        chi2     df       p
-------------+----------------------------------------------------------------
         (1) |       23.07      1     0.0000 #
         (2) |       11.17      1     0.0017 #
-------------+----------------------------------------------------------------
         all |       51.23      2     0.0000
------------------------------------------------------------------------------
                          # Bonferroni-adjusted p-values
```

Saved results

`test` and `testparm` save the following in `r()`:

Scalars

`r(p)`	two-sided p-value	`r(chi2)`	χ^2
`r(F)`	F statistic	`r(ss)`	sum of squares (test)
`r(df)`	test constraints degrees of freedom	`r(rss)`	residual sum of squares
`r(df_r)`	residual degrees of freedom	`r(drop)`	1 if constraints were dropped, 0 otherwise
`r(dropped_i)`	index of ith constraint dropped		

Macros

`r(mtmethod)`	method of adjustment for multiple testing

Matrices

`r(mtest)`	multiple test results

`r(ss)` and `r(rss)` are defined only when `test` is used for testing effects after `anova`.

Methods and formulas

`test` and `testparm` are implemented as ado-files.

`test` and `testparm` perform Wald tests. Let the estimated coefficient vector be $\mathbf{b}$ and the estimated variance–covariance matrix be $\mathbf{V}$. Let $\mathbf{Rb} = \mathbf{r}$ denote the set of q linear hypotheses to be tested jointly.

The Wald test statistic is (Judge et al. 1985, 20–28)

$$W = (\mathbf{Rb} - \mathbf{r})'(\mathbf{RVR}')^{-1}(\mathbf{Rb} - \mathbf{r})$$

If the estimation command reports its significance levels using Z statistics, a chi-squared distribution with q degrees of freedom,

$$W \sim \chi^2_q$$

is used for computation of the significance level of the hypothesis test.

If the estimation command reports its significance levels using t statistics with d degrees of freedom, an F statistic,

$$F = \frac{1}{q}W$$

is computed, and an F distribution with q numerator degrees of freedom and d denominator degrees of freedom computes the significance level of the hypothesis test.

The two-step constrained estimates b_c displayed by `test` with the `coef` option are the GLS estimates of the unconstrained estimates b subject to the specified constraints $Rb = c$ (Gourieroux and Monfort 1995, chap. 10),

$$\mathbf{b_c} = \mathbf{b} - \mathbf{R}'(\mathbf{RVR}')^{-1}\mathbf{R}(\mathbf{Rb} - \mathbf{r})$$

with variance–covariance matrix

$$\mathbf{V_c} = \mathbf{V} - \mathbf{VR}'(\mathbf{RVR}')^{-1}\mathbf{RV}$$

If `test` displays a Wald test for joint (simultaneous) hypotheses, it can also display all 1-degree-of-freedom tests, with p-values adjusted for multiple testing. Let $p_1, p_2, \ldots, p_k$ be the unadjusted p-values of these 1-degree-of-freedom tests. The Bonferroni-adjusted p-values are defined as $p^b_i = \min(1, kp_i)$. The Šidák-adjusted p-values are $p^s_i = 1 - (1 - p_i)^k$. Holm's method for adjusting p-values is defined as $p^h_i = \min(1, k_i p_i)$, where k_i is the number of p-values at least as large as p_i. Note that $p^h_i < p^b_i$, reflecting that Holm's method is strictly less conservative than the widely used Bonferroni method.

If `test` is used after a `svy` command, it carries out an adjusted Wald test—this adjustment should not be confused with the adjustment for multiple testing. Both adjustments may actually be combined. Specifically, the survey adjustment uses an approximate F statistic $(d-k+1)W/(kd)$, where W is the Wald test statistic, k is the dimension of the hypothesis test, and d = the total number of sampled PSUs minus the total number of strata. Under the null hypothesis, $(d-k+1)F/(kd) \sim F(k, d-k+1)$, where $F(k, d-k+1)$ is an F distribution with k numerator degrees of freedom and $d-k+1$ denominator degrees of freedom. If `nosvyadjust` is specified, the p-value is computed using $W/k \sim F(k, d)$.

See Korn and Graubard (1990) for a detailed description of the Bonferroni adjustment technique and for a discussion of the relative merits of it and of the adjusted and unadjusted Wald tests.

Acknowledgment

The `svy` adjustment code was adopted from another command developed in collaboration with John L. Eltinge, Bureau of Labor Statistics.

References

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Also see

[R] **anova** — Analysis of variance and covariance

[R] **anova postestimation** — Postestimation tools for anova

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **lincom** — Linear combinations of estimators

[R] **lrtest** — Likelihood-ratio test after estimation

[R] **nestreg** — Nested model statistics

[R] **nlcom** — Nonlinear combinations of estimators

[R] **testnl** — Test nonlinear hypotheses after estimation

[U] **13.5 Accessing coefficients and standard errors**

[U] **20 Estimation and postestimation commands**

Title

testnl — Test nonlinear hypotheses after estimation

Syntax

```
testnl exp = exp [= exp ...] [, options]

testnl (exp = exp [= exp ...]) [(exp = exp [= exp ...]) ...] [, options]
```

options	Description
`mtest[(opt)]`	test each condition separately
`nosvyadjust`	carry out the Wald test as $W/k \sim F(k,d)$; for use with `svy` estimation commands
`iterate(#)`	use maximum # of iterations to find the optimal step size

The second syntax means that if more than one expression is specified, each must be surrounded by parentheses.

exp is a possibly nonlinear expression containing

```
_b[coef]
_b[eqno:coef]
[eqno]coef
[eqno]_b[coef]
```

eqno is

```
##
name
```

coef identifies a coefficient in the model. *coef* is typically a variable name, a level indicator, an interaction indicator, or an interaction involving continuous variables. Level indicators identify one level of a factor variable and interaction indicators identify one combination of levels of an interaction; see [U] **11.4.3 Factor variables**. *coef* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

Distinguish between `[]`, which are to be typed, and [ ], which indicate optional arguments.

Menu

Statistics > Postestimation > Tests > Test nonlinear hypotheses

Description

`testnl` tests (linear or nonlinear) hypotheses about the estimated parameters from the most recently fit model.

`testnl` produces Wald-type tests of smooth nonlinear (or linear) hypotheses about the estimated parameters from the most recently fit model. The p-values are based on the delta method, an approximation appropriate in large samples.

`testnl` can be used with `svy` estimation results; see [SVY] **svy postestimation**.

The format `(`*exp*$_1$`=`*exp*$_2$`=`*exp*$_3$`...)` for a simultaneous-equality hypothesis is just a convenient shorthand for a list `(`*exp*$_1$`=`*exp*$_2$`)` `(`*exp*$_1$`=`*exp*$_3$`)`, etc.

`testnl` may also be used to test linear hypotheses. `test` is faster if you want to test only linear hypotheses; see [R] **test**. `testnl` is the only option for testing linear and nonlinear hypotheses simultaneously.

Options

`mtest`[`(`*opt*`)`] specifies that tests be performed for each condition separately. *opt* specifies the method for adjusting p-values for multiple testing. Valid values for *opt* are

`bonferroni`	Bonferroni's method
`holm`	Holm's method
`sidak`	Šidák's method
`noadjust`	no adjustment is to be made

Specifying `mtest` without an argument is equivalent to specifying `mtest(noadjust)`.

`nosvyadjust` is for use with `svy` estimation commands; see [SVY] **svy estimation**. It specifies that the Wald test be carried out without the default adjustment for the design degrees of freedom. That is, the test is carried out as $W/k \sim F(k,d)$ rather than as $(d-k+1)W/(kd) \sim F(k,d-k+1)$, where $k =$ the dimension of the test and $d =$ the total number of sampled PSUs minus the total number of strata.

`iterate(#)` specifies the maximum number of iterations used to find the optimal step size in the calculation of numerical derivatives of the test expressions. By default, the maximum number of iterations is 100, but convergence is usually achieved after only a few iterations. You should rarely have to use this option.

Remarks

Remarks are presented under the following headings:

Introduction
Using testnl to perform linear tests
Specifying constraints
Dropped constraints
Output
Multiple constraints
Manipulability

Introduction

▷ Example 1

We have just estimated the parameters of an earnings model on cross-sectional time-series data using one of Stata's more sophisticated estimators:

```
. use http://www.stata-press.com/data/r12/earnings
(NLS Women 14-24 in 1968)
. xtgee ln_w grade age c.age#c.age, corr(exchangeable) nolog
GEE population-averaged model                   Number of obs      =      1326
Group variable:                       idcode    Number of groups   =       269
Link:                               identity    Obs per group: min =         1
Family:                             Gaussian                   avg =       4.9
Correlation:                   exchangeable                    max =         9
                                                Wald chi2(3)       =    327.33
Scale parameter:                    .0976738    Prob > chi2        =    0.0000
```

ln_wage	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
grade	.0749686	.0066111	11.34	0.000	.062011	.0879261
age	.1080806	.0235861	4.58	0.000	.0618526	.1543086
c.age#c.age	-.0016253	.0004739	-3.43	0.001	-.0025541	-.0006966
_cons	-.8788933	.2830899	-3.10	0.002	-1.433739	-.3240473

An implication of this model is that peak earnings occur at age `-_b[age]/(2*_b[c.age#c.age])`, which here is equal to 33.2. Say that we have a theory that peak earnings should occur at age `16 + 1/_b[grade]`.

```
. testnl -_b[age]/(2*_b[c.age#c.age]) = 16 + 1/_b[grade]
  (1)  -_b[age]/(2*_b[c.age#c.age]) = 16 + 1/_b[grade]
               chi2(1) =        1.71
           Prob > chi2 =        0.1914
```

These data do not reject our theory. ◁

Using testnl to perform linear tests

`testnl` may be used to test linear constraints, but `test` is faster; see [R] **test**. You could type

```
. testnl _b[x4] = _b[x1]
```

but it would take less computer time if you typed

```
. test _b[x4] = _b[x1]
```

Specifying constraints

The constraints to be tested can be formulated in many different ways. You could type

```
. testnl _b[mpg]*_b[weight] = 1
```

or

```
. testnl _b[mpg] = 1/_b[weight]
```

or you could express the constraint any other way you wished. (To say that testnl allows constraints to be specified in different ways does not mean that the test itself does not depend on the formulation. This point is briefly discussed later.) In formulating the constraints, you must, however, exercise one caution: users of test often refer to the coefficient on a variable by specifying the variable name. For example,

```
. test mpg = 0
```

More formally, they should type

```
. test _b[mpg] = 0
```

but test allows the _b[] surrounding the variable name to be omitted. testnl does not allow this shorthand. Typing

```
. testnl mpg=0
```

specifies the constraint that the value of variable mpg in the first observation is zero. If you make this mistake, sometimes testnl will catch it:

```
. testnl mpg=0
equation (1) contains reference to X rather than _b[X]
r(198);
```

In other cases, testnl may not catch the mistake; then the constraint will be dropped because it does not make sense:

```
. testnl mpg=0
  Constraint (1) dropped
```

(There are reasons other than this for constraints being dropped.) The worst case, however, is

```
. testnl _b[weight]*mpg = 1
```

when what you mean is not that _b[weight] equals the reciprocal of the value of mpg in the first observation, but rather that

```
. testnl _b[weight]*_b[mpg] = 1
```

Sometimes this mistake will be caught by the "contains reference to X rather than _b[X]" error, and sometimes it will not. Be careful.

testnl, like test, can be used after any Stata estimation command, including the survey estimators. When you use it after a multiple-equation command, such as mlogit or heckman, you refer to coefficients by using Stata's standard syntax: [*eqname*]_b[*varname*].

Stata's single-equation estimation output looks like this:

```
             |    Coef   ...
-------------+----------------------------------------------------------------
      weight |   12.27  ...     <-  coefficient is  _b[weight]
         mpg |    3.21  ...
-------------+----------------------------------------------------------------
```

Stata's multiple-equation output looks like this:

```
             |    Coef   ...
-------------+----------------------------------------------------------------
cat1         |           ...
      weight |   12.27   ...    <-  coefficient is  [cat1]_b[weight]
         mpg |    3.21   ...
-------------+----------------------------------------------------------------
8            |           ...
      weight |    5.83   ...    <-  coefficient is  [8]_b[weight]
         mpg |    7.43   ...
-------------+----------------------------------------------------------------
```

Dropped constraints

`testnl` automatically drops constraints when

- They are nonbinding, for example, `_b[mpg]=_b[mpg]`. More subtle cases include

```
_b[mpg]*_b[weight] = 4
_b[weight] = 2
_b[mpg] = 2
```

  In this example, the third constraint is nonbinding because it is implied by the first two.

- They are contradictory, for example, `_b[mpg]=2 and _b[mpg]=3`. More subtle cases include

```
_b[mpg]*_b[weight] = 4
_b[weight] = 2
_b[mpg] = 3
```

  The third constraint contradicts the first two.

Output

`testnl` reports the constraints being tested followed by an F or a χ^2 test:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress price mpg weight c.weight#c.weight foreign
  (output omitted)
. testnl (39*_b[mpg]^2 = _b[foreign]) (_b[mpg]/_b[weight] = 4)
  (1)  39*_b[mpg]^2 = _b[foreign]
  (2)  _b[mpg]/_b[weight] = 4
             F(2, 69) =        0.08
             Prob > F =        0.9195
. logit foreign price weight mpg
  (output omitted)
. testnl (45*_b[mpg]^2 = _b[price]) (_b[mpg]/_b[weight] = 4)
  (1)  45*_b[mpg]^2 = _b[price]
  (2)  _b[mpg]/_b[weight] = 4
              chi2(2) =        2.44
          Prob > chi2 =        0.2946
```

Multiple constraints

▷ Example 2

We illustrate the simultaneous test of a series of constraints using simulated data on labor-market promotion in a given year. We fit a probit model with separate effects for education, experience, and experience-squared for men and women.

```
. use http://www.stata-press.com/data/r12/promotion
. probit promo male male#c.(yedu yexp yexp2), nolog
Probit regression                                 Number of obs   =        775
                                                  LR chi2(7)      =     424.42
                                                  Prob > chi2     =     0.0000
Log likelihood = -245.42768                       Pseudo R2       =     0.4637
```

promo	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
male	.6489974	.203739	3.19	0.001	.2496763	1.048318
male#c.yedu						
0	.9730237	.1056136	9.21	0.000	.7660248	1.180023
1	1.390517	.1527288	9.10	0.000	1.091174	1.68986
male#c.yexp						
0	.4559544	.0901169	5.06	0.000	.2793285	.6325803
1	1.422539	.1544255	9.21	0.000	1.11987	1.725207
male#c.yexp2						
0	-.1027149	.0573059	-1.79	0.073	-.2150325	.0096026
1	-.3749457	.1160113	-3.23	0.001	-.6023236	-.1475677
_cons	.9872018	.1148215	8.60	0.000	.7621559	1.212248

```
Note: 1 failure and 2 successes completely determined.
```

The effects of human capital seem to differ between men and women. A formal test confirms this.

```
. test (yedu#0.male = yedu#1.male) (yexp#0.male = yexp#1.male)
> (yexp2#0.male = yexp2#1.male)
 ( 1)  [promo]0b.male#c.yedu - [promo]1.male#c.yedu = 0
 ( 2)  [promo]0b.male#c.yexp - [promo]1.male#c.yexp = 0
 ( 3)  [promo]0b.male#c.yexp2 - [promo]1.male#c.yexp2 = 0
           chi2(  3) =   35.43
         Prob > chi2 =    0.0000
```

How do we interpret this gender difference? It has repeatedly been stressed (see, for example, Long [1997, 47–50]; Allison [1999]) that comparison of groups in binary response models, and similarly in other latent-variable models, is hampered by an identification problem: with β the regression coefficients for the latent variable and σ the standard deviation of the latent residual, only the β/σ are identified. In fact, in terms of the latent regression, the probit coefficients should be interpreted as β/σ, not as the β. If we cannot claim convincingly that the residual standard deviation σ does not vary between the sexes, equality of the regression coefficients β implies that the coefficients of the probit model for men and women are *proportional* but not necessarily equal. This is a nonlinear hypothesis in terms of the probit coefficients, not a linear one.

```
. testnl _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp#1.male]/_b[yexp#0.male]
> = _b[yexp2#1.male]/_b[yexp2#0.male]
  (1)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp#1.male]/_b[yexp#0.male]
  (2)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp2#1.male]/_b[yexp2#0.male]
               chi2(2) =        9.21
             Prob > chi2 =        0.0100
```

We conclude that we find fairly strong evidence against the proportionality of the coefficients, and hence we have to conclude that success in the labor market is produced in different ways by men and women. (But remember, these were simulated data.)

◁

▷ Example 3

The syntax for specifying the equality of multiple expressions is just a convenient shorthand for specifying a series of constraints, namely, that the first expression equals the second expression, the first expression also equals the third expression, etc. The Wald test performed and the output of `testnl` are the same whether we use the shorthand or we specify the series of constraints. The lengthy specification as a series of constraints can be simplified using the continuation symbols `///`.

```
. testnl (_b[yedu#1.male]/_b[yedu#0.male] =  ///
         _b[yexp#1.male]/_b[yexp#0.male])   ///
        (_b[yedu#1.male]/_b[yedu#0.male] =  ///
         _b[yexp2#1.male]/_b[yexp2#0.male])
  (1)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp#1.male]/_b[yexp#0.male]
  (2)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp2#1.male]/_b[yexp2#0.male]
               chi2(2) =        9.21
             Prob > chi2 =        0.0100
```

Having established differences between men and women, we would like to do multiple testing between the ratios. Because we did not specify hypotheses in advance, we prefer to adjust the p-values of tests using, here, Bonferroni's method.

```
. testnl _b[yedu#1.male]/_b[yedu#0.male] = ///
         _b[yexp#1.male]/_b[yexp#0.male] = ///
         _b[yexp2#1.male]/_b[yexp2#0.male], mtest(b)
  (1)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp#1.male]/_b[yexp#0.male]
  (2)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp2#1.male]/_b[yexp2#0.male]
```

	chi2	df	p
(1)	6.89	1	0.0173 #
(2)	0.93	1	0.6713 #
all	9.21	2	0.0100

 # Bonferroni-adjusted p-values

◁

Manipulability

Although `testnl` allows you to specify constraints in different ways that are mathematically equivalent, as noted above, this does not mean that the tests are the same. This difference is known as the manipulability of the Wald test for nonlinear hypotheses; also see [R] **boxcox**. The test might even be significant for one formulation but not significant for another formulation that is mathematically

equivalent. Trying out different specifications to find a formulation with the desired p-value is totally inappropriate, though it may actually be fun to try. There is no variance under representation because the nonlinear Wald test is actually a standard Wald test for a linearization of the constraint, which depends on the particular specification. We note that the likelihood-ratio test is not manipulable in this sense.

From a statistical point of view, it is best to choose a specification of the constraints that is as linear is possible. Doing so usually improves the accuracy of the approximation of the null-distribution of the test by a χ^2 or an F distribution. The example above used the nonlinear Wald test to test whether the coefficients of human capital variables for men were proportional to those of women. A specification of proportionality of coefficients in terms of ratios of coefficients is fairly nonlinear if the coefficients in the denominator are close to 0. A more linear version of the test results from a bilinear formulation. Thus instead of

```
. testnl _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp#1.male]/_b[yexp#0.male]
  (1)  _b[yedu#1.male]/_b[yedu#0.male] = _b[yexp#1.male]/_b[yexp#0.male]
               chi2(1) =        6.89
          Prob > chi2 =        0.0087
```

perhaps

```
. testnl _b[yedu#1.male]*_b[yexp#0.male] = _b[yedu#0.male]*_b[yexp#1.male]
  (1)  _b[yedu#1.male]*_b[yexp#0.male] = _b[yedu#0.male]*_b[yexp#1.male]
               chi2(1) =       13.95
          Prob > chi2 =        0.0002
```

is better, and in fact it has been suggested that the latter version of the test is more reliable. This assertion is confirmed by performing simulations and is in line with theoretical results of Phillips and Park (1988). There is strong evidence against the proportionality of human capital effects between men and women, implying for this example that differences in the residual variances between the sexes can be ruled out as the explanation of the sex differences in the analysis of labor market participation.

Saved results

`testnl` saves the following in `r()`:

Scalars

`r(df)`	degrees of freedom
`r(df_r)`	residual degrees of freedom
`r(chi2)`	χ^2
`r(p)`	significance
`r(F)`	F statistic

Macros

`r(mtmethod)`	method specified in `mtest()`

Matrices

`r(G)`	derivatives of $R(\mathbf{b})$ with respect to $\mathbf{b}$; see *Methods and formulas* below
`r(R)`	$R(\mathbf{b})-\mathbf{q}$; see *Methods and formulas* below
`r(mtest)`	multiple test results

Methods and formulas

`testnl` is implemented as an ado-file.

After fitting a model, define $\mathbf{b}$ as the resulting $1 \times k$ parameter vector and $\mathbf{V}$ as the $k \times k$ covariance matrix. The (linear or nonlinear) hypothesis is given by $R(\mathbf{b}) = \mathbf{q}$, where R is a function returning a $j \times 1$ vector. The Wald test formula is (Greene 2012, 528)

$$W = \Big\{R(\mathbf{b}) - \mathbf{q}\Big\}' \Big(\mathbf{G}\mathbf{V}\mathbf{G}'\Big)^{-1} \Big\{R(\mathbf{b}) - \mathbf{q}\Big\}$$

where $\mathbf{G}$ is the derivative matrix of $R(\mathbf{b})$ with respect to $\mathbf{b}$. W is distributed as χ^2 if $\mathbf{V}$ is an asymptotic covariance matrix. $F = W/j$ is distributed as F for linear regression.

The adjustment methods for multiple testing are described in [R] **test**. The adjustment for survey design effects is described in [SVY] **svy postestimation**.

References

Allison, P. D. 1999. Comparing logit and probit coefficients across groups. *Sociological Methods and Research* 28: 186–208.

Gould, W. W. 1996. crc43: Wald test of nonlinear hypotheses after model estimation. *Stata Technical Bulletin* 29: 2–4. Reprinted in *Stata Technical Bulletin Reprints*, vol. 5, pp. 15–18. College Station, TX: Stata Press.

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

Long, J. S. 1997. *Regression Models for Categorical and Limited Dependent Variables*. Thousand Oaks, CA: Sage.

Phillips, P. C. B., and J. Y. Park. 1988. On the formulation of Wald tests of nonlinear restrictions. *Econometrica* 56: 1065–1083.

Also see

[R] **contrast** — Contrasts and linear hypothesis tests after estimation

[R] **lincom** — Linear combinations of estimators

[R] **lrtest** — Likelihood-ratio test after estimation

[R] **nlcom** — Nonlinear combinations of estimators

[R] **test** — Test linear hypotheses after estimation

[U] **13.5 Accessing coefficients and standard errors**

[U] **20 Estimation and postestimation commands**

Title

tetrachoric — Tetrachoric correlations for binary variables

Syntax

`tetrachoric` *varlist* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Main	
`stats(`*statlist*`)`	list of statistics; select up to 4 statistics; default is `stats(rho)`
`edwards`	use the noniterative Edwards and Edwards estimator; default is the maximum likelihood estimator
`print(#)`	significance level for displaying coefficients
`star(#)`	significance level for displaying with a star
`bonferroni`	use Bonferroni-adjusted significance level
`sidak`	use Šidák-adjusted significance level
`pw`	calculate all the pairwise correlation coefficients by using all available data (pairwise deletion)
`zeroadjust`	adjust frequencies when one cell has a zero count
`matrix`	display output in matrix form
`notable`	suppress display of correlations
`posdef`	modify correlation matrix to be positive semidefinite

statlist	Description
`rho`	tetrachoric correlation coefficient
`se`	standard error of rho
`obs`	number of observations
`p`	exact two-sided significance level

`by` is allowed; see [D] **by**.
`fweights` are allowed; see [U] **11.1.6 weight**.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Tetrachoric correlations

Description

`tetrachoric` computes estimates of the tetrachoric correlation coefficients of the binary variables in *varlist*. All these variables should be 0, 1, or missing values.

Tetrachoric correlations assume a latent bivariate normal distribution (X_1,X_2) for each pair of variables (v_1,v_2), with a threshold model for the manifest variables, $v_i = 1$ if and only if $X_i > 0$. The means and variances of the latent variables are not identified, but the correlation, r, of X_1 and X_2 can be estimated from the joint distribution of v_1 and v_2 and is called the tetrachoric correlation coefficients.

tetrachoric computes pairwise estimates of the tetrachoric correlations by the (iterative) maximum likelihood estimator obtained from bivariate probit without explanatory variables (see [R] **biprobit**) by using the Edwards and Edwards (1984) noniterative estimator as the initial value.

The pairwise correlation matrix is returned as r(Rho) and can be used to perform a factor analysis or a principal component analysis of binary variables by using the factormat or pcamat commands; see [MV] **factor** and [MV] **pca**.

Options

Main

stats(*statlist*) specifies the statistics to be displayed in the matrix of output. stats(rho) is the default. Up to four statistics may be specified. stats(rho se p obs) would display the tetrachoric correlation coefficient, its standard error, the significance level, and the number of observations. If *varlist* contains only two variables, all statistics are shown in tabular form. stats(), print(), and star() have no effect unless the matrix option is also specified.

edwards specifies that the noniterative Edwards and Edwards estimator be used. The default is the maximum likelihood estimator. If you analyze many binary variables, you may want to use the fast noniterative estimator proposed by Edwards and Edwards (1984). However, if you have skewed variables, the approximation does not perform well.

print(#) specifies the maximum significance level of correlation coefficients to be printed. Correlation coefficients with larger significance levels are left blank in the matrix. Typing tetrachoric ..., print(.10) would list only those correlation coefficients that are significant at the 10% level or lower.

star(#) specifies the maximum significance level of correlation coefficients to be marked with a star. Typing tetrachoric ..., star(.05) would "star" all correlation coefficients significant at the 5% level or lower.

bonferroni makes the Bonferroni adjustment to calculated significance levels. This option affects printed significance levels and the print() and star() options. Thus tetrachoric ..., print(.05) bonferroni prints coefficients with Bonferroni-adjusted significance levels of 0.05 or less.

sidak makes the Šidák adjustment to calculated significance levels. This option affects printed significance levels and the print() and star() options. Thus tetrachoric ..., print(.05) sidak prints coefficients with Šidák-adjusted significance levels of 0.05 or less.

pw specifies that the tetrachoric correlation be calculated by using all available data. By default, tetrachoric uses casewise deletion, where observations are ignored if any of the specified variables in *varlist* are missing.

zeroadjust specifies that when one of the cells has a zero count, a frequency adjustment be applied in such a way as to increase the zero to one-half and maintain row and column totals.

matrix forces tetrachoric to display the statistics as a matrix, even if *varlist* contains only two variables. matrix is implied if more than two variables are specified.

notable suppresses the output.

posdef modifies the correlation matrix so that it is positive semidefinite, that is, a proper correlation matrix. The modified result is the correlation matrix associated with the least-squares approximation of the tetrachoric correlation matrix by a positive-semidefinite matrix. If the correlation matrix is modified, the standard errors and significance levels are not displayed and are returned in r().

Remarks

Remarks are presented under the following headings:

Association in 2-by-2 tables
Factor analysis of dichotomous variables
Tetrachoric correlations with simulated data

Association in 2-by-2 tables

Although a wide variety of measures of association in cross tabulations have been proposed, such measures are essentially equivalent (monotonically related) in the special case of 2×2 tables—there is only 1 degree of freedom for nonindependence. Still, some measures have more desirable properties than others. Here we compare two measures: the standard Pearson correlation coefficient and the tetrachoric correlation coefficient. Given asymmetric row or column margins, Pearson correlations are limited to a range smaller than -1 to 1, although tetrachoric correlations can still span the range from -1 to 1. To illustrate, consider the following set of tables for two binary variables, X and Z:

	Z = 0	Z = 1	
X = 0	$20 - a$	$10 + a$	30
X = 1	a	$10 - a$	10
	20	20	40

For a equal to 0, 1, 2, 5, 8, 9, and 10, the Pearson and tetrachoric correlations for the above table are

a	0	1	2	5	8	9	10
Pearson	0.577	0.462	0.346	0	−0.346	−0.462	−0.577
Tetrachoric	1.000	0.792	0.607	0	−0.607	−0.792	−1.000

The restricted range for the Pearson correlation is especially unfortunate when you try to analyze the association between binary variables by using models developed for continuous data, such as factor analysis and principal component analysis.

The tetrachoric correlation of two variables (Y_1, Y_2) can be thought of as the Pearson correlation of two latent bivariate normal distributed variables (Y_1^*, Y_2^*) with threshold measurement models $Y_i = (Y_i^* > c_i)$ for unknown cutpoints c_i. Or equivalently, $Y_i = (Y_i^{**} > 0)$ where the latent bivariate normal (Y_1^{**}, Y_2^{**}) are shifted versions of (Y_1^*, Y_2^*) so that the cutpoints are zero. Obviously, you must judge whether assuming underlying latent variables is meaningful for the data. If this assumption is justified, tetrachoric correlations have two advantages. First, you have an intuitive understanding of the size of correlations that are substantively interesting in your field of research, and this intuition is based on correlations that range from -1 to 1. Second, because the tetrachoric correlation for binary variables estimates the Pearson correlation of the latent continuous variables (assumed multivariate-normal distributed), you can use the tetrachoric correlations to analyze multivariate relationships between the dichotomous variables. When doing so, remember that you must interpret the model in terms of the underlying continuous variables.

▷ Example 1

To illustrate tetrachoric correlations, we examine three binary variables from the `familyvalues` dataset (described in example 2).

```
. use http://www.stata-press.com/data/r12/familyvalues
(Attitudes on gender, relationships and family)
. tabulate RS075 RS076
```

fam att: women in charge bad	fam att: trad division of labor 0	1	Total
0	1,564	979	2,543
1	119	632	751
Total	1,683	1,611	3,294

```
. correlate RS074 RS075 RS076
(obs=3291)
```

	RS074	RS075	RS076
RS074	1.0000		
RS075	0.0396	1.0000	
RS076	0.1595	0.3830	1.0000

```
. tetrachoric RS074 RS075 RS076
(obs=3291)
```

	RS074	RS075	RS076
RS074	1.0000		
RS075	0.0689	1.0000	
RS076	0.2480	0.6427	1.0000

As usual, the tetrachoric correlation coefficients are larger (in absolute value) and more dispersed than the Pearson correlations.

◁

Factor analysis of dichotomous variables

▷ Example 2

Factor analysis is a popular model for measuring latent continuous traits. The standard estimators are appropriate only for continuous unimodal data. Because of the skewness implied by Bernoulli-distributed variables (especially when the probability is distributed unevenly), a factor analysis of a Pearson correlation matrix can be rather misleading when used in this context. A factor analysis of a matrix of tetrachoric correlations is more appropriate under these conditions (Uebersax 2000). We illustrate this with data on gender, relationship, and family attitudes of spouses using the Households in The Netherlands survey 1995 (Weesie et al. 1995). For attitude variables, it seems reasonable to assume that agreement or disagreement is just a coarse measurement of more nuanced underlying attitudes.

To demonstrate, we examine a few of the variables from the `familyvalues` dataset.

```
. use http://www.stata-press.com/data/r12/familyvalues
(Attitudes on gender, relationships and family)
. describe RS056-RS063
```

variable name	storage type	display format	value label	variable label
RS056	byte	%9.0g		fam att: should be together
RS057	byte	%9.0g		fam att: should fight for relat
RS058	byte	%9.0g		fam att: should avoid conflict
RS059	byte	%9.0g		fam att: woman better nurturer
RS060	byte	%9.0g		fam att: both spouses money goo
RS061	byte	%9.0g		fam att: woman techn school goo
RS062	byte	%9.0g		fam att: man natural breadwinne
RS063	byte	%9.0g		fam att: common leisure good

```
. summarize RS056-RS063
```

Variable	Obs	Mean	Std. Dev.	Min	Max
RS056	3298	.5630685	.4960816	0	1
RS057	3296	.5400485	.4984692	0	1
RS058	3283	.6387451	.4804374	0	1
RS059	3308	.654474	.4756114	0	1
RS060	3302	.3906723	.487975	0	1
RS061	3293	.7102946	.4536945	0	1
RS062	3307	.5857272	.4926705	0	1
RS063	3298	.5379018	.498637	0	1

```
. correlate RS056-RS063
(obs=3221)
```

	RS056	RS057	RS058	RS059	RS060	RS061	RS062
RS056	1.0000						
RS057	0.1350	1.0000					
RS058	0.2377	0.0258	1.0000				
RS059	0.1816	0.0097	0.2550	1.0000			
RS060	-0.1020	-0.0538	-0.0424	0.0126	1.0000		
RS061	-0.1137	0.0610	-0.1375	-0.2076	0.0706	1.0000	
RS062	0.2014	0.0285	0.2273	0.4098	-0.0793	-0.2873	1.0000
RS063	0.2057	0.1460	0.1049	0.0911	0.0179	-0.0233	0.0975

	RS063
RS063	1.0000

Skewness in these data is relatively modest. For comparison, here are the tetrachoric correlations:

```
. tetrachoric RS056-RS063
(obs=3221)
```

	RS056	RS057	RS058	RS059	RS060	RS061	RS062
RS056	1.0000						
RS057	0.2114	1.0000					
RS058	0.3716	0.0416	1.0000				
RS059	0.2887	0.0158	0.4007	1.0000			
RS060	-0.1620	-0.0856	-0.0688	0.0208	1.0000		
RS061	-0.1905	0.1011	-0.2382	-0.3664	0.1200	1.0000	
RS062	0.3135	0.0452	0.3563	0.6109	-0.1267	-0.4845	1.0000
RS063	0.3187	0.2278	0.1677	0.1467	0.0286	-0.0388	0.1538

	RS063
RS063	1.0000

Again we see that the tetrachoric correlations are generally larger in absolute value than the Pearson correlations. The bivariate probit and Edwards and Edwards estimators (the `edwards` option) implemented in `tetrachoric` may return a correlation matrix that is not positive semidefinite—a mathematical property of any real correlation matrix. Positive definiteness is required by commands for analyses of correlation matrices, such as `factormat` and `pcamat`; see [MV] **factor** and [MV] **pca**. The `posdef` option of `tetrachoric` tests for positive definiteness and projects the estimated correlation matrix to a positive-semidefinite matrix if needed.

```
. tetrachoric RS056-RS063, notable posdef
. matrix C = r(Rho)
```

This time, we suppressed the display of the correlations with the `notable` option and requested that the correlation matrix be positive semidefinite with the `posdef` option. Had the correlation matrix not been positive definite, `tetrachoric` would have displayed a warning message and then adjusted the matrix to be positive semidefinite. We placed the resulting tetrachoric correlation matrix into a matrix, `C`, so that we can perform a factor analysis upon it.

`tetrachoric` with the `posdef` option asserted that `C` was positive definite because no warning message was displayed. We can verify this by using a familiar characterization of symmetric positive-definite matrices: all eigenvalues are real and positive.

```
. matrix symeigen eigenvectors eigenvalues = C
. matrix list eigenvalues
eigenvalues[1,8]
           e1         e2         e3         e4         e5         e6         e7
r1  2.5974789  1.3544664  1.0532476  .77980391  .73462018  .57984565  .54754512
           e8
r1  .35299228
```

We can proceed with a factor analysis on the matrix `C`. We use `factormat` and select iterated principal factors as the estimation method; see [MV] **factor**.

```
. factormat C, n(3221) ipf factor(2)
(obs=3221)
Factor analysis/correlation                      Number of obs    =     3221
    Method: iterated principal factors           Retained factors =        2
    Rotation: (unrotated)                        Number of params =       15
```

Factor	Eigenvalue	Difference	Proportion	Cumulative
Factor1	2.06855	1.40178	0.7562	0.7562
Factor2	0.66677	0.47180	0.2438	1.0000
Factor3	0.19497	0.06432	0.0713	1.0713
Factor4	0.13065	0.10967	0.0478	1.1191
Factor5	0.02098	0.10085	0.0077	1.1267
Factor6	-0.07987	0.01037	-0.0292	1.0975
Factor7	-0.09024	0.08626	-0.0330	1.0645
Factor8	-0.17650	.	-0.0645	1.0000

```
    LR test: independent vs. saturated:  chi2(28) = 4620.01 Prob>chi2 = 0.0000
Factor loadings (pattern matrix) and unique variances
```

Variable	Factor1	Factor2	Uniqueness
RS056	0.5528	0.4120	0.5247
RS057	0.1124	0.4214	0.8098
RS058	0.5333	0.0718	0.7105
RS059	0.6961	-0.1704	0.4865
RS060	-0.1339	-0.0596	0.9785
RS061	-0.5126	0.2851	0.6560
RS062	0.7855	-0.2165	0.3361
RS063	0.2895	0.3919	0.7626

◁

▷ Example 3

We noted in example 2 that the matrix of estimates of the tetrachoric correlation coefficients need not be positive definite. Here is an example:

```
. use http://www.stata-press.com/data/r12/familyvalues
(Attitudes on gender, relationships and family)
. tetrachoric RS056-RS063 in 1/20, posdef
(obs=18)
matrix with tetrachoric correlations is not positive semidefinite;
  it has 2 negative eigenvalues
  maxdiff(corr,adj-corr) =  0.2346
  (adj-corr: tetrachoric correlations adjusted to be positive semidefinite)
```

adj-corr	RS056	RS057	RS058	RS059	RS060	RS061	RS062
RS056	1.0000						
RS057	0.5284	1.0000					
RS058	0.3012	0.2548	1.0000				
RS059	0.3251	0.2791	0.0550	1.0000			
RS060	-0.5197	-0.4222	-0.7163	0.0552	1.0000		
RS061	0.3448	0.4815	-0.0958	-0.1857	-0.0980	1.0000	
RS062	0.1066	-0.0375	0.0072	0.3909	-0.2333	-0.7654	1.0000
RS063	0.3830	0.4939	0.4336	0.0075	-0.8937	-0.0337	0.4934

adj-corr	RS063
RS063	1.0000

```
. mata
------------------------------------------------- mata (type end to exit) -----
: C2 = st_matrix("r(Rho)")
: eigenvecs = .
: eigenvals = .
: symeigensystem(C2, eigenvecs, eigenvals)
: eigenvals
                 1              2              3              4
    +-------------------------------------------------------------+
  1 |  3.156592567   2.065279398   1.324911199   .7554904485     |
    +-------------------------------------------------------------+
                 5              6              7              8
    +-------------------------------------------------------------+
  1 |   .4845368741   .2131895139   2.02944e-16  -1.11650e-16     |
    +-------------------------------------------------------------+
: end
------------------------------------------------------------------------------
```

The estimated tetrachoric correlation matrix is rank-2 deficient. With this `C2` matrix, we can only use models of correlation that allow for singular cases.

◁

Tetrachoric correlations with simulated data

▷ Example 4

We use `drawnorm` (see [D] **drawnorm**) to generate a sample of 1,000 observations from a bivariate normal distribution with means -1 and 1, unit variances, and correlation 0.4.

```
. clear
. set seed 11000
. matrix m = (1, -1)
. matrix V = (1, 0.4 \ 0.4, 1)
. drawnorm c1 c2, n(1000) means(m) cov(V)
(obs 1000)
```

Now consider the measurement model assumed by the tetrachoric correlations. We observe only whether `c1` and `c2` are greater than zero,

```
. generate d1 = (c1 > 0)
. generate d2 = (c2 > 0)
. tabulate d1 d2
```

d1	d2 = 0	d2 = 1	Total
0	176	6	182
1	656	162	818
Total	832	168	1,000

We want to estimate the correlation of `c1` and `c2` from the binary variables `d1` and `d2`. Pearson's correlation of the binary variables `d1` and `d2` is 0.170—a seriously biased estimate of the underlying correlation $\rho = 0.4$.

```
. correlate d1 d2
(obs=1000)
             |       d1       d2
-------------+------------------
          d1 |   1.0000
          d2 |   0.1704   1.0000
```

The tetrachoric correlation coefficient of `d1` and `d2` estimates the Pearson correlation of the latent continuous variables, `c1` and `c2`.

```
. tetrachoric d1 d2
   Number of obs =    1000
 Tetrachoric rho =       0.4790
       Std error =       0.0700
Test of Ho: d1 and d2 are independent
 2-sided exact P =       0.0000
```

The estimate of the tetrachoric correlation of `d1` and `d2`, 0.4790, is much closer to the underlying correlation, 0.4, between `c1` and `c2`.

◁

Saved results

`tetrachoric` saves the following in `r()`:

Scalars

`r(rho)`	tetrachoric correlation coefficient between variables 1 and 2
`r(N)`	number of observations
`r(nneg)`	number of negative eigenvalues (`posdef` only)
`r(se_rho)`	standard error of `r(rho)`
`r(p)`	exact two-sided significance level

Macros

`r(method)`	estimator used

Matrices

`r(Rho)`	tetrachoric correlation matrix
`r(Se_Rho)`	standard errors of `r(Rho)`
`r(Nobs)`	number of observations used in computing correlation
`r(P)`	exact two-sided significance level matrix

Methods and formulas

`tetrachoric` is implemented as an ado-file.

`tetrachoric` provides two estimators for the tetrachoric correlation ρ of two binary variables with the frequencies n_{ij}, $i, j = 0, 1$. `tetrachoric` defaults to the slower (iterative) maximum likelihood estimator obtained from bivariate probit without explanatory variables (see [R] **biprobit**) by using the Edwards and Edwards noniterative estimator as the initial value. A fast (noniterative) estimator is also available by specifying the `edwards` option (Edwards and Edwards 1984; Digby 1983)

$$\widehat{\rho} = \frac{\alpha - 1}{\alpha + 1}$$

where

$$\alpha = \left(\frac{n_{00}n_{11}}{n_{01}n_{10}}\right)^{\pi/4} \quad (\pi = 3.14\ldots)$$

if all $n_{ij} > 0$. If $n_{00} = 0$ or $n_{11} = 0$, $\widehat{\rho} = -1$; if $n_{01} = 0$ or $n_{10} = 0$, $\widehat{\rho} = 1$.

The asymptotic variance of the Edwards and Edwards estimator of the tetrachoric correlation is easily obtained by the delta method,

$$\text{avar}(\widehat{\rho}) = \left(\frac{\pi\alpha}{2(1+\alpha)^2}\right)^2 \left(\frac{1}{n_{00}} + \frac{1}{n_{01}} + \frac{1}{n_{10}} + \frac{1}{n_{11}}\right)$$

provided all $n_{ij} > 0$, otherwise it is left undefined (missing). The Edwards and Edwards estimator is fast, but may be inaccurate if the margins are very skewed.

`tetrachoric` reports exact p-values for statistical independence, computed by the `exact` option of [R] **tabulate twoway**.

References

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Digby, P. G. N. 1983. Approximating the tetrachoric correlation coefficient. *Biometrics* 39: 753–757.

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Golub, G. H., and C. F. Van Loan. 1996. *Matrix Computations*. 3rd ed. Baltimore: Johns Hopkins University Press.

Uebersax, J. S. 2000. Estimating a latent trait model by factor analysis of tetrachoric correlations. http://ourworld.compuserve.com/homepages/jsuebersax/irt.htm.

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Also see

[MV] **factor** — Factor analysis

[MV] **pca** — Principal component analysis

[R] **tabulate twoway** — Two-way tables of frequencies

[R] **biprobit** — Bivariate probit regression

[R] **correlate** — Correlations (covariances) of variables or coefficients

[R] **spearman** — Spearman's and Kendall's correlations

Title

tnbreg — Truncated negative binomial regression

Syntax

`tnbreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`ll(#` | *varname*`)`	truncation point; default value is `ll(0)`, zero truncation
`dispersion(mean)`	parameterization of dispersion; the default
`dispersion(constant)`	constant dispersion for all observations
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`nolrtest`	suppress likelihood-ratio test
`irr`	report incidence-rate ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Count outcomes > Truncated negative binomial regression

Description

`tnbreg` estimates the parameters of a truncated negative binomial model by maximum likelihood. The dependent variable *depvar* is regressed on *indepvars*, where *depvar* is a positive count variable whose values are all above the truncation point.

Options

Model

`noconstant`; see [R] **estimation options**.

`ll(`*#* | *varname*`)` specifies the truncation point, which is a nonnegative integer. The default is zero truncation, `ll(0)`.

`dispersion(mean | constant)` specifies the parameterization of the model. `dispersion(mean)`, the default, yields a model with dispersion equal to $1+\alpha\exp(\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j)$; that is, the dispersion is a function of the expected mean: $\exp(\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j)$. `dispersion(constant)` has dispersion equal to $1+\delta$; that is, it is a constant for all observations.

`exposure(`*varname*$_e$`)`, `offset(`*varname*$_o$`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`nolrtest` suppresses fitting the Poisson model. Without this option, a comparison Poisson model is fit, and the likelihood is used in a likelihood-ratio test of the null hypothesis that the dispersion parameter is zero.

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. `irr` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `tnbreg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Grogger and Carson (1991) showed that overdispersion causes inconsistent estimation of the mean in the truncated Poisson model. To solve this problem, they proposed using the truncated negative binomial model as an alternative. If data are truncated but do not exhibit overdispersion, the truncated Poisson model is more appropriate; see [R] **tpoisson**. For an introduction to negative binomial regression, see Cameron and Trivedi (2005, 2010) and Long and Freese (2006). For an introduction to truncated negative binomial models, see Cameron and Trivedi (1998) and Long (1997, chap. 8).

`tnbreg` fits the mean-dispersion and the constant-dispersion parameterizations of truncated negative binomial models. These parameterizations extend those implemented in `nbreg`; see [R] **nbreg**.

▷ Example 1

We illustrate the truncated negative binomial model using the 1997 MedPar dataset (Hilbe 1999). The data are from 1,495 patients in Arizona who were assigned to a diagnostic-related group (DRG) of patients having a ventilator. Length of stay (`los`), the dependent variable, is a positive integer; it cannot have zero values. The data are truncated because there are no observations on individuals who stayed for zero days.

The objective of this example is to determine whether the length of stay was related to the binary variables: `died`, `hmo`, `type1`, `type2`, and `type3`.

The `died` variable was recorded as a 0 unless the patient died, in which case, it was recorded as a 1. The other variables also adopted this encoding. The `hmo` variable was set to 1 if the patient belonged to a health maintenance organization (HMO).

The `type1`–`type3` variables indicated the type of admission used for the patient. The `type1` variable indicated an emergency admit. The `type2` variable indicated an urgent admit—that is, the first available bed. The `type3` variable indicated an elective admission. Because `type1`–`type3` were mutually exclusive, only two of the three could be used in the truncated negative binomial regression shown below.

```
. use http://www.stata-press.com/data/r12/medpar
. tnbreg los died hmo type2-type3, vce(cluster provnum) nolog
Truncated negative binomial regression
Truncation point: 0                               Number of obs   =       1495
Dispersion     = mean                             Wald chi2(4)    =      36.01
Log likelihood = -4737.535                        Prob > chi2     =     0.0000
                                (Std. Err. adjusted for 54 clusters in provnum)
```

los	Coef.	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
died	-.2521884	.061533	-4.10	0.000	-.3727908	-.1315859
hmo	-.0754173	.0533132	-1.41	0.157	-.1799091	.0290746
type2	.2685095	.0666474	4.03	0.000	.137883	.3991359
type3	.7668101	.2183505	3.51	0.000	.338851	1.194769
_cons	2.224028	.034727	64.04	0.000	2.155964	2.292091
/lnalpha	-.630108	.0764019			-.779853	-.480363
alpha	.5325343	.0406866			.4584734	.6185588

Because observations within the same hospital (provnum) are likely to be correlated, we specified the vce(cluster provnum) option. The results show that whether the patient died in the hospital and the type of admission have significant effects on the patient's length of stay.

◁

▷ Example 2

To illustrate truncated negative binomial regression with more complex data than the previous example, similar data were created from 100 hospitals. Each hospital had its own way of tracking patient data. In particular, hospitals only recorded data from patients with a minimum length of stay, denoted by the variable minstay.

Definitions for minimum length of stay varied among hospitals, typically, from 5 to 18 days. The objective of this example is the same as before: to determine whether the length of stay, recorded in los, was related to the binary variables: died, hmo, type1, type2, and type3.

The binary variables encode the same information as in example 1 above. The minstay variable was used to allow for varying truncation points.

```
. use http://www.stata-press.com/data/r12/medproviders
. tnbreg los died hmo type2-type3, ll(minstay) vce(cluster hospital) nolog
Truncated negative binomial regression
Truncation points: minstay                      Number of obs   =       2144
Dispersion     = mean                           Wald chi2(4)    =      15.22
Log likelihood = -7864.0928                     Prob > chi2     =     0.0043
                              (Std. Err. adjusted for 100 clusters in hospital)
------------------------------------------------------------------------------
             |               Robust
         los |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        died |    .078104   .0303603     2.57   0.010     .0185988    .1376091
         hmo |  -.0731132   .0368899    -1.98   0.047    -.1454162   -.0008103
       type2 |    .0294132  .0390165     0.75   0.451    -.0470578    .1058843
       type3 |    .0626349  .0540124     1.16   0.246    -.0432275    .1684972
       _cons |   3.014964   .0291045   103.59   0.000     2.95792     3.072008
-------------+----------------------------------------------------------------
    /lnalpha |  -.9965124   .0829428                     -1.159077   -.8339475
-------------+----------------------------------------------------------------
       alpha |   .3691647   .0306196                      .3137756    .4343314
------------------------------------------------------------------------------
```

In this analysis, two variables have a statistically significant relationship with length of stay. On average, patients who died in the hospital had longer lengths of stay ($p = 0.01$). Because the coefficient for HMO is negative, that is, $b_{\text{HMO}} = -0.073$, on average, patients who were insured by an HMO had shorter lengths of stay ($p = 0.047$). The type of admission was not statistically significant ($p > 0.05$).

◁

Saved results

tnbreg saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_aux)	number of auxiliary parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(r2_p)	pseudo-R-squared
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(ll_c)	log likelihood, comparison model
e(alpha)	value of alpha
e(N_clust)	number of clusters
e(chi2)	χ^2
e(chi2_c)	χ^2 for comparison test
e(p)	significance
e(rank)	rank of e(V)
e(rank0)	rank of e(V) for constant-only model
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	tnbreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(llopt)	contents of ll(), or 0 if not specified
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(dispers)	mean or constant
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

`tnbreg` is implemented as an ado-file.

Methods and formulas are presented under the following headings:

Mean-dispersion model
Constant-dispersion model

Mean-dispersion model

A negative binomial distribution can be regarded as a gamma mixture of Poisson random variables. The number of times an event occurs, y_j, is distributed as Poisson$(\nu_j\mu_j)$. That is, its conditional likelihood is

$$f(y_j \mid \nu_j) = \frac{(\nu_j\mu_j)^{y_j} e^{-\nu_j\mu_j}}{\Gamma(y_j+1)}$$

where $\mu_j = \exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$ and ν_j is an unobserved parameter with a Gamma$(1/\alpha, \alpha)$ density:

$$g(\nu) = \frac{\nu^{(1-\alpha)/\alpha} e^{-\nu/\alpha}}{\alpha^{1/\alpha}\Gamma(1/\alpha)}$$

This gamma distribution has a mean of 1 and a variance of α, where α is our ancillary parameter.

The unconditional likelihood for the jth observation is therefore

$$f(y_j) = \int_0^\infty f(y_j \mid \nu) g(\nu)\, d\nu = \frac{\Gamma(m+y_j)}{\Gamma(y_j+1)\Gamma(m)}\, p_j^m (1-p_j)^{y_j}$$

where $p_j = 1/(1+\alpha\mu_j)$ and $m = 1/\alpha$. Solutions for α are handled by searching for $\ln\alpha$ because α must be greater than zero. The conditional probability of observing y_j events given that y_j is greater than the truncation point τ_j is

$$\Pr(Y = y_j \,|\, y_j > \tau_j, \mathbf{x}_j) = \frac{f(y_j)}{\Pr(Y > \tau_j \,|\, \mathbf{x}_j)}$$

The log likelihood (with weights w_j and offsets) is given by

$$m = 1/\alpha \qquad p_j = 1/(1+\alpha\mu_j) \qquad \mu_j = \exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$$

$$\begin{aligned}\ln L = \sum_{j=1}^{n} w_j \Big[& \ln\{\Gamma(m+y_j)\} - \ln\{\Gamma(y_j+1)\} \\ & - \ln\{\Gamma(m)\} + m\ln(p_j) + y_j\ln(1-p_j) - \ln\{\Pr(Y > \tau_j \,|\, p_j, m)\}\Big]\end{aligned}$$

Constant-dispersion model

The constant-dispersion model assumes that y_j is conditionally distributed as Poisson(μ_j^*), where $\mu_j^* \sim$ Gamma$(\mu_j/\delta, \delta)$ for some dispersion parameter δ [by contrast, the mean-dispersion model assumes that $\mu_j^* \sim$ Gamma$(1/\alpha, \alpha\mu_j)$]. The log likelihood is given by

$$m_j = \mu_j/\delta \qquad p = 1/(1+\delta)$$

$$\ln L = \sum_{j=1}^{n} w_j \Big[\ln\{\Gamma(m_j + y_j)\} - \ln\{\Gamma(y_j + 1)\} - \ln\{\Gamma(m_j)\} + m_j \ln(p) + y_j \ln(1-p) - \ln\{\Pr(Y > \tau_j \,|\, p, m_j)\} \Big]$$

with everything else defined as shown above in the calculations for the mean-dispersion model.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`tnbreg` also supports estimation with survey data. For details on variance–covariance estimates with survey data, see [SVY] **variance estimation**.

Acknowledgment

We gratefully acknowledge the previous work by Joseph Hilbe, Arizona State University; see Hilbe (1999).

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Also see

[R] **tnbreg postestimation** — Postestimation tools for tnbreg

[R] **nbreg** — Negative binomial regression

[R] **poisson** — Poisson regression

[R] **tpoisson** — Truncated Poisson regression

[R] **zinb** — Zero-inflated negative binomial regression

[R] **zip** — Zero-inflated Poisson regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtnbreg** — Fixed-effects, random-effects, & population-averaged negative binomial models

[U] **20 Estimation and postestimation commands**

Title

tnbreg postestimation — Postestimation tools for tnbreg

Description

The following postestimation commands are available after `tnbreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_disp} [if] [in], scores
```

statistic	Description
Main	
`n`	number of events; the default
`ir`	incidence rate
`cm`	conditional mean, $E(y_j \mid y_j > \tau_j)$
`pr(`*n*`)`	probability $\Pr(y_j = n)$
`pr(`*a*`,`*b*`)`	probability $\Pr(a \le y_j \le b)$
`cpr(`*n*`)`	conditional probability $\Pr(y_j = n \mid y_j > \tau_j)$
`cpr(`*a*`,`*b*`)`	conditional probability $\Pr(a \le y_j \le b \mid y_j > \tau_j)$
`xb`	linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`n`, the default, calculates the predicted number of events, which is $\exp(\mathbf{x}_j\boldsymbol{\beta})$ if neither `offset()` nor `exposure()` was specified when the model was fit; $\exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$ if `offset()` was specified; or $\exp(\mathbf{x}_j\boldsymbol{\beta}) \times \text{exposure}_j$ if `exposure()` was specified.

`ir` calculates the incidence rate $\exp(\mathbf{x}_j\boldsymbol{\beta})$, which is the predicted number of events when exposure is 1. This is equivalent to specifying both the `n` and the `nooffset` options.

`cm` calculates the conditional mean,

$$E(y_j \mid y_j > \tau_j) = \frac{E(y_j)}{\Pr(y_j > \tau_j)}$$

where τ_j is the truncation point found in `e(llopt)`.

`pr(`*n*`)` calculates the probability $\Pr(y_j = n)$, where *n* is a nonnegative integer that may be specified as a number or a variable.

`pr(`*a*`,`*b*`)` calculates the probability $\Pr(a \le y_j \le b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b \ge .$) means $+\infty$;
`pr(20,.)` calculates $\Pr(y_j \ge 20)$;
`pr(20,`*b*`)` calculates $\Pr(y_j \ge 20)$ in observations for which $b \ge .$ and calculates $\Pr(20 \le y_j \le b)$ elsewhere.

`pr(.,b)` produces a syntax error. A missing value in an observation of the variable a causes a missing value in that observation for `pr(a,b)`.

`cpr(n)` calculates the conditional probability $\Pr(y_j = n \,|\, y_j > \tau_j)$, where τ_j is the truncation point found in `e(llopt)`. n is an integer greater than the truncation point that may be specified as a number or a variable.

`cpr(a,b)` calculates the conditional probability $\Pr(a \leq y_j \leq b \,|\, y_j > \tau_j)$, where τ_j is the truncation point found in `e(llopt)`. The syntax for this option is analogous to that used for `pr(a,b)` except that a must be greater than the truncation point.

`xb` calculates the linear prediction, which is $\mathbf{x}_j\boldsymbol{\beta}$ if neither `offset()` nor `exposure()` was specified when the model was fit; $\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$ if `offset()` was specified; or $\mathbf{x}_j\boldsymbol{\beta} + \ln(\text{exposure}_j)$ if `exposure()` was specified; see `nooffset` below.

`stdp` calculates the standard error of the linear prediction.

`nooffset` is relevant only if you specified `offset()` or `exposure()` when you fit the model. It modifies the calculations made by `predict` so that they ignore the offset or exposure variable; the linear prediction is treated as $\mathbf{x}_j\boldsymbol{\beta}$ rather than as $\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$ or $\mathbf{x}_j\boldsymbol{\beta} + \ln(\text{exposure}_j)$. Specifying `predict ..., nooffset` is equivalent to specifying `predict ..., ir`.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\ln\alpha)$ for `dispersion(mean)`.

The second new variable will contain $\partial \ln L/\partial(\ln\delta)$ for `dispersion(constant)`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

In the following formulas, we use the same notation as in [R] **tnbreg**.

Methods and formulas are presented under the following headings:

Mean-dispersion model
Constant-dispersion model

Mean-dispersion model

The equation-level scores are given by

$$\text{score}(\mathbf{x}\boldsymbol{\beta})_j = p_j(y_j - \mu_j) - \frac{p_j^{(m+1)}\mu_j}{\Pr(Y > \tau_j \,|\, p_j, m)}$$

$$\text{score}(\omega)_j = -m\left\{\frac{\alpha(\mu_j - y_j)}{1+\alpha\mu_j} - \ln(1+\alpha\mu_j) + \psi(y_j+m) - \psi(m)\right\} - \frac{p_j^m}{\Pr(Y > \tau_j \,|\, p_j, m)}\{m\ln(p_j) + \mu_j p_j\}$$

where $\omega_j = \ln\alpha_j$, $\psi(z)$ is the digamma function, and τ_j is the truncation point found in `e(llopt)`.

Constant-dispersion model

The equation-level scores are given by

$$\text{score}(\mathbf{x}\boldsymbol{\beta})_j = m_j \left\{ \psi(y_j + m_j) - \psi(m_j) + \ln(p) + \frac{p^{m_j} \ln(p)}{\Pr(Y > \tau_j \,|\, p, m_j)} \right\}$$

$$\text{score}(\omega)_j = y_j - (y_j + m_j)(1 - p) - \text{score}(\mathbf{x}\boldsymbol{\beta})_j - \frac{\mu_j p}{\Pr(Y > \tau_j \,|\, p, m_j)}$$

where $\omega_j = \ln\delta_j$ and τ_j is the truncation point found in `e(llopt)`.

Also see

[R] **tnbreg** — Truncated negative binomial regression

[U] **20 Estimation and postestimation commands**

Title

tobit — Tobit regression

Syntax

`tobit` *depvar* [*indepvars*] [*if*] [*in*] [*weight*], `ll`[`(`#`)`] `ul`[`(`#`)`] [*options*]

options	Description
Model	
`noconstant`	suppress constant term
*`ll`[`(`#`)`]	left-censoring limit
*`ul`[`(`#`)`]	right-censoring limit
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(`#`)`	set confidence level; default is `level(95)`
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

*You must specify at least one of `ll`[`(`#`)`] or `ul`[`(`#`)`].

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `jackknife`, `nestreg`, `rolling`, `statsby`, `stepwise`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`aweights`, `fweights`, `pweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Censored regression > Tobit regression

Description

`tobit` fits a model of *depvar* on *indepvars* where the censoring values are fixed.

Options

Model

`noconstant`; see [R] **estimation options**.

`ll`[`(#)`] and `ul`[`(#)`] indicate the lower and upper limits for censoring, respectively. You may specify one or both. Observations with *depvar* $\leq$ `ll()` are left-censored; observations with *depvar* $\geq$ `ul()` are right-censored; and remaining observations are not censored. You do not have to specify the censoring values at all. It is enough to type `ll`, `ul`, or both. When you do not specify a censoring value, `tobit` assumes that the lower limit is the minimum observed in the data (if `ll` is specified) and the upper limit is the maximum (if `ul` is specified).

`offset(`*varname*`)`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `iterate(#)`, [`no`]`log`, `trace`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, and `nonrtolerance`; see [R] **maximize**. These options are seldom used.

Unlike most maximum likelihood commands, `tobit` defaults to `nolog`—it suppresses the iteration log.

The following option is available with `tobit` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Tobit estimation was originally developed by Tobin (1958). A consumer durable was purchased if a consumer's desire was high enough, where desire was measured by the dollar amount spent by the purchaser. If no purchase was made, the measure of desire was censored at zero.

▷ Example 1

We will demonstrate `tobit` with an artificial example, which in the process will allow us to emphasize the assumptions underlying the estimation. We have a dataset containing the mileage ratings and weights of 74 cars. There are no censored variables in this dataset, but we are going to create one. Before that, however, the relationship between mileage and weight in our complete data is

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. generate wgt = weight/1000
. regress mpg wgt
      Source |       SS       df       MS              Number of obs =      74
-------------+------------------------------           F(  1,    72) =  134.62
       Model |  1591.99024     1  1591.99024            Prob > F      =  0.0000
    Residual |  851.469221    72  11.8259614            R-squared     =  0.6515
-------------+------------------------------           Adj R-squared =  0.6467
       Total |  2443.45946    73  33.4720474            Root MSE      =  3.4389

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         wgt |  -6.008687   .5178782   -11.60   0.000    -7.041058   -4.976316
       _cons |   39.44028   1.614003    24.44   0.000     36.22283    42.65774
------------------------------------------------------------------------------
```

(We divided `weight` by 1,000 simply to make discussing the resulting coefficients easier. We find that each additional 1,000 pounds of weight reduces mileage by 6 mpg.)

`mpg` in our data ranges from 12 to 41. Let us now pretend that our data were censored in the sense that we could not observe a mileage rating below 17 mpg. If the true mpg is 17 or less, all we know is that the mpg is less than or equal to 17:

```
. replace mpg=17 if mpg<=17
(14 real changes made)
. tobit mpg wgt, ll
Tobit regression                                  Number of obs   =         74
                                                  LR chi2(1)      =      72.85
                                                  Prob > chi2     =     0.0000
Log likelihood = -164.25438                       Pseudo R2       =     0.1815

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         wgt |  -6.87305   .7002559    -9.82   0.000    -8.268658   -5.477442
       _cons |  41.49856    2.05838    20.16   0.000     37.39621     45.6009
-------------+----------------------------------------------------------------
      /sigma |  3.845701   .3663309                      3.115605    4.575797
------------------------------------------------------------------------------
  Obs. summary:         18  left-censored observations at mpg<=17
                        56     uncensored observations
                         0 right-censored observations
```

The `replace` before estimation was not really necessary—we remapped all the mileage ratings below 17 to 17 merely to reassure you that `tobit` was not somehow using uncensored data. We typed `ll` after `tobit` to inform `tobit` that the data were left-censored. `tobit` found the minimum of `mpg` in our data and assumed that was the censoring point. We could also have dispensed with `replace` and typed `ll(17)`, informing `tobit` that all values of the dependent variable 17 and below are really censored at 17. In either case, at the bottom of the table, we are informed that there are, as a result, 18 left-censored observations.

On these data, our estimate is now a reduction of 6.9 mpg per 1,000 extra pounds of weight as opposed to 6.0. The parameter reported as `/sigma` is the estimated standard error of the regression; the resulting 3.8 is comparable with the estimated root mean squared error reported by `regress` of 3.4.

◁

❑ Technical note

You would never want to throw away information by purposefully censoring variables. The `regress` estimates are in every way preferable to those of `tobit`. Our example is designed solely to illustrate the relationship between `tobit` and `regress`. If you have uncensored data, use `regress`. If your data are censored, you have no choice but to use `tobit`.

❑

▷ Example 2

`tobit` can also fit models that are censored from above. This time, let's assume that we do not observe the actual mileage rating of cars yielding 24 mpg or better—we know only that it is at least 24. (Also assume that we have undone the change to `mpg` we made in the previous example.)

```
. use http://www.stata-press.com/data/r12/auto, clear
(1978 Automobile Data)
. generate wgt = weight/1000
. regress mpg wgt
  (output omitted)
. tobit mpg wgt, ul(24)
Tobit regression                                  Number of obs   =         74
                                                  LR chi2(1)      =      90.72
                                                  Prob > chi2     =     0.0000
Log likelihood =  -129.8279                       Pseudo R2       =     0.2589

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         wgt |  -5.080645     .43493   -11.68   0.000    -5.947459   -4.213831
       _cons |   36.08037   1.432056    25.19   0.000     33.22628    38.93445
-------------+----------------------------------------------------------------
      /sigma |   2.385357   .2444604                      1.898148    2.872566
------------------------------------------------------------------------------

  Obs. summary:          0  left-censored observations
                        51     uncensored observations
                        23 right-censored observations at mpg>=24
```

◁

▷ Example 3

`tobit` can also fit models that are censored from both sides (the so-called two-limit tobit):

```
. tobit mpg wgt, ll(17) ul(24)
Tobit regression                                  Number of obs   =         74
                                                  LR chi2(1)      =      77.60
                                                  Prob > chi2     =     0.0000
Log likelihood = -104.25976                       Pseudo R2       =     0.2712

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         wgt |  -5.764448   .7245417    -7.96   0.000    -7.208457   -4.320438
       _cons |   38.07469   2.255917    16.88   0.000     33.57865    42.57072
-------------+----------------------------------------------------------------
      /sigma |   2.886337   .3952143                      2.098676    3.673998
------------------------------------------------------------------------------

  Obs. summary:         18  left-censored observations at mpg<=17
                        33     uncensored observations
                        23 right-censored observations at mpg>=24
```

◁

Saved results

tobit saves the following in e():

Scalars

e(N)	number of observations
e(N_unc)	number of uncensored observations
e(N_lc)	number of left-censored observations
e(N_rc)	number of right-censored observations
e(llopt)	contents of ll(), if specified
e(ulopt)	contents of ul(), if specified
e(k_aux)	number of auxiliary parameters
e(df_m)	model degrees of freedom
e(df_r)	residual degrees of freedom
e(r2_p)	pseudo-R-squared
e(chi2)	χ^2
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(F)	F statistic
e(p)	significance
e(rank)	rank of e(V)
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	tobit
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset)	linear offset variable
e(chi2type)	LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(predict)	program used to implement predict
e(footnote)	program and arguments to display footnote
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

James Tobin (1918–2002) was an American economist who after education and research at Harvard moved to Yale, where he was on the faculty from 1950 to 1988. He made many outstanding contributions to economics and was awarded the Nobel Prize in 1981 "for his analysis of financial markets and their relations to expenditure decisions, employment, production and prices". He trained in the U.S. Navy with the writer in Herman Wouk, who later fashioned a character after Tobin in the novel *The Caine Mutiny* (1951): "A mandarin-like midshipman named Tobit, with a domed forehead, measured quiet speech, and a mind like a sponge, was ahead of the field by a spacious percentage."

Methods and formulas

`tobit` is implemented as an ado-file.

See *Methods and formulas* in [R] **intreg**.

See Tobin (1958) for the original derivation of the tobit model. An introductory description of the tobit model can be found in, for instance, Wooldridge (2009, 587–595), Davidson and MacKinnon (2004, 484–486), Long (1997, 196–210), and Maddala and Lahiri (2006, 333–336). Cameron and Trivedi (2010, chap. 16) discuss the tobit model using Stata examples.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`tobit` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

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Also see

[R] **tobit postestimation** — Postestimation tools for tobit

[R] **intreg** — Interval regression

[R] **heckman** — Heckman selection model

[R] **ivtobit** — Tobit model with continuous endogenous regressors

[R] **regress** — Linear regression

[R] **truncreg** — Truncated regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtintreg** — Random-effects interval-data regression models

[XT] **xttobit** — Random-effects tobit models

[U] **20 Estimation and postestimation commands**

Title

tobit postestimation — Postestimation tools for tobit

Description

The following postestimation commands are available after `tobit`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`hausman`	Hausman's specification test
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_sigma} [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the linear prediction
`stdf`	standard error of the forecast
`pr(`*a*`,`*b*`)`	$\Pr(a < y_j < b)$
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

where a and b may be numbers or variables; a missing ($a \geq .$) means $-\infty$, and b missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \mid a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated.
a and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`nooffset` is relevant only if you specified `offset(`*varname*`)`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial\sigma$.

Remarks

Following Cong (2000), write the tobit model as

$$y_i^* = \begin{cases} y_i, & \text{if } a < y_i < b \\ a, & \text{if } y_i \leq a \\ b, & \text{if } y_i \geq b \end{cases}$$

y_i is a latent variable; instead, we observe y_i^*, which is bounded between a and b if y_i is outside those bounds.

There are four types of marginal effects that may be of interest in the tobit model, depending on the application:

1. The β coefficients themselves measure how the unobserved variable y_i changes with respect to changes in the regressors.
2. The marginal effects of the truncated expected value $E(y_i^*|a < y_i^* < b)$ measure the changes in y_i with respect to changes in the regressors among the subpopulation for which y_i is not at a boundary.
3. The marginal effects of the censored expected value $E(y_i^*)$ describe how the observed variable y_i^* changes with respect to the regressors.
4. The marginal effects of $\Pr(\mathrm{a} < \mathrm{y_i^*} < \mathrm{b})$ describe how the probability of being uncensored changes with respect to the regressors.

In the next example, we show how to obtain each of these.

▷ Example 1

In example 3 of [R] **tobit**, we fit a two-limit tobit model of `mpg` on `wgt`.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. generate wgt = weight/1000
```

```
. tobit mpg wgt, ll(17) ul(24)
Tobit regression                                  Number of obs   =         74
                                                  LR chi2(1)      =      77.60
                                                  Prob > chi2     =     0.0000
Log likelihood = -104.25976                       Pseudo R2       =     0.2712

------------------------------------------------------------------------------
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         wgt |  -5.764448   .7245417    -7.96   0.000    -7.208457   -4.320438
       _cons |   38.07469   2.255917    16.88   0.000     33.57865    42.57072
-------------+----------------------------------------------------------------
       /sigma |   2.886337   .3952143                      2.098676    3.673998
------------------------------------------------------------------------------
  Obs. summary:         18  left-censored observations at mpg<=17
                        33     uncensored observations
                        23 right-censored observations at mpg>=24
```

`tobit` reports the β coefficients for the latent regression model. The marginal effect of x_k on y is simply the corresponding β_k, because $E(y|x)$ is linear in x. Thus a 1,000-pound increase in a car's weight (which is a 1-unit increase in `wgt`) would lower fuel economy by 5.8 mpg.

To estimate the means of the marginal effects on the expected value of the censored outcome, conditional on weight being each of three values (2,000; 3,000; and 4,000 pounds), we type

```
. margins, dydx(wgt) predict(ystar(17,24)) at(wgt=(2 3 4))
Conditional marginal effects                      Number of obs   =         74
Model VCE    : OIM

Expression   : E(mpg*|17<mpg<24), predict(ystar(17,24))
dy/dx w.r.t. : wgt

1._at        : wgt             =           2

2._at        : wgt             =           3

3._at        : wgt             =           4

------------------------------------------------------------------------------
             |            Delta-method
             |      dy/dx   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
wgt          |
         _at |
          1  |   -1.0861    .311273    -3.49   0.000    -1.696184   -.4760162
          2  |  -4.45315   .4772541    -9.33   0.000    -5.388551    -3.51775
          3  |  -1.412822   .3289702    -4.29   0.000    -2.057591    -.768052
------------------------------------------------------------------------------
```

The $E(y^*|x)$ is nonlinear in x, so the marginal effect for a continuous covariate is not the same as the change in y^* induced by a one-unit change in x. Recall that the marginal effect at a point is the slope of the tangent line at that point. In our example, we estimate the mean of the marginal effects for different values of `wgt`. The estimated mean of the marginal effects is -1.1 mpg for a 2,000 pound car; -4.5 mpg for a 3,000 pound car; and -1.4 mpg for a 4,000 pound car.

To estimate the means of the marginal effects on the expected value of the truncated outcome at the same levels of wgt, we type

```
. margins, dydx(wgt) predict(e(17,24)) at(wgt=(2 3 4))
Conditional marginal effects                      Number of obs   =         74
Model VCE    : OIM
Expression   : E(mpg|17<mpg<24), predict(e(17,24))
dy/dx w.r.t. : wgt
1._at        : wgt             =           2
2._at        : wgt             =           3
3._at        : wgt             =           4
```

	dy/dx	Delta-method Std. Err.	z	P>|z|	[95% Conf.	Interval]
wgt						
_at						
1	-1.166572	.0827549	-14.10	0.000	-1.328768	-1.004375
2	-2.308842	.4273727	-5.40	0.000	-3.146477	-1.471207
3	-1.288896	.0889259	-14.49	0.000	-1.463188	-1.114604

The mean of the marginal effects of a change in wgt on y_i (which is bounded between 17 and 24) is about -1.2 mpg for a 2,000 pound car; -2.3 mpg for a 3,000 pound car; and -1.3 for a 4,000 pound car.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

References

Cong, R. 2000. sg144: Marginal effects of the tobit model. *Stata Technical Bulletin* 56: 27–34. Reprinted in *Stata Technical Bulletin Reprints*, vol. 10, pp. 189–197. College Station, TX: Stata Press.

McDonald, J. F., and R. A. Moffitt. 1980. The use of tobit analysis. *Review of Economics and Statistics* 62: 318–321.

Also see

[R] **tobit** — Tobit regression

[U] **20 Estimation and postestimation commands**

Title

total — Estimate totals

Syntax

`total` *varlist* [*if*] [*in*] [*weight*] [, *options*]

options	Description
if/in/over	
`over(`*varlist*[`, nolabel`]`)`	group over subpopulations defined by *varlist*; optionally, suppress group labels
SE/Cluster	
`vce(`*vcetype*`)`	*vcetype* may be `analytic`, `cluster` *clustvar*, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noheader`	suppress table header
`nolegend`	suppress table legend
display_options	control column formats and line width
`coeflegend`	display legend instead of statistics

`bootstrap`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `pweights`, and `iweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Summaries, tables, and tests > Summary and descriptive statistics > Totals

Description

`total` produces estimates of totals, along with standard errors.

Options

if/in/over

`over(`*varlist* [`, nolabel`]`)` specifies that estimates be computed for multiple subpopulations, which are identified by the different values of the variables in *varlist*.

When this option is supplied with one variable name, such as `over(`*varname*`)`, the value labels of *varname* are used to identify the subpopulations. If *varname* does not have labeled values (or there are unlabeled values), the values themselves are used, provided that they are nonnegative integers. Noninteger values, negative values, and labels that are not valid Stata names are substituted with a default identifier.

When `over()` is supplied with multiple variable names, each subpopulation is assigned a unique default identifier.

`nolabel` specifies that value labels attached to the variables identifying the subpopulations be ignored.

SE/Cluster

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(analytic)`, the default, uses the analytically derived variance estimator associated with the sample total.

Reporting

`level(#)`; see [R] **estimation options**.

`noheader` prevents the table header from being displayed. This option implies `nolegend`.

`nolegend` prevents the table legend identifying the subpopulations from being displayed.

display_options: `cformat(%`*fmt*`)` and `nolstretch`; see [R] **estimation options**.

The following option is available with `total` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

▷ Example 1

Suppose that we collected data on incidence of heart attacks. The variable `heartatk` indicates whether a person ever had a heart attack (1 means yes; 0 means no). We can then estimate the total number of persons who have had heart attacks for each `sex` in the population represented by the data we collected.

```
. use http://www.stata-press.com/data/r12/total
. total heartatk [pw=swgt], over(sex)
Total estimation                  Number of obs    =    4946
         Male: sex = Male
       Female: sex = Female
------------------------------------------------------------
             Over |      Total   Std. Err.   [95% Conf. Interval]
------------------+-----------------------------------------
heartatk         |
             Male |     944559   104372.3      739943     1149175
           Female |     581590   82855.59    419156.3    744023.7
------------------------------------------------------------
```

◁

Saved results

total saves the following in e():

Scalars

e(N)	number of observations
e(N_over)	number of subpopulations
e(N_clust)	number of clusters
e(k_eq)	number of equations in e(b)
e(df_r)	sample degrees of freedom
e(rank)	rank of e(V)

Macros

e(cmd)	total
e(cmdline)	command as typed
e(varlist)	*varlist*
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(cluster)	name of cluster variable
e(over)	*varlist* from over()
e(over_labels)	labels from over() variables
e(over_namelist)	names from e(over_labels)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(marginsnotok)	predictions disallowed by margins

Matrices

e(b)	vector of total estimates
e(V)	(co)variance estimates
e(_N)	vector of numbers of nonmissing observations
e(error)	error code corresponding to e(b)

Functions

e(sample)	marks estimation sample

Methods and formulas

total is implemented as an ado-file.

Methods and formulas are presented under the following headings:

The total estimator
Survey data
The survey total estimator
The poststratified total estimator
Subpopulation estimation

The total estimator

Let y denote the variable on which to calculate the total and $y_j, j = 1, \ldots, n$, denote an individual observation on y. Let w_j be the frequency weight (or iweight), and if no weight is specified, define $w_j = 1$ for all j. See the next section for pweighted data. The sum of the weights is an estimate of the population size:

$$\widehat{N} = \sum_{j=1}^{n} w_j$$

If the population values of y are denoted by $Y_j, j = 1, \ldots, N$, the associated population total is

$$Y = \sum_{j=1}^{N} Y_j = N\overline{y}$$

where $\overline{y}$ is the population mean. The total is estimated as

$$\widehat{Y} = \widehat{N}\overline{y}$$

The variance estimator for the total is

$$\widehat{V}(\widehat{Y}) = \widehat{N}^2\widehat{V}(\overline{y})$$

where $\widehat{V}(\overline{y})$ is the variance estimator for the mean; see [R] **mean**. The standard error of the total is the square root of the variance.

If x, x_j, $\overline{x}$, and $\widehat{X}$ are similarly defined for another variable (observed jointly with y), the covariance estimator between $\widehat{X}$ and $\widehat{Y}$ is

$$\widehat{\mathrm{Cov}}(\widehat{X}, \widehat{Y}) = \widehat{N}^2\widehat{\mathrm{Cov}}(\overline{x}, \overline{y})$$

where $\widehat{\mathrm{Cov}}(\overline{x}, \overline{y})$ is the covariance estimator between two means; see [R] **mean**.

Survey data

See [SVY] **variance estimation** and [SVY] **poststratification** for discussions that provide background information for the following formulas.

The survey total estimator

Let Y_j be a survey item for the jth individual in the population, where $j = 1, \ldots, M$ and M is the size of the population. The associated population total for the item of interest is

$$Y = \sum_{j=1}^{M} Y_j$$

Let y_j be the survey item for the jth sampled individual from the population, where $j = 1, \ldots, m$ and m is the number of observations in the sample.

The estimator $\widehat{Y}$ for the population total Y is

$$\widehat{Y} = \sum_{j=1}^{m} w_j y_j$$

where w_j is a sampling weight. The estimator for the number of individuals in the population is

$$\widehat{M} = \sum_{j=1}^{m} w_j$$

The score variable for the total estimator is the variable itself,

$$z_j(\widehat{Y}) = y_j$$

The poststratified total estimator

Let P_k denote the set of sampled observations that belong to poststratum k, and define $I_{P_k}(j)$ to indicate if the jth observation is a member of poststratum k, where $k = 1, \ldots, L_P$ and L_P is the number of poststrata. Also, let M_k denote the population size for poststratum k. P_k and M_k are identified by specifying the `poststrata()` and `postweight()` options on `svyset`; see [SVY] **svyset**.

The estimator for the poststratified total is

$$\widehat{Y}^P = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{Y}_k = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j)\, w_j y_j$$

where

$$\widehat{M}_k = \sum_{j=1}^{m} I_{P_k}(j) w_j$$

The score variable for the poststratified total is

$$z_j(\widehat{Y}^P) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left(y_j - \frac{\widehat{Y}_k}{\widehat{M}_k} \right)$$

Subpopulation estimation

Let S denote the set of sampled observations that belong to the subpopulation of interest, and define $I_S(j)$ to indicate if the jth observation falls within the subpopulation.

The estimator for the subpopulation total is

$$\widehat{Y}^S = \sum_{j=1}^{m} I_S(j)\, w_j y_j$$

and its score variable is

$$z_j(\widehat{Y}^S) = I_S(j)\, y_j$$

The estimator for the poststratified subpopulation total is

$$\widehat{Y}^{PS} = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \widehat{Y}^S_k = \sum_{k=1}^{L_P} \frac{M_k}{\widehat{M}_k} \sum_{j=1}^{m} I_{P_k}(j) I_S(j)\, w_j y_j$$

and its score variable is

$$z_j(\widehat{Y}^{PS}) = \sum_{k=1}^{L_P} I_{P_k}(j) \frac{M_k}{\widehat{M}_k} \left\{ I_S(j)\, y_j - \frac{\widehat{Y}^S_k}{\widehat{M}_k} \right\}$$

References

Cochran, W. G. 1977. *Sampling Techniques*. 3rd ed. New York: Wiley.

Stuart, A., and J. K. Ord. 1994. *Kendall's Advanced Theory of Statistics: Distribution Theory, Vol I*. 6th ed. London: Arnold.

Also see

[R] **total postestimation** — Postestimation tools for total

[R] **mean** — Estimate means

[R] **proportion** — Estimate proportions

[R] **ratio** — Estimate ratios

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **direct standardization** — Direct standardization of means, proportions, and ratios

[SVY] **poststratification** — Poststratification for survey data

[SVY] **subpopulation estimation** — Subpopulation estimation for survey data

[SVY] **svy estimation** — Estimation commands for survey data

[SVY] **variance estimation** — Variance estimation for survey data

[U] **20 Estimation and postestimation commands**

Title

total postestimation — Postestimation tools for total

Description

The following postestimation commands are available after `total`:

Command	Description
`estat`	VCE
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Remarks

▷ Example 1

Continuing with our data on incidence of heart attacks from example 1 in [R] **total**, we want to test whether there are twice as many heart attacks among men than women in the population.

```
. use http://www.stata-press.com/data/r12/total
. total heartatk [pw=swgt], over(sex)
  (output omitted)
. test _b[Male] = 2*_b[Female]
 ( 1)  [heartatk]Male - 2 [heartatk]Female = 0
       F(  1,  4945) =    1.25
            Prob > F =    0.2643
```

Thus we do not reject our hypothesis that the total number of heart attacks for men is twice that for women in the population.

◁

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **total** — Estimate totals

[U] **20 Estimation and postestimation commands**

Title

tpoisson — Truncated Poisson regression

Syntax

`tpoisson` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
`ll(#` | *varname*`)`	truncation point; default value is `ll(0)`, zero truncation
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`irr`	report incidence-rate ratios
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`vce()` and weights are not allowed with the `svy` prefix; see [SVY] **svy**.
`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Count outcomes > Truncated Poisson regression

Description

`tpoisson` estimates the parameters of a truncated Poisson model by maximum likelihood. The dependent variable *depvar* is regressed on *indepvars*, where *depvar* is a positive count variable whose values are all above the truncation point.

Options

Model

`noconstant`; see [R] **estimation options**.

`ll(`*#* | *varname*`)` specifies the truncation point, which is a nonnegative integer. The default is zero truncation, `ll(0)`.

`exposure(`*varname*$_e$`)`, `offset(`*varname*$_o$`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated. `irr` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `tpoisson` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

Truncated Poisson regression is used to model the number of occurrences of an event when that number is restricted to be above the truncation point. If the dependent variable is not truncated, standard Poisson regression may be more appropriate; see [R] **poisson**. Truncated Poisson regression was first proposed by Grogger and Carson (1991). For an introduction to Poisson regression, see Cameron and Trivedi (2005, 2010) and Long and Freese (2006). For an introduction to truncated Poisson models, see Cameron and Trivedi (1998) and Long (1997, chap. 8).

Suppose that the patients admitted to a hospital for a given condition form a random sample from a population of interest and that each admitted patient stays at least one day. You are interested in modeling the length of stay of patients in days. The sample is truncated at zero because you only have data on individuals who stayed at least one day. `tpoisson` accounts for the truncated sample, whereas `poisson` does not.

Truncation is not the same as censoring. Right-censored Poisson regression was implemented in Stata by Raciborski (2011).

▷ Example 1

Consider the Simonoff (2003) dataset of running shoes for a sample of runners who registered an online running log. A running-shoe marketing executive is interested in knowing how the number of running shoes purchased relates to other factors such as gender, marital status, age, education, income, typical number of runs per week, average miles run per week, and the preferred type of running. These data are naturally truncated at zero. A truncated Poisson model is fit to the number of shoes owned on runs per week, miles run per week, gender, age, and marital status.

No options are needed because zero truncation is the default for `tpoisson`.

```
. use http://www.stata-press.com/data/r12/runshoes
. tpoisson shoes rpweek mpweek male age married
Iteration 0:   log likelihood = -88.328151
Iteration 1:   log likelihood = -86.272639
Iteration 2:   log likelihood = -86.257999
Iteration 3:   log likelihood = -86.257994
Truncated Poisson regression                    Number of obs   =         60
Truncation point: 0                             LR chi2(5)      =      22.75
                                                Prob > chi2     =     0.0004
Log likelihood = -86.257994                     Pseudo R2       =     0.1165
------------------------------------------------------------------------------
       shoes |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      rpweek |   .1575811   .1097893     1.44   0.151    -.057602    .3727641
      mpweek |   .0210673   .0091113     2.31   0.021     .0032094   .0389252
        male |   .0446134   .2444626     0.18   0.855    -.4345246   .5237513
         age |   .0185565   .0137786     1.35   0.178     -.008449   .045562
     married |  -.1283912   .2785044    -0.46   0.645    -.6742498   .4174674
       _cons |  -1.205844   .6619774    -1.82   0.069    -2.503296   .0916078
------------------------------------------------------------------------------
```

Using the zero-truncated Poisson regression with these data, only the coefficient on average miles per week is statistically significant at the 5% level.

◁

▷ Example 2

Semiconductor manufacturing requires that silicon wafers be coated with a layer of metal oxide. The depth of this layer is strictly controlled. In this example, a critical oxide layer is designed for 300 ± 20 angstroms (Å).

After the oxide layer is coated onto a wafer, the wafer enters a photolithography step in which the lines representing the electrical connections are printed on the oxide and later etched and filled with metal. The widths of these lines are measured. In this example, they are controlled to 90 ± 5 micrometers (μm).

After these and other steps, each wafer is electrically tested at probe. If too many failures are discovered, the wafer is rejected and sent for engineering analysis. In this example, the maximum number of probe failures tolerated for this product is 10.

A major failure at probe has been encountered—88 wafers had more than 10 failures each. The 88 wafers that failed were tested using 4 probe machines. The engineer suspects that the failures were a result of faulty probe machines, poor depth control, or poor line widths. The line widths and depths in these data are the actual measurement minus its specification target, 300 Å for the oxide depths and 90 μm for the line widths.

The following table tabulates the average failure rate for each probe using Stata's `mean` command; see [R] **mean**.

```
. use http://www.stata-press.com/data/r12/probe
. mean failures, over(probe) nolegend
Mean estimation                     Number of obs    =        88
```

Over	Mean	Std. Err.	[95% Conf.	Interval]
failures				
1	15.875	1.186293	13.51711	18.23289
2	14.95833	.5912379	13.78318	16.13348
3	16.47059	.9279866	14.62611	18.31506
4	23.09677	.9451117	21.21826	24.97529

The 95% confidence intervals in this table suggest that there are about 5–11 additional failures per wafer on probe 4. These are unadjusted for varying line widths and oxide depths. Possibly, probe 4 received the wafers with larger line widths or extreme oxide depths.

Truncated Poisson regression more clearly identifies the root causes for the increased failures by estimating the differences between probes adjusted for the line widths and oxide depths. It also allows us to determine whether the deviations from specifications in line widths or oxide depths might be contributing to the problem.

```
. tpoisson failures i.probe depth width, ll(10) nolog
Truncated Poisson regression                    Number of obs   =         88
Truncation point: 10                            LR chi2(5)      =      73.70
                                                Prob > chi2     =     0.0000
Log likelihood = -239.35746                     Pseudo R2       =     0.1334
```

failures	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
probe						
2	-.1113037	.1019786	-1.09	0.275	-.3111781	.0885707
3	.0114339	.1036032	0.11	0.912	-.1916245	.2144924
4	.4254115	.0841277	5.06	0.000	.2605242	.5902989
depth	-.0005034	.0033375	-0.15	0.880	-.0070447	.006038
width	.0330225	.015573	2.12	0.034	.0025001	.063545
_cons	2.714025	.0752617	36.06	0.000	2.566515	2.861536

The coefficients listed for the probes are testing the null hypothesis: H_0: probe$_i$ = probe$_1$, where i equals 2, 3, and 4. Because the only coefficient that is statistically significant is the one for testing for H_0: probe$_4$ = probe$_1$, $p < 0.001$, and because the p-values for the other probes are not statistically significant, that is, $p \geq 0.275$, the implication is that there is a difference between probe 4 and the other machines. Because the coefficient for this test is positive, 0.425, the conclusion is that the

average failure rate for probe 4, after adjusting for line widths and oxide depths, is higher than the other probes. Possibly, probe 4 needs calibration or the head used with this machine is defective.

Line-width control is statistically significant, $p = 0.034$, but variation in oxide depths is not causing the increased failure rate. The engineer concluded that the sudden increase in failures is the result of two problems. First, probe 4 is malfunctioning, and second, there is a possible lithography or etching problem.

◁

Saved results

`tpoisson` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(r2_p)`	pseudo-R-squared
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

`e(cmd)`	`tpoisson`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(llopt)`	contents of `ll()`, or `0` if not specified
`e(wtype)`	weight type
`e(wexp)`	weight expression
`e(title)`	title in estimation output
`e(clustvar)`	name of cluster variable
`e(offset)`	linear offset variable
`e(chi2type)`	`Wald` or `LR`; type of model χ^2 test
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(opt)`	type of optimization
`e(which)`	`max` or `min`; whether optimizer is to perform maximization or minimization
`e(ml_method)`	type of `ml` method
`e(user)`	name of likelihood-evaluator program
`e(technique)`	maximization technique
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(Cns)`	constraints matrix
`e(ilog)`	iteration log (up to 20 iterations)
`e(gradient)`	gradient vector
`e(V)`	variance–covariance matrix of the estimators
`e(V_modelbased)`	model-based variance

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`tpoisson` is implemented as an ado-file.

The conditional probability of observing y_j events given that $y_j > \tau_j$, where τ_j is the truncation point, is given by

$$\Pr(Y = y_j \,|\, y_j > \tau_j, \mathbf{x}_j) = \frac{\exp(-\lambda)\lambda^{y_j}}{y_j!\Pr(Y > \tau_j \,|\, \mathbf{x}_j)}$$

The log likelihood (with weights w_j and offsets) is given by

$$\xi_j = \mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$$

$$f(y_j) = \frac{\exp\{-\exp(\xi_j)\}\exp(\xi_j y_j)}{y_j!\Pr(Y > \tau_j \,|\, \xi_j)}$$

$$\ln L = \sum_{j=1}^{n} w_j \left[-\exp(\xi_j) + \xi_j y_j - \ln(y_j!) - \ln\left\{\Pr(Y > \tau_j \,|\, \xi_j)\right\}\right]$$

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`tpoisson` also supports estimation with survey data. For details on variance–covariance estimates with survey data, see [SVY] **variance estimation**.

Acknowledgment

We gratefully acknowledge the previous work by Joseph Hilbe, Arizona State University; see Hilbe (1999).

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Also see

[R] **tpoisson postestimation** — Postestimation tools for tpoisson

[R] **poisson** — Poisson regression

[R] **tnbreg** — Truncated negative binomial regression

[R] **nbreg** — Negative binomial regression

[R] **zinb** — Zero-inflated negative binomial regression

[R] **zip** — Zero-inflated Poisson regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtpoisson** — Fixed-effects, random-effects, and population-averaged Poisson models

[U] **20 Estimation and postestimation commands**

Title

tpoisson postestimation — Postestimation tools for tpoisson

Description

The following postestimation commands are available after `tpoisson`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]
```

statistic	Description
Main	
`n`	number of events; the default
`ir`	incidence rate
`cm`	conditional mean, $E(y_j \mid y_j > \tau_j)$
`pr(`*n*`)`	probability $\Pr(y_j = n)$
`pr(`*a*`,`*b*`)`	probability $\Pr(a \leq y_j \leq b)$
`cpr(`*n*`)`	conditional probability $\Pr(y_j = n \mid y_j > \tau_j)$
`cpr(`*a*`,`*b*`)`	conditional probability $\Pr(a \leq y_j \leq b \mid y_j > \tau_j)$
`xb`	linear prediction
`stdp`	standard error of the linear prediction
`score`	first derivative of the log likelihood with respect to $\mathbf{x}_j\boldsymbol{\beta}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`n`, the default, calculates the predicted number of events, which is $\exp(\mathbf{x}_j\boldsymbol{\beta})$ if neither `offset()` nor `exposure()` was specified when the model was fit; $\exp(\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j)$ if `offset()` was specified; or $\exp(\mathbf{x}_j\boldsymbol{\beta}) \times \text{exposure}_j$ if `exposure()` was specified.

`ir` calculates the incidence rate $\exp(\mathbf{x}_j\boldsymbol{\beta})$, which is the predicted number of events when exposure is 1. This is equivalent to specifying both the `n` and the `nooffset` options.

`cm` calculates the conditional mean,

$$E(y_j \mid y_j > \tau_j) = \frac{E(y_j)}{\Pr(y_j > \tau_j)}$$

where τ_j is the truncation point found in `e(llopt)`.

`pr(`*n*`)` calculates the probability $\Pr(y_j = n)$, where *n* is a nonnegative integer that may be specified as a number or a variable.

`pr(`*a*`,`*b*`)` calculates the probability $\Pr(a \leq y_j \leq b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b \geq .$) means $+\infty$;
`pr(20,.)` calculates $\Pr(y_j \geq 20)$;
`pr(20,`*b*`)` calculates $\Pr(y_j \geq 20)$ in observations for which $b \geq .$ and calculates $\Pr(20 \leq y_j \leq b)$ elsewhere.

`pr(.,`*b*`)` produces a syntax error. A missing value in an observation of the variable *a* causes a missing value in that observation for `pr(`*a*`,`*b*`)`.

`cpr(`*n*`)` calculates the conditional probability $\Pr(y_j = n \,|\, y_j > \tau_j)$, where τ_j is the truncation point found in `e(llopt)`. *n* is an integer greater than the truncation point that may be specified as a number or a variable.

`cpr(`*a*`,`*b*`)` calculates the conditional probability $\Pr(a \leq y_j \leq b \,|\, y_j > \tau_j)$, where τ_j is the truncation point found in `e(llopt)`. The syntax for this option is analogous to that used for `pr(`*a*`,`*b*`)` except that *a* must be greater than the truncation point.

`xb` calculates the linear prediction, which is $\mathbf{x}_j\boldsymbol{\beta}$ if neither `offset()` nor `exposure()` was specified when the model was fit; $\mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j$ if `offset()` was specified; or $\mathbf{x}_j\boldsymbol{\beta} + \ln(\text{exposure}_j)$ if `exposure()` was specified; see `nooffset` below.

`stdp` calculates the standard error of the linear prediction.

`score` calculates the equation-level score, $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

`nooffset` is relevant only if you specified `offset()` or `exposure()` when you fit the model. It modifies the calculations made by `predict` so that they ignore the offset or exposure variable; the linear prediction is treated as $\mathbf{x}_j\boldsymbol{\beta}$ rather than as $\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j$ or $\mathbf{x}_j\boldsymbol{\beta}+\ln(\text{exposure}_j)$. Specifying `predict ..., nooffset` is equivalent to specifying `predict ..., ir`.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

In the following formula, we use the same notation as in [R] **tpoisson**.

The equation-level scores are given by

$$\text{score}(\mathbf{x}\boldsymbol{\beta})_j = y_j - e^{\xi_j} - \frac{e^{-e^{\xi_j}}e^{\xi_j}}{\Pr(Y > \tau_j \,|\, \xi_j)}$$

where τ_j is the truncation point found in `e(llopt)`.

Also see

[R] **tpoisson** — Truncated Poisson regression

[U] **20 Estimation and postestimation commands**

Title

translate — Print and translate logs

Syntax

Print log and SMCL files

`print` *filename* [`, like(`*ext*`) name(`*windowname*`)` *override_options*]

Translate log files to SMCL files and vice versa

`translate` *filename*$_{\text{in}}$ *filename*$_{\text{out}}$ [`, translator(`*tname*`) name(`*windowname*`)`

override_options `replace`]

View translator parameter settings

`translator query` [*tname*]

Change translator parameter settings

`translator set` [*tname setopt setval*]

Return translator parameter settings to default values

`translator reset` *tname*

List current mappings from one extension to another

`transmap query` [*.ext*]

Specify that files with one extension be treated the same as files with another extension

`transmap define` *.ext*$_{\text{new}}$ *.ext*$_{\text{old}}$

filename in `print`, in addition to being a filename to be printed, may be specified as `@Results` to mean the Results window and `@Viewer` to mean the Viewer window.

filename$_{\text{in}}$ in `translate` may be specified just as *filename* in `print`.

tname in `translator` specifies the name of a translator; see the `translator()` option under *Options for translate*.

Description

`print` prints log, SMCL, and text files. Although there is considerable flexibility in how `print` (and `translate`, which `print` uses) can be set to work, they have already been set up and should just work:

```
. print mylog.smcl
. print mylog.log
```

Unix users may discover that they need to do a bit of setup before `print` works; see *Printing files, Unix* below. International Unix users may also wish to modify the default paper size. All users can tailor `print` and `translate` to their needs.

`print` may also be used to print the current contents of the Results window or the Viewer. For instance, the current contents of the Results window could be printed by typing

```
. print @Results
```

`translate` translates log and SMCL files from one format to another, the other typically being suitable for printing. `translate` can also translate SMCL logs (logs created by typing, say, `log using mylog`) to plain text:

```
. translate mylog.smcl mylog.log
```

You can use `translate` to recover a log when you have forgotten to start one. You may type

```
. translate @Results mylog.txt
```

to capture as plain text what is currently shown in the Results window.

This entry provides a general overview of `print` and `translate` and covers in detail the printing and translation of text (nongraphic) files.

`translator query`, `translator set`, and `translator reset` show, change, and restore the default values of the settings for each translator.

`transmap define` and `transmap query` create and show mappings from one file extension to another for use with `print` and `translate`.

For example, `print myfile.txt` knows to use a translator appropriate for printing text files because of the `.txt` extension. However, it does not know what to do with `.xyz` files. If you have `.xyz` files and always wish to treat them as `.txt` files, you can type `transmap define .xyz .txt`.

Options for print

`like(`*ext*`)` specifies how the file should be translated to a form suitable for printing. The default is to determine the translation method from the extension of *filename*. Thus `mylog.smcl` is translated according to the rule for translating `smcl` files, `myfile.txt` is translated according to the rule for translating `txt` files, and so on. (These rules are, in fact, `translate`'s `smcl2prn` and `txt2prn` translators, but put that aside for the moment.)

Rules for the following extensions are predefined:

`.txt`	assume input file contains plain text
`.log`	assume input file contains Stata log text
`.smcl`	assume input file contains SMCL

To print a file that has an extension different from those listed above, you can define a new extension, but you do not have to do that. Assume that you wish to print the file `read.me`, which you know to contain plain text. If you were just to type `print read.me`, you would be told that Stata cannot translate `.me` files. (You would actually be told that the translator for `me2prn` was not found.) You could type `print read.me, like(txt)` to tell `print` to print `read.me` like a `.txt` file.

On the other hand, you could type

```
. transmap define .me .txt
```

to tell Stata that `.me` files are always to be treated like `.txt` files. If you did that, Stata would remember the new rule, even in future sessions.

When you specify the `like()` option, you override the recorded rules. So, if you were to type `print mylog.smcl, like(txt)`, the file would be printed as plain text (meaning that all the SMCL commands would show).

`name(`*windowname*`)` specifies which window to print when printing a Viewer. The default is for Stata to print the topmost Viewer [Unix(GUI) users: See the second technical note in *Printing files, Unix*]. The `name()` option is ignored when printing the Results window.

The window name is located inside parentheses in the window title. For example, if the title for a Viewer window is *Viewer (#1) [help print]*, the name for the window is `#1`.

override_options refers to `translate`'s options for overriding default values. `print` uses `translate` to translate the file into a format suitable for sending to the printer, and thus `translate`'s *override_options* may also be used with `print`. The settings available vary between each translator (for example, `smcl2ps` will have different settings than `smcl2txt`) and may also differ across operating systems (for example, Windows may have different printing options than Mac OS X). To find out what you can override when printing `.smcl` files, type

```
. translator query smcl2prn
(output omitted)
```

In the omitted output, you might learn that there is an `rmargin` # tunable value, which specifies the right margin in inches. You could specify the *override_option* `rmargin(#)` to temporarily override the default value, or you could type `translator set smcl2prn rmargin` # beforehand to permanently reset the value.

Alternatively, on some computers with some translators, you might discover that nothing can be set.

Options for translate

`translator(`*tname*`)` specifies the name of the translator to be used to translate the file. The available translators are

tname	Input	Output
`smcl2ps`	SMCL	PostScript
`log2ps`	Stata text log	PostScript
`txt2ps`	generic text file	PostScript
`Viewer2ps`	Viewer window	PostScript
`Results2ps`	Results window	PostScript
`smcl2prn`	SMCL	default printer format
`log2prn`	Stata text log	default printer format
`txt2prn`	generic text log	default printer format
`Results2prn`	Results window	default printer format
`Viewer2prn`	Viewer window	default printer format
`smcl2txt`	SMCL	generic text file
`smcl2log`	SMCL	Stata text log
`Results2txt`	Results window	generic text file
`Viewer2txt`	Viewer window	generic text file
`smcl2pdf`	SMCL	PDF
`log2pdf`	Stata text log	PDF
`txt2pdf`	generic text log	PDF
`Results2pdf`	Results window	PDF
`Viewer2pdf`	Viewer window	PDF

If `translator()` is not specified, `translate` determines which translator to use from extensions of the filenames specified. Typing `translate myfile.smcl myfile.ps` would use the `smcl2ps` translator. Typing `translate myfile.smcl myfile.ps, translate(smcl2prn)` would override the default and use the `smcl2prn` translator.

Actually, when you type `translate` *a*`.`*b* *c*`.`*d*, `translate` looks up `.`*b* in the `transmap` extension-synonym table. If `.`*b* is not found, the translator *b*`2`*d* is used. If `.`*b* is found in the table, the mapped extension is used (call it *b*′), and then the translator *b*′`2`*d* is used. For example,

Command	Translator used
`. translate myfile.smcl myfile.ps`	`smcl2ps`
`. translate myfile.odd myfile.ps`	`odd2ps`, which does not exist, so error
`. transmap define .odd .txt`	
`. translate myfile.odd myfile.ps`	`txt2ps`

You can list the mappings that `translate` uses by typing `transmap query`.

`name(`*windowname*`)` specifies which window to translate when translating a Viewer. The default is for Stata to translate the topmost Viewer. The `name()` option is ignored when translating the Results window.

The window name is located inside parentheses in the window title. For example, if the title for a Viewer window is *Viewer (#1) [help print]*, the name for the window is `#1`.

override_options override any of the default options of the specified or implied translator. To find out what you can override for, say, `log2ps`, type

```
. translator query log2ps
(output omitted)
```

In the omitted output, you might learn that there is an `rmargin` # tunable value, which, for `log2ps`, specifies the right margin in inches. You could specify the *override_option* `rmargin(#)` to temporarily override the default value or type `translator set log2ps rmargin` # beforehand to permanently reset the value.

`replace` specifies that *filename*$_{\text{out}}$ be replaced if it already exists.

Remarks

Remarks are presented under the following headings:

Printing files
Printing files, Mac and Windows
Printing files, Unix
Translating files from one format to another

Printing files

Printing should be easy; just type

```
. print mylog.smcl
. print mylog.log
```

You can use `print` to print SMCL files, plain text files, and even the contents of the Results and Viewer windows:

```
. print @Results
```

```
. print @Viewer
. print @Viewer, name(#2)
```

For information about printing and translating graph files, see [G-2] **graph print** and see [G-2] **graph export**.

Printing files, Mac and Windows

When you type `print`, you are using the same facility that you would be using if you had selected **Print** from the **File** menu. If you try to print a file that Stata does not know about, Stata will complain:

```
. print read.me
translator me2prn not found
(perhaps you need to specify the like() option)
r(111);
```

Then you could type

```
. print read.me, like(txt)
```

to indicate that you wanted `read.me` sent to the printer in the same fashion as if the file were named `readme.txt`, or you could type

```
. transmap define .me .txt
. print read.me
```

Here you are telling Stata once and for all that you want files ending in `.me` to be treated in the same way as files ending in `.txt`. Stata will remember this mapping, even across sessions. To clear the `.me` mapping, type

```
. transmap define .me
```

To see all the mappings, type

```
. transmap query
```

To print to a file, use the `translate` command, not `print`:

```
. translate mylog.smcl mylog.prn
```

`translate` prints to a file by using the Windows print driver when the new filename ends in `.prn`. Under Mac, the `prn` translators are the same as the `pdf` translators. We suggest that you simply use the `.pdf` file extension when printing to a file.

Printing files, Unix

Stata assumes that you have a PostScript printer attached to your Unix computer and that the Unix command `lpr(1)` can be used to send PostScript files to it, but you can change this. On your Unix system, typing

```
mycomputer$ lpr < filename
```

may not be sufficient to print PostScript files. For instance, perhaps on your system you would need to type

```
mycomputer$ lpr -Plexmark < filename
```

or

```
mycomputer$ lpr -Plexmark filename
```

or something else. To set the print command to be `lpr -Plexmark` *filename* and to state that the printer expects to receive PostScript files, type

```
. printer define prn ps "lpr -Plexmark @"
```

To set the print command to `lpr -Plexmark <` *filename* and to state that the printer expects to receive plain text files, type

```
. printer define prn txt "lpr -Plexmark < @"
```

That is, just type the command necessary to send files to your printer and include an `@` sign where the filename should be substituted. Two file formats are available: `ps` and `txt`. The default setting, as shipped from the factory, is

```
. printer define prn ps "lpr < @"
```

We will return to the `printer` command in the technical note that follows because it has some other capabilities you should know about.

In any case, after you redefine the default printer, the following should just work:

```
. print mylog.smcl
. print mylog.log
```

If you try to print a file that Stata does not know about, it will complain:

```
. print read.me
translator me2prn not found
r(111);
```

Here you could type

```
. print read.me, like(txt)
```

to indicate that you wanted `read.me` sent to the printer in the same fashion as if the file were named `readme.txt`, or you could type

```
. transmap define .me .txt
. print read.me
```

Here you are telling Stata once and for all that you want files ending in `.me` to be treated in the same way as files ending in `.txt`. Stata will remember this setting for `.me`, even across sessions.

If you want to clear the `.me` setting, type

```
. transmap define .me
```

If you want to see all your settings, type

```
. transmap query
```

❑ Technical note

The syntax of the `printer` command is

`printer define` *printername* [{ `ps` | `txt` } `"`*Unix command with* `@"`]

`printer query` [*printername*]

You may define multiple printers. By default, `print` uses the printer named `prn`, but `print` has the syntax

`print` *filename* [`, like(`*ext*`) printer(`*printername*`)` *override_options*]

so, if you define multiple printers, you may route your output to them.

For instance, if you have a second printer on your system, you might type

```
. printer define lexmark ps "lpr -Plexmark < @"
```

After doing that, you could type

```
. print myfile.smcl, printer(lexmark)
```

Any printers that you set will be remembered even across sessions. You can delete printers:

```
. printer define lexmark
```

You can list all the defined printers by typing `printer query`, and you can list the definition of a particular printer, say, `prn`, by typing `printer query prn`.

The default printer `prn` we have predefined for you is

```
. printer define prn ps "lpr < @"
```

meaning that we assume that it is a PostScript printer and that the Unix command `lpr(1)`, without options, is sufficient to cause files to print. Feel free to change the default definition. If you change it, the change will be remembered across sessions. ❑

❑ Technical note

Unix(GUI) users should note that X-Windows does not have the concept of a window z-order, which prevents Stata from determining which window is the topmost window. Instead, Stata determines which window is topmost based on which window has the focus. However, some window managers will set the focus to a window without bringing the window to the top. What Stata considers the topmost window may not appear topmost visually. For this reason, you should always use the `name()` option to ensure that the correct window is printed. ❑

❑ Technical note

When you select the Results window to print from the **Print** menu or toolbar button, the result is the same as if you were to issue the `print` command. When you select a Viewer window to print from the **Print** menu or toolbar button, the result is the same as if you were to issue the `print` command with a `name()` option. ❑

The translation to PostScript format is done by `translate` and, in particular, is performed by the translators `smcl2ps`, `log2ps`, and `txt2ps`. There are many tunable parameters in each of these translators. You can display the current values of these tunable parameters for, say, `smcl2ps` by typing

```
. translator query smcl2ps
(output omitted)
```

and you can set any of the tunable parameters (for instance, setting `smcl2ps`'s `rmargin` value to 1) by typing

```
. translator set smcl2ps rmargin 1
(output omitted)
```

Any settings you make will be remembered across sessions. You can reset `smcl2ps` to be as it was when Stata was shipped by typing

```
. translator reset smcl2ps
```

Translating files from one format to another

If you have a SMCL log, which you might have created by previously typing `log using mylog`, you can translate it to an text log by typing

```
. translate myfile.smcl myfile.log
```

and you can translate it to a PostScript file by typing

```
. translate myfile.smcl myfile.ps
```

`translate` translates files from one format to another, and, in fact, `print` uses `translate` to produce a file suitable for sending to the printer.

When you type

```
. translate a.b c.d
```

`translate` looks for the predefined translator *b*2*d* and uses that to perform the translation. If there is a `transmap` synonym for *b*, however, the mapped value b' is used: b'2*d*.

Only certain translators exist, and they are listed under the description of the `translate()` option in *Options for translate* above, or you can type

```
. translator query
```

for a complete (and perhaps more up-to-date) list.

Anyway, `translate` forms the name *b*2*d* or b'2*d*, and if the translator does not exist, `translate` issues an error message. With the `translator()` option, you can specify exactly which translator to use, and then it does not matter how your files are named.

The only other thing to know is that some translators have tunable parameters that affect how they perform their translation. You can type

```
. translator query translator_name
```

to find out what those parameters are. Some translators have no tunable parameters, and some have many:

```
. translator query smcl2ps
```

header	on							
headertext								
logo	on							
user								
projecttext								
cmdnumber	on							
fontsize	9			lmargin	1.00			
pagesize	letter			rmargin	1.00			
pagewidth	8.50			tmargin	1.00			
pageheight	11.00			bmargin	1.00			
scheme	monochrome							
cust1_result_color	0	0	0	cust2_result_color	0	0	0	
cust1_standard_color	0	0	0	cust2_standard_color	0	0	0	
cust1_error_color	0	0	0	cust2_error_color	255	0	0	
cust1_input_color	0	0	0	cust2_input_color	0	0	0	
cust1_link_color	0	0	0	cust2_link_color	0	0	255	
cust1_hilite_color	0	0	0	cust2_hilite_color	0	0	0	
cust1_result_bold	on			cust2_result_bold	on			
cust1_standard_bold	off			cust2_standard_bold	off			
cust1_error_bold	on			cust2_error_bold	on			
cust1_input_bold	off			cust2_input_bold	off			
cust1_link_bold	off			cust2_link_bold	off			
cust1_hilite_bold	on			cust2_hilite_bold	on			
cust1_link_underline	on			cust2_link_underline	on			
cust1_hilite_underline	off			cust2_hilite_underline	off			

You can temporarily override any setting by specifying the *setopt*(*setval*) option on the `translate` (or `print`) command. For instance, you can type

```
. translate ..., ... cmdnumber(off)
```

or you can reset the value permanently by typing

```
. translator set smcl2ps setopt setval
```

For instance,

```
. translator set smcl2ps cmdnumber off
```

If you reset a value, Stata will remember the change, even in future sessions.

Mac and Windows users: The `smcl2ps` (and the other `*2ps` translators) are not used by `print`, even when you have a PostScript printer attached to your computer. Instead, the Mac or Windows print driver is used. Resetting `smcl2ps` values will not affect printing; instead, you change the defaults in the Printers Control Panel in Windows and by selecting **Page Setup...** from the **File** menu in Mac. You can, however, `translate` files yourself using the `smcl2ps` translator and the other `*2ps` translators.

Saved results

`transmap query` *.ext* saves in macro `r(suffix)` the mapped extension (without the leading period) or saves *ext* if the *ext* is not mapped.

`translator query` *translatorname* saves *setval* in macro `r(`*setopt*`)` for every *setopt*, *setval* pair.

`printer query` *printername* (Unix only) saves in macro `r(suffix)` the "filetype" of the input that the printer expects (currently "`ps`" or "`txt`") and, in macro `r(command)`, the command to send output to the printer.

Methods and formulas

`print` is implemented as an ado-file.

Also see

[R] **log** — Echo copy of session to file

[G-2] **graph export** — Export current graph

[G-2] **graph print** — Print a graph

[G-2] **graph set** — Set graphics options

[P] **smcl** — Stata Markup and Control Language

[U] **15 Saving and printing output—log files**

Title

treatreg — Treatment-effects model

Syntax

Basic syntax

```
treatreg depvar [indepvars], treat(depvar_t = indepvars_t) [twostep]
```

Full syntax for maximum likelihood estimates only

```
treatreg depvar [indepvars] [if] [in] [weight],
  treat(depvar_t = indepvars_t [, noconstant]) [treatreg_ml_options]
```

Full syntax for two-step consistent estimates only

```
treatreg depvar [indepvars] [if] [in],
  treat(depvar_t = indepvars_t [, noconstant]) twostep [treatreg_ts_options]
```

treatreg_ml_options	Description
Model	
*`treat()`	equation for treatment effects
`noconstant`	suppress constant term
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`first`	report first-step probit estimates
`noskip`	perform likelihood-ratio test
`hazard(`*newvar*`)`	create *newvar* containing hazard from treatment equation
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

*`treat(`*depvar_t* `=` *indepvars_t* `[, noconstant])` is required.

treatreg_ts_options	Description
Model	
*treat()	equation for treatment effects
*twostep	produce two-step consistent estimate
noconstant	suppress constant term
SE	
vce(*vcetype*)	*vcetype* may be conventional, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
first	report first-step probit estimates
hazard(*newvar*)	create *newvar* containing hazard from treatment equation
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
coeflegend	display legend instead of statistics

*treat(*depvar*$_t$ = *indepvars*$_t$ [, noconstant]) and twostep are required.

indepvars and *indepvars*$_t$ may contain factor variables; see [U] **11.4.3 Factor variables**.
depvar, *indepvars*, *depvar*$_t$, and *indepvars*$_t$ may contain time-series operators; see [U] **11.4.4 Time-series varlists**.
bootstrap, by, jackknife, rolling, statsby, and svy are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the bootstrap prefix; see [R] **bootstrap**.
aweights are not allowed with the jackknife prefix; see [R] **jackknife**.
twostep, vce(), first, noskip, hazard(), and weights are not allowed with the svy prefix; see [SVY] **svy**.
pweights, aweights, fweights, and iweights are allowed with maximum likelihood estimation; see [U] **11.1.6 weight**. No weights are allowed if twostep is specified.
coeflegend does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

treatreg for maximum likelihood estimates

Statistics > Sample-selection models > Treatment-effects model (ML)

treatreg for two-step consistent estimates

Statistics > Sample-selection models > Treatment-effects model (two-step)

Description

treatreg fits a treatment-effects model by using either a two-step consistent estimator or full maximum likelihood. The treatment-effects model considers the effect of an endogenously chosen binary treatment on another endogenous continuous variable, conditional on two sets of independent variables.

Options for maximum likelihood estimates

Model

`treat(`*depvar*$_t$ `=` *indepvars*$_t$ [`, noconstant`]`)` specifies the variables and options for the treatment equation. It is an integral part of specifying a treatment-effects model and is required.

`noconstant`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`first` specifies that the first-step probit estimates of the treatment equation be displayed before estimation.

`noskip` specifies that a full maximum-likelihood model with only a constant for the regression equation be fit. This model is not displayed but is used as the base model to compute a likelihood-ratio test for the model test statistic displayed in the estimation header. By default, the overall model test statistic is an asymptotically equivalent Wald test that all the parameters in the regression equation are zero (except the constant). For many models, this option can substantially increase estimation time.

`hazard(`*newvar*`)` will create a new variable containing the hazard from the treatment equation. The hazard is computed from the estimated parameters of the treatment equation.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: `difficult`, `technique(`*algorithm_spec*`)`, `iterate(#)`, [`no`]`log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(`*init_specs*`)`; see [R] **maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default *vcetype* to `vce(opg)`.

The following option is available with `treatreg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Options for two-step consistent estimates

Model

`treat(`*depvar*$_t$ `=` *indepvars*$_t$ [`, noconstant`]`)` specifies the variables and options for the treatment equation. It is an integral part of specifying a treatment-effects model and is required.

`twostep` specifies that two-step consistent estimates of the parameters, standard errors, and covariance matrix be produced, instead of the default maximum likelihood estimates.

`noconstant`; see [R] **estimation options**.

SE

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory and that use bootstrap or jackknife methods; see [R] ***vce_option***.

`vce(conventional)`, the default, uses the conventionally derived variance estimator for the two-step estimator of the treatment-effects model.

Reporting

`level(#)`; see [R] **estimation options**.

`first` specifies that the first-step probit estimates of the treatment equation be displayed before estimation.

`hazard(`*newvar*`)` will create a new variable containing the hazard from the treatment equation. The hazard is computed from the estimated parameters of the treatment equation.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `treatreg` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

The treatment-effects model estimates the effect of an endogenous binary treatment, z_j, on a continuous, fully observed variable y_j, conditional on the independent variables x_j and w_j. The primary interest is in the regression function

$$y_j = \mathbf{x}_j\boldsymbol{\beta} + \delta z_j + \epsilon_j$$

where z_j is an endogenous dummy variable indicating whether the treatment is assigned or not. The binary decision to obtain the treatment z_j is modeled as the outcome of an unobserved latent variable, z_j^*. It is assumed that z_j^* is a linear function of the exogenous covariates $\mathbf{w}_j$ and a random component u_j. Specifically,

$$z_j^* = \mathbf{w}_j\boldsymbol{\gamma} + u_j$$

and the observed decision is

$$z_j = \begin{cases} 1, & \text{if } z_j^* > 0 \\ 0, & \text{otherwise} \end{cases}$$

where ϵ and u are bivariate normal with mean zero and covariance matrix

$$\begin{bmatrix} \sigma^2 & \rho\sigma \\ \rho\sigma & 1 \end{bmatrix}$$

There are many variations of this model in the literature. Maddala (1983) derives the maximum likelihood and two-step estimators of the version implemented here and also gives a brief review of several empirical applications of this model. Barnow, Cain, and Goldberger (1981) provide another useful derivation of this model. Barnow, Cain, and Goldberger (1981) concentrate on deriving the conditions for which the self-selection bias of the simple OLS estimator of the treatment effect, δ, is nonzero and of a specific sign.

▷ Example 1

We will illustrate `treatreg` with part of the Mroz dataset distributed with Berndt (1996). This dataset contains 753 observations on women's labor supply. Our subsample is of 250 observations, with 150 market laborers and 100 nonmarket laborers.

```
. use http://www.stata-press.com/data/r12/labor
. describe
Contains data from http://www.stata-press.com/data/r12/labor.dta
  obs:           250
 vars:            15                          18 Apr 2011 05:01
 size:        15,000
```

variable name	storage type	display format	value label	variable label
lfp	float	%9.0g		1 if woman worked in 1975
whrs	float	%9.0g		wife's hours of work
kl6	float	%9.0g		# of children younger than 6
k618	float	%9.0g		# of children between 6 and 18
wa	float	%9.0g		wife's age
we	float	%9.0g		wife's education attainment
ww	float	%9.0g		wife's wage
hhrs	float	%9.0g		husband's hours worked in 1975
ha	float	%9.0g		husband's age
he	float	%9.0g		husband's educational attainment
hw	float	%9.0g		husband's wage
faminc	float	%9.0g		family income
wmed	float	%9.0g		wife's mother's educational attainment
wfed	float	%9.0g		wife's father's educational attainment
cit	float	%9.0g		1 if live in large city

```
Sorted by:
. summarize
```

Variable	Obs	Mean	Std. Dev.	Min	Max
lfp	250	.6	.4908807	0	1
whrs	250	799.84	915.6035	0	4950
kl6	250	.236	.5112234	0	3
k618	250	1.364	1.370774	0	8
wa	250	42.92	8.426483	30	60
we	250	12.352	2.164912	5	17
ww	250	2.27523	2.59775	0	14.631
hhrs	250	2234.832	600.6702	768	5010
ha	250	45.024	8.171322	30	60
he	250	12.536	3.106009	3	17
hw	250	7.494435	4.636192	1.0898	40.509
faminc	250	23062.54	12923.98	3305	91044
wmed	250	9.136	3.536031	0	17
wfed	250	8.608	3.751082	0	17
cit	250	.624	.4853517	0	1

We will assume that the wife went to college if her educational attainment is more than 12 years. Let `wc` be the dummy variable indicating whether the individual went to college. With this definition, our sample contains the following distribution of college education:

```
. generate wc = 0
. replace wc = 1 if we > 12
(69 real changes made)
. tab wc
```

wc	Freq.	Percent	Cum.
0	181	72.40	72.40
1	69	27.60	100.00
Total	250	100.00	

We will model the wife's wage as a function of her age, whether the family was living in a big city, and whether she went to college. An ordinary least-squares estimation produces the following results:

```
. regress ww wa cit wc
```

Source	SS	df	MS		
Model	93.2398568	3	31.0799523	Number of obs =	250
Residual	1587.08776	246	6.45157627	F(3, 246) =	4.82
				Prob > F =	0.0028
Total	1680.32762	249	6.74830369	R-squared =	0.0555
				Adj R-squared =	0.0440
				Root MSE =	2.54

ww	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
wa	-.0104985	.0192667	-0.54	0.586	-.0484472	.0274502
cit	.1278922	.3389058	0.38	0.706	-.5396351	.7954195
wc	1.332192	.3644344	3.66	0.000	.6143819	2.050001
_cons	2.278337	.8432385	2.70	0.007	.6174488	3.939225

Is 1.332 a consistent estimate of the marginal effect of a college education on wages? If individuals choose whether to attend college and the error term of the model that gives rise to this choice is correlated with the error term in the wage equation, then the answer is no. (See Barnow, Cain, and Goldberger [1981] for a good discussion of the existence and sign of selectivity bias.) We might suspect that individuals with higher abilities, either innate or due to the circumstances of their birth, would be more likely to go to college and to earn higher wages. Such ability is, of course, unobserved. Furthermore, if the error term in our model for going to college is correlated with ability, and the error term in our wage equation is correlated with ability, the two terms should be positively correlated. These conditions make the problem of signing the selectivity bias equivalent to an omitted-variable problem. In the case at hand, because we would expect the correlation between the omitted variable and a college education to be positive, we suspect that OLS is biased upward.

To account for the bias, we fit the treatment-effects model. We model the wife's college decision as a function of her mother's and her father's educational attainment. Thus we are interested in fitting the model

$$\texttt{ww} = \beta_0 + \beta_1\texttt{wa} + \beta_2\texttt{cit} + \delta\texttt{wc} + \epsilon$$

$$wc^* = \gamma_0 + \gamma_1\texttt{wmed} + \gamma_2\texttt{wfed} + u$$

where

$$\texttt{wc} = \begin{cases} 1, & wc^* > 0, \text{ that is, wife went to college} \\ 0, & \text{otherwise} \end{cases}$$

and where ϵ and u have a bivariate normal distribution with zero mean and covariance matrix

$$\begin{bmatrix} \sigma^2 & \rho\sigma \\ \rho\sigma & 1 \end{bmatrix}$$

The following output gives the maximum likelihood estimates of the parameters of this model:

```
. treatreg ww wa cit, treat(wc=wmed wfed)
Iteration 0:   log likelihood = -707.07237
Iteration 1:   log likelihood = -707.07215
Iteration 2:   log likelihood = -707.07215
Treatment-effects model -- MLE                  Number of obs   =        250
                                                Wald chi2(3)    =       4.11
Log likelihood = -707.07215                     Prob > chi2     =     0.2501
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
ww						
wa	-.0110424	.0199652	-0.55	0.580	-.0501735	.0280887
cit	.127636	.3361938	0.38	0.704	-.5312917	.7865638
wc	1.271327	.7412951	1.72	0.086	-.1815842	2.724239
_cons	2.318638	.9397573	2.47	0.014	.4767478	4.160529
wc						
wmed	.1198055	.0320056	3.74	0.000	.0570757	.1825352
wfed	.0961886	.0290868	3.31	0.001	.0391795	.1531977
_cons	-2.631876	.3309128	-7.95	0.000	-3.280453	-1.983299
/athrho	.0178668	.1899898	0.09	0.925	-.3545063	.3902399
/lnsigma	.9241584	.0447455	20.65	0.000	.8364588	1.011858
rho	.0178649	.1899291			-.3403659	.371567
sigma	2.519747	.1127473			2.308179	2.750707
lambda	.0450149	.4786442			-.8931105	.9831404

```
LR test of indep. eqns. (rho = 0):   chi2(1) =     0.01   Prob > chi2 = 0.9251
```

In the input, we specified that the continuous dependent variable, `ww` (wife's wage), is a linear function of `cit` and `wa`. Note the syntax for the treatment variable. The treatment `wc` is not included in the first variable list; it is specified in the `treat()` option. In this example, `wmed` and `wfed` are specified as the exogenous covariates in the treatment equation.

The output has the form of many two-equation estimators in Stata. We note that our conjecture that the OLS estimate was biased upward is verified. But it is perhaps more interesting that the size of the bias is negligible, and the likelihood-ratio test at the bottom of the output indicates that we cannot reject the null hypothesis that the two error terms are uncorrelated. This result might be due to several specification errors. We ignored the selectivity bias due to the endogeneity of entering the labor market. We have also written both the wage equation and the college-education equation in linear form, ignoring any higher power terms or interactions.

The results for the two ancillary parameters require explanation. For numerical stability during optimization, `treatreg` does not directly estimate ρ or σ. Instead, `treatreg` estimates the inverse hyperbolic tangent of ρ,

$$\operatorname{atanh}\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

and $\ln\sigma$. Also, `treatreg` reports $\lambda = \rho\sigma$, along with an estimate of the standard error of the estimate and confidence interval.

◁

▷ Example 2

Stata also produces a two-step estimator of the model with the `twostep` option. Maximum likelihood estimation of the parameters can be time consuming with large datasets, and the two-step estimates may provide a good alternative in such cases. Continuing with the women's wage model, we can obtain the two-step estimates with consistent covariance estimates by typing

```
. treatreg ww wa cit, treat(wc=wmed wfed) twostep
Treatment-effects model -- two-step estimates   Number of obs      =       250
                                                Wald chi2(3)       =      3.67
                                                Prob > chi2        =    0.2998
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
ww						
wa	-.0111623	.020152	-0.55	0.580	-.0506594	.0283348
cit	.1276102	.33619	0.38	0.704	-.53131	.7865305
wc	1.257995	.8007428	1.57	0.116	-.3114319	2.827422
_cons	2.327482	.9610271	2.42	0.015	.4439031	4.21106
wc						
wmed	.1198888	.0319862	3.75	0.000	.0571971	.1825806
wfed	.0960764	.0290583	3.31	0.001	.0391233	.1530295
_cons	-2.631496	.3308389	-7.95	0.000	-3.279928	-1.983063
hazard						
lambda	.0548738	.5283928	0.10	0.917	-.9807571	1.090505
rho	0.02178					
sigma	2.5198211					

The reported `lambda` (λ) is the parameter estimate on the hazard from the augmented regression, which is derived in Maddala (1983) and presented in *Methods and formulas* below.

◁

❑ Technical note

The difference in expected earnings between participants and nonparticipants is

$$E\left(y_j \mid z_j = 1\right) - E\left(y_j \mid z_j = 0\right) \;=\; \delta + \rho\sigma \left[\frac{\phi(\mathbf{w}_j\boldsymbol{\gamma})}{\Phi(\mathbf{w}_j\boldsymbol{\gamma})\{1 - \Phi(\mathbf{w}_j\boldsymbol{\gamma})\}} \right]$$

where ϕ is the standard normal density and Φ is the standard normal cumulative distribution function. If the correlation between the error terms, ρ, is zero, the problem reduces to one estimable by OLS and the difference is simply δ. Because ρ is positive in the example, least squares overestimates the treatment effect, δ.

❑

Saved results

treatreg (maximum likelihood) saves the following in e():

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_aux)	number of auxiliary parameters
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(N_clust)	number of clusters
e(lambda)	λ
e(selambda)	standard error of λ
e(sigma)	estimate of sigma
e(chi2)	χ^2
e(chi2_c)	χ^2 for comparison test
e(p_c)	p-value for comparison test
e(p)	significance
e(rho)	ρ
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	treatreg
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(hazard)	variable containing hazard
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(method)	ml
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(footnote)	program used to implement the footnote display
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

`treatreg` (two-step) saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(df_m)`	model degrees of freedom
`e(lambda)`	λ
`e(selambda)`	standard error of λ
`e(sigma)`	estimate of sigma
`e(chi2)`	χ^2
`e(p)`	significance
`e(rho)`	ρ
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`treatreg`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(title)`	title in estimation output
`e(chi2type)`	`Wald` or `LR`; type of model χ^2 test
`e(vce)`	*vcetype* specified in `vce()`
`e(vcetype)`	title used to label Std. Err.
`e(hazard)`	variable specified in `hazard()`
`e(method)`	`ml` or `twostep`
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(footnote)`	program used to implement the footnote display
`e(marginsok)`	predictions allowed by `margins`
`e(marginsnotok)`	predictions disallowed by `margins`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`treatreg` is implemented as an ado-file. Maddala (1983, 117–122) derives both the maximum likelihood and the two-step estimator implemented here. Greene (2012, 890–894) also provides an introduction to the treatment-effects model.

The primary regression equation of interest is

$$y_j = \mathbf{x}_j\boldsymbol{\beta} + \delta z_j + \epsilon_j$$

where z_j is a binary decision variable that is assumed to stem from an unobservable latent variable:

$$z_j^* = \mathbf{w}_j\boldsymbol{\gamma} + u_j$$

The decision to obtain the treatment is made according to the rule

$$z_j = \begin{cases} 1, & \text{if } z_j^* > 0 \\ 0, & \text{otherwise} \end{cases}$$

where ϵ and u are bivariate normal with mean zero and covariance matrix

$$\begin{bmatrix} \sigma^2 & \rho\sigma \\ \rho\sigma & 1 \end{bmatrix}$$

The likelihood function for this model is given in Maddala (1983, 122). Greene (2000, 180) discusses the standard method of reducing a bivariate normal to a function of a univariate normal and the correlation ρ. The following is the log likelihood for observation j,

$$\ln L_j = \begin{cases} \ln\Phi\left\{\dfrac{\mathbf{w}_j\boldsymbol{\gamma} + (y_j - \mathbf{x}_j\boldsymbol{\beta} - \delta)\rho/\sigma}{\sqrt{1-\rho^2}}\right\} - \dfrac{1}{2}\left(\dfrac{y_j - \mathbf{x}_j\boldsymbol{\beta} - \delta}{\sigma}\right)^2 - \ln(\sqrt{2\pi}\sigma), & z_j = 1 \\ \ln\Phi\left\{\dfrac{-\mathbf{w}_j\boldsymbol{\gamma} - (y_j - \mathbf{x}_j\boldsymbol{\beta})\rho/\sigma}{\sqrt{1-\rho^2}}\right\} - \dfrac{1}{2}\left(\dfrac{y_j - \mathbf{x}_j\boldsymbol{\beta}}{\sigma}\right)^2 - \ln(\sqrt{2\pi}\sigma), & z_j = 0 \end{cases}$$

where $\Phi(\cdot)$ is the cumulative distribution function of the standard normal distribution.

In the maximum likelihood estimation, σ and ρ are not directly estimated. Rather $\ln\sigma$ and $\operatorname{atanh}\rho$ are directly estimated, where

$$\operatorname{atanh}\rho = \frac{1}{2}\ln\left(\frac{1+\rho}{1-\rho}\right)$$

The standard error of $\lambda = \rho\sigma$ is approximated through the delta method, which is given by

$$\operatorname{Var}(\lambda) \approx \mathbf{D}\operatorname{Var}\{(\operatorname{atanh}\rho \;\; \ln\sigma)\}\,\mathbf{D}'$$

where $\mathbf{D}$ is the Jacobian of λ with respect to $\operatorname{atanh}\rho$ and $\ln\sigma$.

With maximum likelihood estimation, this command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

The maximum likelihood version of `treatreg` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

Maddala (1983, 120–122) also derives the two-step estimator. In the first stage, probit estimates are obtained of the treatment equation

$$\Pr(z_j = 1 \mid \mathbf{w}_j) = \Phi(\mathbf{w}_j\boldsymbol{\gamma})$$

From these estimates, the hazard, h_j, for each observation j is computed as

$$h_j = \begin{cases} \phi(\mathbf{w}_j\widehat{\boldsymbol{\gamma}})/\Phi(\mathbf{w}_j\widehat{\boldsymbol{\gamma}}), & z_j = 1 \\ -\phi(\mathbf{w}_j\widehat{\boldsymbol{\gamma}})/\{1 - \Phi(\mathbf{w}_j\widehat{\boldsymbol{\gamma}})\}, & z_j = 0 \end{cases}$$

where ϕ is the standard normal density function. If

$$d_j = h_j(h_j + \widehat{\boldsymbol{\gamma}}\,\mathbf{w}_j)$$

then

$$E\left(y_j \mid z_j\right) = \mathbf{x}_j\boldsymbol{\beta} + \delta\mathbf{z}_j + \rho\sigma h_j$$
$$\mathrm{Var}\left(y_j \mid z_j\right) = \sigma^2\left(1 - \rho^2 d_j\right)$$

The two-step parameter estimates of $\boldsymbol{\beta}$ and δ are obtained by augmenting the regression equation with the hazard h. Thus the regressors become $[\,\mathbf{x}\ \mathbf{z}\ h\,]$, and the additional parameter estimate β_h is obtained on the variable containing the hazard. A consistent estimate of the regression disturbance variance is obtained using the residuals from the augmented regression and the parameter estimate on the hazard

$$\widehat{\sigma}^{\,2} = \frac{\mathbf{e}'\mathbf{e} + \beta_h^2 \sum_{j=1}^{N} d_j}{N}$$

The two-step estimate of ρ is then

$$\widehat{\rho} = \frac{\beta_h}{\widehat{\sigma}}$$

To understand how the consistent estimates of the coefficient covariance matrix based on the augmented regression are derived, let $\mathbf{A} = [\,\mathbf{x}\ \mathbf{z}\ h\,]$ and $\mathbf{D}$ be a square diagonal matrix of size N with $(1 - \widehat{\rho}^{\,2} d_j)$ on the diagonal elements. The conventional VCE is

$$\mathbf{V}_{\mathrm{twostep}} = \widehat{\sigma}^{\,2}(\mathbf{A}'\mathbf{A})^{-1}(\mathbf{A}'\mathbf{D}\mathbf{A} + \mathbf{Q})(\mathbf{A}'\mathbf{A})^{-1}$$

where

$$\mathbf{Q} = \widehat{\rho}^{\,2}(\mathbf{A}'\mathbf{D}\mathbf{A})\mathbf{V}_{\mathbf{p}}(\mathbf{A}'\mathbf{D}\mathbf{A})$$

and $\mathbf{V}_{\mathbf{p}}$ is the variance–covariance estimate from the probit estimation of the treatment equation.

References

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Also see

[R] **treatreg postestimation** — Postestimation tools for treatreg

[R] **heckman** — Heckman selection model

[R] **probit** — Probit regression

[R] **regress** — Linear regression

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

treatreg postestimation — Postestimation tools for treatreg

Description

The following postestimation commands are available after `treatreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`[1]	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[2]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`[1]	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `estat ic` and `suest` are not appropriate after `treatreg, twostep`.

[2] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

After ML or twostep

```
predict [type] newvar [if] [in] [, statistic]
```

After ML

```
predict [type] { stub* | newvar_reg newvar_treat newvar_athrho newvar_lnsigma }
    [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`yctrt`	$E(y_j \mid \text{treatment} = 1)$
`ycntrt`	$E(y_j \mid \text{treatment} = 0)$
`ptrt`	$\Pr(\text{treatment} = 1)$
`xbtrt`	linear prediction for treatment equation
`stdptrt`	standard error of the linear prediction for treatment equation

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction, $\mathbf{x}_j\mathbf{b}$.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for one observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`yctrt` calculates the expected value of the dependent variable conditional on the presence of the treatment: $E(y_j \mid \text{treatment} = 1)$.

`ycntrt` calculates the expected value of the dependent variable conditional on the absence of the treatment: $E(y_j \mid \text{treatment} = 0)$.

`ptrt` calculates the probability of the presence of the treatment: $\Pr(\text{treatment} = 1) = \Pr(\mathbf{w}_j\boldsymbol{\gamma} + u_j > 0)$.

`xbtrt` calculates the linear prediction for the treatment equation.

`stdptrt` calculates the standard error of the linear prediction for the treatment equation.

`scores`, not available with `twostep`, calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\boldsymbol{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial(\boldsymbol{w}_j\boldsymbol{\gamma})$.

The third new variable will contain $\partial \ln L/\partial \operatorname{atanh} \rho$.

The fourth new variable will contain $\partial \ln L/\partial \ln\sigma$.

Remarks

Example 1

The default statistic produced by `predict` after `treatreg` is the expected value of the dependent variable from the underlying distribution of the regression model. For example 1 in [R] **treatreg**, this model is

$$\texttt{ww} = \beta_0 + \beta_1\texttt{wa} + \beta_2\texttt{cit} + \delta\texttt{wc} + \epsilon$$

Several other interesting aspects of the treatment-effects model can be explored with `predict`. We continue with our wage model, the wife's expected wage, conditional on attending college, can be obtained with the `yctrt` option. The wife's expected wages, conditional on not attending college, can be obtained with the `ycntrt` option. Thus the difference in expected wages between participants and nonparticipants is the difference between `yctrt` and `ycntrt`. For the case at hand, we have the following calculation:

```
. predict wwctrt, yctrt
. predict wwcntrt, ycntrt
. generate diff = wwctrt - wwcntrt
. summarize diff
    Variable |        Obs        Mean    Std. Dev.       Min        Max
-------------+---------------------------------------------------------
        diff |        250    1.356912    .0134202    1.34558   1.420173
```

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **treatreg** — Treatment-effects model

[U] **20 Estimation and postestimation commands**

Title

truncreg — Truncated regression

Syntax

`truncreg` *depvar* [*indepvars*] [*if*] [*in*] [*weight*] [`,` *options*]

options	Description
Model	
`noconstant`	suppress constant term
`ll(`*varname*`|#)`	lower limit for left-truncation
`ul(`*varname*`|#)`	upper limit for right-truncation
`offset(`*varname*`)`	include *varname* in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`noskip`	perform likelihood-ratio test
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.

depvar and *indepvars* may contain time-series operators; see [U] **11.4.4 Time-series varlists**.

`bootstrap`, `by`, `jackknife`, `mi estimate`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

`vce(bootstrap)` and `vce(jackknife)` are not allowed with the `mi estimate` prefix; see [MI] **mi estimate**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`aweights` are not allowed with the `jackknife` prefix; see [R] **jackknife**.

`vce()`, `noskip`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`aweights`, `fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Truncated regression

Description

truncreg fits a regression model of *depvar* on *indepvars* from a sample drawn from a restricted part of the population. Under the normality assumption for the whole population, the error terms in the truncated regression model have a truncated normal distribution, which is a normal distribution that has been scaled upward so that the distribution integrates to one over the restricted range.

Options

Model

noconstant; see [R] **estimation options**.

ll(*varname* | #) and ul(*varname* | #) indicate the lower and upper limits for truncation, respectively. You may specify one or both. Observations with *depvar* $\leq$ ll() are left-truncated, observations with *depvar* $\geq$ ul() are right-truncated, and the remaining observations are not truncated. See [R] **tobit** for a more detailed description.

offset(*varname*), constraints(*constraints*), collinear; see [R] **estimation options**.

SE/Robust

vce(*vcetype*) specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

level(#); see [R] **estimation options**.

noskip specifies that a full maximum-likelihood model with only a constant for the regression equation be fit. This model is not displayed but is used as the base model to compute a likelihood-ratio test for the model test statistic displayed in the estimation header. By default, the overall model test statistic is an asymptotically equivalent Wald test of all the parameters in the regression equation being zero (except the constant). For many models, this option can substantially increase estimation time.

nocnsreport; see [R] **estimation options**.

display_options: noomitted, vsquish, noemptycells, baselevels, allbaselevels, cformat(%*fmt*), pformat(%*fmt*), sformat(%*fmt*), and nolstretch; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used, but you may use the ltol(#) option to relax the convergence criterion; the default is 1e-6 during specification searches.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with truncreg but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

Truncated regression fits a model of a dependent variable on independent variables from a restricted part of a population. Truncation is essentially a characteristic of the distribution from which the sample data are drawn. If x has a normal distribution with mean μ and standard deviation σ, the density of the truncated normal distribution is

$$f(x \mid a < x < b) = \frac{f(x)}{\Phi\left(\frac{b-\mu}{\sigma}\right) - \Phi\left(\frac{a-\mu}{\sigma}\right)} = \frac{\frac{1}{\sigma}\phi\left(\frac{x-\mu}{\sigma}\right)}{\Phi\left(\frac{b-\mu}{\sigma}\right) - \Phi\left(\frac{a-\mu}{\sigma}\right)}$$

where ϕ and Φ are the density and distribution functions of the standard normal distribution.

Compared with the mean of the untruncated variable, the mean of the truncated variable is greater if the truncation is from below, and the mean of the truncated variable is smaller if the truncation is from above. Moreover, truncation reduces the variance compared with the variance in the untruncated distribution.

▷ Example 1

We will demonstrate `truncreg` with part of the Mroz dataset distributed with Berndt (1996). This dataset contains 753 observations on women's labor supply. Our subsample is of 250 observations, with 150 market laborers and 100 nonmarket laborers.

```
. use http://www.stata-press.com/data/r12/laborsub
. describe
Contains data from http://www.stata-press.com/data/r12/laborsub.dta
  obs:           250
 vars:             6                          25 Sep 2010 18:36
 size:         1,750
-------------------------------------------------------------------------------
              storage  display     value
variable name   type   format      label      variable label
-------------------------------------------------------------------------------
lfp             byte   %9.0g                  1 if woman worked in 1975
whrs            int    %9.0g                  Wife's hours of work
kl6             byte   %9.0g                  # of children younger than 6
k618            byte   %9.0g                  # of children between 6 and 18
wa              byte   %9.0g                  Wife's age
we              byte   %9.0g                  Wife's educational attainment
-------------------------------------------------------------------------------
Sorted by:
. summarize, sep(0)
    Variable |       Obs        Mean    Std. Dev.       Min        Max
-------------+--------------------------------------------------------
         lfp |       250          .6    .4908807         0          1
        whrs |       250      799.84    915.6035         0       4950
         kl6 |       250        .236    .5112234         0          3
        k618 |       250       1.364    1.370774         0          8
          wa |       250       42.92    8.426483        30         60
          we |       250      12.352    2.164912         5         17
```

We first perform ordinary least-squares estimation on the market laborers.

```
. regress whrs kl6 k618 wa we if whrs > 0
      Source |       SS       df       MS              Number of obs =     150
-------------+------------------------------           F(  4,   145) =    2.80
       Model |  7326995.15     4  1831748.79            Prob > F      =  0.0281
    Residual |  94793104.2   145  653745.546           R-squared     =  0.0717
-------------+------------------------------           Adj R-squared =  0.0461
       Total |  102120099    149  685369.794            Root MSE      =  808.55

------------------------------------------------------------------------------
        whrs |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         kl6 |  -421.4822   167.9734    -2.51   0.013    -753.4748   -89.48953
        k618 |  -104.4571   54.18616    -1.93   0.056    -211.5538    2.639668
          wa |  -4.784917   9.690502    -0.49   0.622     -23.9378    14.36797
          we |   9.353195   31.23793     0.30   0.765    -52.38731    71.0937
       _cons |   1629.817   615.1301     2.65   0.009     414.0371    2845.597
------------------------------------------------------------------------------
```

Now we use `truncreg` to perform truncated regression with truncation from below zero.

```
. truncreg whrs kl6 k618 wa we, ll(0)
(note: 100 obs. truncated)

Fitting full model:

Iteration 0:   log likelihood = -1205.6992
Iteration 1:   log likelihood = -1200.9873
Iteration 2:   log likelihood = -1200.9159
Iteration 3:   log likelihood = -1200.9157
Iteration 4:   log likelihood = -1200.9157

Truncated regression
Limit:   lower =          0                     Number of obs =     150
         upper =       +inf                     Wald chi2(4)  =   10.05
Log likelihood = -1200.9157                     Prob > chi2   =  0.0395

------------------------------------------------------------------------------
        whrs |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         kl6 |  -803.0042   321.3614    -2.50   0.012    -1432.861   -173.1474
        k618 |   -172.875   88.72898    -1.95   0.051    -346.7806    1.030579
          wa |  -8.821123   14.36848    -0.61   0.539    -36.98283    19.34059
          we |   16.52873   46.50375     0.36   0.722    -74.61695    107.6744
       _cons |    1586.26    912.355     1.74   0.082    -201.9233    3374.442
-------------+----------------------------------------------------------------
      /sigma |   983.7262   94.44303    10.42   0.000     798.6213    1168.831
------------------------------------------------------------------------------
```

If we assume that our data were censored, the tobit model is

```
. tobit whrs kl6 k618 wa we, ll(0)
Tobit regression                                  Number of obs   =        250
                                                  LR chi2(4)      =      23.03
                                                  Prob > chi2     =     0.0001
Log likelihood = -1367.0903                       Pseudo R2       =     0.0084

------------------------------------------------------------------------------
        whrs |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
         kl6 |  -827.7657   214.7407    -3.85   0.000    -1250.731   -404.8008
        k618 |  -140.0192   74.22303    -1.89   0.060    -286.2129    6.174547
          wa |  -24.97919   13.25639    -1.88   0.061    -51.08969    1.131317
          we |   103.6896   41.82393     2.48   0.014     21.31093    186.0683
       _cons |   589.0001   841.5467     0.70   0.485    -1068.556    2246.556
-------------+----------------------------------------------------------------
       /sigma |   1309.909   82.73335                      1146.953    1472.865
------------------------------------------------------------------------------

  Obs. summary:        100  left-censored observations at whrs<=0
                       150     uncensored observations
                         0 right-censored observations
```

◁

❑ Technical note

Whether truncated regression is more appropriate than the ordinary least-squares estimation depends on the purpose of that estimation. If we are interested in the mean of wife's working hours conditional on the subsample of market laborers, least-squares estimation is appropriate. However if we are interested in the mean of wife's working hours regardless of market or nonmarket labor status, least-squares estimates could be seriously misleading.

Truncation and censoring are different concepts. A sample has been censored if no observations have been systematically excluded but some of the information contained in them has been suppressed. In a truncated distribution, only the part of the distribution above (or below, or between) the truncation points is relevant to our computations. We need to scale it up by the probability that an observation falls in the range that interests us to make the distribution integrate to one. The censored distribution used by tobit, however, is a mixture of discrete and continuous distributions. Instead of rescaling over the observable range, we simply assign the full probability from the censored regions to the censoring points. The truncated regression model is sometimes less well behaved than the tobit model. Davidson and MacKinnon (1993) provide an example where truncation results in more inconsistency than censoring.

❑

Saved results

truncreg saves the following in e():

Scalars

e(N)	number of observations
e(N_bf)	number of obs. before truncation
e(chi2)	model χ^2
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_aux)	number of auxiliary parameters
e(df_m)	model degrees of freedom
e(ll)	log likelihood
e(ll_0)	log likelihood, constant-only model
e(N_clust)	number of clusters
e(sigma)	estimate of sigma
e(p)	significance
e(rank)	rank of e(V)
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	truncreg
e(cmdline)	command as typed
e(llopt)	contents of ll(), if specified
e(ulopt)	contents of ul(), if specified
e(depvar)	name of dependent variable
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset1)	offset
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance
e(means)	means of independent variables
e(dummy)	indicator for dummy variables

Functions

e(sample)	marks estimation sample

Methods and formulas

truncreg is implemented as an ado-file. Greene (2012, 833–839) and Davidson and MacKinnon (1993, 534–537) provide introductions to the truncated regression model.

Let $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}$ be the model. $\mathbf{y}$ represents continuous outcomes either observed or not observed. Our model assumes that $\epsilon \sim N(\mathbf{0}, \sigma^2\mathbf{I})$.

Let a be the lower limit and b be the upper limit. The log likelihood is

$$\ln L = -\frac{n}{2}\log(2\pi\sigma^2) - \frac{1}{2\sigma^2}\sum_{j=1}^{n}(y_j - \mathbf{x}_j\boldsymbol{\beta})^2 - \sum_{j=1}^{n}\log\left\{\Phi\left(\frac{b - \mathbf{x}_j\boldsymbol{\beta}}{\sigma}\right) - \Phi\left(\frac{a - \mathbf{x}_j\boldsymbol{\beta}}{\sigma}\right)\right\}$$

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`truncreg` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

Berndt, E. R. 1996. *The Practice of Econometrics: Classic and Contemporary*. New York: Addison–Wesley.

Cong, R. 1999. sg122: Truncated regression. *Stata Technical Bulletin* 52: 47–52. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 248–255. College Station, TX: Stata Press.

Davidson, R., and J. G. MacKinnon. 1993. *Estimation and Inference in Econometrics*. New York: Oxford University Press.

Greene, W. H. 2012. *Econometric Analysis*. 7th ed. Upper Saddle River, NJ: Prentice Hall.

Also see

[R] **truncreg postestimation** — Postestimation tools for truncreg

[R] **regress** — Linear regression

[R] **tobit** — Tobit regression

[MI] **estimation** — Estimation commands for use with mi estimate

[SVY] **svy estimation** — Estimation commands for survey data

[U] **20 Estimation and postestimation commands**

Title

truncreg postestimation — Postestimation tools for truncreg

Description

The following postestimation commands are available after `truncreg`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_lnsigma} [if] [in], scores
```

statistic	Description
Main	
`xb`	linear prediction; the default
`stdp`	standard error of the prediction
`stdf`	standard error of the forecast
`pr(`*a*`,`*b*`)`	$\Pr(a < y_j < b)$
`e(`*a*`,`*b*`)`	$E(y_j \mid a < y_j < b)$
`ystar(`*a*`,`*b*`)`	$E(y_j^*)$, $y_j^* = \max\{a, \min(y_j, b)\}$

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

where a and b may be numbers or variables; a missing ($a \geq .$) means $-\infty$, and b missing ($b \geq .$) means $+\infty$; see [U] **12.2.1 Missing values**.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

`stdf` calculates the standard error of the forecast, which is the standard error of the point prediction for 1 observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by `stdf` are always larger than those produced by `stdp`; see *Methods and formulas* in [R] **regress postestimation**.

`pr(`*a*`,`*b*`)` calculates $\Pr(a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the probability that $y_j|\mathbf{x}_j$ would be observed in the interval (a, b).

a and *b* may be specified as numbers or variable names; *lb* and *ub* are variable names;
`pr(20,30)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,`*ub*`)` calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < ub)$; and
`pr(20,`*ub*`)` calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$.

a missing ($a \geq .$) means $-\infty$; `pr(.,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$;
`pr(`*lb*`,30)` calculates $\Pr(-\infty < \mathbf{x}_j\mathbf{b} + u_j < 30)$ in observations for which $lb \geq .$
and calculates $\Pr(lb < \mathbf{x}_j\mathbf{b} + u_j < 30)$ elsewhere.

b missing ($b \geq .$) means $+\infty$; `pr(20,.)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$;
`pr(20,`*ub*`)` calculates $\Pr(+\infty > \mathbf{x}_j\mathbf{b} + u_j > 20)$ in observations for which $ub \geq .$
and calculates $\Pr(20 < \mathbf{x}_j\mathbf{b} + u_j < ub)$ elsewhere.

`e(`*a*`,`*b*`)` calculates $E(\mathbf{x}_j\mathbf{b} + u_j \mid a < \mathbf{x}_j\mathbf{b} + u_j < b)$, the expected value of $y_j|\mathbf{x}_j$ conditional on $y_j|\mathbf{x}_j$ being in the interval (a, b), meaning that $y_j|\mathbf{x}_j$ is truncated.
a and *b* are specified as they are for `pr()`.

`ystar(`*a*`,`*b*`)` calculates $E(y_j^*)$, where $y_j^* = a$ if $\mathbf{x}_j\mathbf{b} + u_j \leq a$, $y_j^* = b$ if $\mathbf{x}_j\mathbf{b} + u_j \geq b$, and $y_j^* = \mathbf{x}_j\mathbf{b} + u_j$ otherwise, meaning that y_j^* is censored. *a* and *b* are specified as they are for `pr()`.

`nooffset` is relevant only if you specified `offset(`*varname*`)`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\mathbf{b}$ rather than as $\mathbf{x}_j\mathbf{b} + \text{offset}_j$.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial \ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L/\partial\sigma$.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **truncreg** — Truncated regression

[U] **20 Estimation and postestimation commands**

Title

ttest — Mean-comparison tests

Syntax

One-sample mean-comparison test

```
ttest varname == # [if] [in] [, level(#)]
```

Two-sample mean-comparison test (unpaired)

```
ttest varname1 == varname2 [if] [in], unpaired [unequal welch level(#)]
```

Two-sample mean-comparison test (paired)

```
ttest varname1 == varname2 [if] [in] [, level(#)]
```

Two-group mean-comparison test

```
ttest varname [if] [in], by(groupvar) [options1]
```

Immediate form of one-sample mean-comparison test

```
ttesti #obs #mean #sd #val [, level(#)]
```

Immediate form of two-sample mean-comparison test

```
ttesti #obs1 #mean1 #sd1 #obs2 #mean2 #sd2 [, options2]
```

options$_1$	Description
Main	
* `by(`*groupvar*`)`	variable defining the groups
`unequal`	unpaired data have unequal variances
`welch`	use Welch's approximation
`level(#)`	set confidence level; default is `level(95)`

*`by(`*groupvar*`)` is required.

options$_2$	Description
Main	
`unequal`	unpaired data have unequal variances
`welch`	use Welch's approximation
`level(#)`	set confidence level; default is `level(95)`

`by` is allowed with `test`; see [D] **by**.

Menu

one-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > One-sample mean-comparison test

two-sample, unpaired

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-sample mean-comparison test

two-sample, paired

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Mean-comparison test, paired data

two-group

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-group mean-comparison test

immediate command: one-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > One-sample mean-comparison calculator

immediate command: two-sample

Statistics > Summaries, tables, and tests > Classical tests of hypotheses > Two-sample mean-comparison calculator

Description

`ttest` performs t tests on the equality of means. In the first form, `ttest` tests that *varname* has a mean of *#*. In the second form, `ttest` tests that *varname*$_1$ and *varname*$_2$ have the same mean, assuming *unpaired* data. In the third form, `ttest` tests that *varname*$_1$ and *varname*$_2$ have the same mean, assuming *paired* data. In the fourth form, `ttest` tests that *varname* has the same mean within the two groups defined by *groupvar*.

`ttesti` is the immediate form of `ttest`; see [U] **19 Immediate commands**.

For the equivalent of a two-sample t test with sampling weights (`pweights`), use the `svy: mean` command with the `over()` option, and then use `lincom`; see [R] **mean** and [SVY] **svy postestimation**.

Options

Main

`by(`*groupvar*`)` specifies the *groupvar* that defines the two groups that `ttest` will use to test the hypothesis that their means are equal. Specifying `by(`*groupvar*`)` implies an unpaired (two sample) t test. Do not confuse the `by()` option with the `by` prefix; you can specify both.

`unpaired` specifies that the data be treated as unpaired. The `unpaired` option is used when the two sets of values to be compared are in different variables.

`unequal` specifies that the unpaired data not be assumed to have equal variances.

`welch` specifies that the approximate degrees of freedom for the test be obtained from Welch's formula (1947) rather than from Satterthwaite's approximation formula (1946), which is the default when `unequal` is specified. Specifying `welch` implies `unequal`.

`level(#)` specifies the confidence level, as a percentage, for confidence intervals. The default is `level(95)` or as set by `set level`; see [U] **20.7 Specifying the width of confidence intervals**.

Remarks

▷ Example 1: One-sample mean-comparison test

In the first form, `ttest` tests whether the mean of the sample is equal to a known constant under the assumption of unknown variance. Assume that we have a sample of 74 automobiles. We know each automobile's average mileage rating and wish to test whether the overall average for the sample is 20 miles per gallon.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. ttest mpg==20
One-sample t test
```

Variable	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
mpg	74	21.2973	.6725511	5.785503	19.9569	22.63769

```
    mean = mean(mpg)                                          t =   1.9289
Ho: mean = 20                                 degrees of freedom =       73

    Ha: mean < 20               Ha: mean != 20                 Ha: mean > 20
 Pr(T < t) = 0.9712         Pr(|T| > |t|) = 0.0576          Pr(T > t) = 0.0288
```

The test indicates that the underlying mean is not 20 with a significance level of 5.8%.

◁

▷ Example 2: Two-sample mean-comparison test

We are testing the effectiveness of a new fuel additive. We run an experiment with 12 cars. We run the cars without and with the fuel treatment. The results of the experiment are as follows:

Without treatment	With treatment	Without treatment	With treatment
20	24	18	17
23	25	24	28
21	21	20	24
25	22	24	27
18	23	23	21
17	18	19	23

By creating two variables called `mpg1` and `mpg2` representing mileage without and with the treatment, respectively, we can test the equality of means by typing

```
. use http://www.stata-press.com/data/r12/fuel
. ttest mpg1==mpg2
Paired t test
```

Variable	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
mpg1	12	21	.7881701	2.730301	19.26525	22.73475
mpg2	12	22.75	.9384465	3.250874	20.68449	24.81551
diff	12	-1.75	.7797144	2.70101	-3.46614	-.0338602

```
     mean(diff) = mean(mpg1 - mpg2)                               t =  -2.2444
 Ho: mean(diff) = 0                            degrees of freedom =       11

 Ha: mean(diff) < 0           Ha: mean(diff) != 0           Ha: mean(diff) > 0
 Pr(T < t) = 0.0232         Pr(|T| > |t|) = 0.0463          Pr(T > t) = 0.9768
```

We find that the means are statistically different from each other at any level greater than 4.6%. ◁

▷ Example 3: Group mean-comparison test

Let's pretend that the preceding data were collected by running 24 cars: 12 cars with the additive and 12 without. Although we might be tempted to enter the data in the same way, we should resist (see the technical note below). Instead, we enter the data as 24 observations on `mpg` with an additional variable, `treated`, taking on 1 if the car received the fuel treatment and 0 otherwise:

```
. use http://www.stata-press.com/data/r12/fuel3
. ttest mpg, by(treated)
Two-sample t test with equal variances
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
0	12	21	.7881701	2.730301	19.26525	22.73475
1	12	22.75	.9384465	3.250874	20.68449	24.81551
combined	24	21.875	.6264476	3.068954	20.57909	23.17091
diff		-1.75	1.225518		-4.291568	.7915684

```
    diff = mean(0) - mean(1)                                      t =  -1.4280
Ho: diff = 0                                     degrees of freedom =       22
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0837         Pr(|T| > |t|) = 0.1673          Pr(T > t) = 0.9163
```

This time we do not find a statistically significant difference.

If we were not willing to assume that the variances were equal and wanted to use Welch's formula, we could type

```
. ttest mpg, by(treated) welch
Two-sample t test with unequal variances
```

Group	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
0	12	21	.7881701	2.730301	19.26525	22.73475
1	12	22.75	.9384465	3.250874	20.68449	24.81551
combined	24	21.875	.6264476	3.068954	20.57909	23.17091
diff		-1.75	1.225518		-4.28369	.7836902

```
    diff = mean(0) - mean(1)                                      t =  -1.4280
Ho: diff = 0                     Welch's degrees of freedom =  23.2465
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0833         Pr(|T| > |t|) = 0.1666          Pr(T > t) = 0.9167
```

◁

❑ Technical note

In two-group randomized designs, subjects will sometimes refuse the assigned treatment but still be measured for an outcome. In this case, take care to specify the group properly. You might be tempted to let *varname* contain missing where the subject refused and thus let `ttest` drop such observations from the analysis. Zelen (1979) argues that it would be better to specify that the subject belongs to the group in which he or she was randomized, even though such inclusion will dilute the measured effect.

❑

❑ Technical note

There is a second, inferior way to organize the data in the preceding example. Remember, we ran a test on 24 cars, 12 without the additive and 12 with. Nevertheless, we could have entered the data in the same way as we did when we had 12 cars, each run without and with the additive, by creating two variables—`mpg1` and `mpg2`.

This method is inferior because it suggests a connection that is not there. For the 12-car experiment, there was most certainly a connection—it was the same car. In the 24-car experiment, however, it is arbitrary which mpg results appear next to which. Nevertheless, if our data are organized like this, `ttest` can accommodate us.

```
. use http://www.stata-press.com/data/r12/fuel
. ttest mpg1==mpg2, unpaired
Two-sample t test with equal variances
```

Variable	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
mpg1	12	21	.7881701	2.730301	19.26525	22.73475
mpg2	12	22.75	.9384465	3.250874	20.68449	24.81551
combined	24	21.875	.6264476	3.068954	20.57909	23.17091
diff		-1.75	1.225518		-4.291568	.7915684

```
    diff = mean(mpg1) - mean(mpg2)                                t =  -1.4280
Ho: diff = 0                                     degrees of freedom =       22

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.0837         Pr(|T| > |t|) = 0.1673          Pr(T > t) = 0.9163
```

❑

▷ Example 4

`ttest` can be used to test the equality of a pair of means; see [R] **oneway** for testing the equality of more than two means.

Suppose that we have data on the 50 states. The dataset contains the median age of the population (`medage`) and the region of the country (`region`) for each state. Region 1 refers to the Northeast, region 2 to the North Central, region 3 to the South, and region 4 to the West. Using `oneway`, we can test the equality of all four means.

```
. use http://www.stata-press.com/data/r12/census
(1980 Census data by state)
. oneway medage region
```

Source	SS	df	MS	F	Prob > F
Between groups	46.3961903	3	15.4653968	7.56	0.0003
Within groups	94.1237947	46	2.04616945		
Total	140.519985	49	2.8677548		

```
Bartlett's test for equal variances:  chi2(3) =  10.5757  Prob>chi2 = 0.014
```

We find that the means are different, but we are interested only in testing whether the means for the Northeast (`region==1`) and West (`region==4`) are different. We could use `oneway`,

```
. oneway medage region if region==1 | region==4
                        Analysis of Variance
    Source              SS         df      MS            F     Prob > F
------------------------------------------------------------------------
Between groups       46.241247       1    46.241247     20.02     0.0002
 Within groups       46.1969169     20   2.30984584
------------------------------------------------------------------------
    Total            92.4381638     21   4.40181733
Bartlett's test for equal variances:  chi2(1) =   2.4679  Prob>chi2 = 0.116
```

or we could use `ttest`:

```
. ttest medage if region==1 | region==4, by(region)
Two-sample t test with equal variances
------------------------------------------------------------------------------
   Group |     Obs        Mean    Std. Err.   Std. Dev.   [95% Conf. Interval]
---------+--------------------------------------------------------------------
      NE |       9    31.23333    .3411581    1.023474    30.44662    32.02005
    West |      13    28.28462    .4923577    1.775221    27.21186    29.35737
---------+--------------------------------------------------------------------
combined |      22    29.49091    .4473059    2.098051    28.56069    30.42113
---------+--------------------------------------------------------------------
    diff |            2.948718    .6590372                1.57399    4.323445
------------------------------------------------------------------------------
    diff = mean(NE) - mean(West)                                  t =   4.4743
Ho: diff = 0                                     degrees of freedom =       20
    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.9999         Pr(|T| > |t|) = 0.0002          Pr(T > t) = 0.0001
```

The significance levels of both tests are the same.

◁

Immediate form

▷ Example 5

`ttesti` is like `ttest`, except that we specify summary statistics rather than variables as arguments. For instance, we are reading an article that reports the mean number of sunspots per month as 62.6 with a standard deviation of 15.8. There are 24 months of data. We wish to test whether the mean is 75:

```
. ttesti 24 62.6 15.8 75
One-sample t test
------------------------------------------------------------------------------
         |     Obs        Mean    Std. Err.   Std. Dev.   [95% Conf. Interval]
---------+--------------------------------------------------------------------
       x |      24        62.6    3.225161        15.8    55.92825    69.27175
------------------------------------------------------------------------------
    mean = mean(x)                                            t =  -3.8448
Ho: mean = 75                                    degrees of freedom =       23
    Ha: mean < 75                Ha: mean != 75                 Ha: mean > 75
 Pr(T < t) = 0.0004         Pr(|T| > |t|) = 0.0008          Pr(T > t) = 0.9996
```

◁

▷ Example 6

There is no immediate form of `ttest` with paired data because the test is also a function of the covariance, a number unlikely to be reported in any published source. For nonpaired data, however, we might type

```
. ttesti 20 20 5  32 15 4
Two-sample t test with equal variances
```

	Obs	Mean	Std. Err.	Std. Dev.	[95% Conf.	Interval]
x	20	20	1.118034	5	17.65993	22.34007
y	32	15	.7071068	4	13.55785	16.44215
combined	52	16.92308	.6943785	5.007235	15.52905	18.3171
diff		5	1.256135		2.476979	7.523021

```
    diff = mean(x) - mean(y)                                      t =   3.9805
Ho: diff = 0                     degrees of freedom =       50

    Ha: diff < 0                 Ha: diff != 0                 Ha: diff > 0
 Pr(T < t) = 0.9999         Pr(|T| > |t|) = 0.0002          Pr(T > t) = 0.0001
```

If we had typed `ttesti 20 20 5  32 15 4, unequal`, the test would have assumed unequal variances. ◁

Saved results

`ttest` and `ttesti` save the following in `r()`:

Scalars

`r(N_1)`	sample size n_1	`r(sd_1)`	standard deviation for first variable
`r(N_2)`	sample size n_2	`r(sd_2)`	standard deviation for second variable
`r(p_l)`	lower one-sided p-value	`r(sd)`	combined standard deviation
`r(p_u)`	upper one-sided p-value	`r(mu_1)`	$\bar{x}_1$ mean for population 1
`r(p)`	two-sided p-value	`r(mu_2)`	$\bar{x}_2$ mean for population 2
`r(se)`	estimate of standard error	`r(df_t)`	degrees of freedom
`r(t)`	t statistic		

Methods and formulas

`ttest` and `ttesti` are implemented as ado-files.

See, for instance, Hoel (1984, 140–161) or Dixon and Massey (1983, 121–130) for an introduction and explanation of the calculation of these tests. Acock (2010, 155–166) and Hamilton (2009, 157–162) describe t tests using applications in Stata.

The test for $\mu = \mu_0$ for unknown σ is given by

$$t = \frac{(\overline{x} - \mu_0)\sqrt{n}}{s}$$

The statistic is distributed as Student's t with $n-1$ degrees of freedom (Gosset [Student, pseud.] 1908).

The test for $\mu_x = \mu_y$ when σ_x and σ_y are unknown but $\sigma_x = \sigma_y$ is given by

$$t = \frac{\overline{x} - \overline{y}}{\left\{\frac{(n_x-1)s_x^2+(n_y-1)s_y^2}{n_x+n_y-2}\right\}^{1/2}\left(\frac{1}{n_x}+\frac{1}{n_y}\right)^{1/2}}$$

The result is distributed as Student's t with $n_x + n_y - 2$ degrees of freedom.

You could perform `ttest` (without the `unequal` option) in a regression setting given that regression assumes a homoskedastic error model. To compare with the `ttest` command, denote the underlying observations on x and y by x_j, $j = 1, \ldots, n_x$, and y_j, $j = 1, \ldots, n_y$. In a regression framework, typing `ttest` without the `unequal` option is equivalent to

1. creating a new variable z_j that represents the stacked observations on x and y (so that $z_j = x_j$ for $j = 1, \ldots, n_x$ and $z_{n_x+j} = y_j$ for $j = 1, \ldots, n_y$)
2. and then estimating the equation $z_j = \beta_0 + \beta_1 d_j + \epsilon_j$, where $d_j = 0$ for $j = 1, \ldots, n_x$ and $d_j = 1$ for $j = n_x + 1, \ldots, n_x + n_y$ (that is, $d_j = 0$ when the z observations represent x, and $d_j = 1$ when the z observations represent y).

The estimated value of β_1, b_1, will equal $\overline{y} - \overline{x}$, and the reported t statistic will be the same t statistic as given by the formula above.

The test for $\mu_x = \mu_y$ when σ_x and σ_y are unknown and $\sigma_x \neq \sigma_y$ is given by

$$t = \frac{\overline{x} - \overline{y}}{\left(s_x^2/n_x + s_y^2/n_y\right)^{1/2}}$$

The result is distributed as Student's t with ν degrees of freedom, where ν is given by (with Satterthwaite's [1946] formula)

$$\frac{\left(s_x^2/n_x + s_y^2/n_y\right)^2}{\frac{\left(s_x^2/n_x\right)^2}{n_x-1} + \frac{\left(s_y^2/n_y\right)^2}{n_y-1}}$$

With Welch's formula (1947), the number of degrees of freedom is given by

$$-2 + \frac{\left(s_x^2/n_x + s_y^2/n_y\right)^2}{\frac{\left(s_x^2/n_x\right)^2}{n_x+1} + \frac{\left(s_y^2/n_y\right)^2}{n_y+1}}$$

The test for $\mu_x = \mu_y$ for matched observations (also known as paired observations, correlated pairs, or permanent components) is given by

$$t = \frac{\overline{d}\sqrt{n}}{s_d}$$

where $\overline{d}$ represents the mean of $x_i - y_i$ and s_d represents the standard deviation. The test statistic t is distributed as Student's t with $n - 1$ degrees of freedom.

You can also use `ttest` without the `unpaired` option in a regression setting because a paired comparison includes the assumption of constant variance. The `ttest` with an unequal variance assumption does not lend itself to an easy representation in regression settings and is not discussed here. $(x_j - y_j) = \beta_0 + \epsilon_j$.

William Sealy Gosset (1876–1937) was born in Canterbury, England. He studied chemistry and mathematics at Oxford and worked as a chemist with the brewers Guinness in Dublin. Gosset became interested in statistical problems, which he discussed with Karl Pearson and later with Fisher and Neyman. He published several important papers under the pseudonym "Student", and he lent that name to the t test he invented.

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Also see

[R] **bitest** — Binomial probability test

[R] **ci** — Confidence intervals for means, proportions, and counts

[R] **mean** — Estimate means

[R] **oneway** — One-way analysis of variance

[R] **prtest** — One- and two-sample tests of proportions

[R] **sdtest** — Variance-comparison tests

[MV] **hotelling** — Hotelling's T-squared generalized means test

Title

update — Update Stata

Syntax

Report on update level of currently installed Stata

```
update
```

Set update source

```
update from location
```

Compare update level of currently installed Stata with that of source

```
update query [ , from(location) ]
```

Perform update if necessary

```
update all [ , from(location) detail force exit ]
```

Set automatic updates (Mac and Windows only)

```
set update_query { on | off }
set update_interval #
set update_prompt { on | off }
```

Menu

Help > Check for Updates

Description

The `update` command reports on the current update level and installs official updates to Stata. Official updates are updates to Stata as it was originally shipped from StataCorp, not the additions to Stata published in, for instance, the *Stata Journal* (SJ). Those additions are installed using the `net` command and updated using the `adoupdate` command; see [R] **net** and [R] **adoupdate**.

`update` without arguments reports on the update level of the currently installed Stata.

`update from` sets an update source, where *location* is a directory name or URL. If you are on the Internet, type `update from http://www.stata.com`.

`update query` compares the update level of the currently installed Stata with that available from the update source and displays a report.

`update all` updates all necessary files. This is what you should type to check for and install updates.

`set update_query` determines if `update query` is to be automatically performed when Stata is launched. Only Mac and Windows platforms can be set for automatic updating.

`set update_interval #` sets the number of days to elapse before performing the next automatic `update query`. The default # is 7. The interval starts from the last time an `update query` was performed (automatically or manually). Only Mac and Windows platforms can be set for automatic updating.

`set update_prompt` determines whether a dialog is to be displayed before performing an automatic `update query`. The dialog allows you to perform an `update query` now, perform one the next time Stata is launched, perform one after the next interval has passed, or disable automatic `update query`. Only Mac and Windows platforms can be set for automatic updating.

Options

`from(`*location*`)` specifies the location of the update source. You can specify the `from()` option on the individual `update` commands or use the `update from` command. Which you do makes no difference. You typically do not need to use this option.

`detail` specifies to display verbose output during the update process.

`force` specifies to force downloading of all files even if, based on the date comparison, Stata does not think it is necessary. There is seldom a reason to specify this option.

`exit` instructs Stata to exit when the update has successfully completed. There is seldom a reason to specify this option.

Remarks

`update` updates the official components of Stata from the official source: http://www.stata.com. If you are connected to the Internet, the easy thing to do is to type

```
. update all
```

and follow the instructions. If Stata is up to date, `update all` will do nothing. Otherwise, it will download whatever is necessary and install the files. If you just want to know what updates are available, type

```
. update query
```

`update query` will check if any updates are available and report that information. If updates are available, it will recommend that you type `update all`.

If you want to report the current update level, type

```
. update
```

`update` will report the update level of the Stata installation. `update` will also show you the date that updates were last checked and if any updates were available at that time.

Saved results

`update` without a subcommand, `update from`, and `update query` save the following in `r()`:

Scalars

`r(inst_exe)`	date of executable installed (*)
`r(avbl_exe)`	date of executable available over web (*) (**)
`r(inst_ado)`	date of ado-files installed (*)
`r(avbl_ado)`	date of ado-files available over web (*) (**)
`r(inst_utilities)`	date of utilities installed (*)
`r(avbl_utilities)`	date of utilities available over web (*) (**)
`r(inst_docs)`	date of documentation installed (*)
`r(avbl_docs)`	date of documentation available over web (*) (**)

Macros

`r(name_exe)`	name of the Stata executable
`r(dir_exe)`	directory in which executable is stored
`r(dir_ado)`	directory in which ado-files are stored
`r(dir_utilities)`	directory in which utilities are stored
`r(dir_docs)`	directory in which PDF documentation is stored

Notes:

* Dates are stored as integers counting the number of days since January 1, 1960; see [D] **datetime**.

** These dates are not saved by `update` without a subcommand because `update` by itself reports information solely about the local computer and does not check what is available on the web.

Also see

[R] **adoupdate** — Update user-written ado-files

[R] **net** — Install and manage user-written additions from the Internet

[R] **ssc** — Install and uninstall packages from SSC

[P] **sysdir** — Query and set system directories

[U] **28 Using the Internet to keep up to date**

[GSM] **19 Updating and extending Stata—Internet functionality**

[GSU] **19 Updating and extending Stata—Internet functionality**

[GSW] **19 Updating and extending Stata—Internet functionality**

Title

vce_option **—** Variance estimators

Syntax

estimation_cmd ... [, `vce(`*vcetype*`)` ...]

vcetype	Description
Likelihood based	
`oim`	observed information matrix (OIM)
`opg`	outer product of the gradient (OPG) vectors
Sandwich estimators	
`robust`	Huber/White/sandwich estimator
`cluster` *clustvar*	clustered sandwich estimator
Replication based	
`bootstrap` [, *bootstrap_options*]	bootstrap estimation
`jackknife` [, *jackknife_options*]	jackknife estimation

Description

This entry describes the `vce()` option, which is common to most estimation commands. `vce()` specifies how to estimate the variance–covariance matrix (VCE) corresponding to the parameter estimates. The standard errors reported in the table of parameter estimates are the square root of the variances (diagonal elements) of the VCE.

Options

SE/Robust

`vce(oim)` is usually the default for models fit using maximum likelihood. `vce(oim)` uses the observed information matrix (OIM); see [R] **ml**.

`vce(opg)` uses the sum of the outer product of the gradient (OPG) vectors; see [R] **ml**. This is the default VCE when the `technique(bhhh)` option is specified; see [R] **maximize**.

`vce(robust)` uses the robust or sandwich estimator of variance. This estimator is robust to some types of misspecification so long as the observations are independent; see [U] **20.20 Obtaining robust variance estimates**.

If the command allows `pweights` and you specify them, `vce(robust)` is implied; see [U] **20.22.3 Sampling weights**.

`vce(cluster` *clustvar*`)` specifies that the standard errors allow for intragroup correlation, relaxing the usual requirement that the observations be independent. That is, the observations are independent across groups (clusters) but not necessarily within groups. *clustvar* specifies to which group each observation belongs, for example, `vce(cluster personid)` in data with repeated observations on individuals. `vce(cluster` *clustvar*`)` affects the standard errors and variance–covariance matrix of the estimators but not the estimated coefficients; see [U] **20.20 Obtaining robust variance estimates**.

`vce(bootstrap` [`,` *bootstrap_options*]`)` uses a bootstrap; see [R] **bootstrap**. After estimation with `vce(bootstrap)`, see [R] **bootstrap postestimation** to obtain percentile-based or bias-corrected confidence intervals.

`vce(jackknife` [`,` *jackknife_options*]`)` uses the delete-one jackknife; see [R] **jackknife**.

Remarks

Remarks are presented under the following headings:

Prefix commands
Passing options in vce()

Prefix commands

Specifying `vce(bootstrap)` or `vce(jackknife)` is often equivalent to using the corresponding prefix command. Here is an example using `jackknife` with `regress`.

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)

. regress mpg turn trunk, vce(jackknife)
(running regress on estimation sample)

Jackknife replications (74)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
........................
```

Linear regression				Number of obs	= 74
				Replications	= 74
				F(2, 73)	= 66.26
				Prob > F	= 0.0000
				R-squared	= 0.5521
				Adj R-squared	= 0.5395
				Root MSE	= 3.9260

mpg	Coef.	Jackknife Std. Err.	t	P>|t|	[95% Conf.	Interval]
turn	-.7610113	.150726	-5.05	0.000	-1.061408	-.4606147
trunk	-.3161825	.1282326	-2.47	0.016	-.5717498	-.0606152
_cons	55.82001	5.031107	11.09	0.000	45.79303	65.84699

```
. jackknife: regress mpg turn trunk
(running regress on estimation sample)
Jackknife replications (74)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
........................
Linear regression                               Number of obs      =        74
                                                Replications       =        74
                                                F(   2,     73)    =     66.26
                                                Prob > F           =    0.0000
                                                R-squared          =    0.5521
                                                Adj R-squared      =    0.5395
                                                Root MSE           =    3.9260

------------------------------------------------------------------------------
             |             Jackknife
         mpg |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        turn |  -.7610113    .150726    -5.05   0.000    -1.061408   -.4606147
       trunk |  -.3161825   .1282326    -2.47   0.016    -.5717498   -.0606152
       _cons |   55.82001   5.031107    11.09   0.000     45.79303    65.84699
------------------------------------------------------------------------------
```

Here it does not matter whether we specify the `vce(jackknife)` option or instead use the `jackknife` prefix.

However, `vce(jackknife)` should be used in place of the `jackknife` prefix whenever available because they are not always equivalent. For example, to use the `jackknife` prefix with `clogit` properly, you must tell `jackknife` to omit whole groups rather than individual observations. Specifying `vce(jackknife)` does this automatically.

```
. use http://www.stata-press.com/data/r12/clogitid
. jackknife, cluster(id): clogit y x1 x2, group(id)
  (output omitted)
```

This extra information is automatically communicated to `jackknife` by `clogit` when the `vce()` option is specified.

```
. clogit y x1 x2, group(id) vce(jackknife)
(running clogit on estimation sample)
Jackknife replications (66)
----+--- 1 ---+--- 2 ---+--- 3 ---+--- 4 ---+--- 5
..................................................    50
................
Conditional (fixed-effects) logistic regression   Number of obs    =        369
                                                  Replications     =         66
                                                  F(   2,     65)  =       4.58
                                                  Prob > F         =     0.0137
Log likelihood = -123.41386                       Pseudo R2        =     0.0355

                                  (Replications based on 66 clusters in id)
------------------------------------------------------------------------------
             |             Jackknife
           y |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
          x1 |    .653363   .3010608     2.17   0.034      .052103    1.254623
          x2 |   .0659169   .0487858     1.35   0.181    -.0315151    .1633489
------------------------------------------------------------------------------
```

Passing options in vce()

If you wish to specify more options to the bootstrap or jackknife estimation, you can include them within the `vce()` option. Below we request 300 bootstrap replications and save the replications in `bsreg.dta`:

```
. use http://www.stata-press.com/data/r12/auto
(1978 Automobile Data)
. regress mpg turn trunk, vce(bootstrap, nodots seed(123) rep(300) saving(bsreg))
Linear regression                               Number of obs      =        74
                                                Replications       =       300
                                                Wald chi2(2)       =    127.28
                                                Prob > chi2        =    0.0000
                                                R-squared          =    0.5521
                                                Adj R-squared      =    0.5395
                                                Root MSE           =    3.9260

------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
         mpg |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        turn |  -.7610113   .1361786    -5.59   0.000    -1.027916   -.4941062
       trunk |  -.3161825   .1145728    -2.76   0.006     -.540741   -.0916239
       _cons |   55.82001    4.69971    11.88   0.000     46.60875    65.03127
------------------------------------------------------------------------------

. bstat using bsreg
Bootstrap results                               Number of obs      =        74
                                                Replications       =       300

      command:  regress mpg turn trunk

------------------------------------------------------------------------------
             |   Observed   Bootstrap                         Normal-based
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
        turn |  -.7610113   .1361786    -5.59   0.000    -1.027916   -.4941062
       trunk |  -.3161825   .1145728    -2.76   0.006     -.540741   -.0916239
       _cons |   55.82001    4.69971    11.88   0.000     46.60875    65.03127
------------------------------------------------------------------------------
```

Methods and formulas

By default, Stata's maximum likelihood estimators display standard errors based on variance estimates given by the inverse of the negative Hessian (second derivative) matrix. If `vce(robust)`, `vce(cluster` *clustvar*`)`, or `pweights` is specified, standard errors are based on the robust variance estimator (see [U] **20.20 Obtaining robust variance estimates**); likelihood-ratio tests are not appropriate here (see [SVY] **survey**), and the model χ^2 is from a Wald test. If `vce(opg)` is specified, the standard errors are based on the outer product of the gradients; this option has no effect on likelihood-ratio tests, though it does affect Wald tests.

If `vce(bootstrap)` or `vce(jackknife)` is specified, the standard errors are based on the chosen replication method; here the model χ^2 or F statistic is from a Wald test using the respective replication-based covariance matrix. The t distribution is used in the coefficient table when the `vce(jackknife)` option is specified. `vce(bootstrap)` and `vce(jackknife)` are also available with some commands that are not maximum likelihood estimators.

Also see

[R] **bootstrap** — Bootstrap sampling and estimation

[R] **jackknife** — Jackknife estimation

[XT] ***vce_options*** — Variance estimators

[U] **20 Estimation and postestimation commands**

Title

view — View files and logs

Syntax

Display file in Viewer

```
view [file] ["]filename["] [, asis adopath]
```

Bring up browser pointed to specified URL

```
view browse ["]url["]
```

Display help results in Viewer

```
view help [topic_or_command_name]
```

Display search results in Viewer

```
view search keywords
```

Display news results in Viewer

```
view news
```

Display net results in Viewer

```
view net [netcmd]
```

Display ado-results in Viewer

```
view ado [adocmd]
```

Display update results in Viewer

```
view update [updatecmd]
```

Programmer's analog to view file and view browse

```
view view_d
```

Programmer's analog to view help

```
view help_d
```

Programmer's analog to view search

```
view search_d
```

Programmer's analog to view net

```
view net_d
```

Programmer's analog to view ado

```
view ado_d
```

Programmer's analog to view update

```
view update_d
```

Menu

File > View...

Description

`view` displays file contents in the Viewer.

`view file` displays the specified file. `file` is optional, so if you had a SMCL session log created by typing `log using mylog`, you could view it by typing `view mylog.smcl`. `view file` can properly display `.smcl` files (logs and the like), `.sthlp` files, and text files. `view file`'s `asis` option specifies that the file be displayed as plain text, regardless of the *filename*'s extension.

`view browse` opens your browser pointed to *url*. Typing `view browse http://www.stata.com` would bring up your browser pointed to the http://www.stata.com website.

`view help` does the same as the `help` command—see [R] **help**—but displays the result in the Viewer. For example, to review the help for Stata's `print` command, you could type `view help print`.

`view search` does the same as the `search` command—see [R] **search**—but displays the result in the Viewer. For instance, to search the online help for information on robust regression, you could type `view search robust regression`.

`view news` does the same as the `news` command—see [R] **news**—but displays the results in the Viewer. (`news` displays the latest news from http://www.stata.com.)

`view net` does the same as the `net` command—see [R] **net**—but displays the result in the Viewer. For instance, typing `view net search hausman test` would search the Internet for additions to Stata related to the Hausman test. Typing `view net from http://www.stata.com` would go to the Stata download site at http://www.stata.com.

`view ado` does the same as the `ado` command—see [R] **net**—but displays the result in the Viewer. For instance, typing `view ado dir` would show a list of files you have installed.

`view update` does the same as the `update` command—see [R] **update**—but displays the result in the Viewer. Typing `view update` would show the dates of what you have installed, and from there you could click to compare those dates with the latest updates available. Typing `view update query` would skip the first step and show the comparison.

The `view *_d` commands are more useful in programming contexts than they are interactively.

`view view_d` displays a dialog box from which you may type the name of a file or a URL to be displayed in the Viewer.

`view help_d` displays a help dialog box from which you may obtain interactive help on any Stata command.

`view search_d` displays a search dialog box from which you may obtain interactive help based on keywords.

`view net_d` displays a search dialog box from which you may search the Internet for additions to Stata (which you could then install).

`view ado_d` displays a dialog box from which you may search the user-written routines you have previously installed.

`view update_d` displays an update dialog box in which you may type the source from which updates are to be obtained.

Options

`asis`, allowed with `view file`, specifies that the file be displayed as text, regardless of the *filename*'s extension. `view file`'s default action is to display files ending in `.smcl` and `.sthlp` as SMCL; see [P] **smcl**.

`adopath`, allowed with `view file`, specifies that Stata search the `S_ADO` path for *filename* and display it, if found.

Remarks

Most users access the Viewer by selecting **File > View...** and proceeding from there. The `view` command allows you to skip that step. Some common interactive uses of `view` are

```
. view mysession.smcl
. view mysession.log

. view help print
. view help regress

. view news
. view browse http://www.stata.com

. view net search hausman test

. view net
. view ado

. view update query
```

Also, programmers find `view` useful for creating special effects.

Also see

[R] **help** — Display online help

[R] **net** — Install and manage user-written additions from the Internet

[R] **news** — Report Stata news

[R] **search** — Search Stata documentation

[R] **update** — Update Stata

[D] **type** — Display contents of a file

[GSM] **3 Using the Viewer**

[GSU] **3 Using the Viewer**

[GSW] **3 Using the Viewer**

Title

vwls — Variance-weighted least squares

Syntax

`vwls` *depvar indepvars* [*if*] [*in*] [*weight*] [, *options*]

options	Description
Model	
`noconstant`	suppress constant term
`sd(`*varname*`)`	variable containing estimate of conditional standard deviation
Reporting	
`level(#)`	set confidence level; default is `level(95)`
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
`coeflegend`	display legend instead of statistics

indepvars may contain factor variables; see [U] **11.4.3 Factor variables**.
`bootstrap`, `by`, `jackknife`, `rolling`, and `statsby` are allowed; see [U] **11.1.10 Prefix commands**.
Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.
`fweights` are allowed; see [U] **11.1.6 weight**.
`coeflegend` does not appear in the dialog box.
See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Linear models and related > Other > Variance-weighted least squares

Description

`vwls` estimates a linear regression using variance-weighted least squares. It differs from ordinary least-squares (OLS) regression in that it does not assume homogeneity of variance, but requires that the conditional variance of *depvar* be estimated prior to the regression. The estimated variance need not be constant across observations. `vwls` treats the estimated variance as if it were the true variance when it computes the standard errors of the coefficients.

You must supply an estimate of the conditional standard deviation of *depvar* to `vwls` by using the `sd(`*varname*`)` option, or you must have grouped data with the groups defined by the *indepvars* variables. In the latter case, `vwls` treats all *indepvars* as categorical variables, computes the mean and standard deviation of *depvar* separately for each subgroup, and computes the regression of the subgroup means on *indepvars*.

`regress` with analytic weights can be used to produce another kind of "variance-weighted least squares"; see *Remarks* for an explanation of the difference.

Options

Model

`noconstant`; see [R] **estimation options**.

`sd(`*varname*`)` is an estimate of the conditional standard deviation of *depvar* (that is, it can vary observation by observation). All values of *varname* must be > 0. If you specify `sd()`, you cannot use `fweights`.

If `sd()` is not given, the data will be grouped by *indepvars*. Here *indepvars* are treated as categorical variables, and the means and standard deviations of *depvar* for each subgroup are calculated and used for the regression. Any subgroup for which the standard deviation is zero is dropped.

Reporting

`level(#)`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

The following option is available with `vwls` but is not shown in the dialog box:

`coeflegend`; see [R] **estimation options**.

Remarks

The `vwls` command is intended for use with two special—and different—types of data. The first contains data that consist of measurements from physical science experiments in which all error is due solely to measurement errors and the sizes of the measurement errors are known.

You can also use variance-weighted least-squares linear regression for certain problems in categorical data analysis, such as when all the independent variables are categorical and the outcome variable is either continuous or a quantity that can sensibly be averaged. If each of the subgroups defined by the categorical variables contains a reasonable number of subjects, then the variance of the outcome variable can be estimated independently within each subgroup. For the purposes of estimation, `vwls` treats each subgroup as one observation, with the dependent variable being the subgroup mean of the outcome variable.

The `vwls` command fits the model

$$y_i = \mathbf{x}_i\boldsymbol{\beta} + \varepsilon_i$$

where the errors ε_i are independent normal random variables with the distribution $\varepsilon_i \sim N(0, \nu_i)$. The independent variables $\mathbf{x}_i$ are assumed to be known without error.

As described above, `vwls` assumes that you already have estimates s_i^2 for the variances ν_i. The error variance is not estimated in the regression. The estimates s_i^2 are used to compute the standard errors of the coefficients; see *Methods and formulas* below.

In contrast, weighted OLS regression assumes that the errors have the distribution $\varepsilon_i \sim N(0, \sigma^2/w_i)$, where the w_i are known weights and σ^2 is an unknown parameter that is estimated in the regression. This is the difference from variance-weighted least squares: in weighted OLS, the magnitude of the error variance is estimated in the regression using all the data.

Example 1

An artificial, but informative, example illustrates the difference between variance-weighted least squares and weighted OLS.

We measure the quantities x_i and y_i and estimate that the standard deviation of y_i is s_i. We enter the data into Stata:

```
. use http://www.stata-press.com/data/r12/vwlsxmpl
. list
```

	x	y	s
1.	1	1.2	.5
2.	2	1.9	.5
3.	3	3.2	1
4.	4	4.3	1
5.	5	4.9	1
6.	6	6.0	2
7.	7	7.2	2
8.	8	7.9	2

Because we want observations with smaller variance to carry larger weight in the regression, we compute an OLS regression with analytic weights proportional to the inverse of the squared standard deviations:

```
. regress y x [aweight=s^(-2)]
(sum of wgt is   1.1750e+01)
```

Source	SS	df	MS		
Model	22.6310183	1	22.6310183	Number of obs	= 8
Residual	.193355117	6	.032225853	F(1, 6)	= 702.26
				Prob > F	= 0.0000
				R-squared	= 0.9915
				Adj R-squared	= 0.9901
Total	22.8243734	7	3.26062477	Root MSE	= .17952

y	Coef.	Std. Err.	t	P>|t|	[95% Conf.	Interval]
x	.9824683	.0370739	26.50	0.000	.8917517	1.073185
_cons	.1138554	.1120078	1.02	0.349	-.1602179	.3879288

If we compute a variance-weighted least-squares regression by using `vwls`, we get the same results for the coefficient estimates but very different standard errors:

```
. vwls y x, sd(s)
```

```
Variance-weighted least-squares regression          Number of obs   =       8
Goodness-of-fit chi2(6)     =    0.28               Model chi2(1)   =   33.24
Prob > chi2                 =  0.9996               Prob > chi2     =  0.0000
```

y	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
x	.9824683	.170409	5.77	0.000	.6484728	1.316464
_cons	.1138554	.51484	0.22	0.825	-.8952124	1.122923

Although the values of y_i were nicely linear with x_i, the `vwls` regression used the large estimates for the standard deviations to compute large standard errors for the coefficients. For weighted OLS regression, however, the scale of the analytic weights has no effect on the standard errors of the coefficients—only the relative proportions of the analytic weights affect the regression.

If we are sure of the sizes of our error estimates for y_i, using `vwls` is valid. However, if we can estimate only the relative proportions of error among the y_i, then `vwls` is not appropriate.

◁

▷ Example 2

Let's now consider an example of the use of `vwls` with categorical data. Suppose that we have blood pressure data for $n = 400$ subjects, categorized by gender and race (black or white). Here is a description of the data:

```
. use http://www.stata-press.com/data/r12/bp
. table gender race, c(mean bp sd bp freq) row col format(%8.1f)
```

	Race		
Gender	White	Black	Total
Female	117.1	118.5	117.8
	10.3	11.6	10.9
	100	100	200
Male	122.1	125.8	124.0
	10.6	15.5	13.3
	100	100	200
Total	119.6	122.2	120.9
	10.7	14.1	12.6
	200	200	400

Performing a variance-weighted regression using `vwls` gives

```
. vwls bp gender race
Variance-weighted least-squares regression          Number of obs   =     400
Goodness-of-fit chi2(1)     =    0.88               Model chi2(2)   =   27.11
Prob > chi2                 =  0.3486               Prob > chi2     =  0.0000
```

bp	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
gender	5.876522	1.170241	5.02	0.000	3.582892	8.170151
race	2.372818	1.191683	1.99	0.046	.0371631	4.708473
_cons	116.6486	.9296297	125.48	0.000	114.8266	118.4707

By comparison, an OLS regression gives the following result:

```
. regress bp gender race
      Source |       SS       df       MS              Number of obs =     400
-------------+------------------------------           F(  2,   397) =   15.24
       Model |  4485.66639     2  2242.83319            Prob > F      =  0.0000
    Residual |  58442.7305   397  147.210908            R-squared     =  0.0713
-------------+------------------------------           Adj R-squared =  0.0666
       Total |  62928.3969   399   157.71528            Root MSE      =  12.133

------------------------------------------------------------------------------
          bp |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
      gender |      6.1775   1.213305     5.09   0.000     3.792194    8.562806
        race |      2.5875   1.213305     2.13   0.034     .2021938    4.972806
       _cons |    116.4862   1.050753   110.86   0.000     114.4205     118.552
------------------------------------------------------------------------------
```

Note the larger value for the `race` coefficient (and smaller p-value) in the OLS regression. The assumption of homogeneity of variance in OLS means that the mean for black men pulls the regression line higher than in the `vwls` regression, which takes into account the larger variance for black men and reduces its effect on the regression.

◁

Saved results

`vwls` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(df_m)`	model degrees of freedom
`e(chi2)`	model χ^2
`e(df_gf)`	goodness-of-fit degrees of freedom
`e(chi2_gf)`	goodness-of-fit χ^2
`e(rank)`	rank of `e(V)`

Macros

`e(cmd)`	`vwls`
`e(cmdline)`	command as typed
`e(depvar)`	name of dependent variable
`e(properties)`	`b V`
`e(predict)`	program used to implement `predict`
`e(asbalanced)`	factor variables `fvset` as `asbalanced`
`e(asobserved)`	factor variables `fvset` as `asobserved`

Matrices

`e(b)`	coefficient vector
`e(V)`	variance–covariance matrix of the estimators

Functions

`e(sample)`	marks estimation sample

Methods and formulas

`vwls` is implemented as an ado-file.

Let $\mathbf{y} = (y_1, y_2, \ldots, y_n)'$ be the vector of observations of the dependent variable, where n is the number of observations. When `sd()` is specified, let s_1, s_2, ..., s_n be the standard deviations supplied by `sd()`. For categorical data, when `sd()` is not given, the means and standard deviations of y for each subgroup are computed, and n becomes the number of subgroups, $\mathbf{y}$ is the vector of subgroup means, and s_i are the standard deviations for the subgroups.

Let $\mathbf{V} = \mathrm{diag}(s_1^2, s_2^2, \ldots, s_n^2)$ denote the estimate of the variance of $\mathbf{y}$. Then the estimated regression coefficients are

$$\mathbf{b} = (\mathbf{X}'\mathbf{V}^{-1}\mathbf{X})^{-1}\mathbf{X}'\mathbf{V}^{-1}\mathbf{y}$$

and their estimated covariance matrix is

$$\widehat{\mathrm{Cov}}(\mathbf{b}) = (\mathbf{X}'\mathbf{V}^{-1}\mathbf{X})^{-1}$$

A statistic for the goodness of fit of the model is

$$Q = (\mathbf{y} - \mathbf{X}\mathbf{b})'\,\mathbf{V}^{-1}(\mathbf{y} - \mathbf{X}\mathbf{b})$$

where Q has a χ^2 distribution with $n - k$ degrees of freedom (k is the number of independent variables plus the constant, if any).

References

Gini, R., and J. Pasquini. 2006. Automatic generation of documents. *Stata Journal* 6: 22–39.

Grizzle, J. E., C. F. Starmer, and G. G. Koch. 1969. Analysis of categorical data by linear models. *Biometrics* 25: 489–504.

Press, W. H., S. A. Teukolsky, W. T. Vetterling, and B. P. Flannery. 2007. *Numerical Recipes in C: The Art of Scientific Computing*. 3rd ed. Cambridge: Cambridge University Press.

Also see

[R] **vwls postestimation** — Postestimation tools for vwls

[R] **regress** — Linear regression

[U] **11.1.6 weight**

[U] **20 Estimation and postestimation commands**

Title

vwls postestimation — Postestimation tools for vwls

Description

The following postestimation commands are available after `vwls`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	VCE and estimation sample summary
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`linktest`	link test for model specification
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

See the corresponding entries in the *Base Reference Manual* for details.

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [`, xb stdp`]

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`xb`, the default, calculates the linear prediction.

`stdp` calculates the standard error of the linear prediction.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

Also see

[R] **vwls** — Variance-weighted least squares

[U] **20 Estimation and postestimation commands**

Title

which — Display location and version for an ado-file

Syntax

`which` *fname*[`.`*ftype*] [`, all`]

Description

`which` looks for *fname*`.`*ftype* along the `S_ADO` path. If Stata finds the file, `which` displays the full path and filename, along with, if the file is text, all lines in the file that begin with "`*!`" in the first column. If Stata cannot find the file, `which` issues the message "file not found along ado-path" and sets the return code to 111. *ftype* must be a file type for which Stata usually looks along the ado-path to find. Allowable *ftype*s are

`.ado`, `.class`, `.dlg`, `.idlg`, `.sthlp`, `.ihlp`, `.hlp`, `.key`, `.maint`, `.mata`, `.mlib`, `.mo`, `.mnu`, `.plugin`, `.scheme`, `.stbcal`, and `.style`

If *ftype* is omitted, `which` assumes `.ado`. When searching for `.ado` files, if Stata cannot find the file, Stata then checks to see if *fname* is a built-in Stata command, allowing for valid abbreviations. If it is, the message "built-in command" is displayed; if not, the message "command not found as either built-in or ado-file" is displayed and the return code is set to 111.

For information about internal version control, see [P] **version**.

Option

`all` forces `which` to report the location of all files matching the *fname*`.`*ftype* found along the search path. The default is to report just the first one found.

Remarks

If you write programs, you know that you make changes to the programs over time. If you are like us, you also end up with multiple versions of the program stored on your disk, perhaps in different directories. You may even have given copies of your programs to other Stata users, and you may not remember which version of a program you or your friends are using. The `which` command helps you solve this problem.

▷ Example 1

The `which` command displays the path for *filename*`.ado` and any lines in the code that begin with "`*!`". For example, we might want information about the `test` command, described in [R] **test**, which is an ado-file written by StataCorp. Here is what happens when we type `which test`:

```
. which test
C:\Program Files\Stata12\ado\base\t\test.ado
*! version 2.2.1  18feb2011
```

`which` displays the path for the `test.ado` file and also a line beginning with "`*!`" that indicates the version of the file. This is how we, at StataCorp, do version control—see [U] **18.11.1 Version** for an explanation of our version control numbers.

We do not need to be so formal. `which` will display anything typed after lines that begin with '`*!`'. For instance, we might write `myprog.ado`:

```
. which myprog
.\myprog.ado
*! first written 1/03/2011
*! bug fix on 1/05/2011 (no variance case)
*! updated 1/24/2011 to include noconstant option
*! still suspicious if variable takes on only two values
```

It does not matter where in the program the lines beginning with `*!` are—`which` will list them (in particular, our "still suspicious" comment was buried about 50 lines down in the code). All that is important is that the `*!` marker appear in the first two columns of a line.

◁

▷ Example 2

If we type `which` *command*, where *command* is a built-in command rather than an ado-file, Stata responds with

```
. which summarize
built-in command:  summarize
```

If *command* was neither a built-in command nor an ado-file, Stata would respond with

```
. which junk
command junk not found as either built-in or ado-file
r(111);
```

◁

Also see

[P] **findfile** — Find file in path

[P] **version** — Version control

[U] **17 Ado-files**

[U] **18.11.1 Version**

Title

xi — Interaction expansion

Syntax

`xi` [`, prefix(`*string*`) noomit`] *term*(*s*)

`xi` [`, prefix(`*string*`) noomit`] `:` *any_stata_command varlist_with_terms* ...

where a *term* has the form

`i.`*varname*		`I.`*varname*
`i.`*varname*$_1$`*i.`*varname*$_2$		`I.`*varname*$_1$`*I.`*varname*$_2$
`i.`*varname*$_1$`*`*varname*$_3$		`I.`*varname*$_1$`*`*varname*$_3$
`i.`*varname*$_1$`|`*varname*$_3$		`I.`*varname*$_1$`|`*varname*$_3$

varname, *varname*$_1$, and *varname*$_2$ denote numeric or string categorical variables. *varname*$_3$ denotes a continuous, numeric variable.

Menu

Data > Create or change data > Other variable-creation commands > Interaction expansion

Most commands in Stata now allow factor variables; see [U] **11.4.3 Factor variables**. To determine if a command allows factor variables, see the information printed below the options table for the command. If the command allows factor variables, it will say something like "*indepvars* may contain factor variables".

We recommend that you use factor variables instead of `xi` if a command allows factor variables.

We include [R] **xi** in our documentation so that readers can consult it when using a Stata command that does not allow factor variables.

Description

`xi` expands terms containing categorical variables into indicator (also called dummy) variable sets by creating new variables and, in the second syntax (`xi:` *any_stata_command*), executes the specified command with the expanded terms. The dummy variables created are

`i.`*varname*	creates dummies for categorical variable *varname*
`i.`*varname*$_1$`*i.`*varname*$_2$	creates dummies for categorical variables *varname*$_1$ and *varname*$_2$: all interactions and main effects
`i.`*varname*$_1$`*`*varname*$_3$	creates dummies for categorical variable *varname*$_1$ and continuous variable *varname*$_3$: all interactions and main effects
`i.`*varname*$_1$`|`*varname*$_3$	creates dummies for categorical variable *varname*$_1$ and continuous variable *varname*$_3$: all interactions and main effect of *varname*$_3$, but no main effect of *varname*$_1$

Options

`prefix(`*string*`)` allows you to choose a prefix other than `_I` for the newly created interaction variables. The prefix cannot be longer than four characters. By default, `xi` will create interaction variables starting with `_I`. When you use `xi`, it drops all previously created interaction variables starting with the prefix specified in the `prefix(`*string*`)` option or with `_I` by default. Therefore, if you want to keep the variables with a certain prefix, specify a different prefix in the `prefix(`*string*`)` option.

`noomit` prevents `xi` from omitting groups. This option provides a way to generate an indicator variable for every category having one or more variables, which is useful when combined with the `noconstant` option of an estimation command.

Remarks

Remarks are presented under the following headings:

Background
Indicator variables for simple effects
Controlling the omitted dummy
Categorical variable interactions
Interactions with continuous variables
Using xi: Interpreting output
How xi names variables
xi as a command rather than a command prefix
Warnings

`xi` provides a convenient way to include dummy or indicator variables when fitting a model (say, with `regress` or `logistic`). For instance, assume that the categorical variable `agegrp` contains 1 for ages 20–24, 2 for ages 25–39, 3 for ages 40–44, etc. Typing

```
. xi: logistic outcome weight i.agegrp bp
```

estimates a logistic regression of `outcome` on `weight`, dummies for each `agegrp` category, and `bp`. That is, `xi` searches out and expands terms starting with "`i.`" or "`I.`" but ignores the other variables. `xi` will expand both numeric and string categorical variables, so if you had a string variable `race` containing "white", "black", and "other", typing

```
. xi: logistic outcome weight bp i.agegrp i.race
```

would include indicator variables for the race group as well.

The `i.` indicator variables `xi` expands may appear anywhere in the *varlist*, so

```
. xi: logistic outcome i.agegrp weight i.race bp
```

would fit the same model.

You can also create interactions of categorical variables; typing

```
xi: logistic outcome weight bp i.agegrp*i.race
```

fits a model with indicator variables for all `agegrp` and `race` combinations, including the `agegrp` and `race` main-effect terms (that is, the terms that are created when you just type `i.agegrp i.race`).

You can interact dummy variables with continuous variables; typing

```
xi: logistic outcome bp i.agegrp*weight i.race
```

fits a model with indicator variables for all `agegrp` categories interacted with `weight`, plus the main-effect terms `weight` and `i.agegrp`.

You can get the interaction terms without the `agegrp` main effect (but with the `weight` main effect) by typing

```
xi: logistic outcome bp i.agegrp|weight i.race
```

You can also include multiple interactions:

```
xi: logistic outcome bp i.agegrp*weight i.agegrp*i.race
```

We will now back up and describe the construction of dummy variables in more detail.

Background

The terms *continuous*, *categorical*, and *indicator* or *dummy* variables are used below. Continuous variables measure something—such as height or weight—and at least conceptually can take on any real number over some range. Categorical variables, on the other hand, take on a finite number of values, each denoting membership in a subclass—for example, excellent, good, and poor, which might be coded 0, 1, 2, or 1, 2, 3, or even "Excellent", "Good", and "Poor". An indicator or dummy variable—the terms are used interchangeably—is a special type of two-valued categorical variable that contains values 0, denoting false, and 1, denoting true. The information contained in any k-valued categorical variable can be equally well represented by k indicator variables. Instead of one variable recording values representing excellent, good, and poor, you can have three indicator variables, indicating the truth or falseness of "result is excellent", "result is good", and "result is poor".

`xi` provides a convenient way to convert categorical variables to dummy or indicator variables when you fit a model (say, with `regress` or `logistic`).

▷ Example 1

For instance, assume that the categorical variable `agegrp` contains 1 for ages 20–24, 2 for ages 25–39, and 3 for ages 40–44. (There is no one over 44 in our data.) As it stands, `agegrp` would be a poor candidate for inclusion in a model even if we thought age affected the outcome. The reason is that the coding would restrict the effect of being in the second age group to be twice the effect of being in the first, and, similarly, the effect of being in the third to be three times the first. That is, if we fit the model,

$$y = \beta_0 + \beta_1 \texttt{agegrp} + X\beta_2$$

the effect of being in the first age group is β_1, the second $2\beta_1$, and the third $3\beta_1$. If the coding 1, 2, and 3 is arbitrary, we could just as well have coded the age groups 1, 4, and 9, making the effects β_1, $4\beta_1$, and $9\beta_1$.

The solution is to convert the categorical variable `agegrp` to a set of indicator variables, a_1, a_2, and a_3, where a_i is 1 if the individual is a member of the ith age group and 0 otherwise. We can then fit the model

$$y = \beta_0 + \beta_{11}a_1 + \beta_{12}a_2 + \beta_{13}a_3 + X\beta_2$$

The effect of being in age group 1 is now β_{11}; 2, β_{12}; and 3, β_{13}; and these results are independent of our (arbitrary) coding. The only difficulty at this point is that the model is unidentified in the sense that there are an infinite number of $(\beta_0, \beta_{11}, \beta_{12}, \beta_{13})$ that fit the data equally well.

To see this, pretend that $(\beta_0, \beta_{11}, \beta_{12}, \beta_{13}) = (1, 1, 3, 4)$. The predicted values of y for the various age groups are

$$y = \begin{cases} 1 + 1 + X\beta_2 = 2 + X\beta_2 & \text{(age group 1)} \\ 1 + 3 + X\beta_2 = 4 + X\beta_2 & \text{(age group 2)} \\ 1 + 4 + X\beta_2 = 5 + X\beta_2 & \text{(age group 3)} \end{cases}$$

Now pretend that $(\beta_0, \beta_{11}, \beta_{12}, \beta_{13}) = (2, 0, 2, 3)$. The predicted values of y are

$$y = \begin{cases} 2 + 0 + X\beta_2 = 2 + X\beta_2 & \text{(age group 1)} \\ 2 + 2 + X\beta_2 = 4 + X\beta_2 & \text{(age group 2)} \\ 2 + 3 + X\beta_2 = 5 + X\beta_2 & \text{(age group 3)} \end{cases}$$

These two sets of predictions are indistinguishable: for age group 1, $y = 2 + X\beta_2$ regardless of the coefficient vector used, and similarly for age groups 2 and 3. This arises because we have three equations and four unknowns. Any solution is as good as any other, and, for our purposes, we merely need to choose one of them. The popular selection method is to set the coefficient on the first indicator variable to 0 (as we have done in our second coefficient vector). This is equivalent to fitting the model

$$y = \beta_0 + \beta_{12}a_2 + \beta_{13}a_3 + X\beta_2$$

How we select a particular coefficient vector (identifies the model) does not matter. It does, however, affect the *interpretation* of the coefficients.

For instance, we could just as well choose to omit the second group. In our artificial example, this would yield $(\beta_0, \beta_{11}, \beta_{12}, \beta_{13}) = (4, -2, 0, 1)$ instead of $(2, 0, 2, 3)$. These coefficient vectors are the same in the sense that

$$y = \begin{cases} 2 + 0 + X\beta_2 = 2 + X\beta_2 = 4 - 2 + X\beta_2 & \text{(age group 1)} \\ 2 + 2 + X\beta_2 = 4 + X\beta_2 = 4 + 0 + X\beta_2 & \text{(age group 2)} \\ 2 + 3 + X\beta_2 = 5 + X\beta_2 = 4 + 1 + X\beta_2 & \text{(age group 3)} \end{cases}$$

But what does it mean that β_{13} can just as well be 3 or 1? We obtain $\beta_{13} = 3$ when we set $\beta_{11} = 0$, so $\beta_{13} = \beta_{13} - \beta_{11}$ and β_{13} measures the difference between age groups 3 and 1.

In the second case, we obtain $\beta_{13} = 1$ when we set $\beta_{12} = 0$, so $\beta_{13} - \beta_{12} = 1$ and β_{13} measures the difference between age groups 3 and 2. There is no inconsistency. According to our $\beta_{12} = 0$ model, the difference between age groups 3 and 1 is $\beta_{13} - \beta_{11} = 1 - (-2) = 3$, the same result we got in the $\beta_{11} = 0$ model.

◁

▷ Example 2

The issue of interpretation is important because it can affect the way we discuss results. Imagine that we are studying recovery after a coronary bypass operation. Assume that the age groups are children under 13 (we have two of them), young adults under 25 (we have a handful of them), adults under 46 (of which we have even more), mature adults under 56, older adults under 65, and elderly adults. We follow the prescription of omitting the first group, so all our results are reported relative to children under 13. While there is nothing statistically wrong with this, readers will be suspicious when we make statements like "compared with young children, older and elder adults . . . ". Moreover, we will probably have to end each statement with "although results are not statistically significant" because we have only two children in our comparison group. Of course, even with results reported in this way, we can do reasonable comparisons (say, with mature adults), but we will have to do extra work to perform the appropriate linear hypothesis test using Stata's `test` command.

Here it would be better to force the omitted group to be more reasonable, such as mature adults. There is, however, a generic rule for automatic comparison group selection that, although less popular, tends to work better than the omit-the-first-group rule. That rule is to omit the most prevalent group. The most prevalent is usually a reasonable baseline.

◁

In any case, the prescription for categorical variables is

1. Convert each k-valued categorical variable to k indicator variables.
2. Drop one of the k indicator variables; any one will do, but dropping the first is popular, dropping the most prevalent is probably better in terms of having the computer guess at a reasonable interpretation, and dropping a specified one often eases interpretation the most.
3. Fit the model on the remaining $k - 1$ indicator variables.

`xi` automates this procedure.

We will now consider each of `xi`'s features in detail.

Indicator variables for simple effects

When you type `i.`*varname*, `xi` internally tabulates *varname* (which may be a string or a numeric variable) and creates indicator (dummy) variables for each observed value, omitting the indicator for the smallest value. For instance, say that `agegrp` takes on the values 1, 2, 3, and 4. Typing

```
xi: logistic outcome i.agegrp
```

creates indicator variables named `_Iagegrp_2`, `_Iagegrp_3`, and `_Iagegrp_4`. (`xi` chooses the names and tries to make them readable; `xi` guarantees that the names are unique.) The expanded logistic model is

```
. logistic outcome _Iagegrp_2 _Iagegrp_3 _Iagegrp_4
```

Afterward, you can drop the new variables `xi` leaves behind by typing '`drop _I*`' (note the capitalization).

`xi` provides the following features when you type `i.`*varname*:

- *varname* may be string or numeric.
- Dummy variables are created automatically.
- By default, the dummy-variable set is identified by dropping the dummy corresponding to the smallest value of the variable (how to specify otherwise is discussed below).
- The new dummy variables are left in your dataset. By default, the names of the new dummy variables start with `_I`; therefore, you can drop them by typing '`drop _I*`'. You do not have to do this; each time you use `xi`, any automatically generated dummies with the same prefix as the one specified in the `prefix(`*string*`)` option, or `_I` by default, are dropped and new ones are created.
- The new dummy variables have variable labels so that you can determine what they correspond to by typing '`describe`'.
- `xi` may be used with any Stata command (not just `logistic`).

Controlling the omitted dummy

By default, `i.`*varname* omits the dummy corresponding to the smallest value of *varname*; for a string variable, this is interpreted as dropping the first in an alphabetical, case-sensitive sort. `xi` provides two alternatives to dropping the first: `xi` will drop the dummy corresponding to the most prevalent value of *varname*, or `xi` will let you choose the particular dummy to be dropped.

To change `xi`'s behavior to dropping the most prevalent dummy, type

```
. char _dta[omit] prevalent
```

although whether you type "prevalent" or "yes" or anything else does not matter. Setting this characteristic affects the expansion of all categorical variables in the dataset. If you resave your dataset, the prevalent preference will be remembered. If you want to change the behavior back to the default drop-the-first rule, type

```
. char _dta[omit]
```

to clear the characteristic.

Once you set `_dta[omit]`, `i.`*varname* omits the dummy corresponding to the most prevalent value of *varname*. Thus the coefficients on the dummies have the interpretation of change from the most prevalent group. For example,

```
. char _dta[omit] prevalent
. xi: regress y i.agegrp
```

might create `_Iagegrp_1` through `_Iagegrp_4`, resulting in `_Iagegrp_2` being omitted if `agegrp` $=$ 2 is most common (as opposed to the default dropping of `_Iagegrp_1`). The model is then

$$\texttt{y} = b_0 + b_1\,\texttt{\_Iagegrp\_1} + b_3\,\texttt{\_Iagegrp\_3} + b_4\,\texttt{\_Iagegrp\_4} + u$$

Then

Predicted `y` for `agegrp` 1 $= b_0 + b_1$	Predicted `y` for `agegrp` 3 $= b_0 + b_3$
Predicted `y` for `agegrp` 2 $= b_0$	Predicted `y` for `agegrp` 4 $= b_0 + b_4$

Thus the model's reported t or Z statistics are for a test of whether each group is different from the most prevalent group.

Perhaps you wish to omit the dummy for `agegrp` 3 instead. You do this by setting the variable's `omit` characteristic:

```
. char agegrp[omit] 3
```

This overrides `_dta[omit]` if you have set it. Now when you type

```
. xi: regress y i.agegrp
```

`_Iagegrp_3` will be omitted, and you will fit the model

$$\texttt{y} = b'_0 + b'_1\,\texttt{\_Iagegrp\_1} + b'_2\,\texttt{\_Iagegrp\_2} + b'_4\,\texttt{\_Iagegrp\_4} + u$$

Later if you want to return to the default omission, type

```
. char agegrp[omit]
```

to clear the characteristic.

In summary, `i.`*varname* omits the first group by default, but if you define

```
. char _dta[omit] prevalent
```

the default behavior changes to dropping the most prevalent group. Either way, if you define a characteristic of the form

```
. char varname[omit] #
```

or, if *varname* is a string,

```
. char varname[omit] string-literal
```

the specified value will be omitted.

Examples:

```
. char agegrp[omit] 1
. char race[omit] White      (for race, a string variable)
. char agegrp[omit]          (to restore default for agegrp)
```

Categorical variable interactions

`i.`*varname*$_1$`*i.`*varname*$_2$ creates the dummy variables associated with the interaction of the categorical variables *varname*$_1$ and *varname*$_2$. The identification rules — which categories are omitted — are the same as those for `i.`*varname*. For instance, assume that `agegrp` takes on four values and `race` takes on three values. Typing

```
. xi: regress y i.agegrp*i.race
```

results in

model:	dummies for:
$y = a + b_2$ `_Iagegrp_2` $+ b_3$ `_Iagegrp_3` $+ b_4$ `_Iagegrp_4`	(`agegrp`)
$+ c_2$ `_Irace_2` $+ c_3$ `_Irace_3`	(`race`)
$+ d_{22}$ `_IageXrac_2_2` $+ d_{23}$ `_IageXrac_2_3`	
$+ d_{32}$ `_IageXrac_3_2` $+ d_{33}$ `_IageXrac_3_3`	(`agegrp*race`)
$+ d_{42}$ `_IageXrac_4_2` $+ d_{43}$ `_IageXrac_4_3`	
$+ u$	

That is, typing

```
. xi: regress y i.agegrp*i.race
```

is the same as typing

```
. xi: regress y i.agegrp i.race i.agegrp*i.race
```

Although there are many other ways the interaction could have been parameterized, this method has the advantage that you can test the joint significance of the interactions by typing

```
. testparm _IageXrac*
```

When you perform the estimation step, whether you specify `i.agegrp*i.race` or `i.race*i.agegrp` makes no difference (other than in the names given to the interaction terms; in the first case, the names will begin with `_IageXrac`; in the second, `_IracXage`). Thus

```
. xi: regress y i.race*i.agegrp
```

fits the same model.

You may also include multiple interactions simultaneously:

```
. xi: regress y i.agegrp*i.race i.agegrp*i.sex
```

The model fit is

model:	dummies for:
$y = a + b_2$ _Iagegrp_2 $+ b_3$ _Iagegrp_3 $+ b_4$ _Iagegrp_4	(agegrp)
$+ c_2$ _Irace_2 $+ c_3$ _Irace_3	(race)
$+ d_{22}$ _IageXrac_2_2 $+ d_{23}$ _IageXrac_2_3	
$+ d_{32}$ _IageXrac_3_2 $+ d_{33}$ _IageXrac_3_3	(agegrp*race)
$+ d_{42}$ _IageXrac_4_2 $+ d_{43}$ _IageXrac_4_3	
$+ e_2$ _Isex_2	(sex)
$+ f_{22}$ _IageXsex_2_2 $+ f_{23}$ _IageXsex_2_3 $+ f_{24}$ _IageXsex_2_4	(agegrp*sex)
$+ u$	

The agegrp dummies are (correctly) included only once.

Interactions with continuous variables

i.*varname*$_1$*i.*varname*$_2$ (as distinguished from i.*varname*$_1$*i.*varname*$_2$—note the second i.) specifies an interaction of a categorical variable with a continuous variable. For instance,

```
. xi: regress y i.agegr*wgt
```

results in the model

$y = a + b_2$ _Iagegrp_2 $+ b_3$ _Iagegrp_3 $+ b_4$ _Iagegrp_4	(agegrp dummies)
$+ c$ wgt	(continuous wgt effect)
$+ d_2$ _IageXwgt_2 $+ d_3$ _IageXwgt_3 $+ d_4$ _IageXwgt_4	(agegrp*wgt interactions)
$+ u$	

A variation on this notation, using | rather than *, omits the agegrp dummies. Typing

```
. xi: regress y i.agegrp|wgt
```

fits the model

$y = a' + c'$ wgt	(continuous wgt effect)
$+ d'_2$ _IageXwgt_2 $+ d'_3$ _IageXwgt_3 $+ d'_4$ _IageXwgt_4	(agegrp*wgt interactions)
$+ u'$	

The predicted values of y are

agegrp*wgt model	agegrp|wgt model	
$y = a + c$ wgt	$a' + c'$ wgt	if agegrp $= 1$
$a + c$ wgt $+ b_2 + d_2$ wgt	$a' + c'$wgt $+ d'_2$ wgt	if agegrp $= 2$
$a + c$ wgt $+ b_3 + d_3$ wgt	$a' + c'$wgt $+ d'_3$ wgt	if agegrp $= 3$
$a + c$ wgt $+ b_4 + d_4$ wgt	$a' + c'$wgt $+ d'_4$ wgt	if agegrp $= 4$

That is, typing

```
. xi: regress y i.agegrp*wgt
```

is equivalent to typing

```
. xi: regress y i.agegrp i.agegrp|wgt
```

In either case, you do not need to specify separately the continuous variable `wgt`; it is included automatically.

Using xi: Interpreting output

```
. xi: regress mpg i.rep78
i.rep78               _Irep78_1-5   (naturally coded; _Irep78_1 omitted)
  (output from regress appears)
```

Interpretation: `i.rep78` expanded to the dummies `_Irep78_1`, `_Irep78_2`, ..., `_Irep78_5`. The numbers on the end are "natural" in the sense that `_Irep78_1` corresponds to `rep78` = 1, `_Irep78_2` to `rep78` = 2, and so on. Finally, the dummy for `rep78` = 1 was omitted.

```
. xi: regress mpg i.make
i.make                _Imake_1-74   (_Imake_1 for make==AMC Concord omitted)
  (output from regress appears)
```

Interpretation: `i.make` expanded to `_Imake_1`, `_Imake_2`, ..., `_Imake_74`. The coding is not natural because `make` is a string variable. `_Imake_1` corresponds to one make, `_Imake_2` to another, and so on. You can find out the coding by typing `describe`. `_Imake_1` for the AMC Concord was omitted.

How xi names variables

By default, `xi` assigns to the dummy variables it creates names having the form

_I*stub*_*groupid*

You may subsequently refer to the entire set of variables by typing '`I`*stub*`*`'. For example,

name	=	_I	+	*stub*	+	_	+	*groupid*	Entire set
_Iagegrp_1		_I		agegrp		_		1	_Iagegrp*
_Iagegrp_2		_I		agegrp		_		2	_Iagegrp*
_IageXwgt_1		_I		ageXwgt		_		1	_IageXwgt*
_IageXrac_1_2		_I		ageXrac		_		1_2	_IageXrac*
_IageXrac_2_1		_I		ageXrac		_		2_1	_IageXrac*

If you specify a prefix in the `prefix(`*string*`)` option, say, `_S`, then `xi` will name the variables starting with the prefix

_S*stub*_*groupid*

xi as a command rather than a command prefix

`xi` can be used as a command prefix or as a command by itself. In the latter form, `xi` merely creates the indicator and interaction variables. Typing

```
. xi: regress y i.agegrp*wgt
i.agegrp              _Iagegrp_1-4   (naturally coded; _Iagegrp_1 omitted)
i.agegrp*wgt          _IageXwgt_1-4   (coded as above)
 (output from regress appears)
```

is equivalent to typing

```
. xi i.agegrp*wgt
i.agegrp              _Iagegrp_1-4   (naturally coded; _Iagegrp_1 omitted)
i.agegrp*wgt          _IageXwgt_1-4   (coded as above)
. regress y _Iagegrp* _IageXwgt*
 (output from regress appears)
```

Warnings

1. `xi` creates new variables in your dataset; most are `byte`s, but interactions with continuous variables will have the storage type of the underlying continuous variable. You may get the message "insufficient memory". If so, you will need to increase the amount of memory allocated to Stata's data areas; see [U] **6 Managing memory**.
2. When using `xi` with an estimation command, you may get the message "matsize too small". If so, see [R] **matsize**.

Saved results

`xi` saves the following characteristics:

`_dta[__xi__Vars__Prefix__]`	prefix names
`_dta[__xi__Vars__To__Drop__]`	variables created

Methods and formulas

`xi` is implemented as an ado-file.

References

Hendrickx, J. 1999. dm73: Using categorical variables in Stata. *Stata Technical Bulletin* 52: 2–8. Reprinted in *Stata Technical Bulletin Reprints*, vol. 9, pp. 51–59. College Station, TX: Stata Press.

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Also see

[U] **11.1.10 Prefix commands**

[U] **20 Estimation and postestimation commands**

Title

zinb — Zero-inflated negative binomial regression

Syntax

```
zinb depvar [indepvars] [if] [in] [weight] ,
    inflate(varlist[ , offset(varname) ] | _cons) [options ]
```

options	Description
Model	
* `inflate( )`	equation that determines whether the count is zero
`noconstant`	suppress constant term
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
`probit`	use probit model to characterize excess zeros; default is logit
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`irr`	report incidence-rate ratios
`vuong`	perform Vuong test
`zip`	perform ZIP likelihood-ratio test
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

* `inflate(`*varlist*`[ , offset(`*varname*`) ] | _cons)` is required.

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()`, `vuong`, `zip`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Count outcomes > Zero-inflated negative binomial regression

Description

`zinb` estimates a zero-inflated negative binomial (ZINB) regression of *depvar* on *indepvars*, where *depvar* is a nonnegative count variable.

Options

Model

`inflate(`*varlist*`[ , offset(`*varname*`)] | _cons)` specifies the equation that determines whether the observed count is zero. Conceptually, omitting `inflate()` would be equivalent to fitting the model with `nbreg`.

`inflate(`*varlist*`[, offset(`*varname*`)])` specifies the variables in the equation. You may optionally include an offset for this *varlist*.

`inflate(_cons)` specifies that the equation determining whether the count is zero contains only an intercept. To run a zero-inflated model of *depvar* with only an intercept in both equations, type `zinb` *depvar*`, inflate(_cons)`.

`noconstant`, `exposure(`*varname*$_e$`)`, `offset(`*varname*$_o$`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

`probit` requests that a probit, instead of logit, model be used to characterize the excess zeros in the data.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. `irr` may be specified at estimation or when replaying previously estimated results.

`vuong` specifies that the Vuong (1989) test of ZINB versus negative binomial be reported. This test statistic has a standard normal distribution with large positive values favoring the ZINB model and large negative values favoring the negative binomial model.

`zip` requests that a likelihood-ratio test comparing the ZINB model with the zero-inflated Poisson model be included in the output.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with zinb but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

See Long (1997, 242–247) and Greene (2012, 821–826) for a discussion of zero-modified count models. For information about the test developed by Vuong (1989), see Greene (2012, 823–824) and Long (1997). Greene (1994) applied the test to zero-inflated Poisson and negative binomial models, and there is a description of that work in Greene (2012).

Negative binomial regression fits models of the number of occurrences (counts) of an event. You could use nbreg for this (see [R] **nbreg**), but in some count-data models, you might want to account for the prevalence of zero counts in the data.

For instance, you could count how many fish each visitor to a park catches. Many visitors may catch zero, because they do not fish (as opposed to being unsuccessful). You may be able to model whether a person fishes depending on several covariates related to fishing activity and model how many fish a person catches depending on several covariates having to do with the success of catching fish (type of lure/bait, time of day, temperature, season, etc.). This is the type of data for which the zinb command is useful.

The zero-inflated (or zero-altered) negative binomial model allows overdispersion through the splitting process that models the outcomes as zero or nonzero.

▷ Example 1

We have data on the number of fish caught by visitors to a national park. Some of the visitors do not fish, but we do not have the data on whether a person fished; we have data merely on how many fish were caught, together with several covariates. Because our data have a preponderance of zeros (142 of 250), we use the zinb command to model the outcome.

```
. use http://www.stata-press.com/data/r12/fish
. zinb count persons livebait, inf(child camper) vuong
Fitting constant-only model:
Iteration 0:   log likelihood = -519.33992
  (output omitted)
Iteration 8:   log likelihood = -442.66299
Fitting full model:
Iteration 0:   log likelihood = -442.66299  (not concave)
  (output omitted)
Iteration 8:   log likelihood = -401.54776
```

```
Zero-inflated negative binomial regression        Number of obs   =       250
                                                  Nonzero obs     =       108
                                                  Zero obs        =       142

Inflation model = logit                           LR chi2(2)      =     82.23
Log likelihood  = -401.5478                       Prob > chi2     =    0.0000
```

	Coef.	Std. Err.	z	P>|z|	[95% Conf.	Interval]
count						
persons	.9742984	.1034938	9.41	0.000	.7714543	1.177142
livebait	1.557523	.4124424	3.78	0.000	.7491503	2.365895
_cons	-2.730064	.476953	-5.72	0.000	-3.664874	-1.795253
inflate						
child	3.185999	.7468551	4.27	0.000	1.72219	4.649808
camper	-2.020951	.872054	-2.32	0.020	-3.730146	-.3117567
_cons	-2.695385	.8929071	-3.02	0.003	-4.44545	-.9453189
/lnalpha	.5110429	.1816816	2.81	0.005	.1549535	.8671323
alpha	1.667029	.3028685			1.167604	2.380076

```
Vuong test of zinb vs. standard negative binomial: z =     5.59  Pr>z = 0.0000
```

In general, Vuong test statistics that are significantly positive favor the zero-inflated models, whereas those that are significantly negative favor the non–zero-inflated models. Thus, in the above model, the zero inflation is significant. ◁

Saved results

`zinb` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_zero)`	number of zero observations
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_aux)`	number of auxiliary parameters
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(df_c)`	degrees of freedom for comparison test
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance of model test
`e(chi2_cp)`	χ^2 for test of $\alpha = 0$
`e(vuong)`	Vuong test statistic
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	zinb
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(inflate)	logit or probit
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset1)	offset
e(offset2)	offset for inflate()
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_cpt)	Wald or LR; type of model χ^2 test corresponding to e(chi2_cp)
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

zinb is implemented as an ado-file.

Several models in the literature are (correctly) described as zero inflated. The zinb command maximizes the log likelihood $\ln L$, defined by

$$
\begin{aligned}
m &= 1/\alpha \\
p_j &= 1/(1+\alpha\mu_j) \\
\xi_j^{\beta} &= \mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j^{\beta} \\
\xi_j^{\gamma} &= \mathbf{z}_j\boldsymbol{\gamma} + \text{offset}_j^{\gamma} \\
\mu_j &= \exp(\xi_j^{\beta}) \\
\ln L &= \sum_{j\in S} w_j \ln\left[F(\xi_j^{\gamma}) + \left\{1 - F(\xi_j^{\gamma})\right\}p_j^m\right] \\
&\qquad + \sum_{j\notin S} w_j\Big[\ln\left\{1 - F(\xi_j^{\gamma})\right\} + \ln\Gamma(m+y_j) - \ln\Gamma(y_j+1) \\
&\qquad\qquad - \ln\Gamma(m) + m\ln p_j + y_j\ln(1-p_j)\Big]
\end{aligned}
$$

where w_j are the weights, F is the inverse of the logit link (or the inverse of the probit link if `probit` was specified), and S is the set of observations for which the outcome $y_j = 0$.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`zinb` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

Greene, W. H. 1994. Accounting for excess zeros and sample selection in Poisson and negative binomial regression models. Working paper EC-94-10, Department of Economics, Stern School of Business, New York University. http://ideas.repec.org/p/ste/nystbu/94-10.html.

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Vuong, Q. H. 1989. Likelihood ratio tests for model selection and non-nested hypotheses. *Econometrica* 57: 307–333.

Also see

[R] **zinb postestimation** — Postestimation tools for zinb

[R] **zip** — Zero-inflated Poisson regression

[R] **nbreg** — Negative binomial regression

[R] **poisson** — Poisson regression

[R] **tnbreg** — Truncated negative binomial regression

[R] **tpoisson** — Truncated Poisson regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtnbreg** — Fixed-effects, random-effects, & population-averaged negative binomial models

[U] **20 Estimation and postestimation commands**

Title

zinb postestimation — Postestimation tools for zinb

Description

The following postestimation commands are available after `zinb`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_inflate newvar_lnalpha} [if] [in], scores
```

statistic	Description
Main	
`n`	number of events; the default
`ir`	incidence rate
`pr`	probability of a degenerate zero
`pr(`*n*`)`	probability $\Pr(y_j = n)$
`pr(`*a*`,`*b*`)`	probability $\Pr(a \leq y_j \leq b)$
`xb`	linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`n`, the default, calculates the predicted number of events, which is $(1-p_j)\exp(\mathbf{x}_j\boldsymbol{\beta})$ if neither `offset()` nor `exposure()` was specified when the model was fit, where p_j is the predicted probability of a zero outcome; $(1-p_j)\exp\{(\mathbf{x}_j\boldsymbol{\beta})+\text{offset}_j\}$ if `offset()` was specified; or $(1-p_j)\{\exp(\mathbf{x}_j\boldsymbol{\beta})\times\text{exposure}_j\}$ if `exposure()` was specified.

`ir` calculates the incidence rate $\exp(\mathbf{x}_j\boldsymbol{\beta})$, which is the predicted number of events when exposure is 1. This is equivalent to specifying both the `n` and the `nooffset` options.

`pr` calculates the probability $\Pr(y_j=0)$, where this zero was obtained from the degenerate distribution $F(\mathbf{z}_j\boldsymbol{\gamma})$. If `offset()` was specified within the `inflate()` option, then $F(\mathbf{z}_j\boldsymbol{\gamma}+\text{offset}_j^{\gamma})$ is calculated.

`pr(`*n*`)` calculates the probability $\Pr(y_j=n)$, where *n* is a nonnegative integer that may be specified as a number or a variable. Note that `pr` is not equivalent to `pr(0)`.

`pr(`*a*`,`*b*`)` calculates the probability $\Pr(a\le y_j\le b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b\ge$.) means $+\infty$;
`pr(20,.)` calculates $\Pr(y_j\ge 20)$;
`pr(20,`*b*`)` calculates $\Pr(y_j\ge 20)$ in observations for which $b\ge$. and calculates $\Pr(20\le y_j\le b)$ elsewhere.

`pr(.,`*b*`)` produces a syntax error. A missing value in an observation of the variable *a* causes a missing value in that observation for `pr(`*a*`,`*b*`)`.

`xb` calculates the linear prediction, which is $\mathbf{x}_j\boldsymbol{\beta}$ if neither `offset()` nor `exposure()` was specified; $\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j$ if `offset()` was specified; or $\mathbf{x}_j\boldsymbol{\beta}+\ln(\text{exposure}_j)$ if `exposure()` was specified; see `nooffset` below.

`stdp` calculates the standard error of the linear prediction.

`nooffset` is relevant only if you specified `offset()` or `exposure()` when you fit the model. It modifies the calculations made by `predict` so that they ignore the offset or exposure variable; the linear prediction is treated as $\mathbf{x}_j\boldsymbol{\beta}$ rather than as $\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j$ or $\mathbf{x}_j\boldsymbol{\beta}+\ln(\text{exposure}_j)$. Specifying `predict ..., nooffset` is equivalent to specifying `predict ..., ir`.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial\ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial\ln L/\partial(\mathbf{z}_j\boldsymbol{\gamma})$.

The third new variable will contain $\partial\ln L/\partial\ln\alpha$.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

The probabilities calculated using the `pr(`*n*`)` option are the probability $\Pr(y_i = n)$. These are calculated using

$$\Pr(0|\mathbf{x}_i) = \omega_i + (1 - \omega_i)\, p_2(0|\mathbf{x}_i)$$

$$\Pr(n|\mathbf{x}_i) = (1 - \omega_i)\, p_2(n|\mathbf{x}_i) \qquad \text{for } n = 1, 2, \ldots$$

where ω_i is the probability of obtaining an observation from the degenerate distribution whose mass is concentrated at zero, and $p_2(n|\mathbf{x}_i)$ is the probability of $y_i = n$ from the nondegenerate, negative binomial distribution. ω_i can be obtained from the `pr` option.

See Cameron and Trivedi (1998, sec. 4.7) for further details.

Reference

Cameron, A. C., and P. K. Trivedi. 1998. *Regression Analysis of Count Data*. Cambridge: Cambridge University Press.

Also see

[R] **zinb** — Zero-inflated negative binomial regression

[U] **20 Estimation and postestimation commands**

Title

zip — Zero-inflated Poisson regression

Syntax

```
zip depvar [indepvars] [if] [in] [weight] ,
    inflate(varlist[ , offset(varname) ] | _cons) [options]
```

options	Description
Model	
* `inflate( )`	equation that determines whether the count is zero
`noconstant`	suppress constant term
`exposure(`*varname*$_e$`)`	include ln(*varname*$_e$) in model with coefficient constrained to 1
`offset(`*varname*$_o$`)`	include *varname*$_o$ in model with coefficient constrained to 1
`constraints(`*constraints*`)`	apply specified linear constraints
`collinear`	keep collinear variables
`probit`	use probit model to characterize excess zeros; default is logit
SE/Robust	
`vce(`*vcetype*`)`	*vcetype* may be `oim`, `robust`, `cluster` *clustvar*, `opg`, `bootstrap`, or `jackknife`
Reporting	
`level(#)`	set confidence level; default is `level(95)`
`irr`	report incidence-rate ratios
`vuong`	perform Vuong test
`nocnsreport`	do not display constraints
display_options	control column formats, row spacing, line width, and display of omitted variables and base and empty cells
Maximization	
maximize_options	control the maximization process; seldom used
`coeflegend`	display legend instead of statistics

* `inflate(`*varlist*`[ , offset(`*varname*`) ] | _cons)` is required.

indepvars and *varlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

`bootstrap`, `by`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the `bootstrap` prefix; see [R] **bootstrap**.

`vce()`, `vuong`, and weights are not allowed with the `svy` prefix; see [SVY] **svy**.

`fweights`, `iweights`, and `pweights` are allowed; see [U] **11.1.6 weight**.

`coeflegend` does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Menu

Statistics > Count outcomes > Zero-inflated Poisson regression

Description

`zip` estimates a zero-inflated Poisson (ZIP) regression of *depvar* on *indepvars*, where *depvar* is a nonnegative count variable.

Options

Model

`inflate(`*varlist*`[ , offset(`*varname*`)] | _cons)` specifies the equation that determines whether the observed count is zero. Conceptually, omitting `inflate()` would be equivalent to fitting the model with `poisson`; see [R] **poisson**.

`inflate(`*varlist*`[, offset(`*varname*`)])` specifies the variables in the equation. You may optionally include an offset for this *varlist*.

`inflate(_cons)` specifies that the equation determining whether the count is zero contains only an intercept. To run a zero-inflated model of *depvar* with only an intercept in both equations, type `zip` *depvar*`, inflate(_cons)`.

`noconstant`, `exposure(`*varname*$_e$`)`, `offset(`*varname*$_o$`)`, `constraints(`*constraints*`)`, `collinear`; see [R] **estimation options**.

`probit` requests that a probit, instead of logit, model be used to characterize the excess zeros in the data.

SE/Robust

`vce(`*vcetype*`)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory, that are robust to some kinds of misspecification, that allow for intragroup correlation, and that use bootstrap or jackknife methods; see [R] ***vce_option***.

Reporting

`level(#)`; see [R] **estimation options**.

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, e^b rather than b. Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. `irr` may be specified at estimation or when replaying previously estimated results.

`vuong` specifies that the Vuong (1989) test of ZIP versus Poisson be reported. This test statistic has a standard normal distribution with large positive values favoring the ZIP model and large negative values favoring the Poisson model.

`nocnsreport`; see [R] **estimation options**.

display_options: `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `cformat(%`*fmt*`)`, `pformat(%`*fmt*`)`, `sformat(%`*fmt*`)`, and `nolstretch`; see [R] **estimation options**.

Maximization

maximize_options: difficult, technique(*algorithm_spec*), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(*init_specs*); see [R] **maximize**. These options are seldom used.

Setting the optimization type to technique(bhhh) resets the default *vcetype* to vce(opg).

The following option is available with zip but is not shown in the dialog box:

coeflegend; see [R] **estimation options**.

Remarks

See Long (1997, 242–247) and Greene (2012, 821–826) for a discussion of zero-modified count models. For information about the test developed by Vuong (1989), see Greene (2012, 823–824) and Long (1997). Greene (1994) applied the test to ZIP and ZINB models, as described in Greene (2012, 824).

Poisson regression fits models of the number of occurrences (counts) of an event. You could use poisson for this (see [R] **poisson**), but in some count-data models, you might want to account for the prevalence of zero counts in the data.

For instance, you might count how many fish each visitor to a park catches. Many visitors may catch zero, because they do not fish (as opposed to being unsuccessful). You may be able to model whether a person fishes depending on several covariates related to fishing activity and model how many fish a person catches depending on several covariates having to do with the success of catching fish (type of lure/bait, time of day, temperature, season, etc.). This is the type of data for which the zip command is useful.

The zero-inflated (or zero-altered) Poisson model allows overdispersion through the splitting process that models the outcomes as zero or nonzero.

▷ Example 1

We have data on the number of fish caught by visitors to a national park. Some of the visitors do not fish, but we do not have the data on whether a person fished; we merely have data on how many fish were caught together with several covariates. Because our data have a preponderance of zeros (142 of 250), we use the zip command to model the outcome.

```
. use http://www.stata-press.com/data/r12/fish
. zip count persons livebait, inf(child camper) vuong
Fitting constant-only model:
Iteration 0:   log likelihood =  -1347.807
Iteration 1:   log likelihood = -1305.3245
  (output omitted)
Iteration 4:   log likelihood = -1103.9425
Fitting full model:
Iteration 0:   log likelihood = -1103.9425
Iteration 1:   log likelihood =  -896.2346
  (output omitted)
Iteration 5:   log likelihood = -850.70142
```

```
Zero-inflated Poisson regression                Number of obs   =       250
                                                Nonzero obs     =       108
                                                Zero obs        =       142

Inflation model = logit                         LR chi2(2)      =    506.48
Log likelihood  = -850.7014                     Prob > chi2     =    0.0000

------------------------------------------------------------------------------
             |      Coef.   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
count        |
     persons |   .8068853   .0453288    17.80   0.000     .7180424    .8957281
    livebait |   1.757289   .2446082     7.18   0.000     1.277866    2.236713
       _cons |  -2.178472   .2860289    -7.62   0.000    -2.739078   -1.617865
-------------+----------------------------------------------------------------
inflate      |
       child |   1.602571   .2797719     5.73   0.000     1.054228    2.150913
      camper |  -1.015698    .365259    -2.78   0.005    -1.731593   -.2998038
       _cons |  -.4922872   .3114562    -1.58   0.114     -1.10273    .1181558
------------------------------------------------------------------------------
Vuong test of zip vs. standard Poisson:           z =     3.95  Pr>z = 0.0000
```

In general, Vuong test statistics that are significantly positive favor the zero-inflated models, while those that are significantly negative favor the non–zero-inflated models. Thus, in the above model, the zero inflation is significant.

◁

Saved results

`zip` saves the following in `e()`:

Scalars

`e(N)`	number of observations
`e(N_zero)`	number of zero observations
`e(k)`	number of parameters
`e(k_eq)`	number of equations in `e(b)`
`e(k_eq_model)`	number of equations in overall model test
`e(k_dv)`	number of dependent variables
`e(df_m)`	model degrees of freedom
`e(ll)`	log likelihood
`e(ll_0)`	log likelihood, constant-only model
`e(ll_c)`	log likelihood, comparison model
`e(df_c)`	degrees of freedom for comparison test
`e(N_clust)`	number of clusters
`e(chi2)`	χ^2
`e(p)`	significance of model test
`e(vuong)`	Vuong test statistic
`e(rank)`	rank of `e(V)`
`e(ic)`	number of iterations
`e(rc)`	return code
`e(converged)`	`1` if converged, `0` otherwise

Macros

e(cmd)	zip
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(inflate)	logit or probit
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(offset1)	offset
e(offset2)	offset for inflate()
e(chi2type)	Wald or LR; type of model χ^2 test
e(vce)	*vcetype* specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

e(b)	coefficient vector
e(Cns)	constraints matrix
e(ilog)	iteration log (up to 20 iterations)
e(gradient)	gradient vector
e(V)	variance–covariance matrix of the estimators
e(V_modelbased)	model-based variance

Functions

e(sample)	marks estimation sample

Methods and formulas

zip is implemented as an ado-file.

Several models in the literature are (correctly) described as zero inflated. The zip command maximizes the log-likelihood $\ln L$, defined by

$$
\begin{aligned}
\xi_j^{\beta} &= \mathbf{x}_j\boldsymbol{\beta} + \text{offset}_j^{\beta} \\
\xi_j^{\gamma} &= \mathbf{z}_j\boldsymbol{\gamma} + \text{offset}_j^{\gamma} \\
\ln L &= \sum_{j\in S} w_j \ln\left[F(\xi_j^{\gamma}) + \left\{1 - F(\xi_j^{\gamma})\right\}\exp(-\lambda_j)\right] + \\
&\qquad \sum_{j\notin S} w_j\left[\ln\left\{1 - F(\xi_j^{\gamma})\right\} - \lambda_j + \xi_j^{\beta} y_j - \ln(y_j!)\right]
\end{aligned}
$$

where w_j are the weights, F is the inverse of the logit link (or the inverse of the probit link if `probit` was specified), and S is the set of observations for which the outcome $y_j = 0$.

This command supports the Huber/White/sandwich estimator of the variance and its clustered version using `vce(robust)` and `vce(cluster` *clustvar*`)`, respectively. See [P] **_robust**, particularly *Maximum likelihood estimators* and *Methods and formulas*.

`zip` also supports estimation with survey data. For details on VCEs with survey data, see [SVY] **variance estimation**.

References

Greene, W. H. 1994. Accounting for excess zeros and sample selection in Poisson and negative binomial regression models. Working paper EC-94-10, Department of Economics, Stern School of Business, New York University. http://ideas.repec.org/p/ste/nystbu/94-10.html.

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Vuong, Q. H. 1989. Likelihood ratio tests for model selection and non-nested hypotheses. *Econometrica* 57: 307–333.

Also see

[R] **zip postestimation** — Postestimation tools for zip

[R] **zinb** — Zero-inflated negative binomial regression

[R] **nbreg** — Negative binomial regression

[R] **poisson** — Poisson regression

[R] **tnbreg** — Truncated negative binomial regression

[R] **tpoisson** — Truncated Poisson regression

[SVY] **svy estimation** — Estimation commands for survey data

[XT] **xtpoisson** — Fixed-effects, random-effects, and population-averaged Poisson models

[U] **20 Estimation and postestimation commands**

Title

zip postestimation — Postestimation tools for zip

Description

The following postestimation commands are available after `zip`:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat`	AIC, BIC, VCE, and estimation sample summary
`estat (svy)`	postestimation statistics for survey data
`estimates`	cataloging estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`lrtest`[1]	likelihood-ratio test
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`predict`	predictions, residuals, influence statistics, and other diagnostic measures
`predictnl`	point estimates, standard errors, testing, and inference for generalized predictions
`pwcompare`	pairwise comparisons of estimates
`suest`	seemingly unrelated estimation
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

[1] `lrtest` is not appropriate with `svy` estimation results.

See the corresponding entries in the *Base Reference Manual* for details, but see [SVY] **estat** for details about `estat` (svy).

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]

predict [type] {stub* | newvar_reg newvar_inflate} [if] [in], scores
```

statistic	Description
Main	
`n`	number of events; the default
`ir`	incidence rate
`pr`	probability of a degenerate zero
`pr(`*n*`)`	probability $\Pr(y_j = n)$
`pr(`*a*`,`*b*`)`	probability $\Pr(a \leq y_j \leq b)$
`xb`	linear prediction
`stdp`	standard error of the linear prediction

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Menu

Statistics > Postestimation > Predictions, residuals, etc.

Options for predict

Main

`n`, the default, calculates the predicted number of events, which is $(1-p_j)\exp(\mathbf{x}_j\boldsymbol{\beta})$ if neither `offset()` nor `exposure()` was specified when the model was fit, where p_j is the predicted probability of a zero outcome; $(1-p_j)\exp\{(\mathbf{x}_j\boldsymbol{\beta})+\text{offset}_j\}$ if `offset()` was specified; or $(1-p_j)\{\exp(\mathbf{x}_j\boldsymbol{\beta})\times\text{exposure}_j\}$ if `exposure()` was specified.

`ir` calculates the incidence rate $\exp(\mathbf{x}_j\boldsymbol{\beta})$, which is the predicted number of events when exposure is 1. This is equivalent to specifying both the `n` and the `nooffset` options.

`pr` calculates the probability $\Pr(y_j=0)$, where this zero was obtained from the degenerate distribution $F(\mathbf{z}_j\boldsymbol{\gamma})$. If `offset()` was specified within the `inflate()` option, then $F(\mathbf{z}_j\boldsymbol{\gamma}+\text{offset}_j^{\gamma})$ is calculated.

`pr(`*n*`)` calculates the probability $\Pr(y_j=n)$, where *n* is a nonnegative integer that may be specified as a number or a variable. Note that `pr` is not equivalent to `pr(0)`.

`pr(`*a*`,`*b*`)` calculates the probability $\Pr(a\le y_j\le b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b\ge .$) means $+\infty$;
`pr(20,.)` calculates $\Pr(y_j\ge 20)$;
`pr(20,`*b*`)` calculates $\Pr(y_j\ge 20)$ in observations for which $b\ge .$ and calculates $\Pr(20\le y_j\le b)$ elsewhere.

`pr(.,`*b*`)` produces a syntax error. A missing value in an observation of the variable *a* causes a missing value in that observation for `pr(`*a*`,`*b*`)`.

`xb` calculates the linear prediction, which is $\mathbf{x}_j\boldsymbol{\beta}$ if neither `offset()` nor `exposure()` was specified; $\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j$ if `offset()` was specified; or $\mathbf{x}_j\boldsymbol{\beta}+\ln(\text{exposure}_j)$ if `exposure()` was specified; see `nooffset` below.

`stdp` calculates the standard error of the linear prediction.

`nooffset` is relevant only if you specified `offset()` or `exposure()` when you fit the model. It modifies the calculations made by `predict` so that they ignore the offset or exposure variable; the linear prediction is treated as $\mathbf{x}_j\boldsymbol{\beta}$ rather than as $\mathbf{x}_j\boldsymbol{\beta}+\text{offset}_j$ or $\mathbf{x}_j\boldsymbol{\beta}+\ln(\text{exposure}_j)$. Specifying `predict ..., nooffset` is equivalent to specifying `predict ..., ir`.

`scores` calculates equation-level score variables.

The first new variable will contain $\partial\ln L/\partial(\mathbf{x}_j\boldsymbol{\beta})$.

The second new variable will contain $\partial\ln L/\partial(\mathbf{z}_j\boldsymbol{\gamma})$.

Methods and formulas

All postestimation commands listed above are implemented as ado-files.

The probabilities calculated using the `pr(`*n*`)` option are the probability $\Pr(y_i = n)$. These are calculated using

$$\Pr(0|\mathbf{x}_i) = \omega_i + (1 - \omega_i)\,\exp(-\lambda_i)$$

$$\Pr(n|\mathbf{x}_i) = (1 - \omega_i)\frac{\lambda_i^n \exp(-\lambda_i)}{n!} \qquad \text{for } n = 1, 2, \ldots$$

where ω_i is the probability of obtaining an observation from the degenerate distribution whose mass is concentrated at zero. ω_i can be obtained from the `pr` option.

See Cameron and Trivedi (1998, sec. 4.7) for further details.

Reference

Cameron, A. C., and P. K. Trivedi. 1998. *Regression Analysis of Count Data*. Cambridge: Cambridge University Press.

Also see

[R] **zip** — Zero-inflated Poisson regression

[U] **20 Estimation and postestimation commands**

Author index

This is the author index for the 4-volume *Stata Base Reference Manual*.

A

Abramowitz, M., [R] **contrast**, [R] **orthog**
Abrams, K. R., [R] **meta**
Abramson, J. H., [R] **kappa**
Abramson, Z. H., [R] **kappa**
Achen, C. H., [R] **scobit**
Acock, A. C., [R] **alpha**, [R] **anova**, [R] **correlate**, [R] **nestreg**, [R] **oneway**, [R] **prtest**, [R] **ranksum**, [R] **ttest**
Adkins, L. C., [R] **heckman**, [R] **regress**, [R] **regress postestimation**
Afifi, A. A., [R] **anova**, [R] **stepwise**
Agresti, A., [R] **ci**, [R] **expoisson**, [R] **tabulate twoway**
Aigner, D., [R] **frontier**
Aiken, L. S., [R] **pcorr**
Aitchison, J., [R] **ologit**, [R] **oprobit**
Aitken, A. C., [R] **reg3**
Aivazian, S. A., [R] **ksmirnov**
Akaike, H., [R] **BIC note**, [R] **estat**, [R] **glm**
Aldrich, J. H., [R] **logit**, [R] **probit**
Alexandersson, A., [R] **regress**
Alf, E., Jr., [R] **rocfit**, [R] **rocreg**
Alldredge, J. R., [R] **pk**, [R] **pkcross**
Allen, M. J., [R] **alpha**
Allison, P. D., [R] **rologit**, [R] **testnl**
Alonzo, T. A., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Altman, D. G., [R] **anova**, [R] **fracpoly**, [R] **kappa**, [R] **kwallis**, [R] **meta**, [R] **mfp**, [R] **nptrend**, [R] **oneway**
Ambler, G., [R] **fracpoly**, [R] **mfp**, [R] **regress**
Amemiya, T., [R] **glogit**, [R] **intreg**, [R] **ivprobit**, [R] **nlogit**, [R] **tobit**
Andersen, E. B., [R] **clogit**
Andersen, P. K., [R] **glm**
Anderson, J. A., [R] **ologit**, [R] **slogit**
Anderson, R. E., [R] **rologit**
Anderson, R. L., [R] **anova**
Anderson, S., [R] **pkequiv**
Anderson, T. W., [R] **ivregress postestimation**
Andrews, D. F., [R] **rreg**
Andrews, D. W. K., [R] **ivregress**
Ängquist, L., [R] **bootstrap**, [R] **permute**
Angrist, J. D., [R] **ivregress**, [R] **ivregress postestimation**, [R] **qreg**, [R] **regress**
Anscombe, F. J., [R] **binreg postestimation**, [R] **glm**, [R] **glm postestimation**
Arbuthnott, J., [R] **signrank**
Archer, K. J., [R] **logistic**, [R] **logistic postestimation**, [R] **logit**, [R] **logit postestimation**
Arellano, M., [R] **gmm**
Arminger, G., [R] **suest**
Armitage, P., [R] **ameans**, [R] **expoisson**, [R] **pkcross**, [R] **sdtest**
Armstrong, R. D., [R] **qreg**
Arthur, M., [R] **symmetry**
Atkinson, A. C., [R] **boxcox**, [R] **nl**
Azen, S. P., [R] **anova**

B

Babiker, A., [R] **sampsi**
Babin, B. J., [R] **rologit**
Baker, R. J., [R] **glm**
Baker, R. M., [R] **ivregress postestimation**
Bakker, A., [R] **mean**
Balaam, L. N., [R] **pkcross**
Baltagi, B. H., [R] **hausman**
Bamber, D., [R] **rocfit**, [R] **rocregplot**, [R] **roctab**
Bancroft, T. A., [R] **stepwise**
Barnard, G. A., [R] **spearman**, [R] **ttest**
Barnett, A. G., [R] **glm**
Barnow, B. S., [R] **treatreg**
Barrison, I. G., [R] **binreg**
Bartlett, M. S., [R] **oneway**
Bartus, T., [R] **margins**
Basmann, R. L., [R] **ivregress**, [R] **ivregress postestimation**
Bassett, G., Jr., [R] **qreg**
Basu, A., [R] **glm**
Baum, C. F., [R] **gmm**, [R] **heckman**, [R] **heckprob**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **margins**, [R] **net**, [R] **net search**, [R] **regress postestimation**, [R] **regress postestimation time series**, [R] **ssc**
Bayart, D., [R] **qc**
Beale, E. M. L., [R] **stepwise**, [R] **test**
Beaton, A. E., [R] **rreg**
Becketti, S., [R] **fracpoly**, [R] **runtest**, [R] **spearman**
Beggs, S., [R] **rologit**
Belanger, A. J., [R] **sktest**
Belsley, D. A., [R] **estat**, [R] **regress postestimation**
Bendel, R. B., [R] **stepwise**
Benedetti, J. K., [R] **tetrachoric**
Beniger, J. R., [R] **cumul**
Bera, A. K., [R] **sktest**
Beran, R. J., [R] **regress postestimation time series**
Berk, K. N., [R] **stepwise**
Berk, R. A., [R] **rreg**
Berkson, J., [R] **logit**, [R] **probit**
Bern, P. H., [R] **nestreg**
Bernasco, W., [R] **tetrachoric**
Berndt, E. K., [R] **glm**
Berndt, E. R., [R] **treatreg**, [R] **truncreg**
Bernstein, I. H., [R] **alpha**
Berry, G., [R] **ameans**, [R] **expoisson**, [R] **sdtest**
Bewley, R., [R] **reg3**
Beyer, W. H., [R] **qc**

Bickeböller, H., [R] **symmetry**
Bickel, P. J., [R] **rreg**
Birdsall, T. G., [R] **logistic postestimation**
Black, W. C., [R] **rologit**
Blackwell, J. L., III, [R] **areg**
Bland, M., [R] **ranksum**, [R] **sdtest**, [R] **signrank**, [R] **spearman**
Bleda, M.-J., [R] **alpha**
Bliss, C. I., [R] **probit**
Bloch, D. A., [R] **brier**
Bloomfield, P., [R] **qreg**
Blundell, R., [R] **gmm**, [R] **ivprobit**
BMDP, [R] **symmetry**
Boice, J. D., Jr., [R] **bitest**
Boland, P. J., [R] **ttest**
Bolduc, D., [R] **asmprobit**
Bollen, K. A., [R] **regress postestimation**
Bond, S., [R] **gmm**
Bonferroni, C. E., [R] **correlate**
Borenstein, M., [R] **meta**
Bound, J., [R] **ivregress postestimation**
Bowker, A. H., [R] **symmetry**
Box, G. E. P., [R] **anova**, [R] **boxcox**, [R] **lnskew0**
Box, J. F., [R] **anova**
Boyd, N. F., [R] **kappa**
Brackstone, G., [R] **swilk**
Bradley, R. A., [R] **signrank**
Brady, A. R., [R] **logistic**, [R] **spikeplot**
Brant, R., [R] **ologit**
Breslow, N. E., [R] **clogit**, [R] **dstdize**, [R] **symmetry**
Breusch, T. S., [R] **mvreg**, [R] **regress postestimation**, [R] **regress postestimation time series**, [R] **sureg**
Brier, G. W., [R] **brier**
Brillinger, D. R., [R] **jackknife**
Brook, R. H., [R] **brier**
Brown, D. R., [R] **anova**, [R] **contrast**, [R] **loneway**, [R] **oneway**, [R] **pwcompare**
Brown, L. D., [R] **ci**
Brown, M. B., [R] **sdtest**, [R] **tetrachoric**
Brown, S. E., [R] **symmetry**
Bru, B., [R] **poisson**
Buchner, D. M., [R] **ladder**
Buis, M. L., [R] **logistic**, [R] **logit**, [R] **margins**
Bunch, D. S., [R] **asmprobit**
Burke, W. J., [R] **tobit**
Burnam, M. A., [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Burr, I. W., [R] **qc**
Buskens, V., [R] **tabstat**

C

Cai, T., [R] **rocreg**
Cai, T. T., [R] **ci**
Cain, G. G., [R] **treatreg**
Cameron, A. C., [R] **asclogit**, [R] **asmprobit**, [R] **bootstrap**, [R] **gmm**, [R] **heckman**, [R] **intreg**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **mprobit**, [R] **nbreg**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**, [R] **qreg**, [R] **regress**, [R] **regress postestimation**, [R] **simulate**, [R] **sureg**, [R] **tnbreg**, [R] **tobit**, [R] **tpoisson**, [R] **zinb postestimation**, [R] **zip postestimation**
Campbell, M. J., [R] **ci**, [R] **kappa**, [R] **logistic postestimation**, [R] **poisson**, [R] **tabulate twoway**
Cappellari, L., [R] **asmprobit**
Cardell, S., [R] **rologit**
Carlile, T., [R] **kappa**
Carlin, J., [R] **ameans**
Carroll, R. J., [R] **boxcox**, [R] **rreg**, [R] **sdtest**
Carson, R. T., [R] **tnbreg**, [R] **tpoisson**
Carter, S., [R] **frontier**, [R] **lrtest**, [R] **nbreg**
Caudill, S. B., [R] **frontier**
Caulcutt, R., [R] **qc**
Chadwick, J., [R] **poisson**
Chakraborti, S., [R] **ksmirnov**
Chamberlain, G., [R] **clogit**, [R] **gmm**
Chambers, J. M., [R] **diagnostic plots**, [R] **grmeanby**, [R] **lowess**
Chang, I. M., [R] **margins**
Charlett, A., [R] **fracpoly**
Chatfield, M., [R] **anova**
Chatterjee, S., [R] **poisson**, [R] **regress**, [R] **regress postestimation**
Chen, X., [R] **logistic**, [R] **logistic postestimation**, [R] **logit**
Chiburis, R., [R] **heckman**, [R] **heckprob**, [R] **oprobit**
Choi, B. C. K., [R] **rocfit**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **roctab**
Chow, G. C., [R] **contrast**
Chow, S.-C., [R] **pk**, [R] **pkcross**, [R] **pkequiv**, [R] **pkexamine**, [R] **pkshape**
Christakis, N., [R] **rologit**
Clarke, R. D., [R] **poisson**
Clarke-Pearson, D. L., [R] **roccomp**, [R] **rocreg**, [R] **roctab**
Clarkson, D. B., [R] **tabulate twoway**
Clayton, D. G., [R] **cloglog**, [R] **cumul**
Clerget-Darpoux, F., [R] **symmetry**
Cleveland, W. S., [R] **diagnostic plots**, [R] **lowess**, [R] **lpoly**, [R] **sunflower**
Cleves, M. A., [R] **binreg**, [R] **dstdize**, [R] **logistic**, [R] **logit**, [R] **roccomp**, [R] **rocfit**, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **roctab**, [R] **sdtest**, [R] **symmetry**
Clogg, C. C., [R] **suest**
Clopper, C. J., [R] **ci**
Cobb, G. W., [R] **anova**
Cochran, W. G., [R] **ameans**, [R] **anova**, [R] **correlate**, [R] **dstdize**, [R] **mean**, [R] **oneway**, [R] **poisson**, [R] **probit**, [R] **proportion**, [R] **ranksum**, [R] **ratio**, [R] **signrank**, [R] **total**

Coelli, T. J., [R] **frontier**
Cohen, J., [R] **kappa**, [R] **pcorr**
Cohen, P., [R] **pcorr**
Coleman, J. S., [R] **poisson**
Collett, D., [R] **clogit**, [R] **logistic**, [R] **logistic postestimation**
Cone-Wesson, B., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Cong, R., [R] **tobit**, [R] **tobit postestimation**, [R] **treatreg**, [R] **truncreg**
Conover, W. J., [R] **centile**, [R] **ksmirnov**, [R] **kwallis**, [R] **nptrend**, [R] **sdtest**, [R] **spearman**, [R] **tabulate twoway**
Conroy, R. M., [R] **intreg**
Cook, A., [R] **ci**
Cook, N. R., [R] **rocreg**
Cook, R. D., [R] **boxcox**, [R] **regress postestimation**
Coster, D., [R] **contrast**
Coull, B. A., [R] **ci**
Cox, D. R., [R] **boxcox**, [R] **exlogistic**, [R] **expoisson**, [R] **lnskew0**
Cox, G. M., [R] **anova**
Cox, N. J., [R] **ci**, [R] **cumul**, [R] **diagnostic plots**, [R] **histogram**, [R] **inequality**, [R] **kappa**, [R] **kdensity**, [R] **ladder**, [R] **lowess**, [R] **lpoly**, [R] **net**, [R] **net search**, [R] **regress postestimation**, [R] **search**, [R] **serrbar**, [R] **sktest**, [R] **smooth**, [R] **spikeplot**, [R] **ssc**, [R] **stem**, [R] **summarize**, [R] **sunflower**, [R] **tabulate oneway**, [R] **tabulate twoway**
Cragg, J. G., [R] **ivregress postestimation**
Cramér, H., [R] **tabulate twoway**
Cramer, J. S., [R] **logit**
Cronbach, L. J., [R] **alpha**
Croux, C., [R] **rreg**
Cui, J., [R] **symmetry**
Cummings, P., [R] **binreg**, [R] **glm**
Curts-García, J., [R] **smooth**
Cuzick, J., [R] **kappa**, [R] **nptrend**

D

D'Agostino, R. B., [R] **sktest**
D'Agostino, R. B., Jr., [R] **sktest**
Daniel, C., [R] **diagnostic plots**, [R] **oneway**
Danuso, F., [R] **nl**
DasGupta, A., [R] **ci**
Davey Smith, G., [R] **meta**
David, H. A., [R] **spearman**, [R] **summarize**
Davidson, R., [R] **boxcox**, [R] **cnsreg**, [R] **gmm**, [R] **intreg**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **mlogit**, [R] **nl**, [R] **nlsur**, [R] **reg3**, [R] **regress**, [R] **regress postestimation time series**, [R] **tobit**, [R] **truncreg**
Davison, A. C., [R] **bootstrap**
Day, N. E., [R] **clogit**, [R] **dstdize**, [R] **symmetry**
de Irala-Estévez, J., [R] **logistic**
De Luca, G., [R] **biprobit**, [R] **heckprob**, [R] **probit**
de Wolf, I., [R] **rologit**
Deaton, A., [R] **nlsur**
Deb, P., [R] **nbreg**
Dehon, C., [R] **correlate**
del Mar Zamora, M., [R] **heckprob**
DeLong, D. M., [R] **roccomp**, [R] **rocreg**, [R] **roctab**
DeLong, E. R., [R] **roccomp**, [R] **rocreg**, [R] **roctab**
DeMaris, A., [R] **regress postestimation**
Dewey, M. E., [R] **correlate**
Digby, P. G. N., [R] **tetrachoric**
Dixon, W. J., [R] **ttest**
Dobson, A. J., [R] **glm**
Dodd, L. E., [R] **rocreg**
Dohoo, I., [R] **regress**
Doll, R., [R] **poisson**
Donald, S. G., [R] **ivregress postestimation**
Donner, A., [R] **loneway**
Donoho, D. L., [R] **lpoly**
Dore, C. J., [R] **fracpoly**
Dorfman, D. D., [R] **rocfit**, [R] **rocreg**
Draper, N., [R] **eivreg**, [R] **oneway**, [R] **regress**, [R] **stepwise**
Drukker, D. M., [R] **asmprobit**, [R] **boxcox**, [R] **frontier**, [R] **lrtest**, [R] **nbreg**, [R] **tobit**, [R] **treatreg**
Duan, N., [R] **heckman**
Duncan, A. J., [R] **qc**
Dunlop, D. D., [R] **sampsi**
Dunn, G., [R] **kappa**
Dunnett, C. W., [R] **mprobit**, [R] **pwcompare**
Dunnington, G. W., [R] **regress**
Dupont, W. D., [R] **logistic**, [R] **mkspline**, [R] **sunflower**
Durbin, J., [R] **ivregress postestimation**, [R] **regress postestimation time series**
Duren, P., [R] **regress**
Duval, R. D., [R] **bootstrap**, [R] **jackknife**, [R] **rocreg**, [R] **rocregplot**

E

Edgington, E. S., [R] **runtest**
Edwards, A. L., [R] **anova**
Edwards, A. W. F., [R] **tetrachoric**
Edwards, J. H., [R] **tetrachoric**
Efron, B., [R] **bootstrap**, [R] **qreg**
Efroymson, M. A., [R] **stepwise**
Egger, M., [R] **meta**
Eisenhart, C., [R] **correlate**, [R] **runtest**
Ellis, C. D., [R] **poisson**
Eltinge, J. L., [R] **test**
Emerson, J. D., [R] **lv**, [R] **stem**
Ender, P., [R] **marginsplot**
Engel, A., [R] **marginsplot**
Engle, R. F., [R] **regress postestimation time series**
Erdreich, L. S., [R] **roccomp**, [R] **rocfit**, [R] **roctab**
Eubank, R. L., [R] **lpoly**
Evans, M. A., [R] **pk**, [R] **pkcross**
Everitt, B. S., [R] **gllamm**, [R] **glm**

Ewens, W. J., [R] **symmetry**
Ezekiel, M., [R] **regress postestimation**

F

Fan, J., [R] **lpoly**
Fan, Y.-A., [R] **tabulate twoway**
Fang, K.-T., [R] **asmprobit**
Farbmacher, H., [R] **tpoisson**
Feiveson, A. H., [R] **nlcom**, [R] **ranksum**
Feldt, L. S., [R] **anova**
Ferri, H. A., [R] **kappa**
Fieller, E. C., [R] **pkequiv**
Fienberg, S. E., [R] **kwallis**, [R] **tabulate twoway**
Filon, L. N. G., [R] **correlate**
Findley, D. F., [R] **estat**
Findley, T. W., [R] **ladder**
Finlay, K., [R] **ivprobit**, [R] **ivregress**, [R] **ivtobit**
Finney, D. J., [R] **probit**, [R] **tabulate twoway**
Fiorio, C. V., [R] **kdensity**
Fiser, D. H., [R] **logistic postestimation**
Fishell, E., [R] **kappa**
Fisher, L. D., [R] **anova**, [R] **dstdize**, [R] **oneway**
Fisher, N. I., [R] **regress postestimation time series**
Fisher, R. A., [R] **anova**, [R] **ranksum**, [R] **signrank**, [R] **tabulate twoway**
Flannery, B. P., [R] **dydx**, [R] **vwls**
Fleiss, J. L., [R] **dstdize**, [R] **kappa**, [R] **sampsi**
Fletcher, K., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Folsom, R. C., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Ford, J. M., [R] **frontier**
Forsythe, A. B., [R] **sdtest**
Forthofer, R. N., [R] **dstdize**
Foster, A., [R] **regress**
Fourier, J. B. J., [R] **cumul**
Fox, J., [R] **kdensity**, [R] **lv**
Fox, W. C., [R] **logistic postestimation**
Francia, R. S., [R] **swilk**
Freese, J., [R] **asroprobit**, [R] **clogit**, [R] **cloglog**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **mprobit**, [R] **nbreg**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**, [R] **regress**, [R] **regress postestimation**, [R] **tnbreg**, [R] **tpoisson**, [R] **zinb**, [R] **zip**
Frison, L., [R] **sampsi**
Frölich, M., [R] **qreg**
Frome, E. L., [R] **qreg**
Frydenberg, M., [R] **dstdize**, [R] **roccomp**, [R] **roctab**
Fu, V. K., [R] **ologit**
Fuller, W. A., [R] **regress**, [R] **spearman**

G

Gail, M. H., [R] **rocreg**, [R] **rocreg postestimation**
Gall, J.-R. L., [R] **logistic**, [R] **logistic postestimation**
Gallant, A. R., [R] **ivregress**, [R] **nl**
Galton, F., [R] **correlate**, [R] **cumul**, [R] **regress**, [R] **summarize**
Gan, F. F., [R] **diagnostic plots**
Garrett, J. M., [R] **fracpoly**, [R] **logistic**, [R] **logistic postestimation**, [R] **regress postestimation**
Garsd, A., [R] **exlogistic**
Gasser, T., [R] **lpoly**
Gastwirth, J. L., [R] **sdtest**
Gates, R., [R] **asmprobit**
Gauss, J. C. F., [R] **regress**
Gauvreau, K., [R] **dstdize**, [R] **logistic**, [R] **sampsi**
Geisser, S., [R] **anova**
Gel, Y. R., [R] **sdtest**
Gelbach, J., [R] **ivprobit**, [R] **ivtobit**
Gelman, R., [R] **margins**
Genest, C., [R] **swilk**
Gentle, J. E., [R] **anova**, [R] **nl**
Genton, M. G., [R] **sktest**
Genz, A., [R] **asmprobit**
Gerkins, V. R., [R] **symmetry**
Geweke, J., [R] **asmprobit**
Gibbons, J. D., [R] **ksmirnov**, [R] **spearman**
Giesen, D., [R] **tetrachoric**
Gijbels, I., [R] **lpoly**
Gillham, N. W., [R] **regress**
Gillispie, C. C., [R] **regress**
Gini, R., [R] **vwls**
Gleason, J. R., [R] **anova**, [R] **bootstrap**, [R] **ci**, [R] **correlate**, [R] **loneway**, [R] **summarize**, [R] **ttest**
Gleser, G., [R] **alpha**
Glidden, D. V., [R] **logistic**
Gnanadesikan, R., [R] **cumul**, [R] **diagnostic plots**
Godfrey, L. G., [R] **regress postestimation time series**
Goeden, G. B., [R] **kdensity**
Goerg, S. J., [R] **ksmirnov**
Goldberger, A. S., [R] **intreg**, [R] **tobit**, [R] **treatreg**
Goldstein, R., [R] **brier**, [R] **correlate**, [R] **inequality**, [R] **nl**, [R] **ologit**, [R] **oprobit**, [R] **ranksum**, [R] **regress postestimation**
Golub, G. H., [R] **orthog**, [R] **tetrachoric**
Good, P. I., [R] **permute**, [R] **symmetry**, [R] **tabulate twoway**
Goodall, C., [R] **lowess**, [R] **rreg**
Goodman, L. A., [R] **tabulate twoway**
Gordon, M. G., [R] **binreg**
Gorga, M. P., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Gorman, J. W., [R] **stepwise**
Gosset [Student, pseud.], W. S., [R] **ttest**
Gosset, W. S., [R] **ttest**
Gould, W. W., [R] **bootstrap**, [R] **dydx**, [R] **frontier**, [R] **grmeanby**, [R] **jackknife**, [R] **kappa**, [R] **logistic**, [R] **margins**, [R] **maximize**, [R] **mkspline**, [R] **ml**, [R] **net search**, [R] **nlcom**, [R] **ologit**, [R] **oprobit**, [R] **predictnl**, [R] **qreg**, [R] **regress**, [R] **rreg**, [R] **simulate**, [R] **sktest**, [R] **smooth**, [R] **swilk**, [R] **testnl**

Gourieroux, C., [R] **hausman**, [R] **suest**, [R] **test**
Graubard, B. I., [R] **margins**, [R] **ml**, [R] **test**
Graybill, F. A., [R] **centile**
Green, D. M., [R] **logistic postestimation**
Greene, W. H., [R] **asclogit**, [R] **asmprobit**, [R] **biprobit**, [R] **clogit**, [R] **cnsreg**, [R] **frontier**, [R] **gmm**, [R] **heckman**, [R] **heckprob**, [R] **hetprob**, [R] **ivregress**, [R] **logit**, [R] **lrtest**, [R] **margins**, [R] **mkspline**, [R] **mlogit**, [R] **nlogit**, [R] **nlsur**, [R] **pcorr**, [R] **probit**, [R] **reg3**, [R] **regress**, [R] **regress postestimation time series**, [R] **sureg**, [R] **testnl**, [R] **treatreg**, [R] **truncreg**, [R] **zinb**, [R] **zip**
Greenfield, S., [R] **alpha**, [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Greenhouse, S. W., [R] **anova**
Greenland, S., [R] **ci**, [R] **glogit**, [R] **mkspline**, [R] **ologit**, [R] **poisson**
Gregoire, A., [R] **kappa**
Griffith, J. L., [R] **brier**
Griffith, R., [R] **gmm**
Griffiths, W. E., [R] **cnsreg**, [R] **estat**, [R] **glogit**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **probit**, [R] **regress**, [R] **regress postestimation**, [R] **test**
Grizzle, J. E., [R] **vwls**
Grogger, J. T., [R] **tnbreg**, [R] **tpoisson**
Gronau, R., [R] **heckman**
Gropper, D. M., [R] **frontier**
Guan, W., [R] **bootstrap**
Gutierrez, R. G., [R] **frontier**, [R] **lpoly**, [R] **lrtest**, [R] **nbreg**

H

Haan, P., [R] **asmprobit**, [R] **mlogit**, [R] **mprobit**
Hadi, A. S., [R] **poisson**, [R] **regress**, [R] **regress postestimation**
Hadorn, D. C., [R] **brier**
Hahn, J., [R] **ivregress postestimation**
Hair, J. F., Jr., [R] **rologit**
Hajian-Tilaki, K. O., [R] **rocreg**
Hajivassiliou, V. A., [R] **asmprobit**
Hald, A., [R] **qreg**, [R] **regress**, [R] **signrank**, [R] **summarize**
Hall, A. D., [R] **frontier**
Hall, A. R., [R] **gmm**, [R] **gmm postestimation**, [R] **ivregress**, [R] **ivregress postestimation**
Hall, B. H., [R] **glm**
Hall, N. S., [R] **anova**
Hall, P., [R] **bootstrap**, [R] **regress postestimation time series**
Hall, R. E., [R] **glm**
Hall, W. J., [R] **roccomp**, [R] **rocfit**, [R] **roctab**
Hallock, K., [R] **qreg**
Halvorsen, K. T., [R] **tabulate twoway**
Hamerle, A., [R] **clogit**
Hamilton, J. D., [R] **gmm**
Hamilton, L. C., [R] **bootstrap**, [R] **diagnostic plots**, [R] **ladder**, [R] **lv**, [R] **mlogit**, [R] **regress**, [R] **regress postestimation**, [R] **rreg**, [R] **simulate**, [R] **summarize**, [R] **ttest**
Hampel, F. R., [R] **rreg**
Hanley, J. A., [R] **roccomp**, [R] **rocfit**, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **roctab**
Hansen, L. P., [R] **gmm**, [R] **ivregress**, [R] **ivregress postestimation**
Hao, L., [R] **qreg**
Harbord, R. M., [R] **roccomp**, [R] **roctab**
Hardin, J. W., [R] **binreg**, [R] **biprobit**, [R] **estat**, [R] **glm**, [R] **glm postestimation**, [R] **regress postestimation**
Haritou, A., [R] **suest**
Harkness, J., [R] **ivprobit**, [R] **ivtobit**
Harrell, F. E., Jr., [R] **mkspline**, [R] **ologit**
Harris, R. L., [R] **qc**
Harris, T., [R] **qreg**
Harrison, D. A., [R] **histogram**, [R] **tabulate oneway**, [R] **tabulate twoway**
Harrison, J. A., [R] **dstdize**
Harvey, A. C., [R] **hetprob**
Hastie, T. J., [R] **grmeanby**, [R] **slogit**
Hauck, W. W., [R] **pkequiv**
Haughton, J., [R] **inequality**
Hausman, J. A., [R] **glm**, [R] **hausman**, [R] **ivregress postestimation**, [R] **nlogit**, [R] **rologit**, [R] **suest**
Hayashi, F., [R] **gmm**, [R] **ivregress**, [R] **ivregress postestimation**
Hayes, R. J., [R] **permute**
Hays, R. D., [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Heagerty, P. J., [R] **anova**, [R] **dstdize**, [R] **oneway**
Heckman, J., [R] **biprobit**, [R] **heckman**, [R] **heckman postestimation**, [R] **heckprob**
Hedges, L. V., [R] **meta**
Heiss, F., [R] **nlogit**
Henderson, B. E., [R] **symmetry**
Hendrickx, J., [R] **mlogit**, [R] **xi**
Hensher, D. A., [R] **nlogit**
Hickam, D. H., [R] **brier**
Higgins, J. E., [R] **anova**
Higgins, J. P. T., [R] **meta**
Hilbe, J. M., [R] **cloglog**, [R] **estat**, [R] **glm**, [R] **glm postestimation**, [R] **logistic**, [R] **logit**, [R] **nbreg**, [R] **poisson**, [R] **probit**, [R] **sampsi**, [R] **simulate**, [R] **tnbreg**, [R] **tpoisson**
Hill, A. B., [R] **poisson**
Hill, R. C., [R] **cnsreg**, [R] **estat**, [R] **glogit**, [R] **heckman**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **probit**, [R] **regress**, [R] **regress postestimation**, [R] **test**
Hills, M., [R] **cloglog**, [R] **cumul**
Hinkley, D. V., [R] **bootstrap**
Hirji, K. F., [R] **exlogistic**, [R] **expoisson**

Hoaglin, D. C., [R] **diagnostic plots**, [R] **lv**, [R] **regress postestimation**, [R] **smooth**, [R] **stem**
Hochberg, Y., [R] **oneway**
Hocking, R. R., [R] **stepwise**
Hoel, P. G., [R] **bitest**, [R] **ttest**
Hoffmann, J. P., [R] **glm**
Hole, A. R., [R] **asmprobit**, [R] **clogit**, [R] **mlogit**, [R] **mprobit**
Holloway, L., [R] **brier**
Holm, S., [R] **test**
Holmes, S., [R] **bootstrap**
Hood, W. C., [R] **ivregress**
Hosmer, D. W., Jr., [R] **clogit**, [R] **clogit postestimation**, [R] **glm**, [R] **glogit**, [R] **lincom**, [R] **logistic**, [R] **logistic postestimation**, [R] **logit**, [R] **logit postestimation**, [R] **lrtest**, [R] **mlogit**, [R] **predictnl**, [R] **stepwise**
Hotelling, H., [R] **roccomp**, [R] **rocfit**, [R] **roctab**
Huang, C., [R] **sunflower**
Huang, D. S., [R] **nlsur**, [R] **sureg**
Huber, P. J., [R] **qreg**, [R] **rreg**, [R] **suest**
Hunter, D. R., [R] **qreg**
Hurd, M., [R] **intreg**, [R] **tobit**
Hutto, C., [R] **exlogistic**
Huynh, H., [R] **anova**

I

Iglewicz, B., [R] **lv**
Isaacs, D., [R] **fracpoly**
Ishiguro, M., [R] **BIC note**

J

Jackman, R. W., [R] **regress postestimation**
Jacobs, K. B., [R] **symmetry**
Jaeger, D. A., [R] **ivregress postestimation**
James, B. R., [R] **rocreg**, [R] **rocreg postestimation**
James, K. L., [R] **rocreg**, [R] **rocreg postestimation**
Janes, H., [R] **rocfit**, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Jann, B., [R] **estimates store**, [R] **ksmirnov**, [R] **saved results**, [R] **tabulate twoway**
Jarque, C. M., [R] **sktest**
Jeffreys, H., [R] **ci**, [R] **spearman**
Jenkins, S. P., [R] **asmprobit**, [R] **do**, [R] **inequality**
Joe, H., [R] **tabulate twoway**
Johnson, D. E., [R] **anova**, [R] **contrast**, [R] **pwcompare**
Johnson, M. E., [R] **sdtest**
Johnson, M. M., [R] **sdtest**
Johnson, N. L., [R] **ksmirnov**, [R] **nbreg**, [R] **poisson**
Jolliffe, D., [R] **inequality**, [R] **qreg**, [R] **regress**
Jolliffe, I. T., [R] **brier**
Jones, A., [R] **heckman**, [R] **logit**, [R] **probit**
Jones, D. R., [R] **meta**
Jones, M. C., [R] **kdensity**, [R] **lpoly**
Judge, G. G., [R] **estat**, [R] **glogit**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **probit**, [R] **regress postestimation**, [R] **test**
Judson, D. H., [R] **poisson**, [R] **tabulate twoway**, [R] **tpoisson**
Juul, S., [R] **dstdize**, [R] **roccomp**, [R] **roctab**

K

Kahn, H. A., [R] **dstdize**
Kaiser, J., [R] **ksmirnov**, [R] **permute**, [R] **signrank**
Kalmijn, M., [R] **tetrachoric**
Keane, M. P., [R] **asmprobit**
Keeler, E. B., [R] **brier**
Kemp, A. W., [R] **nbreg**, [R] **poisson**
Kempthorne, P. J., [R] **regress postestimation**
Kendall, M. G., [R] **centile**, [R] **spearman**, [R] **tabulate twoway**, [R] **tobit**
Kennedy, W. J., Jr., [R] **anova**, [R] **nl**, [R] **regress**, [R] **stepwise**
Kettenring, J. R., [R] **diagnostic plots**
Keynes, J. M., [R] **ameans**
Khandker, S. R., [R] **inequality**
Kiernan, M., [R] **kappa**
Kirkwood, B. R., [R] **dstdize**, [R] **summarize**
Kish, L., [R] **loneway**
Kitagawa, G., [R] **BIC note**
Klar, J., [R] **logistic postestimation**
Kleiber, C., [R] **inequality**
Klein, L. R., [R] **reg3**, [R] **regress postestimation time series**
Klein, M., [R] **binreg**, [R] **clogit**, [R] **logistic**, [R] **lrtest**, [R] **mlogit**, [R] **ologit**
Kleinbaum, D. G., [R] **binreg**, [R] **clogit**, [R] **logistic**, [R] **lrtest**, [R] **mlogit**, [R] **ologit**
Kleiner, B., [R] **diagnostic plots**, [R] **lowess**
Kmenta, J., [R] **eivreg**, [R] **ivregress**, [R] **regress**
Koch, G. G., [R] **anova**, [R] **kappa**, [R] **vwls**
Koehler, K. J., [R] **diagnostic plots**
Koenker, R., [R] **qreg**, [R] **regress postestimation**
Kohler, U., [R] **kdensity**, [R] **regress**, [R] **regress postestimation**
Kolmogorov, A. N., [R] **ksmirnov**
Kontopantelis, E., [R] **meta**
Koopmans, T. C., [R] **ivregress**
Korn, E. L., [R] **margins**, [R] **ml**, [R] **test**
Kotz, S., [R] **inequality**, [R] **ksmirnov**, [R] **nbreg**, [R] **nlogit**, [R] **poisson**
Kreuter, F., [R] **kdensity**, [R] **regress**, [R] **regress postestimation**
Krushelnytskyy, B., [R] **inequality**, [R] **qreg**
Kruskal, W. H., [R] **kwallis**, [R] **ranksum**, [R] **spearman**, [R] **tabulate twoway**
Kuehl, R. O., [R] **anova**, [R] **contrast**, [R] **oneway**
Kuh, E., [R] **estat**, [R] **regress postestimation**
Kumbhakar, S. C., [R] **frontier**

Kung, D. S., [R] **qreg**
Kutner, M. H., [R] **pkcross**, [R] **pkequiv**, [R] **pkshape**, [R] **regress postestimation**

L

Lachenbruch, P. A., [R] **diagnostic plots**
Lacy, M. G., [R] **permute**
Lafontaine, F., [R] **boxcox**
Lahiri, K., [R] **tobit**
Lai, S., [R] **exlogistic**
Laird, N. M., [R] **expoisson**
Lambert, D., [R] **zip**
Lambert, P. C., [R] **poisson**
Landis, J. R., [R] **kappa**
Lane, P. W., [R] **margins**
Lange, K., [R] **qreg**
Laplace, P.-S., [R] **regress**
Larsen, W. A., [R] **regress postestimation**
Lash, T. L., [R] **ci**, [R] **glogit**, [R] **poisson**
Lauritzen, S. L., [R] **summarize**
Lee, E. S., [R] **dstdize**
Lee, E. T., [R] **roccomp**, [R] **rocfit**, [R] **roctab**
Lee, T.-C., [R] **estat**, [R] **glogit**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **probit**, [R] **regress postestimation**, [R] **test**
Lee, W. C., [R] **roctab**
Legendre, A.-M., [R] **regress**
Lehmann, E. L., [R] **oneway**
Lemeshow, S., [R] **clogit**, [R] **clogit postestimation**, [R] **glm**, [R] **glogit**, [R] **lincom**, [R] **logistic**, [R] **logistic postestimation**, [R] **logit**, [R] **logit postestimation**, [R] **lrtest**, [R] **mlogit**, [R] **predictnl**, [R] **stepwise**
Leroy, A. M., [R] **qreg**, [R] **regress postestimation**, [R] **rreg**
Levene, H., [R] **sdtest**
Levin, B., [R] **dstdize**, [R] **kappa**, [R] **sampsi**
Levinsohn, J., [R] **frontier**
Levy, D., [R] **sunflower**
Lewis, H. G., [R] **heckman**
Lewis, I. G., [R] **binreg**
Lewis, J. D., [R] **fracpoly**
Li, G., [R] **rreg**
Li, W., [R] **pkcross**, [R] **pkequiv**, [R] **pkshape**
Likert, R. A., [R] **alpha**
Lim, G. C., [R] **cnsreg**, [R] **regress**, [R] **regress postestimation**
Lindley, D. V., [R] **ci**
Lindsey, C., [R] **boxcox**, [R] **lowess**, [R] **regress postestimation**, [R] **stepwise**
Linhart, J. M., [R] **lpoly**
Lipset, S. M., [R] **histogram**
Liu, J.-P., [R] **pk**, [R] **pkcross**, [R] **pkequiv**, [R] **pkexamine**, [R] **pkshape**
Locke, C. S., [R] **pkequiv**
Lokshin, M., [R] **heckman**, [R] **heckprob**, [R] **oprobit**
Long, J. S., [R] **asroprobit**, [R] **clogit**, [R] **cloglog**, [R] **intreg**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **mprobit**, [R] **nbreg**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**, [R] **regress**, [R] **regress postestimation**, [R] **testnl**, [R] **tnbreg**, [R] **tobit**, [R] **tpoisson**, [R] **zinb**, [R] **zip**
Longley, J. D., [R] **kappa**
Longton, G., [R] **rocfit**, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
López-Feldman, A., [R] **inequality**
Lorenz, M. O., [R] **inequality**
Louis, T. A., [R] **tabulate twoway**
Lovell, C. A. K., [R] **frontier**
Lovie, A. D., [R] **spearman**
Lovie, P., [R] **spearman**
Lucas, H. L., [R] **pkcross**
Luce, R. D., [R] **rologit**
Lumley, T. S., [R] **anova**, [R] **dstdize**, [R] **oneway**
Lunt, M., [R] **ologit**, [R] **slogit**
Lütkepohl, H., [R] **estat**, [R] **glogit**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **probit**, [R] **regress postestimation**, [R] **test**

M

Ma, G., [R] **roccomp**, [R] **rocfit**, [R] **roctab**
Machin, D., [R] **ci**, [R] **kappa**, [R] **tabulate twoway**
Mack, T. M., [R] **symmetry**
MacKinnon, J. G., [R] **boxcox**, [R] **cnsreg**, [R] **gmm**, [R] **intreg**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **mlogit**, [R] **nl**, [R] **nlsur**, [R] **reg3**, [R] **regress**, [R] **regress postestimation time series**, [R] **tobit**, [R] **truncreg**
MacRae, K. D., [R] **binreg**
Madansky, A., [R] **runtest**
Maddala, G. S., [R] **nlogit**, [R] **tobit**, [R] **treatreg**
Magnusson, L. M., [R] **ivprobit**, [R] **ivregress**, [R] **ivtobit**
Mallows, C. L., [R] **regress postestimation**
Mander, A., [R] **anova**, [R] **symmetry**
Mann, H. B., [R] **kwallis**, [R] **ranksum**
Manning, W. G., [R] **heckman**
Manski, C. F., [R] **gmm**
Mantel, N., [R] **stepwise**
Marchenko, Y. V., [R] **anova**, [R] **loneway**, [R] **oneway**, [R] **sktest**
Marden, J. I., [R] **rologit**
Markowski, C. A., [R] **sdtest**
Markowski, E. P., [R] **sdtest**
Marschak, J., [R] **ivregress**
Martin, W., [R] **regress**
Martínez, M. A., [R] **logistic**
Mascher, K., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Massey, F. J., Jr., [R] **ttest**
Massey, J. T., [R] **marginsplot**
Master, I. M., [R] **exlogistic**
Mastrucci, M. T., [R] **exlogistic**

Matthews, J. N. S., [R] **ameans**, [R] **expoisson**, [R] **sdtest**
Mátyás, L., [R] **gmm**
Maurer, K., [R] **marginsplot**
Maxwell, A. E., [R] **symmetry**
McCleary, S. J., [R] **regress postestimation**
McClish, D. K., [R] **rocreg**
McCullagh, P., [R] **binreg**, [R] **binreg postestimation**, [R] **glm**, [R] **glm postestimation**, [R] **ologit**, [R] **rologit**
McCulloch, C. E., [R] **logistic**
McDonald, J. A., [R] **sunflower**
McDonald, J. F., [R] **tobit**, [R] **tobit postestimation**
McDowell, A., [R] **marginsplot**
McDowell, A. W., [R] **sureg**
McFadden, D. L., [R] **asclogit**, [R] **asmprobit**, [R] **clogit**, [R] **hausman**, [R] **maximize**, [R] **nlogit**, [R] **suest**
McGill, R., [R] **sunflower**
McGinnis, R. E., [R] **symmetry**
McGuire, T. J., [R] **dstdize**
McKelvey, R. D., [R] **ologit**
McNeil, B. J., [R] **roccomp**, [R] **rocfit**, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **roctab**
McNeil, D., [R] **poisson**
Meeusen, W., [R] **frontier**
Mehta, C. R., [R] **exlogistic**, [R] **exlogistic postestimation**, [R] **expoisson**, [R] **tabulate twoway**
Melly, B., [R] **qreg**
Mensing, R. W., [R] **anova postestimation**
Metz, C. E., [R] **logistic postestimation**
Miao, W., [R] **sdtest**
Michels, K. M., [R] **anova**, [R] **contrast**, [R] **loneway**, [R] **oneway**, [R] **pwcompare**
Mielke, P., [R] **brier**
Miller, A. B., [R] **kappa**
Miller, R. G., Jr., [R] **diagnostic plots**, [R] **oneway**, [R] **pwcompare**
Milliken, G. A., [R] **anova**, [R] **contrast**, [R] **margins**, [R] **pwcompare**
Miranda, A., [R] **gllamm**, [R] **heckprob**, [R] **ivprobit**, [R] **ivtobit**, [R] **logistic**, [R] **logit**, [R] **nbreg**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**
Mitchell, C., [R] **exlogistic**
Mitchell, M. N., [R] **logistic**, [R] **logistic postestimation**, [R] **logit**, [R] **marginsplot**
Moffitt, R. A., [R] **tobit**, [R] **tobit postestimation**
Monfort, A., [R] **hausman**, [R] **suest**, [R] **test**
Monson, R. R., [R] **bitest**
Montoya, D., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Mood, A. M., [R] **centile**
Mooney, C. Z., [R] **bootstrap**, [R] **jackknife**, [R] **rocreg**, [R] **rocregplot**
Moran, J. L., [R] **dstdize**
Morris, C., [R] **bootstrap**
Morris, N. F., [R] **binreg**
Moskowitz, M., [R] **kappa**
Mosteller, F., [R] **jackknife**, [R] **regress**, [R] **regress postestimation**, [R] **rreg**
Moulton, L. H., [R] **permute**
Muellbauer, J., [R] **nlsur**
Mullahy, J., [R] **gmm**, [R] **zinb**, [R] **zip**
Müller, H. G., [R] **lpoly**
Muro, J., [R] **heckprob**
Murphy, A. H., [R] **brier**
Murray-Lyon, I. M., [R] **binreg**
Muñoz, J., [R] **exlogistic**

N

Nachtsheim, C. J., [R] **pkcross**, [R] **pkequiv**, [R] **pkshape**, [R] **regress postestimation**
Nadarajah, S., [R] **nlogit**
Nadaraya, E. A., [R] **lpoly**
Nagler, J., [R] **scobit**
Naiman, D. Q., [R] **qreg**
Nannicini, T., [R] **treatreg**
Narula, S. C., [R] **qreg**
Nee, J. C. M., [R] **kappa**
Neely, S. T., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Nelder, J. A., [R] **binreg**, [R] **binreg postestimation**, [R] **glm**, [R] **glm postestimation**, [R] **margins**, [R] **ologit**
Nelson, C. R., [R] **ivregress postestimation**
Nelson, E. C., [R] **alpha**, [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Nelson, F. D., [R] **logit**, [R] **probit**
Neter, J., [R] **pkcross**, [R] **pkequiv**, [R] **pkshape**, [R] **regress postestimation**
Newey, W. K., [R] **glm**, [R] **gmm**, [R] **ivprobit**, [R] **ivregress**, [R] **ivtobit**
Newman, S. C., [R] **poisson**
Newson, R., [R] **centile**, [R] **glm**, [R] **inequality**, [R] **kwallis**, [R] **mkspline**, [R] **ranksum**, [R] **signrank**, [R] **spearman**, [R] **tabulate twoway**
Newton, H. J., [R] **kdensity**
Neyman, J., [R] **ci**
Nicewander, W. A., [R] **correlate**
Nichols, A., [R] **ivregress**, [R] **reg3**, [R] **treatreg**
Nickell, S. J., [R] **gmm**
Nolan, D., [R] **diagnostic plots**
Norton, S. J., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Nunnally, J. C., [R] **alpha**

O

O'Fallon, W. M., [R] **logit**
Oehlert, G. W., [R] **nlcom**, [R] **rocreg postestimation**, [R] **rocregplot**

Olivier, D., [R] **expoisson**
Olkin, I., [R] **kwallis**
Olson, J. M., [R] **symmetry**
Ord, J. K., [R] **centile**, [R] **mean**, [R] **proportion**, [R] **qreg**, [R] **ratio**, [R] **summarize**, [R] **total**
Orsini, N., [R] **mkspline**
Ostle, B., [R] **anova postestimation**
Over, M., [R] **regress**

P

Pacheco, J. M., [R] **dstdize**
Pagan, A. R., [R] **frontier**, [R] **mvreg**, [R] **regress postestimation**, [R] **sureg**
Pagano, M., [R] **dstdize**, [R] **logistic**, [R] **margins**, [R] **sampsi**, [R] **tabulate twoway**
Paik, M. C., [R] **dstdize**, [R] **kappa**, [R] **sampsi**
Pampel, F. C., [R] **logistic**, [R] **logit**, [R] **probit**
Panis, C., [R] **mkspline**
Park, H. J., [R] **regress**
Park, J. Y., [R] **boxcox**, [R] **margins**, [R] **nlcom**, [R] **predictnl**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **testnl**
Parks, W. P., [R] **exlogistic**
Parner, E. T., [R] **glm**
Parzen, E., [R] **estat**, [R] **kdensity**
Pasquini, J., [R] **vwls**
Patel, N. R., [R] **exlogistic**, [R] **exlogistic postestimation**, [R] **expoisson**, [R] **tabulate twoway**
Patterson, H. D., [R] **pkcross**
Paul, C., [R] **logistic**
Pearce, M. S., [R] **logistic**
Pearson, E. S., [R] **ci**, [R] **ttest**
Pearson, K., [R] **correlate**, [R] **tabulate twoway**
Pepe, M. S., [R] **roc**, [R] **roccomp**, [R] **rocfit**, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **roctab**
Peracchi, F., [R] **regress**, [R] **regress postestimation**
Pérez-Hernández, M. A., [R] **kdensity**
Pérez-Hoyos, S., [R] **lrtest**
Perkins, A. M., [R] **ranksum**
Perrin, E., [R] **alpha**, [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Pesarin, F., [R] **tabulate twoway**
Peterson, B., [R] **ologit**
Peterson, W. W., [R] **logistic postestimation**
Petitclerc, M., [R] **kappa**
Petkova, E., [R] **suest**
Petrin, A., [R] **frontier**
Pfeffer, R. I., [R] **symmetry**
Phillips, P. C. B., [R] **boxcox**, [R] **margins**, [R] **nlcom**, [R] **predictnl**, [R] **regress postestimation time series**, [R] **rocreg postestimation**, [R] **rocregplot**, [R] **testnl**
Pickles, A., [R] **gllamm**, [R] **glm**
Pike, M. C., [R] **symmetry**
Pindyck, R. S., [R] **biprobit**, [R] **heckprob**
Pischke, J.-S., [R] **ivregress**, [R] **ivregress postestimation**, [R] **qreg**, [R] **regress**
Pitblado, J. S., [R] **frontier**, [R] **lpoly**, [R] **maximize**, [R] **ml**
Plackett, R. L., [R] **ameans**, [R] **regress**, [R] **rologit**, [R] **summarize**, [R] **ttest**
Plummer, W. D., Jr., [R] **sunflower**
Pocock, S. J., [R] **sampsi**
Poi, B. P., [R] **bootstrap**, [R] **bstat**, [R] **frontier**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **maximize**, [R] **ml**, [R] **nl**, [R] **nlsur**, [R] **reg3**
Poirier, D. J., [R] **biprobit**
Poisson, S. D., [R] **poisson**
Pollock, P. H., III, [R] **histogram**
Ponce de Leon, A., [R] **roccomp**, [R] **roctab**
Porter, T. M., [R] **correlate**
Powers, D. A., [R] **logit**, [R] **probit**
Preece, D. A., [R] **ttest**
Pregibon, D., [R] **glm**, [R] **linktest**, [R] **logistic**, [R] **logistic postestimation**, [R] **logit**, [R] **logit postestimation**
Press, W. H., [R] **dydx**, [R] **vwls**
Punj, G. N., [R] **rologit**

R

Rabe-Hesketh, S., [R] **gllamm**, [R] **glm**, [R] **heckprob**, [R] **ivprobit**, [R] **ivtobit**, [R] **logistic**, [R] **logit**, [R] **nbreg**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**
Raciborski, R., [R] **poisson**, [R] **tpoisson**
Raftery, A., [R] **BIC note**, [R] **estat**, [R] **glm**
Ramalheira, C., [R] **ameans**
Ramsey, J. B., [R] **regress postestimation**
Ratkowsky, D. A., [R] **nl**, [R] **pk**, [R] **pkcross**
Redelmeier, D. A., [R] **brier**
Reeves, D., [R] **meta**
Reichenheim, M. E., [R] **kappa**, [R] **roccomp**, [R] **roctab**
Reid, C., [R] **ci**
Reilly, M., [R] **logistic**
Relles, D. A., [R] **rreg**
Rencher, A. C., [R] **anova postestimation**
Revankar, N. S., [R] **frontier**
Richardson, W., [R] **ttest**
Riffenburgh, R. H., [R] **ksmirnov**, [R] **kwallis**
Riley, A. R., [R] **net search**
Rivers, D., [R] **ivprobit**
Roberson, P. K., [R] **logistic postestimation**
Robyn, D. L., [R] **cumul**
Rodgers, J. L., [R] **correlate**
Rodríguez, G., [R] **nbreg**, [R] **poisson**

Rogers, W. H., [R] **brier**, [R] **glm**, [R] **heckman**, [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **nbreg**, [R] **poisson**, [R] **predictnl**, [R] **qreg**, [R] **regress**, [R] **rocreg**, [R] **rreg**, [R] **sktest**, [R] **slogit**, [R] **suest**
Ronning, G., [R] **clogit**
Rose, J. M., [R] **nlogit**
Rosenthal, R., [R] **contrast**
Rosner, B., [R] **sampsi**
Rosnow, R. L., [R] **contrast**
Ross, G. J. S., [R] **nl**
Rossi, P. E., [R] **sureg**
Rothman, K. J., [R] **ci**, [R] **dstdize**, [R] **glogit**, [R] **poisson**
Rothstein, H. R., [R] **meta**
Rousseeuw, P. J., [R] **qreg**, [R] **regress postestimation**, [R] **rreg**
Rovine, M. J., [R] **correlate**
Royston, P., [R] **bootstrap**, [R] **centile**, [R] **cusum**, [R] **diagnostic plots**, [R] **dotplot**, [R] **dydx**, [R] **estat**, [R] **fracpoly**, [R] **fracpoly postestimation**, [R] **glm**, [R] **kdensity**, [R] **lnskew0**, [R] **lowess**, [R] **mfp**, [R] **ml**, [R] **nl**, [R] **regress**, [R] **sampsi**, [R] **sktest**, [R] **smooth**, [R] **swilk**
Rubin, D. B., [R] **contrast**
Rubin, H., [R] **ivregress postestimation**
Rubinfeld, D. L., [R] **biprobit**, [R] **heckprob**
Rudebusch, G. D., [R] **ivregress postestimation**
Ruppert, D., [R] **boxcox**, [R] **rreg**
Rutherford, E., [R] **poisson**
Rutherford, M. J., [R] **poisson**
Ruud, P. A., [R] **gmm**, [R] **rologit**, [R] **suest**
Ryan, T. P., [R] **qc**

S

Sakamoto, Y., [R] **BIC note**
Salgado-Ugarte, I. H., [R] **kdensity**, [R] **lowess**, [R] **smooth**
Salim, A., [R] **logistic**
Sanders, F., [R] **brier**
Santos Silva, J. M. C., [R] **gmm**
Sargan, J. D., [R] **ivregress postestimation**
Sasieni, P., [R] **dotplot**, [R] **lowess**, [R] **nptrend**, [R] **smooth**
Satterthwaite, F. E., [R] **ttest**
Sauerbrei, W., [R] **bootstrap**, [R] **estat**, [R] **fracpoly**, [R] **mfp**
Savin, N. E., [R] **regress postestimation time series**
Saw, S. L. C., [R] **qc**
Sawa, T., [R] **estat**
Saxl, I., [R] **correlate**
Schaalje, G. B., [R] **anova postestimation**
Schaffer, M. E., [R] **ivregress**, [R] **ivregress postestimation**
Scheffé, H., [R] **anova**, [R] **oneway**
Schlesselman, J. J., [R] **boxcox**
Schlossmacher, E. J., [R] **qreg**
Schmidt, C. H., [R] **brier**
Schmidt, P., [R] **frontier**, [R] **regress postestimation**
Schneider, H., [R] **sdtest**
Schnell, D., [R] **regress**
Schonlau, M., [R] **glm**, [R] **logistic**, [R] **logit**, [R] **poisson**, [R] **regress**
Schuirmann, D. J., [R] **pkequiv**
Schwarz, G., [R] **BIC note**, [R] **estat**
Scott, D. W., [R] **kdensity**
Scott, G. B., [R] **exlogistic**
Scotto, M. G., [R] **diagnostic plots**
Searle, S. R., [R] **contrast**, [R] **margins**, [R] **pwcompare**, [R] **pwmean**
Seed, P. T., [R] **ci**, [R] **correlate**, [R] **logistic postestimation**, [R] **roccomp**, [R] **roctab**, [R] **sampsi**, [R] **sdtest**, [R] **spearman**
Seidler, J., [R] **correlate**
Selvin, S., [R] **poisson**
Sempos, C. T., [R] **dstdize**
Semykina, A., [R] **inequality**, [R] **qreg**
Seneta, E., [R] **correlate**
Senn, S. J., [R] **glm**, [R] **ttest**
Shapiro, S. S., [R] **swilk**
Shavelson, R. J., [R] **alpha**
Shea, J., [R] **ivregress postestimation**
Sheather, S. J., [R] **boxcox**, [R] **lowess**, [R] **lpoly**, [R] **regress postestimation**, [R] **stepwise**
Sheldon, T. A., [R] **meta**
Shewhart, W. A., [R] **qc**
Shiboski, S. C., [R] **logistic**
Shiller, R. J., [R] **tobit**
Shimizu, M., [R] **kdensity**, [R] **lowess**
Shrout, P. E., [R] **kappa**
Šidák, Z., [R] **correlate**, [R] **oneway**
Silverman, B. W., [R] **kdensity**
Silvey, S. D., [R] **ologit**, [R] **oprobit**
Simonoff, J. S., [R] **kdensity**, [R] **tnbreg**, [R] **tpoisson**
Simor, I. S., [R] **kappa**
Singleton, K. J., [R] **gmm**
Sininger, Y., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Skrondal, A., [R] **gllamm**, [R] **glm**
Smeeton, N. C., [R] **ranksum**, [R] **signrank**
Smirnov, N. V., [R] **ksmirnov**
Smith, H., [R] **eivreg**, [R] **oneway**, [R] **regress**, [R] **stepwise**
Smith, J. M., [R] **fracpoly**
Smith, R. J., [R] **ivprobit**
Snedecor, G. W., [R] **ameans**, [R] **anova**, [R] **correlate**, [R] **oneway**, [R] **ranksum**, [R] **signrank**
Snell, E. J., [R] **exlogistic**, [R] **expoisson**
Song, F., [R] **meta**
Soon, T. W., [R] **qc**
Spearman, C., [R] **spearman**
Speed, F. M., [R] **margins**

Speed, T., [R] **diagnostic plots**
Spiegelhalter, D. J., [R] **brier**
Spieldman, R. S., [R] **symmetry**
Spitzer, J. J., [R] **boxcox**
Sprent, P., [R] **ranksum**, [R] **signrank**
Sribney, W. M., [R] **orthog**, [R] **ranksum**, [R] **signrank**, [R] **stepwise**, [R] **test**
Staelin, R., [R] **rologit**
Staiger, D., [R] **ivregress postestimation**
Starmer, C. F., [R] **vwls**
Startz, R., [R] **ivregress postestimation**
Stegun, I. A., [R] **contrast**, [R] **orthog**
Steichen, T. J., [R] **kappa**, [R] **kdensity**, [R] **sunflower**
Steiger, W., [R] **qreg**
Stein, C., [R] **bootstrap**
Stephenson, D. B., [R] **brier**
Stepniewska, K. A., [R] **nptrend**
Sterne, J. A. C., [R] **dstdize**, [R] **meta**, [R] **summarize**
Stevenson, R. E., [R] **frontier**
Stewart, M. B., [R] **intreg**, [R] **oprobit**, [R] **tobit**
Stigler, S. M., [R] **ameans**, [R] **ci**, [R] **correlate**, [R] **kwallis**, [R] **qreg**, [R] **regress**
Stillman, S., [R] **ivregress**, [R] **ivregress postestimation**
Stine, R., [R] **bootstrap**
Stock, J. H., [R] **ivregress**, [R] **ivregress postestimation**
Stoto, M. A., [R] **lv**
Stover, L., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Street, J. O., [R] **rreg**
Stryhn, H., [R] **regress**
Stuart, A., [R] **centile**, [R] **mean**, [R] **proportion**, [R] **qreg**, [R] **ratio**, [R] **summarize**, [R] **symmetry**, [R] **tobit**, [R] **total**
Student, *see* Gosset, W. S.
Stuetzle, W., [R] **sunflower**
Suárez, C., [R] **heckprob**
Sullivan, G., [R] **regress**
Sutton, A. J., [R] **meta**
Swed, F. S., [R] **runtest**
Swets, J. A., [R] **logistic postestimation**
Szroeter, J., [R] **regress postestimation**

T

Taka, M. T., [R] **pkcross**
Tamhane, A. C., [R] **oneway**, [R] **sampsi**
Taniuchi, T., [R] **kdensity**
Tanner, W. P., Jr., [R] **logistic postestimation**
Tanur, J. M., [R] **kwallis**
Tapia, R. A., [R] **kdensity**
Tarlov, A. R., [R] **alpha**, [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Taylor, C., [R] **gllamm**, [R] **glm**
Teukolsky, S. A., [R] **dydx**, [R] **vwls**
Theil, H., [R] **ivregress**, [R] **reg3**
Thiele, T. N., [R] **summarize**
Thompson, J. C., [R] **diagnostic plots**
Thompson, J. R., [R] **kdensity**, [R] **poisson**
Thompson, M. L., [R] **rocreg**
Thorndike, F., [R] **poisson**
Thurstone, L. L., [R] **rologit**
Tibshirani, R. J., [R] **bootstrap**, [R] **qreg**
Tidmarsh, C. E., [R] **fracpoly**
Tilford, J. M., [R] **logistic postestimation**
Tobías, A., [R] **alpha**, [R] **logistic postestimation**, [R] **lrtest**, [R] **poisson**, [R] **roccomp**, [R] **roctab**, [R] **sdtest**
Tobin, J., [R] **tobit**
Toman, R. J., [R] **stepwise**
Tong, H., [R] **estat**
Toplis, P. J., [R] **binreg**
Tosetto, A., [R] **logistic**, [R] **logit**
Train, K. E., [R] **asmprobit**
Trapido, E., [R] **exlogistic**
Treiman, D. J., [R] **eivreg**, [R] **mlogit**
Trivedi, P. K., [R] **asclogit**, [R] **asmprobit**, [R] **bootstrap**, [R] **gmm**, [R] **heckman**, [R] **intreg**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **logit**, [R] **mprobit**, [R] **nbreg**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**, [R] **qreg**, [R] **regress**, [R] **regress postestimation**, [R] **simulate**, [R] **sureg**, [R] **tnbreg**, [R] **tobit**, [R] **tpoisson**, [R] **zinb postestimation**, [R] **zip postestimation**
Tsiatis, A. A., [R] **exlogistic**
Tufte, E. R., [R] **stem**
Tukey, J. W., [R] **jackknife**, [R] **ladder**, [R] **linktest**, [R] **lv**, [R] **regress**, [R] **regress postestimation**, [R] **rreg**, [R] **smooth**, [R] **spikeplot**, [R] **stem**
Tukey, P. A., [R] **diagnostic plots**, [R] **lowess**
Tyler, J. H., [R] **regress**

U

Uebersax, J. S., [R] **tetrachoric**
Uhlendorff, A., [R] **asmprobit**, [R] **mlogit**, [R] **mprobit**
University Group Diabetes Program, [R] **glogit**
Utts, J. M., [R] **ci**

V

Valman, H. B., [R] **fracpoly**
van Belle, G., [R] **anova**, [R] **dstdize**, [R] **oneway**
Van de Ven, W. P. M. M., [R] **biprobit**, [R] **heckprob**
van den Broeck, J., [R] **frontier**
Van Kerm, P., [R] **inequality**, [R] **kdensity**
Van Loan, C. F., [R] **orthog**, [R] **tetrachoric**
Van Pragg, B. M. S., [R] **biprobit**, [R] **heckprob**
Velleman, P. F., [R] **regress postestimation**, [R] **smooth**
Verardi, V., [R] **correlate**, [R] **rreg**
Vetterling, W. T., [R] **dydx**, [R] **vwls**
Vidmar, S., [R] **ameans**
Vittinghoff, E., [R] **logistic**
Vohr, B. R., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**

von Bortkewitsch, L., [R] **poisson**
von Eye, A., [R] **correlate**
Von Storch, H., [R] **brier**
Vondráček, J., [R] **correlate**
Vuong, Q. H., [R] **ivprobit**, [R] **zinb**, [R] **zip**

W

Wacholder, S., [R] **binreg**
Wagner, H. M., [R] **qreg**
Wallis, W. A., [R] **kwallis**
Walters, S. J., [R] **ci**, [R] **kappa**, [R] **tabulate twoway**
Wand, M. P., [R] **kdensity**
Wang, D., [R] **ci**, [R] **dstdize**, [R] **prtest**
Wang, Y., [R] **asmprobit**
Wang, Z., [R] **logistic postestimation**, [R] **lrtest**, [R] **stepwise**
Ware, J. E., Jr., [R] **alpha**, [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Waterson, E. J., [R] **binreg**
Watson, G. S., [R] **lpoly**, [R] **regress postestimation time series**
Watson, M. W., [R] **ivregress**
Weber, S., [R] **correlate**
Webster, A. D., [R] **fracpoly**
Wedderburn, R. W. M., [R] **glm**
Weesie, J., [R] **alpha**, [R] **constraint**, [R] **hausman**, [R] **ladder**, [R] **logistic postestimation**, [R] **reg3**, [R] **regress**, [R] **regress postestimation**, [R] **rologit**, [R] **simulate**, [R] **suest**, [R] **sureg**, [R] **tabstat**, [R] **tabulate twoway**, [R] **test**, [R] **tetrachoric**
Weisberg, H. F., [R] **summarize**
Weisberg, S., [R] **boxcox**, [R] **regress**, [R] **regress postestimation**
Weiss, M., [R] **estimates table**
Weisstein, E. W., [R] **rocreg postestimation**
Welch, B. L., [R] **ttest**
Wellington, J. F., [R] **qreg**
Wells, K. B., [R] **lincom**, [R] **mlogit**, [R] **mprobit**, [R] **mprobit postestimation**, [R] **predictnl**, [R] **slogit**
Welsch, R. E., [R] **estat**, [R] **regress postestimation**
West, K. D., [R] **glm**, [R] **gmm**, [R] **ivregress**
West, S. G., [R] **pcorr**
Westlake, W. J., [R] **pkequiv**
White, H., [R] **regress**, [R] **regress postestimation**, [R] **rocreg**, [R] **suest**
White, I. R., [R] **simulate**
White, K. J., [R] **boxcox**, [R] **regress postestimation time series**
Whitehouse, E., [R] **inequality**
Whiting, P., [R] **roccomp**, [R] **roctab**
Whitney, D. R., [R] **kwallis**, [R] **ranksum**
Widen, J. E., [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
Wieand, S., [R] **rocreg**, [R] **rocreg postestimation**
Wiggins, V. L., [R] **regress postestimation**, [R] **regress postestimation time series**
Wilcox, D. W., [R] **ivregress postestimation**
Wilcoxon, F., [R] **kwallis**, [R] **ranksum**, [R] **signrank**
Wilde, J., [R] **gmm**
Wilk, M. B., [R] **cumul**, [R] **diagnostic plots**, [R] **swilk**
Wilks, D. S., [R] **brier**
Williams, R., [R] **glm**, [R] **ologit**, [R] **oprobit**, [R] **pcorr**, [R] **stepwise**
Wilson, E. B., [R] **ci**
Wilson, S. R., [R] **bootstrap**
Windmeijer, F., [R] **gmm**
Winer, B. J., [R] **anova**, [R] **contrast**, [R] **loneway**, [R] **oneway**, [R] **pwcompare**
Wolfe, F., [R] **correlate**, [R] **spearman**
Wolfe, R., [R] **ologit**, [R] **oprobit**, [R] **tabulate twoway**
Wolfson, C., [R] **kappa**
Wolpin, K. I., [R] **asmprobit**
Wood, F. S., [R] **diagnostic plots**
Woodard, D. E., [R] **contrast**
Wooldridge, J. M., [R] **gmm**, [R] **intreg**, [R] **ivprobit**, [R] **ivregress**, [R] **ivregress postestimation**, [R] **ivtobit**, [R] **margins**, [R] **regress**, [R] **regress postestimation**, [R] **regress postestimation time series**, [R] **tobit**
Working, H., [R] **roccomp**, [R] **rocfit**, [R] **roctab**
Wright, J. H., [R] **ivregress**, [R] **ivregress postestimation**
Wright, J. T., [R] **binreg**
Wright, P. G., [R] **ivregress**
Wu, C. F. J., [R] **qreg**
Wu, D.-M., [R] **ivregress postestimation**

X

Xie, Y., [R] **logit**, [R] **probit**
Xu, J., [R] **cloglog**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **ologit**, [R] **oprobit**, [R] **probit**

Y

Yates, J. F., [R] **brier**
Yee, T. W., [R] **slogit**
Yellott, J. I., Jr., [R] **rologit**
Yen, W. M., [R] **alpha**
Yogo, M., [R] **ivregress**, [R] **ivregress postestimation**

Z

Zabell, S., [R] **kwallis**
Zavoina, W., [R] **ologit**
Zelen, M., [R] **ttest**
Zellner, A., [R] **frontier**, [R] **nlsur**, [R] **reg3**, [R] **sureg**
Zelterman, D., [R] **tabulate twoway**
Zheng, X., [R] **gllamm**
Zimmerman, F., [R] **regress**

Zubkoff, M., [R] **alpha**, [R] **lincom**, [R] **mlogit**,
[R] **mprobit**, [R] **mprobit postestimation**,
[R] **predictnl**, [R] **slogit**
Zucchini, W., [R] **rocreg**
Zwiers, F. W., [R] **brier**

Subject index

This is the subject index for the 4-volume *Base Reference Manual*. Readers may also want to consult the combined subject index (and the combined author index) in the *Quick Reference and Index*.

Semicolons set off the most important entries from the rest. Sometimes no entry will be set off with semicolons, meaning that all entries are equally important.

A

`about` command, [R] **about**
absorption in regression, [R] **areg**
`acprplot` command, [R] **regress postestimation**
added-variable plots, [R] **regress postestimation**
adjusted
  margins, [R] **margins**, [R] **marginsplot**
  means, [R] **contrast**, [R] **margins**, [R] **marginsplot**
  partial residual plot, [R] **regress postestimation**
`ado`, `view` subcommand, [R] **view**
`ado` command, [R] **net**
`ado_d`, `view` subcommand, [R] **view**
`ado describe` command, [R] **net**
`ado dir` command, [R] **net**
ado-files,
  editing, [R] **doedit**
  installing, [R] **net**, [R] **sj**, [R] **ssc**
  location of, [R] **which**
  official, [R] **update**
  searching for, [R] **search**, [R] **ssc**
  updating user-written, [R] **adoupdate**
`adosize`, `set` subcommand, [R] **set**
`ado uninstall` command, [R] **net**
`adoupdate` command, [R] **adoupdate**
agreement, interrater, [R] **kappa**
AIC, [R] **BIC note**, [R] **estat**, [R] **estimates stats**, [R] **glm**
Akaike information criterion, *see* AIC
`all`, `update` subcommand, [R] **update**
alpha coefficient, Cronbach's, [R] **alpha**
`alpha` command, [R] **alpha**
alternative-specific
  conditional logit (McFadden's choice) model, [R] **asclogit**
  multinomial probit regression, [R] **asmprobit**
  rank-ordered probit regression, [R] **asroprobit**
`alternatives`, `estat` subcommand, [R] **asclogit postestimation**, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
`ameans` command, [R] **ameans**
analysis of covariance, *see* ANCOVA
analysis of variance, *see* ANOVA
analysis-of-variance test of normality, [R] **swilk**
ANCOVA, [R] **anova**
ANOVA, [R] **anova**, [R] **contrast**, [R] **loneway**, [R] **oneway**
  Kruskal–Wallis, [R] **kwallis**
ANOVA, *continued*
  plots, [R] **marginsplot**
  repeated measures, [R] **anova**
`anova` command, [R] **anova**, [R] **anova postestimation**
ARCH effects, testing for, [R] **regress postestimation time series**
`archlm`, `estat` subcommand, [R] **regress postestimation time series**
`areg` command, [R] **areg**, [R] **areg postestimation**
`asclogit` command, [R] **asclogit**, [R] **asclogit postestimation**
`asmprobit` command, [R] **asmprobit**, [R] **asmprobit postestimation**
`asroprobit` command, [R] **asroprobit**, [R] **asroprobit postestimation**
association, measures of, [R] **tabulate twoway**
asymmetry, *see* skewness
AUC, [R] **logistic postestimation**, *also see* pk (pharmacokinetic data), *also see* ROC analysis
augmented
  component-plus-residual plot, [R] **regress postestimation**
  partial residual plot, [R] **regress postestimation**
autocorrelation, [R] **regress postestimation time series**, *also see* HAC variance estimate
autoregressive conditional heteroskedasticity, testing for, [R] **regress postestimation time series**
`autotabgraphs`, `set` subcommand, [R] **set**
average
  marginal effects, [R] **margins**, [R] **marginsplot**
  partial effects (APEs), [R] **margins**, [R] **marginsplot**
  predictions, [R] **margins**, [R] **marginsplot**
averages, *see* means
`avplot` and `avplots` commands, [R] **regress postestimation**

B

Bartlett's test for equal variances, [R] **oneway**
`base`, `fvset` subcommand, [R] **fvset**
Bayesian information criterion, *see* BIC
`bcskew0` command, [R] **lnskew0**
Berndt–Hall–Hall–Hausman algorithm, [R] **ml**
beta coefficients, [R] **regress**
BFGS algorithm, [R] **ml**
`bgodfrey`, `estat` subcommand, [R] **regress postestimation time series**
BHHH algorithm, [R] **ml**
bias corrected and accelerated, [R] **bootstrap postestimation**, [R] **bstat**
BIC, [R] **BIC note**, [R] **estat**, [R] **estimates stats**, [R] **glm**
binary outcome model, *see* outcomes, binary
binomial
  distribution, confidence intervals, [R] **ci**
  family regression, [R] **binreg**
  probability test, [R] **bitest**

binreg command, [R] **binreg**, [R] **binreg postestimation**
bioequivalence tests, [R] **pk**, [R] **pkequiv**
biopharmaceutical data, *see* pk (pharmacokinetic data)
biprobit command, [R] **biprobit**, [R] **biprobit postestimation**
bitest and bitesti commands, [R] **bitest**
bivariate probit regression, [R] **biprobit**
biweight regression estimates, [R] **rreg**
blogit command, [R] **glogit**, [R] **glogit postestimation**
Bonferroni's multiple-comparison adjustment, *see* multiple comparisons, Bonferroni's method
bootstrap
  sampling and estimation, [R] **bootstrap**, [R] **bsample**, [R] **bstat**, [R] **qreg**, [R] **rocreg**, [R] **simulate**
  standard errors, [R] ***vce_option***
bootstrap prefix command, [R] **bootstrap**, [R] **bootstrap postestimation**
bootstrap, estat subcommand, [R] **bootstrap postestimation**
Boston College archive, *see* SSC archive
Box–Cox
  power transformations, [R] **lnskew0**
  regression, [R] **boxcox**
boxcox command, [R] **boxcox**, [R] **boxcox postestimation**
Box's conservative epsilon, [R] **anova**
bprobit command, [R] **glogit**, [R] **glogit postestimation**
Breusch–Godfrey test, [R] **regress postestimation time series**
Breusch–Pagan test of independence, [R] **mvreg**, [R] **sureg**
Breusch–Pagan/Cook–Weisberg test for heteroskedasticity, [R] **regress postestimation**
brier command, [R] **brier**
Brier score decomposition, [R] **brier**
browse, view subcommand, [R] **view**
Broyden–Fletcher–Goldfarb–Shanno algorithm, [R] **ml**
bsample command, [R] **bsample**
bsqreg command, [R] **qreg**, [R] **qreg postestimation**
bstat command, [R] **bstat**

C

c(cformat) c-class value, [R] **set cformat**
c(pformat) c-class value, [R] **set cformat**
c(seed) c-class value, [R] **set emptycells**, [R] **set seed**
c(sformat) c-class value, [R] **set cformat**
c(showbaselevels) c-class value, [R] **set showbaselevels**
c(showemptycells) c-class value, [R] **set showbaselevels**
c(showomitted) c-class value, [R] **set showbaselevels**
calculator, [R] **display**
case–control data, [R] **clogit**, [R] **logistic**, [R] **rocreg**, [R] **symmetry**
categorical, *also see* factor variables
  contrasts after anova, [R] **contrast**
  covariates, [R] **anova**
  data, agreement, measures for, [R] **kappa**
  graphs, [R] **grmeanby**, [R] **spikeplot**
  outcomes, *see* outcomes, categorical, *also see* outcomes, binary, *also see* outcomes, ordinal
  regression, *also see* outcomes subentry
    absorbing one categorical variable, [R] **areg**
  tabulations, [R] **table**, [R] **tabstat**, [R] **tabulate oneway**, [R] **tabulate twoway**, [R] **tabulate, summarize()**
  variable creation, [R] **tabulate oneway**, [R] **xi**
cchart command, [R] **qc**
cd, net subcommand, [R] **net**
censored-normal regression, *see* interval regression
centile command, [R] **centile**
centiles, *see* percentiles, displaying
central tendency, measures of, *see* means, *see* medians
cformat, set subcommand, [R] **set**, [R] **set cformat**
check, ml subcommand, [R] **ml**
checksum, set subcommand, [R] **set**
chelp command, [R] **help**
chi-squared
  hypothesis test, [R] **hausman**, [R] **lrtest**, [R] **sdtest**, [R] **tabulate twoway**, [R] **test**, [R] **testnl**
  probability plot, [R] **diagnostic plots**
  quantile plot, [R] **diagnostic plots**
  test of independence, [R] **tabulate twoway**
choice models, [R] **asclogit**, [R] **asmprobit**, [R] **asroprobit**, [R] **clogit**, [R] **cloglog**, [R] **exlogistic**, [R] **glm**, [R] **glogit**, [R] **heckprob**, [R] **hetprob**, [R] **ivprobit**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **mprobit**, [R] **nlogit**, [R] **ologit**, [R] **oprobit**, [R] **probit**, [R] **rologit**, [R] **scobit**, [R] **slogit**, [R] **suest**
Chow test, [R] **anova**, [R] **contrast**, [R] **lrtest**
ci and cii commands, [R] **ci**
classification
  data, *see* ROC analysis
  interrater agreement, [R] **kappa**
  table, [R] **logistic postestimation**
classification, estat subcommand, [R] **logistic postestimation**
clear,
  estimates subcommand, [R] **estimates store**
  fvset subcommand, [R] **fvset**
  ml subcommand, [R] **ml**
clearing estimation results, [R] **estimates store**
clogit command, [R] **bootstrap**, [R] **clogit**, [R] **clogit postestimation**, [R] **exlogistic**, [R] **rologit**
cloglog command, [R] **cloglog**, [R] **cloglog postestimation**
close,
  cmdlog subcommand, [R] **log**
  log subcommand, [R] **log**

cluster estimator of variance, [R] *vce_option*
alternative-specific
conditional logit model, [R] **asclogit**
multinomial probit regression, [R] **asmprobit**
rank-ordered probit regression, [R] **asroprobit**
complementary log-log regression, [R] **cloglog**
generalized linear models, [R] **glm**
for binomial family, [R] **binreg**
generalized methods of moments, [R] **gmm**
heckman selection model, [R] **heckman**
instrumental-variables regression, [R] **ivregress**
interval regression, [R] **intreg**
linear regression, [R] **regress**
constrained, [R] **cnsreg**
truncated, [R] **truncreg**
with dummy-variable set, [R] **areg**
logistic regression, [R] **logistic**, [R] **logit**, *also see* logit regression subentry
conditional, [R] **clogit**
multinomial, [R] **mlogit**
ordered, [R] **ologit**
rank-ordered, [R] **rologit**
skewed, [R] **scobit**
stereotype, [R] **slogit**
logit regression, [R] **logit**, *also see* logistic regression subentry
for grouped data, [R] **glogit**
nested, [R] **nlogit**
maximum likelihood estimation, [R] **ml**
multinomial
logistic regression, [R] **mlogit**
probit regression, [R] **mprobit**
negative binomial regression
truncated, [R] **nbreg**
zero-inflated, [R] **zinb**
nonlinear
least-squares estimation, [R] **nl**
systems of equations, [R] **nlsur**
Poisson regression, [R] **poisson**
truncated, [R] **tpoisson**
zero-inflated, [R] **zip**
probit model
heteroskedastic, [R] **hetprob**
probit regression, [R] **probit**
bivariate, [R] **biprobit**
for grouped data, [R] **glogit**
heteroskedastic, [R] **hetprob**
multinomial, [R] **mprobit**
ordered, [R] **oprobit**
with endogenous regressors, [R] **ivprobit**
with sample selection, [R] **heckprob**
summary statistics,
mean, [R] **mean**
proportion, [R] **proportion**
ratio, [R] **ratio**
total, [R] **total**
cluster estimator of variance, *continued*
tobit model, [R] **tobit**
with endogenous regressors, [R] **ivtobit**
treatment-effects model, [R] **treatreg**
truncated
negative binomial regression, [R] **tnbreg**
Poisson regression, [R] **tpoisson**
regression, [R] **truncreg**
with endogenous regressors,
instrumental-variables regression, [R] **ivregress**
probit model, [R] **ivprobit**
tobit model, [R] **ivtobit**
zero-inflated
negative binomial regression, [R] **zinb**
Poisson regression, [R] **zip**
cluster sampling, [R] **bootstrap**, [R] **bsample**, [R] **jackknife**
`cmdlog`
`close` command, [R] **log**
command, [R] **log**
`off` command, [R] **log**
`on` command, [R] **log**
`using` command, [R] **log**
`cnsreg` command, [R] **cnsreg**, [R] **cnsreg postestimation**
coefficient
alpha, [R] **alpha**
of variation, [R] **tabstat**
coefficients (from estimation),
cataloging, [R] **estimates**
linear combinations of, *see* linear combinations of estimators
nonlinear combinations of, *see* nonlinear combinations of estimators
testing equality of, [R] **test**, [R] **testnl**
collinearity,
display of omitted variables, [R] **set showbaselevels**
handling by `regress`, [R] **regress**
retaining collinear variables, [R] **estimation options**, [R] **orthog**
variance inflation factors, [R] **regress postestimation**
command line, launching dialog box from, [R] **db**
commands, reviewing, [R] **#review**
comparative scatterplot, [R] **dotplot**
complementary log-log regression, [R] **cloglog**, [R] **glm**
completely determined outcomes, [R] **logit**
component-plus-residual plot, [R] **regress postestimation**
conditional
logistic regression, [R] **asclogit**, [R] **clogit**, [R] **rologit**, [R] **slogit**
marginal effects, [R] **margins**, [R] **marginsplot**
margins, [R] **margins**, [R] **marginsplot**
confidence interval, set default, [R] **level**
confidence intervals
for bootstrap statistics, [R] **bootstrap postestimation**, [R] **rocreg**, [R] **rocreg postestimation**

confidence intervals, *continued*
for combinations of coefficients,
linear, [R] **lincom**
nonlinear, [R] **nlcom**
for counts, [R] **ci**
for incidence-rate ratios, [R] **glm**, [R] **nbreg**, [R] **poisson**, [R] **tnbreg**, [R] **tpoisson**, [R] **zinb**, [R] **zip**; [R] **nlcom**
for intragroup correlations, [R] **loneway**
for means, [R] **ci**; [R] **ameans**, [R] **mean**, [R] **ttest**
for medians and percentiles, [R] **centile**
for odds ratios, [R] **glm**, [R] **logistic**, [R] **logit**, [R] **ologit**; [R] **nlcom**
for proportions, [R] **ci**, [R] **proportion**
for ratios, [R] **ratio**
for relative-risk ratios, [R] **mlogit**, [R] **nlcom**
for standardized mortality ratios, [R] **dstdize**
for totals, [R] **total**
conjoint analysis, [R] **rologit**
`conren`, `set` subcommand, [R] **set**
console, controlling scrolling of output, [R] **more**
constrained estimation, [R] **constraint**, [R] **estimation options**
alternative-specific
conditional logistic model, [R] **asclogit**
multinomial probit regression, [R] **asmprobit**
rank-ordered probit regression, [R] **asroprobit**
complementary log-log regression, [R] **cloglog**
generalized linear models, [R] **glm**
for binomial family, [R] **binreg**
generalized negative binomial regression, [R] **nbreg**
heckman selection model, [R] **heckman**
interval regression, [R] **intreg**
linear regression, [R] **cnsreg**
seemingly unrelated, [R] **sureg**
stochastic frontier, [R] **frontier**
three-stage least squares, [R] **reg3**
truncated, [R] **truncreg**
logistic regression, [R] **logistic**, [R] **logit**, *also see* logit regression subentry
conditional, [R] **clogit**
multinomial, [R] **mlogit**
ordered, [R] **ologit**
skewed, [R] **scobit**
stereotype, [R] **slogit**
logit regression, [R] **logit**, *also see* logistic regression subentry
for grouped data, [R] **glogit**
nested, [R] **nlogit**
maximum likelihood estimation, [R] **ml**
multinomial
logistic regression, [R] **mlogit**
probit regression, [R] **mprobit**
negative binomial regression, [R] **nbreg**
truncated, [R] **tnbreg**
zero-inflated, [R] **zinb**
constrained estimation, *continued*
Poisson regression, [R] **poisson**
truncated, [R] **tpoisson**
zero-inflated, [R] **zip**
probit regression, [R] **probit**
bivariate, [R] **biprobit**
for grouped data, [R] **glogit**
heteroskedastic, [R] **hetprob**
multinomial, [R] **mprobit**
ordered, [R] **oprobit**
with endogenous regressors, [R] **ivprobit**
with sample selection, [R] **heckprob**
tobit model with endogenous regressors, [R] **ivtobit**
treatment-effects model, [R] **treatreg**
truncated
negative binomial regression, [R] **tnbreg**
Poisson regression, [R] **tpoisson**
regression, [R] **truncreg**
with endogenous regressors
probit regression, [R] **ivprobit**
tobit model, [R] **ivtobit**
zero-inflated
negative binomial regression, [R] **zinb**
Poisson regression, [R] **zip**
`constraint` command, [R] **constraint**
contingency tables, [R] **roctab**, [R] **symmetry**, [R] **table**, [R] **tabulate twoway**
`contrast` command, [R] **anova postestimation**, [R] **contrast**, [R] **contrast postestimation**, [R] **margins, contrast**
contrasts, [R] **contrast**, [R] **margins, contrast**, [R] **marginsplot**
control charts, [R] **qc**
convergence criteria, [R] **maximize**
Cook–Weisberg test for heteroskedasticity, [R] **regress postestimation**
Cook's D, [R] **glm postestimation**, [R] **regress postestimation**
`copy`, `ssc` subcommand, [R] **ssc**
`copycolor`, `set` subcommand, [R] **set**
copyright
boost, [R] **copyright boost**
freetype, [R] **copyright freetype**
icu, [R] **copyright icu**
JagPDF, [R] **copyright jagpdf**
lapack, [R] **copyright lapack**
libpng, [R] **copyright libpng**
scintilla, [R] **copyright scintilla**
ttf2pt1, [R] **copyright ttf2pt1**
zlib, [R] **copyright zlib**
`copyright` command, [R] **copyright**
`correlate` command, [R] **correlate**
correlated errors, *see* robust, Huber/White/sandwich estimator of variance, *also see* autocorrelation
correlation, [R] **correlate**
binary variables, [R] **tetrachoric**
continuous variables, [R] **correlate**

correlation, *continued*
interitem, [R] **alpha**
intracluster, [R] **loneway**
Kendall's rank, [R] **spearman**
matrices, [R] **correlate**, [R] **estat**
pairwise, [R] **correlate**
partial and semipartial, [R] **pcorr**
serial, [R] **runtest**
Spearman's rank, [R] **spearman**
tetrachoric, [R] **tetrachoric**
`correlation`, `estat` subcommand, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
cost frontier model, [R] **frontier**
count data,
confidence intervals for counts, [R] **ci**
estimation, [R] **expoisson**, [R] **glm**, [R] **gmm**, [R] **nbreg**, [R] **poisson**, [R] **tnbreg**, [R] **tpoisson**, [R] **zinb**, [R] **zip**
graphs, [R] **histogram**, [R] **kdensity**, [R] **spikeplot**
interrater agreement, [R] **kappa**
summary statistics of, [R] **table**, [R] **tabstat**, [R] **tabulate oneway**, [R] **tabulate twoway**, [R] **tabulate, summarize()**
symmetry and marginal homogeneity tests, [R] **symmetry**
`count`, `ml` subcommand, [R] **ml**
covariance
matrix of estimators, [R] **estat**, [R] **estimates store**
of variables or coefficients, [R] **correlate**
covariance, analysis of, [R] **anova**
`covariance`, `estat` subcommand, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
covariate patterns, [R] **logistic postestimation**, [R] **logit postestimation**, [R] **probit postestimation**
COVRATIO, [R] **regress postestimation**
`cprplot` command, [R] **regress postestimation**
Cramér's V, [R] **tabulate twoway**
Cronbach's alpha, [R] **alpha**
crossover designs, [R] **pk**, [R] **pkcross**, [R] **pkshape**
cross-tabulations, *see* tables
`cumul` command, [R] **cumul**
cumulative distribution, empirical, [R] **cumul**
cumulative incidence data, [R] **poisson**
`cusum` command, [R] **cusum**

D

data manipulation, [R] **fvrevar**, [R] **fvset**
data,
autocorrelated, *see* autocorrelation
case–control, *see* case–control data
categorical, *see* categorical data, agreement, measures for
matched case–control, *see* matched case–control data
range of, *see* range of data
ranking, *see* ranking data
sampling, *see* sampling
summarizing, *see* summarizing data
data, *continued*
survival-time, *see* survival analysis
time-series, *see* time-series analysis
Davidon–Fletcher–Powell algorithm, [R] **ml**
`db` command, [R] **db**
default settings of system parameters, [R] **query**, [R] **set_defaults**
`define`, `transmap` subcommand, [R] **translate**
delta beta influence statistic, [R] **clogit postestimation**, [R] **logistic postestimation**, [R] **logit postestimation**
delta chi-squared influence statistic, [R] **clogit postestimation**, [R] **logistic postestimation**, [R] **logit postestimation**
delta deviance influence statistic, [R] **clogit postestimation**, [R] **logistic postestimation**, [R] **logit postestimation**
delta method, [R] **margins**, [R] **nlcom**, [R] **predictnl**, [R] **testnl**
density-distribution sunflower plot, [R] **sunflower**
density estimation, kernel, [R] **kdensity**
derivatives, numeric, [R] **dydx**, [R] **testnl**
`describe`,
`ado` subcommand, [R] **net**
`estimates` subcommand, [R] **estimates describe**
`net` subcommand, [R] **net**
`ssc` subcommand, [R] **ssc**
descriptive statistics, [R] **summarize**
CIs for means, proportions, and counts, [R] **ci**
correlations, [R] **correlate**, [R] **pcorr**, [R] **tetrachoric**
displays, [R] **grmeanby**, [R] **lv**
estimation, [R] **mean**, [R] **proportion**, [R] **ratio**, [R] **total**
means, [R] **ameans**, [R] **summarize**
percentiles, [R] **centile**
pharmacokinetic data,
make dataset of, [R] **pkcollapse**
summarize, [R] **pksumm**
tables, [R] **table**, [R] **tabstat**, [R] **tabulate oneway**, [R] **tabulate twoway**, [R] **tabulate, summarize()**
`design`, `fvset` subcommand, [R] **fvset**
design effects, [R] **loneway**
deviance residual, [R] **binreg postestimation**, [R] **fracpoly postestimation**, [R] **glm postestimation**, [R] **logistic postestimation**, [R] **logit postestimation**, [R] **probit postestimation**
`dfbeta` command, [R] **regress postestimation**
DFBETAs, [R] **regress postestimation**
DFITS, [R] **regress postestimation**
DFP algorithm, [R] **ml**
diagnostic plots, [R] **diagnostic plots**, [R] **logistic postestimation**, [R] **regress postestimation**
diagnostics, regression, [R] **regress postestimation**
dialog box, [R] **db**
dichotomous outcome model, *see* outcomes, binary

difference of estimated coefficients, *see* linear combinations of estimators
`difficult` option, [R] **maximize**
`dir`,
  `ado` subcommand, [R] **net**
  `estimates` subcommand, [R] **estimates store**
direct standardization, [R] **dstdize**, [R] **mean**, [R] **proportion**, [R] **ratio**
dispersion, measures of, *see* percentiles, displaying, *see* range of data, *see* standard deviations, displaying, *see* variance, displaying
display
  settings, [R] **set showbaselevels**
  width and length, [R] **log**
`display` command, as a calculator, [R] **display**
`display`, `ml` subcommand, [R] **ml**
displaying, *also see* printing, logs (output)
  previously typed lines, [R] **#review**
  saved results, [R] **saved results**
distributions,
  examining, [R] **ameans**, [R] **centile**, [R] **kdensity**, [R] **mean**, [R] **pksumm**, [R] **summarize**, [R] **total**
  income, [R] **inequality**
  plots, [R] **cumul**, [R] **cusum**, [R] **diagnostic plots**, [R] **dotplot**, [R] **histogram**, [R] **kdensity**, [R] **ladder**, [R] **lv**, [R] **spikeplot**, [R] **stem**
  standard population, [R] **dstdize**
  testing equality of, [R] **ksmirnov**, [R] **kwallis**, [R] **ranksum**, [R] **signrank**
  testing for normality, [R] **sktest**, [R] **swilk**
  transformations
    to achieve normality, [R] **boxcox**, [R] **ladder**
    to achieve zero skewness, [R] **lnskew0**
`do` command, [R] **do**
`dockable`, `set` subcommand, [R] **set**
`dockingguides`, `set` subcommand, [R] **set**
documentation, keyword search on, [R] **search**
`doedit` command, [R] **doedit**
do-files, [R] **do**
  editing, [R] **doedit**
domain sampling, [R] **alpha**
dose–response models, [R] **binreg**, [R] **glm**, [R] **logistic**
`dotplot` command, [R] **dotplot**
`doublebuffer`, `set` subcommand, [R] **set**
`dp`, `set` subcommand, [R] **set**
`drop`, `estimates` subcommand, [R] **estimates store**
`dstdize` command, [R] **dstdize**
dummy variables, *see* indicator variables
Duncan's multiple-comparison adjustment, *see* multiple comparisons, Duncan's method
Dunnett's multiple-comparison adjustment, *see* multiple comparisons, Dunnett's method
Durbin–Watson statistic, [R] **regress postestimation time series**
`durbinalt`, `estat` subcommand, [R] **regress postestimation time series**
Durbin's alternative test, [R] **regress postestimation time series**
`dwatson`, `estat` subcommand, [R] **regress postestimation time series**
`dydx` command, [R] **dydx**

E

`e()` scalars, macros, matrices, functions, [R] **saved results**
`e(sample)`, resetting, [R] **estimates save**
e-class command, [R] **saved results**
editing
  ado-files and do-files, [R] **doedit**
  files while in Stata, [R] **doedit**
eform_option, [R] ***eform_option***
`eivreg` command, [R] **eivreg**, [R] **eivreg postestimation**
empirical cumulative distribution function, [R] **cumul**
`emptycells`, `set` subcommand, [R] **set**, [R] **set emptycells**
ending a Stata session, [R] **exit**
endless loop, *see* loop, endless
endogeneity test, [R] **ivregress postestimation**
endogenous
  covariates, [R] **gmm**, [R] **ivprobit**, [R] **ivregress**, [R] **ivtobit**, [R] **reg3**
  treatment, [R] **treatreg**
`endogenous`, `estat` subcommand, [R] **ivregress postestimation**
Engle's LM test, [R] **regress postestimation time series**
`eolchar`, `set` subcommand, [R] **set**
Epanechnikov kernel density function, [R] **kdensity**
epidemiology and related,
  Brier score decomposition, [R] **brier**
  interrater agreement, [R] **kappa**
  pharmacokinetic data, *see* pk (pharmacokinetic data)
  ROC analysis, *see* ROC analysis
  standardization, [R] **dstdize**
  symmetry and marginal homogeneity tests, [R] **symmetry**
  tables, [R] **tabulate twoway**
equality tests of
  binomial proportions, [R] **bitest**
  coefficients, [R] **pwcompare**, [R] **test**, [R] **testnl**
  distributions, [R] **ksmirnov**, [R] **kwallis**, [R] **ranksum**, [R] **signrank**
  margins, [R] **margins**, [R] **pwcompare**
  means, [R] **contrast**, [R] **pwmean**, [R] **sampsi**, [R] **ttest**
  medians, [R] **ranksum**
  proportions, [R] **bitest**, [R] **prtest**, [R] **sampsi**
  ROC areas, [R] **roccomp**, [R] **rocreg**
  variances, [R] **sdtest**
equivalence tests, [R] **pk**, [R] **pkequiv**
`ereturn list` command, [R] **saved results**
error-bar charts, [R] **serrbar**

error messages and return codes, [R] **error messages**
searching, [R] **search**
errors-in-variables regression, [R] **eivreg**
`esample`, `estimates` subcommand, [R] **estimates save**
`estat`
`alternatives` command, [R] **asclogit postestimation**, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
`archlm` command, [R] **regress postestimation time series**
`bgodfrey` command, [R] **regress postestimation time series**
`bootstrap` command, [R] **bootstrap postestimation**
`classification` command, [R] **logistic postestimation**
`correlation` command, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
`covariance` command, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
`durbinalt` command, [R] **regress postestimation time series**
`dwatson` command, [R] **regress postestimation time series**
`endogenous` command, [R] **ivregress postestimation**
`facweights` command, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
`firststage` command, [R] **ivregress postestimation**
`gof` command, [R] **logistic postestimation**, [R] **poisson postestimation**
`hettest` command, [R] **regress postestimation**
`ic` command, [R] **estat**
`imtest` command, [R] **regress postestimation**
`mfx` command, [R] **asclogit postestimation**, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
`nproc` command, [R] **rocreg postestimation**
`overid` command, [R] **gmm postestimation**, [R] **ivregress postestimation**
`ovtest` command, [R] **regress postestimation**
`predict` command, [R] **exlogistic postestimation**
`se` command, [R] **exlogistic postestimation**, [R] **expoisson postestimation**
`summarize` command, [R] **estat**
`szroeter` command, [R] **regress postestimation**
`vce` command, [R] **estat**
`vif` command, [R] **regress postestimation**
`estimates`
`clear` command, [R] **estimates store**
command, [R] **suest**
introduction, [R] **estimates**
`describe` command, [R] **estimates describe**
`dir` command, [R] **estimates store**
`drop` command, [R] **estimates store**
`esample` command, [R] **estimates save**
`for` command, [R] **estimates for**
`notes` command, [R] **estimates notes**
`estimates`, *continued*
`query` command, [R] **estimates store**
`replay` command, [R] **estimates replay**
`restore` command, [R] **estimates store**
`save` command, [R] **estimates save**
`stats` command, [R] **estimates stats**
`store` command, [R] **estimates store**
`table` command, [R] **estimates table**
`title` command, [R] **estimates title**
`use` command, [R] **estimates save**
estimation
options, [R] **estimation options**
results,
clearing, [R] **estimates store**
storing and restoring, [R] **estimates store**
tables of, [R] **estimates table**
sample, summarizing, [R] **estat**
estimators,
covariance matrix of, [R] **correlate**, [R] **estat**
linear combinations of, [R] **lincom**
nonlinear combinations of, [R] **nlcom**
exact statistics,
binary confidence intervals, [R] **ci**, [R] **exlogistic**, [R] **roctab**
centiles, [R] **centile**
indirect standardization, [R] **dstdize**
one-way anova, [R] **oneway**
regression, [R] **exlogistic**, [R] **expoisson**
test,
binomial probability, [R] **bitest**
equality of distributions, [R] **ksmirnov**
equality of medians, [R] **ranksum**
Fisher's, [R] **tabulate twoway**
symmetry and marginal homogeneity, [R] **symmetry**
tetrachoric correlations, [R] **tetrachoric**
`exit` command, [R] **exit**
exiting Stata, *see* `exit` command
`exlogistic` command, [R] **exlogistic**, [R] **exlogistic postestimation**
exogeneity test, *see* endogeneity test
exploded logit model, [R] **rologit**
`expoisson` command, [R] **expoisson**, [R] **expoisson postestimation**
exponentiated coefficients, [R] ***eform_option***

F

factor
analysis, [R] **alpha**
variables, [R] **fvrevar**, [R] **fvset**
factor-variable settings, [R] **fvset**
factorial design, [R] **anova**
`facweights`, `estat` subcommand, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
failure-time models, *also see* survival analysis
FAQs, search, [R] **search**
`fastscroll`, `set` subcommand, [R] **set**

feasible generalized least squares, *see* FGLS
fences, [R] **lv**
FGLS (feasible generalized least squares), [R] **reg3**
files, downloading, [R] **adoupdate**, [R] **net**, [R] **sj**, [R] **ssc**, [R] **update**
`findit` command, [R] **search**
`firststage`, `estat` subcommand, [R] **ivregress postestimation**
Fisher's exact test, [R] **tabulate twoway**
fixed-effects models, [R] **anova**, [R] **areg**, [R] **asclogit**, [R] **clogit**
flexible functional form, [R] **boxcox**, [R] **fracpoly**, [R] **mfp**
`floatresults`, `set` subcommand, [R] **set**
`floatwindows`, `set` subcommand, [R] **set**
`footnote`, `ml` subcommand, [R] **ml**
`for`, `estimates` subcommand, [R] **estimates for**
forecast, standard error of, [R] **regress postestimation**
format settings, [R] **set cformat**
`fracgen` command, [R] **fracpoly**
`fracplot` command, [R] **fracpoly postestimation**
`fracpoly` prefix command, [R] **fracpoly**, [R] **fracpoly postestimation**
`fracpred` command, [R] **fracpoly postestimation**
fraction defective, [R] **qc**
fractional polynomial regression, [R] **fracpoly**
  multivariable, [R] **mfp**
frequencies,
  graphical representation, [R] **histogram**, [R] **kdensity**
  table of, [R] **table**, [R] **tabstat**, [R] **tabulate oneway**, [R] **tabulate twoway**, [R] **tabulate, summarize()**
`from`,
  `net` subcommand, [R] **net**
  `update` subcommand, [R] **update**
`from()` option, [R] **maximize**
`frontier` command, [R] **frontier**, [R] **frontier postestimation**
frontier models, [R] **frontier**
functions,
  combinations of estimators, [R] **lincom**, [R] **nlcom**
  cumulative distribution, [R] **cumul**
  derivatives and integrals of, [R] **dydx**
  estimable, [R] **margins**
  evaluator program, [R] **gmm**, [R] **nl**, [R] **nlsur**
  fractional polynomial, [R] **fracpoly**, [R] **mfp**
  index, [R] **logistic postestimation**, [R] **logit postestimation**, [R] **probit postestimation**
  kernel, [R] **kdensity**, [R] **lpoly**
  link, [R] **glm**
  maximizing likelihood, [R] **maximize**, [R] **ml**
  obtaining help for, [R] **help**
  orthogonalization, [R] **orthog**
  piecewise cubic and piecewise linear, [R] **mkspline**
  prediction, [R] **predict**, [R] **predictnl**
  production and cost, [R] **frontier**
  variance, [R] **glm**
`fvrevar` command, [R] **fvrevar**
`fvset`
  `base` command, [R] **fvset**
  `clear` command, [R] **fvset**
  `design` command, [R] **fvset**
  `report` command, [R] **fvset**

G

generalized
  least squares, *see* FGLS
  linear latent and mixed models, *see* GLLAMM
  linear models, *see* GLM
  method of moments, *see* `gmm` command
  negative binomial regression, [R] **nbreg**
`get`, `net` subcommand, [R] **net**
`gladder` command, [R] **ladder**
GLLAMM, [R] **gllamm**
`gllamm` command, [R] **gllamm**
GLM, [R] **binreg**, [R] **glm**
`glm` command, [R] **glm**, [R] **glm postestimation**
`glogit` command, [R] **glogit**, [R] **glogit postestimation**
`gmm` command, [R] **gmm**, [R] **gmm postestimation**
`gnbreg` command, [R] **nbreg**, [R] **nbreg postestimation**
`gof`, `estat` subcommand, [R] **logistic postestimation**, [R] **poisson postestimation**
Goodman and Kruskal's gamma, [R] **tabulate twoway**
goodness-of-fit tests, [R] **brier**, [R] **diagnostic plots**, [R] **ksmirnov**, [R] **logistic postestimation**, [R] **poisson postestimation**, [R] **regress postestimation**, *also see* deviance residual, *also see* normal distribution and normality, test for
`gprobit` command, [R] **glogit**, [R] **glogit postestimation**
`gradient` option, [R] **maximize**
`graph`, `ml` subcommand, [R] **ml**
`graphics`, `set` subcommand, [R] **set**
graphs,
  added-variable plot, [R] **regress postestimation**
  adjusted partial residual plot, [R] **regress postestimation**
  augmented component-plus-residual plot, [R] **regress postestimation**
  augmented partial residual plot, [R] **regress postestimation**
  binary variable cumulative sum, [R] **cusum**
  component-plus-residual, [R] **regress postestimation**
  cumulative distribution, [R] **cumul**
  density, [R] **kdensity**
  density-distribution sunflower, [R] **sunflower**
  derivatives, [R] **dydx**, [R] **testnl**
  diagnostic, [R] **diagnostic plots**
  dotplot, [R] **dotplot**
  error-bar charts, [R] **serrbar**
  fractional polynomial, [R] **fracpoly postestimation**
  histograms, [R] **histogram**, [R] **kdensity**
  integrals, [R] **dydx**

graphs, *continued*
interaction plots, [R] **marginsplot**
ladder-of-power histograms, [R] **ladder**
letter-value display, [R] **lv**
leverage-versus-(squared)-residual, [R] **regress postestimation**
logistic diagnostic, [R] **logistic postestimation**
lowess smoothing, [R] **lowess**
margins plots, [R] **marginsplot**
means and medians, [R] **grmeanby**
normal probability, [R] **diagnostic plots**
partial-regression leverage, [R] **regress postestimation**
partial residual, [R] **regress postestimation**
profile plots, [R] **marginsplot**
quality control, [R] **qc**
quantile, [R] **diagnostic plots**
quantile–normal, [R] **diagnostic plots**
quantile–quantile, [R] **diagnostic plots**
regression diagnostic, [R] **regress postestimation**
residual versus fitted, [R] **regress postestimation**
residual versus predictor, [R] **regress postestimation**
ROC curve, [R] **logistic postestimation**, [R] **roccomp**, [R] **rocfit postestimation**, [R] **rocregplot**, [R] **roctab**
rootograms, [R] **spikeplot**
smoothing, [R] **kdensity**, [R] **lowess**, [R] **lpoly**
spike plot, [R] **spikeplot**
stem-and-leaf, [R] **stem**
sunflower, [R] **sunflower**
symmetry, [R] **diagnostic plots**
time-versus-concentration curve, [R] **pk**, [R] **pkexamine**
Greenhouse–Geisser epsilon, [R] **anova**
`grmeanby` command, [R] **grmeanby**
group-data regression, [R] **glogit**, [R] **intreg**

H

HAC variance estimate, [R] **binreg**, [R] **glm**, [R] **gmm**, [R] **ivregress**, [R] **nl**
Hansen's *J* statistic, [R] **gmm**, [R] **gmm postestimation**, [R] **ivregress**
harmonic mean, [R] **ameans**
hat matrix, *see* projection matrix, diagonal elements of
`hausman` command, [R] **hausman**
Hausman specification test, [R] **hausman**
health ratios, [R] **binreg**
`heckman` command, [R] **heckman**, [R] **heckman postestimation**
Heckman selection model, [R] **heckman**, [R] **heckprob**
`heckprob` command, [R] **heckprob**, [R] **heckprob postestimation**
Helmert contrasts, [R] **contrast**
`help` command, [R] **help**
help file search, [R] **hsearch**
help system, searching, [R] **hsearch**
`help`, `view` subcommand, [R] **view**
`help_d`, `view` subcommand, [R] **view**
`hessian` option, [R] **maximize**
heteroskedastic probit regression, [R] **hetprob**
heteroskedasticity, *also see* HAC variance estimate
conditional, [R] **regress postestimation time series**
robust variances, *see* robust, Huber/White/sandwich estimator of variance
test for, [R] **hetprob**, [R] **regress postestimation**, [R] **regress postestimation time series**
`hetprob` command, [R] **hetprob**, [R] **hetprob postestimation**
`hettest`, `estat` subcommand, [R] **regress postestimation**
hierarchical
regression, [R] **nestreg**, [R] **stepwise**
samples, [R] **anova**, [R] **gllamm**, [R] **loneway**; [R] **areg**
`histogram` command, [R] **histogram**
histograms, [R] **histogram**
dotplots, [R] **dotplot**
kernel density estimator, [R] **kdensity**
ladder-of-powers, [R] **ladder**
of categorical variables, [R] **histogram**
rootograms, [R] **spikeplot**
stem-and-leaf, [R] **stem**
Holm's multiple-comparison adjustment, *see* multiple comparisons, Holm's method
homogeneity of variances, [R] **oneway**, [R] **sdtest**
homoskedasticity tests, [R] **regress postestimation**
Hosmer and Lemeshow
delta chi-squared influence statistic, *see* delta chi-squared influence statistic
delta deviance influence statistic, *see* delta deviance influence statistic
goodness-of-fit test, [R] **logistic postestimation**
`hot`, `ssc` subcommand, [R] **ssc**
`hsearch` command, [R] **hsearch**
`httpproxy`, `set` subcommand, [R] **netio**, [R] **set**
`httpproxyauth`, `set` subcommand, [R] **netio**, [R] **set**
`httpproxyhost`, `set` subcommand, [R] **netio**, [R] **set**
`httpproxyport`, `set` subcommand, [R] **netio**, [R] **set**
`httpproxypw`, `set` subcommand, [R] **netio**, [R] **set**
`httpproxyuser`, `set` subcommand, [R] **netio**, [R] **set**
Huber weighting, [R] **rreg**
Huber/White/sandwich estimator of variance, *see* robust, Huber/White/sandwich estimator of variance
Huynh–Feldt epsilon, [R] **anova**
hypertext help, [R] **help**
hypothesis tests, *see* tests

I

`ic`, `estat` subcommand, [R] **estat**
IIA,
assumption, [R] **clogit**, [R] **nlogit**
relaxing assumption, [R] **asclogit**, [R] **asmprobit**, [R] **asroprobit**
test for, [R] **hausman**, [R] **suest**

immediate commands, [R] **bitest**, [R] **ci**, [R] **prtest**, [R] **sampsi**, [R] **sdtest**, [R] **symmetry**, [R] **tabulate twoway**, [R] **ttest**
`imtest`, `estat` subcommand, [R] **regress postestimation**
incidence-rate ratio, [R] **poisson**, [R] **zip**
  differences, [R] **lincom**, [R] **nlcom**
`include_bitmap`, `set` subcommand, [R] **set**
income distributions, [R] **inequality**
independence of irrelevant alternatives, *see* IIA
independence tests, *see* tests
index of probit and logit, [R] **logit postestimation**, [R] **predict**, [R] **probit postestimation**
index search, [R] **search**
indicator variables, [R] **tabulate oneway**, [R] **xi**, *also see* factor variables
indirect standardization, [R] **dstdize**
inequality measures, [R] **inequality**
influence statistics, *see* delta beta influence statistic, *see* delta chi-squared influence statistic, *see* delta deviance influence statistic, *see* DFBETAs
information
  criteria, *see* AIC, *see* BIC
  matrix, [R] **correlate**, [R] **maximize**
  matrix test, [R] **regress postestimation**
`init`, `ml` subcommand, [R] **ml**
inner fence, [R] **lv**
`install`,
  `net` subcommand, [R] **net**
  `ssc` subcommand, [R] **ssc**
installation
  of official updates, [R] **update**
  of SJ and STB, [R] **net**, [R] **sj**
  of user-written commands (updating), [R] **adoupdate**
instrumental-variables regression, [R] **gmm**, [R] **ivprobit**, [R] **ivregress**, [R] **ivtobit**, [R] **nlsur**
`integ` command, [R] **dydx**
integrals, numeric, [R] **dydx**
interaction, [R] **anova**, [R] **contrast**, [R] **fvrevar**, [R] **margins**, [R] **margins, contrast**, [R] **margins, pwcompare**, [R] **marginsplot**, [R] **pwcompare**, [R] **set emptycells**, [R] **xi**
interaction expansion, [R] **xi**
interaction plots, [R] **marginsplot**
internal consistency, test for, [R] **alpha**
Internet,
  commands to control connections to, [R] **netio**
  installation of updates from, [R] **adoupdate**, [R] **net**, [R] **sj**, [R] **update**
  search, [R] **net search**
interquantile range, [R] **qreg**
interquartile range, [R] **lv**
  reporting, [R] **table**, [R] **tabstat**
interrater agreement, [R] **kappa**
interval regression, [R] **intreg**
intracluster correlation, [R] **loneway**
`intreg` command, [R] **intreg**, [R] **intreg postestimation**
IQR, *see* interquartile range
`iqreg` command, [R] **qreg**, [R] **qreg postestimation**
IRLS, [R] **glm**, [R] **reg3**
`istdize` command, [R] **dstdize**
`iterate()` option, [R] **maximize**
iterated least squares, [R] **reg3**, [R] **sureg**
iterations, controlling the maximum number, [R] **maximize**
`ivprobit` command, [R] **ivprobit**, [R] **ivprobit postestimation**
`ivregress` command, [R] **ivregress**, [R] **ivregress postestimation**
`ivtobit` command, [R] **ivtobit**, [R] **ivtobit postestimation**

J

jackknife
  estimation, [R] **jackknife**
  standard errors, [R] ***vce_option***
`jackknife` prefix command, [R] **jackknife**, [R] **jackknife postestimation**
jackknifed residuals, [R] **predict**, [R] **regress postestimation**

K

`kap` command, [R] **kappa**
`kappa` command, [R] **kappa**
`kapwgt` command, [R] **kappa**
`kdensity` command, [R] **kdensity**
Kendall's tau, [R] **spearman**, [R] **tabulate twoway**
kernel density estimator, [R] **kdensity**
kernel-weighted local polynomial estimator, [R] **lpoly**
Kish design effects, [R] **loneway**
Kolmogorov–Smirnov test, [R] **ksmirnov**
KR-20, [R] **alpha**
Kruskal–Wallis test, [R] **kwallis**
`ksmirnov` command, [R] **ksmirnov**
`ktau` command, [R] **spearman**
Kuder–Richardson Formula 20, [R] **alpha**
kurtosis, [R] **lv**, [R] **pksumm**, [R] **regress postestimation**, [R] **sktest**, [R] **summarize**, [R] **tabstat**
`kwallis` command, [R] **kwallis**

L

L-R plots, [R] **regress postestimation**
L1-norm models, [R] **qreg**
LAD regression, [R] **qreg**
`ladder` command, [R] **ladder**
ladder of powers, [R] **ladder**
Lagrange-multiplier test, [R] **regress postestimation time series**
Latin-square designs, [R] **anova**, [R] **pkshape**
LAV regression, [R] **qreg**

least absolute
deviations, [R] **qreg**
residuals, [R] **qreg**
value regression, [R] **qreg**
least squared deviations, *see* linear regression
least squares, *see* linear regression
generalized, *see* FGLS
least-squares means, [R] **margins**, [R] **marginsplot**
letter values, [R] **lv**
`level`, `set` subcommand, [R] **level**, [R] **set**
Levene's robust test statistic, [R] **sdtest**
leverage, [R] **logistic postestimation**, [R] **predict**, [R] **regress postestimation**
obtaining with weighted data, [R] **predict**
leverage-versus-(squared)-residual plot, [R] **regress postestimation**
license, [R] **about**
likelihood, *see* maximum likelihood estimation
likelihood-ratio
chi-squared of association, [R] **tabulate twoway**
test, [R] **lrtest**
Likert summative scales, [R] **alpha**
limited dependent variables, [R] **asclogit**, [R] **asmprobit**, [R] **asroprobit**, [R] **binreg**, [R] **biprobit**, [R] **brier**, [R] **clogit**, [R] **cloglog**, [R] **cusum**, [R] **exlogistic**, [R] **expoisson**, [R] **glm**, [R] **glogit**, [R] **heckprob**, [R] **hetprob**, [R] **ivprobit**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **mprobit**, [R] **nbreg**, [R] **nlogit**, [R] **ologit**, [R] **oprobit**, [R] **poisson**, [R] **probit**, [R] **rocfit**, [R] **rocreg**, [R] **rologit**, [R] **scobit**, [R] **slogit**, [R] **tnbreg**, [R] **tpoisson**, [R] **zinb**, [R] **zip**
limits, [R] **matsize**
`lincom` command, [R] **lincom**
linear
combinations of estimators, [R] **lincom**
hypothesis test after estimation, [R] **contrast**, [R] **lrtest**, [R] **margins**, [R] **pwcompare**, [R] **test**
regression, [R] **anova**, [R] **areg**, [R] **binreg**, [R] **cnsreg**, [R] **eivreg**, [R] **frontier**, [R] **glm**, [R] **gmm**, [R] **heckman**, [R] **intreg**, [R] **ivregress**, [R] **ivtobit**, [R] **mvreg**, [R] **qreg**, [R] **reg3**, [R] **regress**, [R] **rreg**, [R] **sureg**, [R] **tobit**, [R] **vwls**
splines, [R] **mkspline**
`linegap`, `set` subcommand, [R] **set**
`linesize`, `set` subcommand, [R] **log**, [R] **set**
link function, [R] **glm**
`link`, `net` subcommand, [R] **net**
`linktest` command, [R] **linktest**
`list`,
`ereturn` subcommand, [R] **saved results**
`return` subcommand, [R] **saved results**
`sreturn` subcommand, [R] **saved results**
`lnskew0` command, [R] **lnskew0**
local linear, [R] **lpoly**
local polynomial, [R] **lpoly**
locally weighted smoothing, [R] **lowess**
location, measures of, [R] **lv**, [R] **summarize**, [R] **table**
`locksplitters`, `set` subcommand, [R] **set**
`log`
`close` command, [R] **log**
command, [R] **log**, [R] **view**
`off` command, [R] **log**
`on` command, [R] **log**
`query` command, [R] **log**
`using` command, [R] **log**
log files, printing, [R] **translate**, *also see* `log` command
log-linear model, [R] **glm**, [R] **poisson**, [R] **zip**
`log` or `nolog` option, [R] **maximize**
log transformations, [R] **boxcox**, [R] **lnskew0**
logistic and logit regression, [R] **logistic**, [R] **logit**
complementary log-log, [R] **cloglog**
conditional, [R] **asclogit**, [R] **clogit**, [R] **rologit**
exact, [R] **exlogistic**
fixed-effects, [R] **asclogit**, [R] **clogit**
generalized linear model, [R] **glm**
multinomial, [R] **asclogit**, [R] **clogit**, [R] **mlogit**
nested, [R] **nlogit**
ordered, [R] **ologit**
polytomous, [R] **mlogit**
rank-ordered, [R] **rologit**
skewed, [R] **scobit**
stereotype, [R] **slogit**
with grouped data, [R] **glogit**
`logistic` command, [R] **logistic**, [R] **logistic postestimation**
`logit` command, [R] **logit**, [R] **logit postestimation**
logit regression, *see* logistic and logit regression
lognormal distribution, [R] **ameans**
`logtype`, `set` subcommand, [R] **log**, [R] **set**
`loneway` command, [R] **loneway**
loop, endless, *see* endless loop
Lorenz curve, [R] **inequality**
lowess, *see* locally weighted smoothing
`lowess` command, [R] **lowess**
`lpoly` command, [R] **lpoly**
`lroc` command, [R] **logistic postestimation**
`lrtest` command, [R] **lrtest**
`lsens` command, [R] **logistic postestimation**
`lstat` command, *see* `estat classification` command
`lstretch`, `set` subcommand, [R] **set**
`ltolerance()` option, [R] **maximize**
`lv` command, [R] **lv**
`lvr2plot` command, [R] **regress postestimation**

M

MAD regression, [R] **qreg**
main effects, [R] **anova**
`man` command, [R] **help**
Mann–Whitney two-sample statistics, [R] **ranksum**

marginal
  effects, [R] **margins**, [R] **marginsplot**
  homogeneity, test of, [R] **symmetry**
  means, [R] **contrast**, [R] **margins**, [R] **margins, contrast**, [R] **margins, pwcompare**, [R] **marginsplot**, [R] **pwcompare**
`margins` command, [R] **margins**, [R] **margins postestimation**, [R] **margins, contrast**, [R] **margins, pwcompare**, [R] **marginsplot**
`marginsplot` command, [R] **marginsplot**
`matacache`, `set` subcommand, [R] **set**
`matafavor`, `set` subcommand, [R] **set**
`matalibs`, `set` subcommand, [R] **set**
`matalnum`, `set` subcommand, [R] **set**
`matamofirst`, `set` subcommand, [R] **set**
`mataoptimize`, `set` subcommand, [R] **set**
`matastrict`, `set` subcommand, [R] **set**
matched case–control data, [R] **asclogit**, [R] **clogit**, [R] **symmetry**
matched-pairs tests, [R] **signrank**, [R] **ttest**
`matsize`, `set` subcommand, [R] **matsize**, [R] **set**
`max_memory`, `set` subcommand, [R] **set**
`maxdb`, `set` subcommand, [R] **db**, [R] **set**
maximization technique explained, [R] **maximize**, [R] **ml**
`maximize`, `ml` subcommand, [R] **ml**
maximum
  likelihood estimation, [R] **maximize**, [R] **ml**
  number of variables in a model, [R] **matsize**
maximums and minimums, reporting, [R] **lv**, [R] **summarize**, [R] **table**
`maxiter`, `set` subcommand, [R] **maximize**, [R] **set**
`maxvar`, `set` subcommand, [R] **set**
McFadden's choice model, [R] **asclogit**
McNemar's chi-squared test, [R] **clogit**
`mean` command, [R] **mean**, [R] **mean postestimation**
means,
  arithmetic, geometric, and harmonic, [R] **ameans**
  confidence interval and standard error, [R] **ci**
  displaying, [R] **ameans**, [R] **summarize**, [R] **table**, [R] **tabstat**, [R] **tabulate, summarize()**
  estimating, [R] **mean**
  graphing, [R] **grmeanby**
  marginal, [R] **margins**
  pairwise comparisons of, [R] **pwmean**
  pharmacokinetic data, [R] **pksumm**
  robust, [R] **rreg**
  sample size and power for, [R] **sampsi**
  testing equality of, *see* equality tests of means
measurement error, [R] **alpha**, [R] **vwls**
measures of
  association, [R] **tabulate twoway**
  central tendency, *see* means, *see* medians
  dispersion, *see* percentiles, displaying, *see* range of data, *see* standard deviations, displaying, *see* variance, displaying,
  inequality, [R] **inequality**
  location, [R] **lv**, [R] **summarize**
`median` command, [R] **ranksum**
median regression, [R] **qreg**
median test, [R] **ranksum**
medians,
  displaying, [R] **centile**, [R] **lv**, [R] **summarize**, [R] **table**, [R] **tabstat**
  graphing, [R] **grmeanby**
  testing equality of, *see* equality tests of medians
memory, matsize, *see* `matsize`, `set` subcommand
messages and return codes, *see* error messages and return codes
meta-analysis, [R] **meta**
`mfp` prefix command, [R] **mfp**, [R] **mfp postestimation**
`mfx`, `estat` subcommand, [R] **asclogit postestimation**, [R] **asmprobit postestimation**, [R] **asroprobit postestimation**
midsummaries, [R] **lv**
mild outliers, [R] **lv**
Mills' ratio, [R] **heckman**, [R] **heckman postestimation**
`min_memory`, `set` subcommand, [R] **set**
minimum
  absolute deviations, [R] **qreg**
  squared deviations, [R] **areg**, [R] **cnsreg**, [R] **nl**, [R] **regress**, [R] **regress postestimation**
minimums and maximums, *see* maximums and minimums, reporting
missing values, [R] **misstable**
`misstable`
  `nested` command, [R] **misstable**
  `patterns` command, [R] **misstable**
  `summarize` command, [R] **misstable**
  `tree` command, [R] **misstable**
mixed designs, [R] **anova**
`mkspline` command, [R] **mkspline**
`ml`
  `check` command, [R] **ml**
  `clear` command, [R] **ml**
  `count` command, [R] **ml**
  `display` command, [R] **ml**
  `footnote` command, [R] **ml**
  `graph` command, [R] **ml**
  `init` command, [R] **ml**
  `maximize` command, [R] **ml**
  `model` command, [R] **ml**
  `plot` command, [R] **ml**
  `query` command, [R] **ml**
  `report` command, [R] **ml**
  `score` command, [R] **ml**
  `search` command, [R] **ml**
  `trace` command, [R] **ml**
`mleval` command, [R] **ml**
`mlmatbysum` command, [R] **ml**
`mlmatsum` command, [R] **ml**
`mlogit` command, [R] **mlogit**, [R] **mlogit postestimation**
`mlsum` command, [R] **ml**

mlvecsum command, [R] **ml**
MNP, *see* outcomes, multinomial
model, ml subcommand, [R] **ml**
model specification test, *see* specification test
model,
  maximum number of variables in, [R] **matsize**
  sensitivity, [R] **regress postestimation**, [R] **rreg**
modulus transformations, [R] **boxcox**
monotone missing values, [R] **misstable**
Monte Carlo simulations, [R] **permute**, [R] **simulate**
more command and parameter, [R] **more**
more condition, [R] **query**
more, set subcommand, [R] **more**, [R] **set**
mprobit command, [R] **mprobit**, [R] **mprobit postestimation**
multilevel models, [R] **gllamm**
multinomial outcome model, *see* outcomes, multinomial
multiple comparisons, [R] **contrast**, [R] **margins**, [R] **pwcompare**, [R] **pwmean**; [R] **anova postestimation**, [R] **correlate**, [R] **mvreg**, [R] **oneway**, [R] **regress postestimation**, [R] **roccomp**, [R] **spearman**, [R] **test**, [R] **testnl**, [R] **tetrachoric**
  Bonferroni's method, [R] **contrast**, [R] **margins**, [R] **pwcompare**, [R] **pwmean**; [R] **anova postestimation**, [R] **correlate**, [R] **oneway**, [R] **regress postestimation**, [R] **roccomp**, [R] **spearman**, [R] **test**, [R] **testnl**, [R] **tetrachoric**
  Duncan's method, [R] **pwcompare**, [R] **pwmean**
  Dunnett's method, [R] **pwcompare**, [R] **pwmean**
  Holm's method, [R] **anova postestimation**, [R] **regress postestimation**, [R] **test**, [R] **testnl**
  multiple-range method, *see* Dunnett's method subentry
  Scheffé's method, [R] **contrast**, [R] **margins**, [R] **pwcompare**, [R] **pwmean**; [R] **oneway**
  Šidák's method, [R] **contrast**, [R] **margins**, [R] **pwcompare**, [R] **pwmean**; [R] **anova postestimation**, [R] **correlate**, [R] **oneway**, [R] **regress postestimation**, [R] **roccomp**, [R] **spearman**, [R] **test**, [R] **testnl**, [R] **tetrachoric**
  Studentized-range method, *see* Tukey's method subentry
  Student–Newman–Keuls' method, [R] **pwcompare**, [R] **pwmean**
  Tukey's method, [R] **pwcompare**, [R] **pwmean**
multiple regression, *see* linear regression
multiple-range multiple-comparison adjustment, *see* multiple comparisons, Dunnett's method
multivariable fractional polynomial regression, [R] **mfp**
multivariate analysis,
  bivariate probit, [R] **biprobit**
  regression, [R] **mvreg**
  three-stage least squares, [R] **reg3**
  Zellner's seemingly unrelated, [R] **nlsur**, [R] **sureg**
mvreg command, [R] **mvreg**, [R] **mvreg postestimation**

N

natural splines, [R] **mkspline**
nbreg command, [R] **nbreg**, [R] **nbreg postestimation**
needle plot, [R] **spikeplot**
negative binomial regression, [R] **nbreg**
  generalized linear models, [R] **glm**
  truncated, [R] **tnbreg**
  zero-inflated, [R] **zinb**
nested
  designs, [R] **anova**
  effects, [R] **anova**
  logit, [R] **nlogit**
  model statistics, [R] **nestreg**
  regression, [R] **nestreg**
nested, misstable subcommand, [R] **misstable**
nestreg prefix command, [R] **nestreg**
net
  cd command, [R] **net**
  describe command, [R] **net**
  from command, [R] **net**
  get command, [R] **net**
  install command, [R] **net**
  link command, [R] **net**
  query command, [R] **net**
  search command, [R] **net search**
  set ado command, [R] **net**
  set other command, [R] **net**
  sj command, [R] **net**
  stb command, [R] **net**
net, view subcommand, [R] **view**
net_d, view subcommand, [R] **view**
new, ssc subcommand, [R] **ssc**
Newey–West standard errors, [R] **glm**
news command, [R] **news**
news, view subcommand, [R] **view**
Newton–Raphson algorithm, [R] **ml**
niceness, set subcommand, [R] **set**
nl command, [R] **nl**, [R] **nl postestimation**
nlcom command, [R] **nlcom**
nlogit command, [R] **nlogit**, [R] **nlogit postestimation**
nlogitgen command, [R] **nlogit**
nlogittree command, [R] **nlogit**
nlsur command, [R] **nlsur**, [R] **nlsur postestimation**
nolog or log option, [R] **maximize**
nonconformities, quality control, [R] **qc**
nonconstant variance, *see* robust, Huber/White/sandwich estimator of variance
nonlinear
  combinations of estimators, [R] **nlcom**
  hypothesis test after estimation, [R] **lrtest**, [R] **margins**, [R] **margins, contrast**, [R] **margins, pwcompare**, [R] **nlcom**, [R] **predictnl**, [R] **testnl**
  least squares, [R] **nl**
  regression, [R] **boxcox**, [R] **nl**, [R] **nlsur**

nonparametric analysis,
hypothesis tests,
association, [R] **spearman**
cusum, [R] **cusum**
equality of distributions, [R] **ksmirnov**, [R] **kwallis**, [R] **ranksum**, [R] **signrank**
medians, [R] **ranksum**
proportions, [R] **bitest**, [R] **prtest**
random order, [R] **runtest**
trend, [R] **nptrend**
percentiles, [R] **centile**
quantile regression, [R] **qreg**
ROC analysis, [R] **roc**
estimation, [R] **rocreg**
graphs, [R] **rocregplot**
test equality of areas, [R] **roccomp**
without covariates, [R] **roctab**
smoothing, [R] **kdensity**, [R] **lowess**, [R] **lpoly**, [R] **smooth**
tables, [R] **tabulate twoway**
`nonrtolerance` option, [R] **maximize**
normal distribution and normality,
examining distributions for, [R] **diagnostic plots**, [R] **lv**
probability and quantile plots, [R] **diagnostic plots**
test for, [R] **sktest**, [R] **swilk**
transformations to achieve, [R] **boxcox**, [R] **ladder**, [R] **lnskew0**
`notes`, `estimates` subcommand, [R] **estimates notes**
notes on estimation results, [R] **estimates notes**
`notifyuser`, `set` subcommand, [R] **set**
`nproc`, `estat` subcommand, [R] **rocreg postestimation**
`nptrend` command, [R] **nptrend**
NR algorithm, [R] **ml**
`nrtolerance()` option, [R] **maximize**
N-way analysis of variance, [R] **anova**

O

`obs`, `set` subcommand, [R] **set**
observed information matrix, *see* OIM
`odbcmgr`, `set` subcommand, [R] **set**
odds ratio, [R] **asclogit**, [R] **binreg**, [R] **clogit**, [R] **cloglog**, [R] ***eform_option***, [R] **exlogistic postestimation**, [R] **glm**, [R] **glogit**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **scobit**
differences, [R] **lincom**, [R] **nlcom**
`off`,
`cmdlog` subcommand, [R] **log**
`log` subcommand, [R] **log**
OIM, [R] **ml**, [R] ***vce_option***
`ologit` command, [R] **ologit**, [R] **ologit postestimation**
OLS regression, *see* linear regression
omitted variables test, [R] **regress postestimation**
`on`,
`cmdlog` subcommand, [R] **log**
`log` subcommand, [R] **log**
one-way analysis of variance, [R] **kwallis**, [R] **loneway**, [R] **oneway**
`oneway` command, [R] **oneway**
online help, [R] **help**, [R] **hsearch**, [R] **search**
OPG, [R] **ml**, [R] ***vce_option***
`oprobit` command, [R] **oprobit**, [R] **oprobit postestimation**
order statistics, [R] **lv**
ordered
logit, [R] **ologit**
probit, [R] **oprobit**
ordinal outcome model, *see* outcomes, ordinal
ordinary least squares, *see* linear regression
`orthog` command, [R] **orthog**
orthogonal polynomial, [R] **contrast**, [R] **margins, contrast**
orthogonal polynomials, [R] **orthog**
`orthpoly` command, [R] **orthog**
outcomes,
binary,
complementary log-log, [R] **cloglog**
glm for binomial family, [R] **binreg**, [R] **glm**
grouped data, [R] **glogit**
logistic, [R] **exlogistic**, [R] **logistic**, [R] **logit**, [R] **scobit**
probit, [R] **biprobit**, [R] **heckprob**, [R] **hetprob**, [R] **ivprobit**, [R] **probit**
ROC analysis, [R] **rocfit**, [R] **rocreg**
categorical,
logistic, [R] **asclogit**, [R] **clogit**, [R] **mlogit**, [R] **nlogit**, [R] **slogit**
probit, [R] **asmprobit**, [R] **mprobit**
count,
negative binomial, [R] **nbreg**, [R] **tnbreg**, [R] **zinb**
Poisson, [R] **expoisson**, [R] **poisson**, [R] **tpoisson**, [R] **zip**
multinomial, *see* categorical subentry, *see* ordinal subentry, *see* rank subentry
ordinal,
logistic, [R] **ologit**
probit, [R] **oprobit**
polytomous, *see* categorical subentry, *see* ordinal subentry, *see* rank subentry
rank,
logistic, [R] **rologit**
probit, [R] **asroprobit**
outer fence, [R] **lv**
outer product of the gradient, *see* OPG
outliers, [R] **lv**, [R] **qreg**, [R] **regress postestimation**, [R] **rreg**
out-of-sample predictions, [R] **predict**, [R] **predictnl**
`output`, `set` subcommand, [R] **set**
output,
coefficient table,
automatically widen, [R] **set**
display settings, [R] **set showbaselevels**
format settings, [R] **set cformat**

output, *continued*
controlling the scrolling of, [R] **more**
printing, [R] **translate**
recording, [R] **log**
outside values, [R] **lv**
`overid`, `estat` subcommand, [R] **gmm postestimation**, [R] **ivregress postestimation**
overidentifying restrictions test, [R] **gmm postestimation**, [R] **ivregress postestimation**
`ovtest`, `estat` subcommand, [R] **regress postestimation**

P

`pagesize`, `set` subcommand, [R] **more**, [R] **set**
paging of screen output, controlling, [R] **more**
pairwise comparisons, [R] **margins, pwcompare**, [R] **marginsplot**, [R] **pwcompare**, [R] **pwmean**
pairwise correlation, [R] **correlate**
parameters, system, *see* system parameters
partial
correlation, [R] **pcorr**
effects, [R] **margins**, [R] **marginsplot**
regression leverage plot, [R] **regress postestimation**
regression plot, [R] **regress postestimation**
residual plot, [R] **regress postestimation**
Parzen kernel density function, [R] **kdensity**
pattern of missing values, [R] **misstable**
`patterns`, `misstable` subcommand, [R] **misstable**
pausing until key is pressed, [R] **more**
`pchart` command, [R] **qc**
`pchi` command, [R] **diagnostic plots**
`pcorr` command, [R] **pcorr**
PDF files, [R] **translate**
Pearson goodness-of-fit test, [R] **logistic postestimation**, [R] **poisson postestimation**
Pearson product-moment correlation coefficient, [R] **correlate**
Pearson residual, [R] **binreg postestimation**, [R] **glm postestimation**, [R] **logistic postestimation**, [R] **logit postestimation**
percentiles, displaying, [R] **centile**, [R] **lv**, [R] **summarize**, [R] **table**, [R] **tabstat**
permutation tests, [R] **permute**
`permute` prefix command, [R] **permute**
`pformat`, `set` subcommand, [R] **set**, [R] **set cformat**
pharmaceutical statistics, [R] **pk**, [R] **pksumm**
pharmacokinetic data, *see* pk (pharmacokinetic data)
piecewise
cubic functions, [R] **mkspline**
linear functions, [R] **mkspline**
`pinnable`, `set` subcommand, [R] **set**
pk (pharmacokinetic data), [R] **pk**, [R] **pkcollapse**, [R] **pkcross**, [R] **pkequiv**, [R] **pkexamine**, [R] **pkshape**, [R] **pksumm**
`pkcollapse` command, [R] **pkcollapse**
`pkcross` command, [R] **pkcross**
`pkequiv` command, [R] **pkequiv**
`pkexamine` command, [R] **pkexamine**
`.pkg` filename suffix, [R] **net**
`pkshape` command, [R] **pkshape**
`pksumm` command, [R] **pksumm**
Plackett–Luce model, [R] **rologit**
`playsnd`, `set` subcommand, [R] **set**
`plot`, `ml` subcommand, [R] **ml**
`pnorm` command, [R] **diagnostic plots**
`poisson` command, [R] **nbreg**, [R] **poisson**, [R] **poisson postestimation**
Poisson distribution,
confidence intervals, [R] **ci**
regression, *see* Poisson regression
Poisson regression, [R] **nbreg**, [R] **poisson**
generalized linear model, [R] **glm**
truncated, [R] **tpoisson**
zero-inflated, [R] **zip**
polynomials,
fractional, [R] **fracpoly**, [R] **mfp**
orthogonal, [R] **orthog**
smoothing, *see* local polynomial
polytomous outcome model, *see* outcomes, polytomous
populations,
diagnostic plots, [R] **diagnostic plots**
examining, [R] **histogram**, [R] **lv**, [R] **stem**, [R] **summarize**, [R] **table**
standard, [R] **dstdize**
testing equality of, *see* distributions, testing equality of
testing for normality, [R] **sktest**, [R] **swilk**
postestimation command, [R] **contrast**, [R] **estat**, [R] **estimates**, [R] **hausman**, [R] **lincom**, [R] **linktest**, [R] **lrtest**, [R] **margins**, [R] **margins, contrast**, [R] **margins, pwcompare**, [R] **marginsplot**, [R] **nlcom**, [R] **predict**, [R] **predictnl**, [R] **pwcompare**, [R] **suest**, [R] **test**, [R] **testnl**
poverty indices, [R] **inequality**
power of a test, [R] **sampsi**
power transformations, [R] **boxcox**, [R] **lnskew0**
P–P plot, [R] **diagnostic plots**
`predict` command, [R] **predict**, [R] **regress postestimation**
`predict`, `estat` subcommand, [R] **exlogistic postestimation**
prediction, standard error of, [R] **glm**, [R] **predict**, [R] **regress postestimation**
predictions, [R] **predict**, [R] **predictnl**
`predictnl` command, [R] **predictnl**
prefix command, [R] **bootstrap**, [R] **fracpoly**, [R] **jackknife**, [R] **mfp**, [R] **nestreg**, [R] **permute**, [R] **simulate**, [R] **stepwise**, [R] **xi**
Pregibon delta beta influence statistic, *see* delta beta influence statistic
preprocessor commands, [R] **#review**
prevalence studies, *see* case–control data
`print` command, [R] **translate**
`printcolor`, `set` subcommand, [R] **set**

printing, logs (output), [R] **translate**
`probit` command, [R] **probit**, [R] **probit postestimation**
probit regression, [R] **probit**
  alternative-specific multinomial probit, [R] **asmprobit**
  alternative-specific rank-ordered, [R] **asroprobit**
  bivariate, [R] **biprobit**
  generalized linear model, [R] **glm**
  heteroskedastic, [R] **hetprob**
  multinomial, [R] **mprobit**
  ordered, [R] **oprobit**
  two-equation, [R] **biprobit**
  with endogenous regressors, [R] **ivprobit**
  with grouped data, [R] **glogit**
  with sample selection, [R] **heckprob**
`processors`, `set` subcommand, [R] **set**
product-moment correlation, [R] **correlate**
  between ranks, [R] **spearman**
production frontier models, [R] **frontier**
profile plots, [R] **marginsplot**
programs, user-written, *see* ado-files
projection matrix, diagonal elements of, [R] **logistic postestimation**, [R] **logit postestimation**, [R] **probit postestimation**, [R] **regress postestimation**, [R] **rreg**
`proportion` command, [R] **proportion**, [R] **proportion postestimation**
proportional
  hazards models, *see* survival analysis
  odds model, [R] **ologit**, [R] **slogit**
  sampling, [R] **bootstrap**
proportions,
  confidence intervals for, [R] **ci**
  estimating, [R] **proportion**
  sample size and power for, [R] **sampsi**
  testing equality of, [R] **bitest**, [R] **prtest**
`prtest` command, [R] **prtest**
`prtesti` command, [R] **prtest**
pseudo R-squared, [R] **maximize**
pseudosigmas, [R] **lv**
`pwcompare` command, [R] **pwcompare**, [R] **pwcompare postestimation**
`pwcorr` command, [R] **correlate**
`pwmean` command, [R] **pwmean**, [R] **pwmean postestimation**

Q

qc charts, *see* quality control charts
`qchi` command, [R] **diagnostic plots**
`qladder` command, [R] **ladder**
`qnorm` command, [R] **diagnostic plots**
Q–Q plot, [R] **diagnostic plots**
`qqplot` command, [R] **diagnostic plots**
`_qreg` command, [R] **qreg**
`qreg` command, [R] **qreg**, [R] **qreg postestimation**
`qtolerance()` option, [R] **maximize**
qualitative dependent variables, [R] **asclogit**, [R] **asmprobit**, [R] **asroprobit**, [R] **binreg**, [R] **biprobit**, [R] **brier**, [R] **clogit**, [R] **cloglog**, [R] **cusum**, [R] **exlogistic**, [R] **glm**, [R] **glogit**, [R] **heckprob**, [R] **hetprob**, [R] **ivprobit**, [R] **logistic**, [R] **logit**, [R] **mlogit**, [R] **mprobit**, [R] **nlogit**, [R] **ologit**, [R] **oprobit**, [R] **probit**, [R] **rocfit**, [R] **rocreg**, [R] **rologit**, [R] **scobit**, [R] **slogit**
quality control charts, [R] **qc**, [R] **serrbar**
`quantile` command, [R] **diagnostic plots**
quantile–normal plots, [R] **diagnostic plots**
quantile plots, [R] **diagnostic plots**
quantile–quantile plots, [R] **diagnostic plots**
quantile regression, [R] **qreg**
quantiles, *see* percentiles, displaying
`query`,
  `estimates` subcommand, [R] **estimates store**
  `log` subcommand, [R] **log**
  `ml` subcommand, [R] **ml**
  `net` subcommand, [R] **net**
  `translator` subcommand, [R] **translate**
  `transmap` subcommand, [R] **translate**
  `update` subcommand, [R] **update**
`query` command, [R] **query**
quitting Stata, *see* `exit` command

R

`r()` saved results, [R] **saved results**
Ramsey test, [R] **regress postestimation**
random
  order, test for, [R] **runtest**
  sample, [R] **bootstrap**
random-effects models, [R] **anova**, [R] **loneway**
range chart, [R] **qc**
range of data, [R] **lv**, [R] **stem**, [R] **summarize**, [R] **table**, [R] **tabstat**
rank correlation, [R] **spearman**
rank-order statistics, [R] **signrank**, [R] **spearman**
ranking data, [R] **rologit**
rank-ordered logistic regression, *see* outcomes, rank
`ranksum` command, [R] **ranksum**
rate ratio, *see* incidence-rate ratio
`ratio` command, [R] **ratio**, [R] **ratio postestimation**
ratios, estimating, [R] **ratio**
rc (return codes), *see* error messages and return codes
`rchart` command, [R] **qc**
receiver operating characteristic (ROC) analysis, *see* ROC analysis
reexpression, [R] **boxcox**, [R] **ladder**, [R] **lnskew0**
`reg3` command, [R] **reg3**, [R] **reg3 postestimation**
`regress` command, [R] **regress**, [R] **regress postestimation**, [R] **regress postestimation time series**

regression
diagnostics, [R] **predict**; [R] **ladder**, [R] **logistic postestimation**, [R] **regress postestimation**, [R] **regress postestimation time series**
function, estimating, [R] **lpoly**
regression,
constrained, [R] **cnsreg**
creating orthogonal polynomials for, [R] **orthog**
dummy variables, with, [R] **anova**, [R] **areg**, [R] **xi**
fixed-effects, [R] **areg**
fractional polynomial, [R] **fracpoly**, [R] **mfp**
graphing, [R] **logistic**, [R] **regress postestimation**
grouped data, [R] **intreg**
increasing number of variables allowed, [R] **matsize**
instrumental variables, [R] **gmm**, [R] **ivprobit**, [R] **ivregress**, [R] **ivtobit**, [R] **nlsur**
linear, *see* linear regression
system, [R] **mvreg**, [R] **reg3**, [R] **sureg**
truncated, [R] **truncreg**
reliability, [R] **alpha**, [R] **eivreg**, [R] **loneway**
reliability theory, *see* survival analysis
repeated measures ANOVA, [R] **anova**
repeating and editing commands, [R] **#review**
`replay`, `estimates` subcommand, [R] **estimates replay**
`report`, `fvset` subcommand, [R] **fvset**
`report`, `ml` subcommand, [R] **ml**
RESET test, [R] **regress postestimation**
`reset`, `translator` subcommand, [R] **translate**
residual-versus-fitted plot, [R] **regress postestimation**
residual-versus-predictor plot, [R] **regress postestimation**
residuals, [R] **logistic**, [R] **predict**, [R] **regress postestimation**, [R] **rreg**
resistant smoothers, [R] **smooth**
`restore`, `estimates` subcommand, [R] **estimates store**
restricted cubic splines, [R] **mkspline**
results,
saved, [R] **saved results**
saving, [R] **estimates save**
return codes, *see* error messages and return codes
`return list` command, [R] **saved results**
`reventries`, `set` subcommand, [R] **set**
`#review` command, [R] **#review**
`revkeyboard`, `set` subcommand, [R] **set**
risk ratio, [R] **binreg**
`rmsg`, `set` subcommand, [R] **set**
robust regression, [R] **regress**, [R] **rreg**, *also see* robust, Huber/White/sandwich estimator of variance
robust test for equality of variance, [R] **sdtest**
robust, Huber/White/sandwich estimator of variance, [R] ***vce_option***
alternative-specific
conditional logit model, [R] **asclogit**
multinomial probit regression, [R] **asmprobit**
rank-ordered probit regression, [R] **asroprobit**
complementary log-log regression, [R] **cloglog**
robust, Huber/White/sandwich estimator of variance, *continued*
generalized linear models, [R] **glm**
for binomial family, [R] **binreg**
generalized method of moments, [R] **gmm**
heckman selection model, [R] **heckman**
instrumental-variables regression, [R] **ivregress**
interval regression, [R] **intreg**
linear regression, [R] **regress**
constrained, [R] **cnsreg**
truncated, [R] **truncreg**
with dummy-variable set, [R] **areg**
logistic regression, [R] **logistic**, [R] **logit**, *also see* logit regression subentry
conditional, [R] **clogit**
multinomial, [R] **mlogit**
ordered, [R] **ologit**
rank-ordered, [R] **rologit**
skewed, [R] **scobit**
stereotype, [R] **slogit**
logit regression, [R] **logistic**, [R] **logit**, *also see* logistic regression subentry
for grouped data, [R] **glogit**
nested, [R] **nlogit**
maximum likelihood estimation, [R] **ml**
multinomial
logistic regression, [R] **mlogit**
probit regression, [R] **mprobit**
negative binomial regression, [R] **nbreg**
truncated, [R] **tnbreg**
zero-inflated, [R] **zinb**
nonlinear
least-squares estimation, [R] **nl**
systems of equations, [R] **nlsur**
Poisson regression, [R] **poisson**
truncated, [R] **tpoisson**
zero-inflated, [R] **zip**
probit regression, [R] **probit**
bivariate, [R] **biprobit**
for grouped data, [R] **glogit**
heteroskedastic, [R] **hetprob**
multinomial, [R] **mprobit**
ordered, [R] **oprobit**
with endogenous regressors, [R] **ivprobit**
with sample selection, [R] **heckprob**
summary statistics,
mean, [R] **mean**
proportion, [R] **proportion**
ratio, [R] **ratio**
total, [R] **total**
tobit model, [R] **tobit**
with endogenous regressors, [R] **ivtobit**
treatment-effects model, [R] **treatreg**
truncated
negative binomial regression, [R] **tnbreg**
Poisson regression, [R] **tpoisson**
regression, [R] **truncreg**

robust, Huber/White/sandwich estimator of variance, *continued*
with endogenous regressors,
instrumental-variables regression, [R] **ivregress**
probit regression, [R] **ivprobit**
tobit regression, [R] **ivtobit**
zero-inflated
negative binomial regression, [R] **zinb**
Poisson regression, [R] **zip**
robust, other methods of, [R] **qreg**, [R] **rreg**, [R] **smooth**
`robvar` command, [R] **sdtest**
ROC analysis, [R] **roc**
area under ROC curve, [R] **logistic postestimation**
nonparametric analysis without covariates, [R] **roctab**
parametric analysis without covariates, [R] **rocfit**
regression models, [R] **rocreg**
ROC curves after `rocfit`, [R] **rocfit postestimation**
ROC curves after `rocreg`, [R] **rocregplot**
test equality of ROC areas, [R] **roccomp**
`roccomp` command, [R] **roc**, [R] **roccomp**
`rocfit` command, [R] **rocfit**, [R] **rocfit postestimation**
`rocgold` command, [R] **roc**, [R] **roccomp**
`rocplot` command, [R] **rocfit postestimation**
`rocreg` command, [R] **rocreg**, [R] **rocreg postestimation**, [R] **rocregplot**
`rocregplot` command, [R] **rocregplot**
`roctab` command, [R] **roc**, [R] **roctab**
roh, [R] **loneway**
`rologit` command, [R] **rologit**, [R] **rologit postestimation**
rootograms, [R] **spikeplot**
`rreg` command, [R] **rreg**, [R] **rreg postestimation**
`run` command, [R] **do**
`runiform()` function, [R] **set seed**
`runtest` command, [R] **runtest**
`rvfplot` command, [R] **regress postestimation**
`rvpplot` command, [R] **regress postestimation**

S

`s()` saved results, [R] **saved results**
`S_` macros, [R] **saved results**
sample, random, *see* random sample
sample size, [R] **sampsi**
sampling, [R] **bootstrap**, [R] **bsample**, *also see* cluster sampling
`sampsi` command, [R] **sampsi**
sandwich/Huber/White estimator of variance, *see* robust, Huber/White/sandwich estimator of variance
`save`, `estimates` subcommand, [R] **estimates save**
saved results, [R] **saved results**
saving results, [R] **estimates save**
Scheffé's multiple-comparison adjustment, *see* multiple comparisons, Scheffé's method
`scheme`, `set` subcommand, [R] **set**
Schwarz information criterion, *see* BIC
s-class command, [R] **saved results**
`scobit` command, [R] **scobit**, [R] **scobit postestimation**
`score`, `ml` subcommand, [R] **ml**
scores, [R] **predict**
`scrollbufsize`, `set` subcommand, [R] **set**
scrolling of output, controlling, [R] **more**
`sdtest` command, [R] **sdtest**
`sdtesti` command, [R] **sdtest**
`se`, `estat` subcommand, [R] **exlogistic postestimation**, [R] **expoisson postestimation**
search
help, [R] **hsearch**
Internet, [R] **net search**
`search`,
`ml` subcommand, [R] **ml**
`net` subcommand, [R] **net**
`view` subcommand, [R] **view**
`search` command, [R] **search**
`search_d`, `view` subcommand, [R] **view**
`searchdefault`, `set` subcommand, [R] **search**, [R] **set**
`seed`, `set` subcommand, [R] **set**, [R] **set seed**
seemingly unrelated
estimation, [R] **suest**
regression, [R] **nlsur**, [R] **reg3**, [R] **sureg**
`segmentsize`, `set` subcommand, [R] **set**
selection models, [R] **heckman**, [R] **heckprob**
sensitivity, [R] **logistic postestimation**, *also see* ROC analysis
model, [R] **regress postestimation**, [R] **rreg**
serial correlation, *see* autocorrelation
serial independence, test for, [R] **runtest**
`serrbar` command, [R] **serrbar**
session, recording, [R] **log**
`set`
`adosize` command, [R] **set**
`autotabgraphs` command, [R] **set**
`cformat` command, [R] **set**, [R] **set cformat**
`checksum` command, [R] **set**
command, [R] **query**, [R] **set**
`conren` command, [R] **set**
`copycolor` command, [R] **set**
`dockable` command, [R] **set**
`dockingguides` command, [R] **set**
`doublebuffer` command, [R] **set**
`dp` command, [R] **set**
`emptycells` command, [R] **set**, [R] **set emptycells**
`eolchar` command, [R] **set**
`fastscroll` command, [R] **set**
`floatresults` command, [R] **set**
`floatwindows` command, [R] **set**
`graphics` command, [R] **set**
`httpproxy` command, [R] **netio**, [R] **set**
`httpproxyauth` command, [R] **netio**, [R] **set**
`httpproxyhost` command, [R] **netio**, [R] **set**
`httpproxyport` command, [R] **netio**, [R] **set**
`httpproxypw` command, [R] **netio**, [R] **set**

set, *continued*
httpproxyuser command, [R] **netio**, [R] **set**
include_bitmap command, [R] **set**
level command, [R] **level**, [R] **set**
linegap command, [R] **set**
linesize command, [R] **log**, [R] **set**
locksplitters command, [R] **set**
logtype command, [R] **log**, [R] **set**
lstretch command, [R] **set**
matacache command, [R] **set**
matafavor command, [R] **set**
matalibs command, [R] **set**
matalnum command, [R] **set**
matamofirst command, [R] **set**
mataoptimize command, [R] **set**
matastrict command, [R] **set**
matsize command, [R] **matsize**, [R] **set**
max_memory command, [R] **set**
maxdb command, [R] **db**, [R] **set**
maxiter command, [R] **maximize**, [R] **set**
maxvar command, [R] **set**
min_memory command, [R] **set**
more command, [R] **more**, [R] **set**
niceness command, [R] **set**
notifyuser command, [R] **set**
obs command, [R] **set**
odbcmgr command, [R] **set**
output command, [R] **set**
pagesize command, [R] **more**, [R] **set**
pformat command, [R] **set**, [R] **set cformat**
pinnable command, [R] **set**
playsnd command, [R] **set**
printcolor command, [R] **set**
processors command, [R] **set**
reventries command, [R] **set**
revkeyboard command, [R] **set**
rmsg command, [R] **set**
scheme command, [R] **set**
scrollbufsize command, [R] **set**
searchdefault command, [R] **search**, [R] **set**
seed command, [R] **set**, [R] **set seed**
segmentsize command, [R] **set**
sformat command, [R] **set**, [R] **set cformat**
showbaselevels command, [R] **set**, [R] **set showbaselevels**
showemptycells command, [R] **set**, [R] **set showbaselevels**
showomitted command, [R] **set**, [R] **set showbaselevels**
smoothfonts command, [R] **set**
timeout1 command, [R] **netio**, [R] **set**
timeout2 command, [R] **netio**, [R] **set**
trace command, [R] **set**
tracedepth command, [R] **set**
traceexpand command, [R] **set**
tracehilite command, [R] **set**
set, *continued*
traceindent command, [R] **set**
tracenumber command, [R] **set**
tracesep command, [R] **set**
type command, [R] **set**
update_interval command, [R] **set**, [R] **update**
update_prompt command, [R] **set**, [R] **update**
update_query command, [R] **set**, [R] **update**
varabbrev command, [R] **set**
varkeyboard command, [R] **set**
set ado, net subcommand, [R] **net**
set other, net subcommand, [R] **net**
set, translator subcommand, [R] **translate**
set_defaults command, [R] **set_defaults**
settings
display, [R] **set showbaselevels**
format, [R] **set cformat**
sformat, set subcommand, [R] **set**, [R] **set cformat**
sfrancia command, [R] **swilk**
Shapiro–Francia test for normality, [R] **swilk**
Shapiro–Wilk test for normality, [R] **swilk**
shewhart command, [R] **qc**
showbaselevels, set subcommand, [R] **set**, [R] **set showbaselevels**
showemptycells, set subcommand, [R] **set**, [R] **set showbaselevels**
shownrtolerance option, [R] **maximize**
showomitted, set subcommand, [R] **set**, [R] **set showbaselevels**
showstep option, [R] **maximize**
showtolerance option, [R] **maximize**
Šidák's multiple-comparison adjustment, *see* multiple comparisons, Šidák's method
significance levels, [R] **level**, [R] **query**
signrank command, [R] **signrank**
signtest command, [R] **signrank**
simulate prefix command, [R] **simulate**
simulations, Monte Carlo, [R] **simulate**; [R] **permute**
simultaneous
quantile regression, [R] **qreg**
systems, [R] **reg3**
SJ, *see Stata Journal and Stata Technical Bulletin*
sj, net subcommand, [R] **net**
skewed logistic regression, [R] **scobit**
skewness, [R] **summarize**; [R] **lnskew0**, [R] **lv**, [R] **pksumm**, [R] **sktest**, [R] **tabstat**
sktest command, [R] **sktest**
slogit command, [R] **slogit**, [R] **slogit postestimation**
smooth command, [R] **smooth**
smoothfonts, set subcommand, [R] **set**
smoothing, [R] **lpoly**, [R] **smooth**
graphs, [R] **kdensity**, [R] **lowess**
Spearman–Brown prophecy formula, [R] **alpha**
spearman command, [R] **spearman**
Spearman's rho, [R] **spearman**

specification test, [R] **gmm postestimation**, [R] **hausman**, [R] **ivregress postestimation**, [R] **linktest**, [R] **lnskew0**, [R] **regress postestimation**, [R] **suest**
specificity, [R] **logistic postestimation**, *also see* ROC analysis
Spiegelhalter's Z statistic, [R] **brier**
spike plot, [R] **spikeplot**
`spikeplot` command, [R] **spikeplot**
splines
  linear, [R] **mkspline**
  restricted cubic, [R] **mkspline**
split-plot designs, [R] **anova**
spread, [R] **lv**
`sqreg` command, [R] **qreg**, [R] **qreg postestimation**
`sreturn list` command, [R] **saved results**
`ssc`
  `copy` command, [R] **ssc**
  `describe` command, [R] **ssc**
  `hot` command, [R] **ssc**
  `install` command, [R] **ssc**
  `new` command, [R] **ssc**
  `type` command, [R] **ssc**
  `uninstall` command, [R] **ssc**
SSC archive, [R] **ssc**
standard deviations,
  displaying, [R] **lv**, [R] **summarize**, [R] **table**, [R] **tabstat**, [R] **tabulate, summarize()**
  testing equality of, [R] **sdtest**
standard errors,
  for general predictions, [R] **predictnl**
  forecast, [R] **predict**, [R] **regress postestimation**
  mean, [R] **ci**, [R] **mean**
  prediction, [R] **glm**, [R] **predict**, [R] **regress postestimation**
  residuals, [R] **predict**, [R] **regress postestimation**
  robust, *see* robust, Huber/White/sandwich estimator of variance
standardized
  means, [R] **mean**
  proportions, [R] **proportion**
  rates, [R] **dstdize**
  ratios, [R] **ratio**
  residuals, [R] **binreg postestimation**, [R] **glm postestimation**, [R] **logistic postestimation**, [R] **logit postestimation**, [R] **predict**, [R] **regress postestimation**
standardized margins, [R] **margins**
Stata Journal and *Stata Technical Bulletin*
  installation of, [R] **net**, [R] **sj**
  keyword search of, [R] **search**
`stata.key` file, [R] **search**
Statistical Software Components (SSC) archive, [R] **ssc**
`stats`, `estimates` subcommand, [R] **estimates stats**
STB, *see* *Stata Journal and Stata Technical Bulletin*
`stb`, `net` subcommand, [R] **net**
`stcox`, fractional polynomials, [R] **fracpoly**, [R] **mfp**
`stem` command, [R] **stem**
stem-and-leaf displays, [R] **stem**
stepwise estimation, [R] **stepwise**
`stepwise` prefix command, [R] **stepwise**
stereotype logistic regression, [R] **slogit**
stochastic frontier models, [R] **frontier**
`store`, `estimates` subcommand, [R] **estimates store**
storing and restoring estimation results, [R] **estimates store**
strata,
  graphs, [R] **dotplot**
  models, [R] **asclogit**, [R] **asmprobit**, [R] **asroprobit**, [R] **clogit**, [R] **exlogistic**, [R] **expoisson**, [R] **rocreg**, [R] **rologit**
  resampling, [R] **bootstrap**, [R] **bsample**, [R] **bstat**, [R] **permute**
  standardization, [R] **dstdize**
  summary statistics, [R] **mean**, [R] **proportion**, [R] **ratio**, [R] **total**
Studentized residuals, [R] **predict**, [R] **regress postestimation**
Studentized-range multiple-comparison adjustment, *see* multiple comparisons, Tukey's method
Student–Newman–Keuls' multiple-comparison adjustment, *see* multiple comparisons, Student–Newman–Keuls' method
Student's t distribution
  confidence interval for mean, [R] **ci**, [R] **mean**
  testing equality of means, [R] **ttest**
`suest` command, [R] **suest**
`summarize`,
  `estat` subcommand, [R] **estat**
  `misstable` subcommand, [R] **misstable**
`summarize` command, [R] **summarize**; [R] **tabulate, summarize()**
summarizing data, [R] **summarize**, [R] **tabstat**; [R] **lv**, [R] **table**, [R] **tabulate oneway**, [R] **tabulate twoway**, [R] **tabulate, summarize()**
summary statistics, *see* descriptive statistics, displays
summative (Likert) scales, [R] **alpha**
sums, over observations, [R] **summarize**
`sunflower` command, [R] **sunflower**
sunflower plots, [R] **sunflower**
`sureg` command, [R] **sureg**, [R] **sureg postestimation**
survey sampling, *see* cluster sampling
survival analysis, [R] **cloglog**, [R] **exlogistic**, [R] **expoisson**, [R] **gllamm**, [R] **glm**, [R] **intreg**, [R] **logistic**, [R] **logit**, [R] **poisson**, [R] **tobit**
survival-time data, *see* survival analysis
SVAR, postestimation, [R] **regress postestimation time series**
`swilk` command, [R] **swilk**
symbolic forms, [R] **anova**
`symmetry` command, [R] **symmetry**
symmetry plots, [R] **diagnostic plots**
symmetry, test of, [R] **symmetry**
`symmi` command, [R] **symmetry**
`symplot` command, [R] **diagnostic plots**
syntax diagrams explained, [R] **intro**

system
estimators, [R] **gmm**, [R] **ivregress**, [R] **nlsur**, [R] **reg3**, [R] **sureg**
parameters, [R] **query**, [R] **set**, [R] **set_defaults**
`system1` command, [R] **gmm**
`szroeter`, `estat` subcommand, [R] **regress postestimation**
Szroeter's test for heteroskedasticity, [R] **regress postestimation**

T

t distribution
confidence interval for mean, [R] **ci**, [R] **mean**
testing equality of means, [R] **ttest**
`tab1` command, [R] **tabulate oneway**
`tab2` command, [R] **tabulate twoway**
`tabi` command, [R] **tabulate twoway**
`table` command, [R] **table**
`table`, `estimates` subcommand, [R] **estimates table**
tables,
coefficient,
display in exponentiated form, [R] ***eform_option***
display settings, [R] **estimation options**, [R] **set showbaselevels**
format settings, [R] **set cformat**
maximum likelihood display options, [R] **ml**
system parameter settings, [R] **set**
contingency, [R] **table**, [R] **tabulate twoway**
estimation results, [R] **estimates table**
frequency, [R] **tabulate oneway**, [R] **tabulate twoway**; [R] **table**, [R] **tabstat**, [R] **tabulate, summarize()**
missing values, [R] **misstable**
summary statistics, [R] **table**, [R] **tabstat**, [R] **tabulate, summarize()**
`tabstat` command, [R] **tabstat**
`tabulate` command, [R] **tabulate oneway**, [R] **tabulate twoway**
`summarize()`, [R] **tabulate, summarize()**
tau, [R] **spearman**
TDT test, [R] **symmetry**
`technique()` option, [R] **maximize**
`test` command, [R] **anova postestimation**, [R] **test**
`testnl` command, [R] **testnl**
`testparm` command, [R] **test**
tests,
ARCH effect, [R] **regress postestimation time series**
association, [R] **correlate**, [R] **spearman**, [R] **tabulate twoway**
autoregressive conditional heteroskedasticity, [R] **regress postestimation time series**
binomial probability, [R] **bitest**
bioequivalence, *see* bioequivalence tests
Breusch–Godfrey, *see* Breusch–Godfrey test
Breusch–Pagan, [R] **mvreg**, [R] **sureg**
tests, *continued*
chi-squared hypothesis, *see* chi-squared hypothesis test
Chow, *see* Chow test
cusum, [R] **cusum**
Durbin's alternative, *see* Durbin's alternative test
endogeneity, [R] **ivregress postestimation**
Engle's LM, *see* Engle's LM test
equality of
coefficients, [R] **pwcompare**, [R] **test**, [R] **testnl**
distributions, *see* distributions, testing equality of
margins, [R] **margins**, [R] **pwcompare**
means, [R] **contrast**, [R] **pwmean**, [R] **sampsi**, [R] **ttest**
medians, [R] **ranksum**
proportions, [R] **bitest**, [R] **prtest**, [R] **sampsi**
ROC areas, [R] **roccomp**, [R] **rocreg**
variances, [R] **sdtest**
equivalence, [R] **pk**, [R] **pkequiv**
exogeneity, *see* endogeneity subentry
Fisher's exact, *see* Fisher's exact test
goodness-of-fit, *see* goodness-of-fit tests
Hausman specification, *see* Hausman specification test
heteroskedasticity, [R] **regress postestimation**, [R] **sdtest**
independence, [R] **correlate**, [R] **spearman**, [R] **tabulate twoway**, *also see* Breusch–Pagan subentry
independence of irrelevant alternatives, *see* IIA
information matrix, *see* information matrix test
internal consistency, [R] **alpha**
interrater agreement, [R] **kappa**
Kolmogorov–Smirnov, *see* Kolmogorov–Smirnov test
Kruskal–Wallis, *see* Kruskal–Wallis test
kurtosis, [R] **regress postestimation**, [R] **sktest**
likelihood-ratio, [R] **lrtest**
linear hypotheses after estimation, *see* linear hypothesis test after estimation
marginal homogeneity, [R] **symmetry**
margins, [R] **margins**, [R] **pwcompare**
model coefficients, [R] **lrtest**, [R] **test**, [R] **testnl**
model specification, *see* specification test
nonlinear hypotheses after estimation, *see* nonlinear hypothesis test after estimation
normality, *see* normal distribution and normality
omitted variables, *see* omitted variables test
overidentifying restrictions, *see* overidentifying restrictions test
permutation, [R] **permute**
Ramsey, *see* Ramsey test
random order, [R] **runtest**
RESET, *see* RESET test
serial correlation, [R] **regress postestimation time series**
serial independence, [R] **runtest**
Shapiro–Francia, *see* Shapiro–Francia test for normality

tests, *continued*
Shapiro–Wilk, *see* Shapiro–Wilk test for normality
skewness, [R] **regress postestimation**, [R] **sktest**
symmetry, [R] **symmetry**
Szroeter's, *see* Szroeter's test for heteroskedasticity
TDT, [R] **symmetry**
trend, [R] **nptrend**, [R] **symmetry**
variance-comparison, [R] **sdtest**
weak instruments, [R] **ivregress postestimation**
`tetrachoric` command, [R] **tetrachoric**
three-stage least squares, [R] **reg3**
time-series analysis, [R] **regress postestimation time series**
time-versus-concentration curve, [R] **pk**
`timeout1`, `set` subcommand, [R] **netio**, [R] **set**
`timeout2`, `set` subcommand, [R] **netio**, [R] **set**
`title`, `estimates` subcommand, [R] **estimates title**
`tnbreg` command, [R] **tnbreg**, [R] **tnbreg postestimation**
`tobit` command, [R] **tobit**, [R] **tobit postestimation**
tobit regression, [R] **ivtobit**, [R] **tobit**, *also see* `intreg` command, *also see* `truncreg` command
`.toc` filename suffix, [R] **net**
`tolerance()` option, [R] **maximize**
`total` command, [R] **total**, [R] **total postestimation**
totals, estimation, [R] **total**
`tpoisson` command, [R] **tpoisson**, [R] **tpoisson postestimation**
`trace`, `ml` subcommand, [R] **ml**
`trace` option, [R] **maximize**
`trace`, `set` subcommand, [R] **set**
`tracedepth`, `set` subcommand, [R] **set**
`traceexpand`, `set` subcommand, [R] **set**
`tracehilite`, `set` subcommand, [R] **set**
`traceindent`, `set` subcommand, [R] **set**
`tracenumber`, `set` subcommand, [R] **set**
`tracesep`, `set` subcommand, [R] **set**
tracing iterative maximization process, [R] **maximize**
transformations
to achieve normality, [R] **boxcox**, [R] **ladder**
to achieve zero skewness, [R] **lnskew0**
transformations,
log, [R] **lnskew0**
modulus, [R] **boxcox**
power, [R] **boxcox**, [R] **lnskew0**
`translate` command, [R] **translate**
translate logs, [R] **translate**
`translator`
`query` command, [R] **translate**
`reset` command, [R] **translate**
`set` command, [R] **translate**
`transmap`
`define` command, [R] **translate**
`query` command, [R] **translate**
transmission-disequilibrium test, [R] **symmetry**
treatment effects, [R] **treatreg**
`treatreg` command, [R] **treatreg**, [R] **treatreg postestimation**
`tree`, `misstable` subcommand, [R] **misstable**
trend, test for, [R] **nptrend**, [R] **symmetry**
truncated
negative binomial regression, [R] **tnbreg**
Poisson regression, [R] **tpoisson**
regression, [R] **truncreg**
`truncreg` command, [R] **truncreg**, [R] **truncreg postestimation**
`ttest` and `ttesti` commands, [R] **ttest**
Tukey's multiple-comparison adjustment, *see* multiple comparisons, Tukey's method
tuning constant, [R] **rreg**
two-stage least squares, [R] **gmm**, [R] **ivregress**, [R] **nlsur**, [R] **regress**
two-way
analysis of variance, [R] **anova**
scatterplots, [R] **lowess**
`type`,
`set` subcommand, [R] **set**
`ssc` subcommand, [R] **ssc**

U

U statistic, [R] **ranksum**
uniformly distributed random-number function, [R] **set seed**
`uninstall`,
`net` subcommand, [R] **net**
`ssc` subcommand, [R] **ssc**
unique values, counting, [R] **table**, [R] **tabulate oneway**
univariate
distributions, displaying, [R] **cumul**, [R] **diagnostic plots**, [R] **histogram**, [R] **ladder**, [R] **lv**, [R] **stem**
kernel density estimation, [R] **kdensity**
`update`
`all` command, [R] **update**
command, [R] **update**
`from` command, [R] **update**
`query` command, [R] **update**
`update_interval`, `set` subcommand, [R] **set**, [R] **update**
`update_prompt`, `set` subcommand, [R] **set**, [R] **update**
`update_query`, `set` subcommand, [R] **set**, [R] **update**
`update`, `view` subcommand, [R] **view**
`update_d`, `view` subcommand, [R] **view**
updates to Stata, [R] **adoupdate**, [R] **net**, [R] **sj**, [R] **update**
`use`, `estimates` subcommand, [R] **estimates save**
user-written additions,
installing, [R] **net**, [R] **ssc**
searching for, [R] **net search**, [R] **ssc**
`using`,
`cmdlog` subcommand, [R] **log**
`log` subcommand, [R] **log**

V

varabbrev, set subcommand, [R] set
variables,
  categorical, see categorical data, agreement, measures for
  dummy, see indicator variables
  factor, see factor variables
  in model, maximum number, [R] matsize
  orthogonalize, [R] orthog
variance
  estimators, [R] vce_option
  inflation factors, [R] regress postestimation
  stabilizing transformations, [R] boxcox
variance,
  analysis of, [R] anova, [R] loneway, [R] oneway
  displaying, [R] summarize, [R] table, [R] tabstat, [R] tabulate, summarize(); [R] lv
  Huber/White/sandwich estimator, see robust, Huber/White/sandwich estimator of variance
  nonconstant, see robust, Huber/White/sandwich estimator of variance
  testing equality of, [R] sdtest
variance-comparison test, [R] sdtest
variance–covariance matrix of estimators, [R] correlate, [R] estat
variance-weighted least squares, [R] vwls
varkeyboard, set subcommand, [R] set
vce, estat subcommand, [R] estat
vce() option, [R] vce_option
version of ado-file, [R] which
version of Stata, [R] about
view
  ado command, [R] view
  ado_d command, [R] view
  browse command, [R] view
  command, [R] view
  help command, [R] view
  help_d command, [R] view
  net command, [R] view
  net_d command, [R] view
  news command, [R] view
  search command, [R] view
  search_d command, [R] view
  update command, [R] view
  update_d command, [R] view
  view_d command, [R] view
view_d, view subcommand, [R] view
viewing previously typed lines, [R] #review
vif, estat subcommand, [R] regress postestimation
vwls command, [R] vwls, [R] vwls postestimation

W

Wald tests, [R] contrast, [R] predictnl, [R] test, [R] testnl
weak instrument test, [R] ivregress postestimation
weighted least squares, [R] regress
  for grouped data, [R] glogit
  generalized linear models, [R] glm
  generalized method of moments estimation, [R] gmm
  instrumental-variables regression, [R] gmm, [R] ivregress
  nonlinear least-squares estimation, [R] nl
  nonlinear systems of equations, [R] nlsur
  variance, [R] vwls
Welsch distance, [R] regress postestimation
which command, [R] which
White/Huber/sandwich estimator of variance, see robust, Huber/White/sandwich estimator of variance
White's test for heteroskedasticity, [R] regress postestimation
Wilcoxon
  rank-sum test, [R] ranksum
  signed-ranks test, [R] signrank

X

xchart command, [R] qc
xi prefix command, [R] xi

Z

Zellner's seemingly unrelated regression, [R] sureg; [R] reg3, [R] suest
zero-altered, see zero-inflated
zero-inflated
  negative binomial regression, [R] zinb
  Poisson regression, [R] zip
zero-skewness transform, [R] lnskew0
zinb command, [R] zinb, [R] zinb postestimation
zip command, [R] zip, [R] zip postestimation