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an70	Fall NetCourse schedule announced

We have announced our latest NetCourse schedule:

NetCourse 101. An Introduction to Stata

6 weeks (4 lectures)	
Course dates:	August 20 through October 1
Deadline for enrollment:	August 16
Cost:	$ 85
Course leaders:	Mark Esman, Allen McDowell, and Kyle Willman
Prerequisites:	Stata 6, installed and working
Schedule:	
Lecture 1	August 20
Lecture 2	August 27
One-week break	September 2 through September 8
Lecture 3	September 10
Lecture 4	September 17
Closing discussion	
Course ends	October 1

NetCourse 101. An Introduction to Stata

6 weeks (4 lectures)	
Course dates:	September 17 through October 29
Deadline for enrollment:	September 13
Cost:	$85
Course leaders:	Mark Esman, Jeremy Wernow, and Kyle Willman
Prerequisites:	Stata 6, installed and working
Schedule:	
Lecture 1	September 17
Lecture 2	September 24
One-week break	September 30 through October 6
Lecture 3	October 8
Lecture 4	October 15
Closing discussion	
Course ends	October 29

NetCourse 151. Introduction to Stata programming

6 weeks (4 lectures)	
Course dates:	October 1 through November 12
Deadline for enrollment:	September 27
Cost:	$100
Course leaders:	David Drukker, Ken Higbee, and Allen McDowell
Prerequisites:	Stata 6, installed and working
Schedule:	
Lecture 1	October 1
Lecture 2	October 8
One-week break	October 14 through October 20
Lecture 3	October 22
Lecture 4	October 29
Closing discussion	
Course ends	November 12

More information, including an outline of each course, can be obtained by

1. Pointing your browser to *http://www.stata.com*.
2. Clicking on the Headline *Fall NetCourse schedule announced*.

Email *stata@stata.com* for enrollment forms.

NetCourses are courses offered over the Internet via email then run about 6 weeks. Every Friday a "lecture" is emailed to the course participants. After reading the lecture, participants email questions and comments back to the Course Leaders. These emailed questions are remailed to all course participants by the NetCourse software. Course leaders respond to the questions and comments on Tuesday and Thursday. The other participants are encouraged to amplify or otherwise respond to the questions and comments as well. The next lecture is then emailed on Friday and process repeats.

The courses are designed to take roughly 3 hours per week.

All courses have been updated to Stata 6.

dm66.1 | Stata 6 version of recoding variables using grouped values

David Clayton, MRC Biostatistical Research Unit, Cambridge, david.clayton@mrc-bsu.cam.ac.uk
Michael Hills (retired), mhills@regress.demon.co.uk

On the diskette accompanying this issue is a Stata 6 version of `cut` (see Clayton and Hills, 1999).

Reference

Clayton, D. and M. Hills. 1999. dm66: Recoding variables using grouped values. *Stata Technical Bulletin* 49: 6–7.

dm68 | Display of variables in blocks

Jeroen Weesie, Utrecht University, Netherlands, j.weesie@fss.uu.nl

Stata's `list` command to display the values of variables provides two display styles. In the concise *tabular* (`nodisplay`) style, the default with "few" variables, `list` displays a "matrix" or "table" of values, optionally preceded with an observation number, and with the variable names in a header line above the table. If the output does not fit into the output device, Stata wraps *each of the lines* of the output. In the `display` style, the default with "many" variables, `list` lists the values of the variables per case in three columns, preceded with the variable name. The command `listblck` described in this insert provides an alternative style that lists as many variables as fit onto the output device for all cases, wrapping the variables rather than the observations.

The three styles are most easily shown and compared via an example, using Stata's automobile data. If no style is specified, `list` selects the style it thinks is most appropriate.

```
. list make price weight length mpg rep78 trunk displ foreign in 1/5
Observation 1
        make  AMC Concord       price         4099      weight         2930
      length          186         mpg           22       rep78            3
       trunk           11       displ          121     foreign     Domestic
Observation 2
        make    AMC Pacer       price         4749      weight         3350
      length          173         mpg           17       rep78            3
       trunk           11       displ          258     foreign     Domestic
Observation 3
        make   AMC Spirit       price         3799      weight         2640
      length          168         mpg           22       rep78            .
       trunk           12       displ          121     foreign     Domestic
Observation 4
        make Buick Centur..     price         4816      weight         3250
      length          196         mpg           20       rep78            3
       trunk           16       displ          196     foreign     Domestic
Observation 5
        make Buick Electr..     price         7827      weight         4080
      length          222         mpg           15       rep78            4
       trunk           20       displ          350     foreign     Domestic
```

This display style is quite liberal with output space, and lists the variable names for each observation. The `nodisplay` option produces more concise output.

```
. list make price weight length mpg rep78 trunk displ foreign in 1/5, nodisplay
```

```
                  make     price    weight    length       mpg     rep78     t
> runk     displ   foreign
  1.        AMC Concord      4099      2930       186        22         3
>   11       121  Domestic
  2.          AMC Pacer      4749      3350       173        17         3
>   11       258  Domestic
  3.          AMC Spirit     3799      2640       168        22         .
>   12       121  Domestic
  4.      Buick Century      4816      3250       196        20         3
>   16       196  Domestic
  5.      Buick Electra      7827      4080       222        15         4
>   20       350  Domestic
```

While more concise, it has become almost unreadable as well. The command `listblck` provides an alternative display style that may be a reasonable compromise between conciseness and readability.

```
. listblck make price weight length mpg rep78 trunk displ foreign in 1/5
                  make     price    weight    length       mpg     rep78
  1.        AMC Concord      4099      2930       186        22         3
  2.          AMC Pacer      4749      3350       173        17         3
  3.          AMC Spirit     3799      2640       168        22         .
  4.      Buick Century      4816      3250       196        20         3
  5.      Buick Electra      7827      4080       222        15         4
  6.      Buick LeSabre      5788      3670       218        18         3

      trunk     displ   foreign
  1.     11       121  Domestic
  2.     11       258  Domestic
  3.     12       121  Domestic
  4.     16       196  Domestic
  5.     20       350  Domestic
```

Note that `listblck` repeats the observation numbers so that it becomes possible to link related lines in the output. In cases with a meaningful case identifier, it may be more natural to repeat this variable in each table. This is accomplished with the option `repeat(#)`, where # is the number of leading variables to be repeated.

```
. listblck make price weight length mpg rep78 trunk displ foreign in 1/5, noobs rep(1)
            make     price    weight    length       mpg     rep78
      AMC Concord      4099      2930       186        22         3
        AMC Pacer      4749      3350       173        17         3
       AMC Spirit      3799      2640       168        22         .
    Buick Century      4816      3250       196        20         3
    Buick Electra      7827      4080       222        15         4

            make     trunk     displ   foreign
      AMC Concord        11       121  Domestic
        AMC Pacer        11       258  Domestic
       AMC Spirit        12       121  Domestic
    Buick Century        16       196  Domestic
    Buick Electra        20       350  Domestic
```

Syntax

`listblck` [*varlist*] [`if` *exp*] [`in` *range*] [`, repeat(#) width(#) nolabel noobs`]

Description

`listblck` displays the values of variables in *varlist* for selected cases in an alternative "blocks-of-variables" format. If no *varlist* is specified, the values of all the variables are displayed.

Options

`repeat(#)` specifies the number of leading variables repeated at the beginning of each block. The default is 0.

`width(#)` specifies the display linesize. By default, `listblck` uses the current setting of `display linesize`.

`nolabel` causes the numeric codes rather than label values to be displayed.

`noobs` suppresses printing of the observation numbers.

Acknowledgment

This project was supported by grant PGS 50-370 of the Netherlands Organization for Scientific Research.

dm69	Further new matrix commands

Nicholas J. Cox, University of Durham, UK, n.j.cox@durham.ac.uk

Syntax

`matcfa` *argname1 argname2*

`matcfm` *argname1 argname2*

`matchk` *argname*

`matcname` *matrix1 matrix2*

`matdelrc` *matrix* [, `row(`*rowexp*`)` `col(`*colexp*`)`]

`matewd` *matrix1 matrix2 matrix3* [, `format(`*fmt*`)`]

`matewm` *matrix1 matrix2 matrix3* [, `format(`*fmt*`)`]

`matewop` *matrix1 matrix2 matrix3* , `operator(`*op*`)` [`format(`*fmt*`)`]

`matgop` *column_vector row_vector matrix* , `operator(`*op*`)` [`format(`*fmt*`)`]

`matmad` *matrix1 matrix2*

`matmps` *matrix1 scalar matrix2* or `matmps` *scalar matrix1 matrix2*

`matpow` *matrix new_matrix* [, `format(`*fmt*`)` `power(#)` `iterate(#)` `tolerance(#)`]

Description

`matcfa` checks that

`matrix` *new_matrix* `=` *argname1* `+` *argname2*

would execute correctly; that is, *argname1* and *argname2* name matrices with the same dimensions. `matcfa` is likely to be most useful within matrix programs.

`matcfm` checks that

`matrix` *new_matrix* `=` *argname1* `*` *argname2*

would execute correctly; that is, either both arguments are matrices such that the number of columns of *argname1* equals the number of rows of *argname2*, or one of the two arguments is a scalar and the other is a matrix. If not, an error message will be issued. `matcfm` is likely to be most useful within matrix programs.

`matchk` checks that *argname* names an existing matrix. If not, an error message will be issued. `matchk` is likely to be most useful within matrix programs.

`matcname` gives *matrix1* the row and column names of *matrix2*, provided that the two matrices have the same dimensions. If not, an error message will be issued.

Given a matrix, `matdelrc` deletes a specified row, or a specified column, or both. `matdelrc` will not delete (i.e. annihilate) entire row vectors or entire column vectors.

Given matrices $\mathbf{A}$ and $\mathbf{B}$ of the same order, `matewd` calculates and displays the matrix $\mathbf{C}$ having typical element the ratio

$$c_{ij} = a_{ij}/b_{ij}$$

provided that no b_{ij} is equal to 0. $\mathbf{C}$ may overwrite $\mathbf{A}$ or $\mathbf{B}$. $\mathbf{A}$ and $\mathbf{B}$ may be the same matrix.

Given matrices $\mathbf{A}$ and $\mathbf{B}$ of the same order, `matewm` calculates and displays the matrix $\mathbf{C}$ having typical element the product

$$c_{ij} = a_{ij}\ b_{ij}$$

$\mathbf{C}$ may overwrite $\mathbf{A}$ or $\mathbf{B}$. $\mathbf{A}$ and $\mathbf{B}$ may be the same matrix.

Given matrices $\mathbf{A}$ and $\mathbf{B}$ of the same order and a user-supplied binary operator *op*, `matewop` calculates and displays the matrix C having typical element

$$c_{ij} = a_{ij} \quad op \quad b_{ij}$$

provided that no c_{ij} would be missing. $\mathbf{C}$ may overwrite $\mathbf{A}$ or $\mathbf{B}$. $\mathbf{A}$ and $\mathbf{B}$ may be the same matrix.

Given a column vector $\mathbf{a}$ and a row vector $\mathbf{b}$ and a user-supplied binary operator *op*, `matgop` calculates and displays the matrix $\mathbf{C}$ having typical element

$$c_{ij} = a_i \quad op \quad b_j$$

provided that no c_{ij} would be missing.

`matmad` calculates for matrices $\mathbf{A}$ and $\mathbf{B}$ of the same order the maximum absolute difference between elements

$$\max_{i,j}(|a_{ij} - b_{ij}|).$$

`matmad` is likely to be most useful for checking the convergence of iterative matrix calculations within programs. The result is saved as `r(mad)`.

`matmps` calculates the sum of a scalar and a matrix and places it in a second matrix. For a scalar x and a matrix $\mathbf{A}$ the second matrix $\mathbf{B}$ has typical element

$$b_{ij} = x + a_{ij},$$

the order of the arguments being immaterial. *matrix2* may overwrite *matrix1*.

Given a square matrix $\mathbf{A}$ and power p, `matpow` calculates and displays $\mathbf{A}^p$, the pth power of $\mathbf{A}$. The result is placed in a second matrix.

Options

`format(`*fmt*`)` controls the format with which the resulting matrix is printed. The default is `format(%9.3f)`.

Options unique to matdelrc

`col(`*colexp*`)` specifies the column number. *colexp* should be or evaluate to an integer between 1 and the number of columns.

`row(`*rowexp*`)` specifies the row number. *rowexp* should be or evaluate to an integer between 1 and the number of rows.

Option unique to matewop and matgop

`operator(`*op*`)` specifies a binary operator and is a required option.

Options unique to matpow

`iterate(#)` specifies the maximum number of iterations to attempt when powering until convergence. The default is 100.

`power(#)` specifies the power. If not specified, the power is taken as effectively infinite: that is, powering is repeated until convergence (or until the limit imposed by `iterate( )`).

`tolerance(#)` is a technical option indicating the criterion for convergence. This is the largest acceptable absolute difference between each matrix element and that element on the previous iteration. The default is `1e-6` $= 10^{-6}$.

Remarks

This set of programs is a suite: all should be installed together.

`matcfa`, `matcfm`, `matchk` and, to a lesser extent, `matcname` are essentially utilities for programmers that automate basic checking and management tasks. `matcname` may also be of use interactively.

`matewd`, `matewm`, `matewop`, `matgop` and `matmps` implement various matrix operations which go typically beyond mainstream matrix algebra and reflect a more general view of matrices, as implemented in various array-oriented languages such as APL.

`matmad` calculates one of many measures of the distance between two matrices. Another is `mreldif( )`: see [U] **17.8.2 Matrix functions returning scalars**. `matmad` is used within `matpow` to test for convergence.

An example of the use of `matpow` is powering a matrix of transition probabilities. In the examples below, data from Jeffers (1978) are used that give transition probabilities over 20 years between different vegetation types in a raised mire: bog, *Calluna* (ling), woodland and grazed.

See also Weesie (1997) for another set of matrix programs complementing Stata's built-in commands.

Examples

We create a three by three matrix:

```
. mat A = (1,2,3\4,5,6\7,8,9)
. mat li A
A[3,3]
    c1  c2  c3
r1   1   2   3
r2   4   5   6
r3   7   8   9
```

Delete its second row:

```
. matdelrc A, r(2)
. mat li A
A[2,3]
    c1  c2  c3
r1   1   2   3
r3   7   8   9
```

Now delete the second column of the new matrix:

```
. matdelrc A, c(2)
. mat li A
A[2,2]
    c1  c3
r1   1   3
r3   7   9
```

Create a second matrix:

```
. mat B = (1,3\7,9)
. mat li B
B[2,2]
    c1  c2
r1   1   3
r2   7   9
```

Element-wise division:

```
. matewd A B C
symmetric C[2,2]
      c1    c2
r1  1.00
r2  1.00  1.00
```

Element-wise multiplication:

```
. matewm A B C
C[2,2]
       c1     c2
r1   1.00   9.00
r2  49.00  81.00
```

Element-wise comparison:

```
. matewop A B C, o(>)
symmetric C[2,2]
      c1    c2
r1  0.00
r2  0.00  0.00
```

Now do the outer product of a vector with itself transposed:

```
. mat int = (1,2,3,4,5,6,7,8,9,10,11,12)
. mat li int
int[1,12]
     c1   c2   c3   c4   c5   c6   c7   c8   c9  c10  c11  c12
r1    1    2    3    4    5    6    7    8    9   10   11   12
. mat intt = int´
. matgop intt int multtab , o(*)
```

```
symmetric multtab[12,12]
         c1      c2      c3      c4      c5      c6      c7      c8      c9
 r1    1.00
 r2    2.00    4.00
 r3    3.00    6.00    9.00
 r4    4.00    8.00   12.00   16.00
 r5    5.00   10.00   15.00   20.00   25.00
 r6    6.00   12.00   18.00   24.00   30.00   36.00
 r7    7.00   14.00   21.00   28.00   35.00   42.00   49.00
 r8    8.00   16.00   24.00   32.00   40.00   48.00   56.00   64.00
 r9    9.00   18.00   27.00   36.00   45.00   54.00   63.00   72.00   81.00
r10   10.00   20.00   30.00   40.00   50.00   60.00   70.00   80.00   90.00
r11   11.00   22.00   33.00   44.00   55.00   66.00   77.00   88.00   99.00
r12   12.00   24.00   36.00   48.00   60.00   72.00   84.00   96.00  108.00

        c10     c11     c12
r10  100.00
r11  110.00  121.00
r12  120.00  132.00  144.00
```

Finally, we form the transition matrix and raise it to successively higher powers:

```
. mat P = (0.65,0.29,0.06,0\0.3,0.33,0.3,0.07\0,0.28,0.69,0.03\0,0.4,0.2,0.4)
. mat rownames P = Bog Calluna Woodland Grazed
. mat colnames P = Bog Calluna Woodland Grazed
. mat li P
P[4,4]
               Bog   Calluna  Woodland    Grazed
     Bog       .65       .29       .06         0
 Calluna        .3       .33        .3       .07
Woodland         0       .28       .69       .03
  Grazed         0        .4        .2        .4
. matpow P P2, p(2)
P2[4,4]
               Bog   Calluna  Woodland    Grazed
     Bog     0.510     0.301     0.167     0.022
 Calluna     0.294     0.308     0.338     0.060
Woodland     0.084     0.298     0.566     0.052
  Grazed     0.120     0.348     0.338     0.194
. matmad P P2
.206
. matpow P P3, p(3)
P3[4,4]
               Bog   Calluna  Woodland    Grazed
     Bog     0.421     0.303     0.241     0.035
 Calluna     0.283     0.306     0.355     0.056
Woodland     0.144     0.302     0.495     0.059
  Grazed     0.182     0.322     0.384     0.112
. matmad P2 P3
.088025
. matpow P P4, p(4)
P4[4,4]
               Bog   Calluna  Woodland    Grazed
     Bog     0.365     0.304     0.289     0.042
 Calluna     0.276     0.305     0.365     0.054
Woodland     0.184     0.304     0.453     0.059
  Grazed     0.215     0.311     0.395     0.079
. matmad P3 P4
.05667715
. matpow P Pinf
Pinf[4,4]
               Bog   Calluna  Woodland    Grazed
     Bog     0.261     0.304     0.380     0.055
 Calluna     0.261     0.304     0.380     0.055
Woodland     0.261     0.304     0.380     0.055
  Grazed     0.261     0.304     0.380     0.055
```

Acknowledgments

William Gould sketched the main idea of `matdelrc` and made very helpful comments on previous versions.

References

Jeffers, J. N. R. 1978. *An introduction to systems analysis: with ecological applications.* London: Arnold.

Weesie, J. 1997. Some new matrix commands. *Stata Technical Bulletin* 39: 17–20. Reprinted in *Stata Technical Bulletin Reprints*, vol. 7, pp. 43–48.

dm70	Extensions to generate, extended

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Syntax

`egen` [*type*] *newvar* = *fcn*(*stuff*) [`if` *exp*] [`in` *range*] [`,` *options*]

Description

This insert describes 24 additional functions for `egen`.

Help for these extra functions has been placed in a file `egenodd.hlp`. Therefore, to obtain on-line help, issue either `help egenodd` or `whelp egenodd`.

`egen` creates *newvar* of the optionally specified storage type equal to *fcn*(*stuff*). Depending on *fcn*(), *stuff* refers to an expression, a *varlist*, or a *numlist*, and the options are similarly function-dependent.

Note that `egen` may change the sort order of your data.

The new functions

`any(`*varname*`),` `values(`*integer numlist*`)` is *varname* if *varname* is equal to any of the integer values in a supplied *numlist*, and missing otherwise. See also `eqany(`*varlist*`)` and `neqany(`*varlist* `)`.

`atan2(`*sinevar cosinevar*`)` [`,` `radians`] supplies arctangent of *sinevar/cosinevar* as an angle between 0 and 360 degrees, or optionally between 0 and 2π radians.

`concat(`*varlist*`)` [`,` `format(`*fmt*`)` `decode` `maxlength(#)` `punct(`*pchars*`)`] concatenates *varlist* to produce a string variable. Values of string variables are unchanged. Values of numeric variables are converted to string as is or converted using a format under option `format(`*fmt*`)` or decoded under option `decode`, in which case `maxlength()` may also be used to control the maximum length of label used. By default, variables are added end-to-end: `punct(`*pchars*`)` may be used to specify punctuation, such as a space, `punct(" ")`, or a comma, `punct(,)`.

`eqany(`*varlist*`),` `values(`*integer numlist*`)` is 1 if any of the variables in *varlist* is equal to any of the integer values in a supplied *numlist*, and 0 otherwise. See also `any(`*varname*`)` and `neqany(`*varlist*`)`.

`head(`*strvar*`)` [`,` `punct(`*pchars*`)` `trim`] gives the first word of string variable *strvar*. Given *pchars*, by default a single space `" "`, the head is whatever precedes the first occurrence of *pchars*, or the whole of the string if it does not occur. `head()` applied to `"frog toad"` is `"frog"` and to `"frog"` is `"frog"`. `head()` applied to `"frog,toad"` is similarly `"frog"` with `punct(,)`. The `trim` option trims any leading or trailing spaces. See also `last(`*strvar*`)` and `tail(`*strvar*`)`.

`kurt(`*varname*`)` [`,` `by(`*byvarlist*`)`] returns the kurtosis of *varname*.

`last(`*strvar*`)` [`,` `punct(`*pchars*`)` `trim`] gives the last 'word' of string variable *strvar*. Given *pchars*, by default a single space `" "`, the last word is whatever follows the last occurrence of *pchars*, or the whole of the string if it does not occur. `last()` applied to `"frog toad newt"` is `"newt"` and to `"frog"` is `"frog"`. `last()` applied to `"frog,toad"` is similarly `"toad"` with `punct(,)`. The `trim` option trims any leading or trailing spaces. See also `head(`*strvar*`)` and `tail(`*strvar*`)`.

`lgroup(`*varname*`)` [`,` `missing`] returns integers from 1 and higher according to the distinct groups of *varname* in sorted order. Integers will be labeled with the values of *varname*, or its value labels if such exist. This is useful as an alternative to `group()` when labels are needed as well as the bare integer codes. `missing` indicates that missing values in *varname* are to be treated like any other value when assigning groups, instead of missing values being assigned to the group missing.

`mad(`*exp*`)` [`,` `by(`*byvarlist*`)`] returns the median absolute deviation from the median of *exp*.

`mdev(`*exp*`)` [`,` `by(`*byvarlist*`)`] returns the mean absolute deviation from the mean of *exp*.

`mode(`*varname*`)` [`, minmode unique missing by(`*byvarlist*`)`] produces the mode for *varname*, which may be numeric or string. The mode is the value occurring most frequently. If two or more modes exist, the mode produced will be the highest such value (largest numerically or last alphabetically), except that `minmode` specifies use of the lowest such value and `unique` specifies that only unique modes may be produced. Missing values are excluded from determination of the mode unless `missing` is specified. Even so, the value of the mode is recorded for observations for which the values of *varname* are missing unless explicitly excluded, e.g., by `if` *varname* `< .` or `if` *varname* `!= ""`. `by(`*byvarlist*`)` specifies that determination is to be carried out separately for distinct groups defined by *byvarlist*.

`neqany(`*varlist*`), values(`*integer numlist*`)` contains for each observation the number of variables in *varlist* for which values are equal to any of the integer values in a supplied *numlist*. See also `any(`*varname*`)` and `eqany(`*varlist*`)`.

`pc(`*exp*`)` [`, by(`*byvarlist*`)`] returns *exp* scaled to be a percent of total, between 0 and 100. See also `prop(`*exp*`)`.

`pp(`*varname*`)` [`, by(`*byvarlist*`) a(#)`] sorts *varname* smallest to largest and computes the corresponding plotting position $(i-a)/(n-2a+1)$ for $i = 1$ (smallest), $\ldots, n$ (largest) and constant a.] The default `a` $= 0.5$ yields $(i-0.5)/n$, while `a` $= 0$ yields $i/(n+1)$.

`prop(`*exp*`)` [`, by(`*byvarlist*`)`] returns *exp* scaled to be a proportion of total, between 0 and 1. See also `pc(`*exp*`)`.

`rev(`*varname*`)` [`, by(`*byvarlist*`)`] returns the reverse of *varname*, that is, *varname*`[1]` is exchanged with *varname*`[N]`, and so forth.

`rindex(`*strvar*`) , substr(`*string*`)` returns the index of the last (rightmost) occurrence of *string* in the string variable *strvar*.

`rmed(`*varlist*`)` returns the median across variables for each observation. (The number of variables must not exceed the number of observations.)

`rotate(`*varname*`)` [`, start(#) max(#)`] rotates a set of integers 1, ..., *max*. Suppose we have months 1, ..., 12 and we wish to map 7 to 1, 8 to 2, ..., 12 to 6, 1 to 7, ..., 6 to 12. This would be achieved by `start(7) max(12)`.

`seq()` [`, from(#) to(#) block(#) by(`*byvarlist*`)`] returns integer sequences. Values start from `from` (default 1) and increase to `to` (default the maximum number of values) in `block`s (default size 1). If `to` is less than the maximum number, sequences restart at `from`. Numbering may also be separate within groups defined by *byvarlist*, or decreasing if `to` is less than `from`. Sequences depend on the sort order of observations, following three rules: (1) observations excluded by `if` or `in` are not counted, (2) observations are sorted by *byvarlist*, if specified, (3) otherwise, the order is that when called. Note that no *stuff* is specified.

`skew(`*varname*`)` [`, by(`*byvarlist*`)`] returns the skewness of *varname*.

`sub(`*strvar*`), find(`*findstr*`)` [`replace(`*replacestr*`) all word`] replaces occurrences of *findstr* by *replacestr* in the string variable *strvar*. By default only the first such occurrence in each string value is acted upon. `all` specifies that all occurrences in each string value are to be acted upon. If *replacestr* is not specified, it is taken to be empty, that is, *findstr* is deleted. `word` specifies that only occurrences of *findstr* that are complete words are to be acted upon.

`tag(`*varlist*`)` [`, missing`] tags just one observation in each distinct group defined by *varlist*. When all observations in a group have the same value for a summary variable calculated for the group, it will be sufficient to use just one such value for many purposes. The result will be 1 or 0, according to whether the observation is tagged, and never missing: hence if `tag` is the variable produced by `egen tag = tag(`*varlist*`)` the idiom `if tag` is always safe. `missing` specifies that missing values of *varlist* may be included.

`tail(`*strvar*`)` [`, punct(`*pchars*`) trim`] gives the remainder of string variable *strvar*. Given *pchars*, by default a single space `" "`, the tail is whatever follows the first occurrence of *pchars*, which will be the empty string `""` if it does not occur. `tail()` applied to `"frog toad"` is `"toad"` and to `"frog"` is `""`. `tail()` applied to `"frog,toad"` is similarly `"toad"` with `punct(,)`. The `trim` option trims any leading or trailing spaces. See also `head(`*strvar*`)` and `last(`*strvar*`)`.

Remarks

The official Stata command `egen` (see [R] **egen**) is a driver for a set of functions, each defined by a separate program in an ado-file. The principle is that a command `egen` *newvar* `=` *fcn*`(`*stuff*`)` embodies a call to `egen` function *fcn*, itself defined by program *_gfcn*. Hence the functions of `egen` are defined by programs written in the Stata language, in contrast to the functions used by `generate`, which are all part of the Stata executable (see [U] **16 Functions and expressions**). Hence Stata programmers may add `egen` functions to those supplied by official Stata. Examples previously published in the STB are the `rmiss2()` function of Goldstein (1995) and the `cut()` function of Clayton and Hills (1999). The `egen` functions in official Stata supply the interested programmer with useful templates to modify: often only a few lines in your program need differ from an already written program.

The advantage of an egen function is convenience for interactive use. In contrast, it is not usually a good idea to issue egen commands within Stata programs. If this is done, egen spends much of its time doing housekeeping work which should typically be unnecessary within a Stata program. A program that uses the bare minimum of commands will thus be faster than the same program with a corresponding call to egen. However, this is a counsel of perfection; for occasional use, or if you are a novice Stata programmer, the loss of machine time in using egen may be much smaller than the time you might take to modify a program so that it does not use egen.

More positively, it is worth flagging a change made to egen in Stata 6. egen may now produce string variables as results. Note, however, that it remains true that the default variable type produced by egen is that defined by set type (see [R] **generate**). In turn, by default this is float.

Users of generate will know that it is essential when generating a string variable to specify a string data type. If this habit is ingrained, you need not unlearn it when using the string functions included in this insert. However, these functions implement what is intended as a smart approach. They always generate the string variable of the smallest string type that will do the job required. You might specify a string type that is too small, just right or too big; you might specify any data type whatever, including even a numeric data type; or you might not specify any data type. In all these cases, the functions that produce string results are written on the basis that Stata can work out the best string data type required, so that whatever you might specify will be ignored. What happens is that within each egen program, a str1 variable is first generated, and then replaced by the result required. Stata automatically promotes the variable to whatever string type is needed.

Explanations and examples

The egen functions discussed here fall into various classes.

Functions for string variables

• concat(*varlist*)

Concatenation of string variables is already provided in Stata. In context, Stata understands the addition symbol + as specifying concatenation, adding strings end to end. "soft" + "ware" produces "software" and, given string variables s1 and s2, s1 + s2 indicates their concatenation.

The complications that may arise in practice include (1) wanting to concatenate the string versions of numeric variables and (2) wanting to concatenate variables, together with some separator such as a space or a comma. Given numeric variables n1 and n2

```
. gen str1 newstr = ""
. replace newstr = s1 + string(n1) + string(n2) + s2
```

shows how numeric values may be converted to their string equivalents before concatenation and

```
. replace newstr = s1 + " " + s2 + " " + s3
```

shows how spaces may be added in between variables. Here, as often happens, it is supposed that we would rather let Stata work out the particular string data type required. That is, we first generate a variable of type str1, the most compact string type; then the replace command automatically leads to promotion of the variable to the appropriate data type.

If all this is already possible, why then introduce concat()? concat() allows you to do everything in one line in a very concise manner.

```
. egen newstr = concat(s1 n1 n2 s2)
```

carries with it an implicit instruction to convert numeric values to their string equivalents, and the appropriate string data type is worked out within concat() by Stata's automatic promotion. Moreover,

```
. egen newstr = concat(s1 s2 s3), p(" ")
```

specifies that spaces are to be used as separators. (The default is no separation of concatenated strings.)

As an example of punctuation other than a space, consider

```
. egen fullname = concat(surname forename), p(", ")
```

Non-integer numerical values can cause difficulties, but

```
. egen newstr = concat(n1 n2), format(%9.3f) p(" ")
```

specifies the use of format %9.3f. In other words, this is equivalent to

```
. gen str1 newstr = ""
. replace newstr = string(n1,"%9.3f") + " " + string(n2,"%9.3f")
```

See [R] **16.3.5 String functions** for more on `string()`.

As a final flourish, the `decode` option instructs `concat()` to use value labels. With that option, the `maxlength()` option may also be used. For further details on `decode`, see [R] **encode**. Unlike the `decode` command, however, `concat()` uses `string(`*varname*`)`, not `""`, whenever values of *varname* are not associated with value labels, and the `format()` option, whenever specified, applies to this use of `string()`.

• `head(`*strvar*`)`, `last(`*strvar*`)` and `tail(`*strvar*`)` These three functions are for subdividing strings. The approach is to find specified separators using the `index()` string function and then to extract what is desired, which either precedes or follows the separators, using the `substr()` string function (see [U] **16.3.5 String functions**).

By default, substrings are considered to be separated by individual spaces, so we will give definitions in those terms, and generalize shortly.

The *head* of the string is whatever precedes the first space, or the whole of the string if no space occurs. This could also be called the first 'word'. The *tail* of the string is whatever follows the first space. This could be nothing or one or more words. The *last word* in the string is whatever follows the last space, or the whole of the string if no space occurs.

To make this clear, let us look at some examples. The quotation marks here just mark the limits of each string and are not part of the strings.

	head()	tail()	last()
"frog"	"frog"	""	"frog"
"frog toad"	"frog"	"toad"	"toad"
"frog toad newt"	"frog"	"toad newt"	"newt"
"frog toad newt"	"frog"	" toad newt"	"newt"
"frog toad newt"	"frog"	"toad newt"	"newt"

The main subtlety is that these functions are literal, so that the tail of `"frog  toad newt"`, in which two spaces follow `"frog"`, includes the second of those spaces, and is thus `" toad newt"`. Therefore you may prefer to use the `trim()` option to trim the result of any leading and/or trailing spaces, producing in this instance `"toad newt"`.

The `punct(`*pchars*`)` option may be used to specify separators other than spaces. The general definitions of `head()`, `tail()` and `last()` are therefore in terms of whatever separator has been specified, that is, relative to the first or last occurrence of the separator in the string value. Thus with `punct(,)` and the string `"Darwin, Charles Robert"` the head is `"Darwin"` and the tail and the last are both `" Charles Robert"`. Note again the leading space in this example, which may be trimmed with `trim()`. The punctuation (here the comma `,`) is discarded, just as it is with a single space.

pchars, the argument of `punct()`, will usually, but not necessarily, be a single character. If two or more characters are specified, then these must occur together; `punct(:;)` would mean that words are separated by a colon followed by a semi-colon (that is `:;`). It is not implied, in particular, that the colon and semi-colon are alternatives: for that the user must modify the programs presented here or resort to first principles using `tokenize` (see [R] **tokenize**).

With personal names `head()` or `last()` might be applied to extract surnames if strings were like `"Darwin, Charles Robert"` or `"Charles Robert Darwin"` with the surname coming first or last. What then happens with surnames like `"von Neumann"` or `"de la Mare"`? `"von Neumann, John"` is no problem, if the comma is specified as a separator, but `last()` does not contain enough intelligence to handle `"Walter de la Mare"` properly. For that, the best advice is to use programs specially written for person name extraction, such as `extrname` (Gould 1993).

• `rindex(`*strvar*`)`

The existing function `index()` finds the position of the first occurrence of a specified substring within a string. Thus `index("Stata","a")` returns 3, because the first occurrence of `"a"` in `"Stata"` starts at that position. Similarly `index("Stata","at")` is also 3.

`rindex()` (read right `index` if you wish) returns the position of the last occurrence of a substring. Thus if `"Stata"` were the value of a string variable, then `egen rindex = rindex(`*varname*`), sub(a)` would return 5 in that case.

As with `index()`, if a substring does not occur within the string value, then `rindex()` returns 0.

Note, however, that `rindex()` is not a perfect analogue of `index()`. `index()` can be applied to both variables and

individual strings. `rindex()` may only be applied to string variables.

• `sub(`*strvar*`)`

`sub()` substitutes occurrences of one substring with another. An important special case, which is in fact the default, is that the replacement substring is empty: that is, the substring is deleted.

`sub()` applies the extended macro function `subinstr` (see [U] **21.3.6 Extended macro functions**) to each observation in turn. As a consequence it may be rather slow.

If we wished to delete commas from a string variable, we would use

```
. egen nocomma = sub(myvar), f(,) all
```

while if we wished to replace them with spaces, we would have

```
. egen nocomma = sub(myvar), f(,) r(" ") all
```

Note the use of `all` to specify that all commas, not just the first found in each string value, should be replaced.

An important restriction in many problems is to work only on complete words. If we wished to replace `"man"` with `"male"`, then the option `word` would prevent `"woman"` becoming `"womale"`.

Functions for categorical and integer variables

• `any(`*varname*`)`, `eqany(`*varlist*`)` and `neqany(`*varlist*`)`

`any()`, `eqany()` and `neqany()` are for categorical or other variables taking integer values. If we define a subset of values specified by an integer *numlist* (see [U] **14.1.8 numlist**), then `any()` extracts the subset, leaving every other value missing, `eqany()` defines an indicator variable (1 if in subset, 0 otherwise), and `neqany()` counts occurrences of the subset across a set of variables. Therefore, with just one variable `eqany(`*varname*`)` and `neqany(`*varname*`)` are equivalent.

With the auto data supplied with official Stata, we can generate a variable containing the high values of `rep78` and a variable indicating whether `rep78` has a high value:

```
. egen hirep = any(rep78), v(3/5)
. egen ishirep = eqany(rep78), v(3/5)
```

In this case, it is easy to produce the same results with official Stata commands:

```
. gen hirep = rep78 if rep78 == 3 | rep78 == 4 | rep78 == 5
. gen byte ishirep = rep78 == 3 | rep78 == 4 | rep78 == 5
```

but as the specification becomes more complicated, or involves several variables, the `egen` functions here may be more convenient.

• `lgroup(`*varname*`)`

The existing `egen` function `group()` maps the distinct groups of a *varlist* to a categorical variable that takes on integer values from 1 to the number of groups. The order of the groups is that of the sort order of *varlist*. The *varlist* may be of numeric variables, string variables, or a mixture. The resulting variable can be useful for many purposes, including stepping through the distinct groups in an easy and systematic manner and tidying up an untidy ordering. Suppose the actual (and arbitrary) codes present in the data are $1, 2, 4$ and 7, but we desire equally spaced numbers, as when the codes will be values on one axis of a graph. `group( )` will map these to $1, 2, 3$ and 4.

The resulting variable does not have value labels. Therefore the values from 1 upwards carry no indication of meaning. Interpretation requires comparison with the original *varlist*.

`lgroup(`*varname*`)` produces a categorical variable in the same manner as `group()`, but with value labels. These value labels are either the actual values of *varname*, or any value labels of *varname*, if they exist. The values of *varname* could be as long as those of a single `str80` variable, yet value labels may be no longer than 80 characters. Thus `lgroup()` is restricted to taking a single variable.

The `missing` option behaves in the same way as that of `group()`. The default is that missing maps to missing. If missing values are to be treated like any other, and given an integer code, then specify `missing`.

• `rotate(`*varname*`)`

The idea behind `rotate()` is perhaps best explained by a specific example. A rainfall time series with a strong seasonal component is collected for each month over several years for a station in the Northern hemisphere. The months are coded 1 (January) through 12 (December). The scale, however, is clearly circular, and January follows December just as February follows January. A plot of rainfall against month shows a pattern of a dry summer (driest around July) and a wet winter (wettest

around January). But the conventional coding means that on this plot the interesting wet season is split between the left-hand and right-hand edges of the graph. It would be better to have the month axis extend from (say) July to June. Such a rotation would reunite the two parts of the wet season, and is accomplished by

```
. egen newmonth = rotate(month), st(7) max(12)
```

indicating that the new `start` is 7 and the scale wraps around after the `max`imum value of 12.

A special feature of `rotate()` is that any value labels associated with the variable to be rotated will be rotated to match. Thus `newmonth` has July coded as 1, in contrast to `month` which had July coded as 7. If `month` had value label `"July"` associated with value 7, then `newmonth` will have the same value label associated with value 1.

• `seq()`

`seq()` creates a new variable containing one or more sequences of integers. It is principally useful for quick creation of observation identifiers or automatic numbering of levels of factors or categorical variables. `seq()` is based on the separate command `seq` (Cox 1997), but one notable detail has been changed, as noted at the end of this section.

In the simplest case

```
. egen a = seq()
```

is just equivalent to the common idiom

```
. gen a = _n
```

`a` may also be obtained from

```
. range a 1 _N
```

(the actual value of `_N` may also be used).

In more complicated cases, `seq()` with option calls is equivalent to nimble fingerwork with those versatile functions `int` and `mod`.

```
. egen b = seq(), b(2)
```

produces integers in blocks of 2, while

```
. egen c = seq(), t(6)
```

restarts the sequence after 6 is reached.

```
. egen d = seq(), f(10) t(12)
```

shows that sequences may start with integers other than 1, and

```
. egen e = seq(), f(3) t(1)
```

shows that they may decrease.

Suppose we have 12 observations in memory. The results of these commands are shown by

```
. list a b c d e
```

and are

```
     a    b    c    d    e
1.   1    1    1   10    3
2.   2    1    2   11    2
3.   3    2    3   12    1
4.   4    2    4   10    3
5.   5    3    5   11    2
6.   6    3    6   12    1
7.   7    4    1   10    3
8.   8    4    2   11    2
9.   9    5    3   12    1
10.  10   5    4   10    3
11.  11   6    5   11    2
12.  12   6    6   12    1
```

All these sequences could have been generated in one line with `generate` and use of `int` and `mod` functions. The variables `b` through `e` are obtainable by

```
. gen b = 1 + int((_n - 1)/2)
. gen c = 1 + mod(_n - 1, 6)
. gen d = 10 + mod(_n - 1, 3)
. gen e = 3 - mod(_n - 1, 3)
```

Nevertheless `seq()` may save users from puzzling out such solutions, or indeed from typing in the needed values.

In general, the sequences produced depend on the sort order of observations, following three rules:

1: observations excluded by `if` or `in` are not counted.

2: observations are sorted by *byvarlist*, if specified.

3: otherwise, the order is that when called.

Note that `seq` (Cox 1997) did not use Rule 3. The consequence was that the result of applying `seq` was not guaranteed identical from application to application whenever sorting was required, even with identical data, because of the indeterminacy of sorting. That is, if we sort (say) integer values, it is sufficient that all the 1s are together and followed by all the 2s. But there is no guarantee that the order of the 1s, as defined by any other variables, will be identical from sort to sort.

The existing `egen` function `fill()` offers an alternative to `seq()` (see [R] **egen**). In essence, `fill()` requires a minimal example that indicates the kind of sequence required, whereas `seq()` requires the rule to be specified through options. There are sequences that `fill()` can produce that `seq()` cannot, and *vice versa*. `fill()` cannot be combined with `if` or `in`, in contrast to `seq()`.

Functions for statistical or quantitative analysis

- `pp(`*varname*`)`

`pp()` calculates plotting positions. These are so called because of their role in distributional diagnostic plots (see [R] **diagplots**). If data are ranked so that $x_{(1)}, \ldots, x_{(n)}$ are in ascending order, a general form that includes essentially all plotting positions used in practice is $(i - a)/(n - 2a + 1)$ for $i = 1, \ldots, n$ and some constant a. This provides, in essence, an estimate of the proportion of data less than or equal to $x_{(i)}$. Popular choices for a are 0.5, suggested by Hazen, and wired into the official Stata command `quantile`, and 0, suggested by Weibull and Gumbel, and wired into the official Stata commands `pnorm`, `qnorm`, `pchi` and `qchi`.

For many years there has been debate about the relative merits of these plotting position formulas: see Barnett (1975), Cunnane (1978) and Harter (1984). It is agreed that the ideal plotting positions depend on the distribution being fitted, and also on the precise purpose of plotting, whether model validation or parameter estimation. Cunnane (1978) focuses on probability plotting as estimation of quantiles, ideally with no bias and minimum variance. This implies, for example, that the Weibull or Gumbel formula with $a = 0$ is correct for the uniform distribution alone, while $a = 0.375$ should be used for the Gaussian or normal distribution, and $a = 0.44$ for the exponential and Gumbel (extreme value I) distributions. The latter values of a are closer to the Hazen proposal of 0.5 than to the Weibull or Gumbel proposal of 0. Many authors, including Chambers *et al.* (1983) and Meeker and Escobar (1998), use $a = 0.5$ as a general rule.

The purpose therefore of `pp()` is to provide Stata users with a general tool for choosing plotting positions, making it easier to produce customized distributional diagnostic plots, especially for probability distributions not allowed for in official Stata.

The option `by()` allows calculation of plotting positions to proceed separately for different groups, as in

```
. egen ppmpg = pp(mpg), by(rep78) a(0)
```

- `mode(`*varname*`)`

The mode is the most common value of a dataset. This idea can be applied to numeric and string variables alike. It is perhaps most useful for categorical variables (whether defined by integers or strings) or for other integer-valued values, but `mode()` can be applied to variables of any type. Nevertheless, the modes of continuous (or nearly continuous) variables are perhaps better estimated either from inspection of a graph of a frequency distribution or from the results of some density estimation (see [R] **kdensity**).

A key question is what to do if two or more values are equally common. The somewhat arbitrary default of `mode()` is that the highest such value will be reported. Highest means highest in sort order, whether numeric for numeric variables, or alphabetic for string variables. The opposite convention, to report the lowest, is obtained by the `minmode` option. A more stringent convention that only unique modes be reported is obtained by the `unique` option. With that stringent convention, there might not be a unique mode, in which case the result produced will be a missing value.

Missing values need special attention. It is very possible that missing (whether the period . for numeric variables or the empty string "" for string variables) is the most common value in a variable. However, missing values are by default excluded from determination of modes. If you wish to include them, use the `missing` option.

In contrast, `egen mode = mode(`*varname*`)` allows the generation of nonmissing modes for observations for which *varname* is missing. This allows use of the mode as one simple means of imputation for categorical variables. If it is desired that the mode is missing whenever *varname* is missing, that is readily achieved by specifying `if` *varname* `< .` or `if` *varname* `!= ""` or, most generally, `if !missing(`*varname*`)`.

• `rmed(`*varlist*`)`

`rmed()` resembles, for example, the existing `egen` function `rmean()`, but it produces medians across variables rather than means. The procedure used to calculate the median depends on placing all the values in a single observation (row of the data) into a temporary variable (column of the data). Therefore it is essential that the number of variables in the data be no greater than the number of observations. (If it is greater, then increasing the number of observations may be a way forward, assuming that sufficient memory is available. See [R] **obs**.)

• `mad(`*exp*`)` and `mdev(`*exp*`)`

`mad()` and `mdev()` produce alternative measures of spread. The median absolute deviation from the median and even the mean deviation will both be more resistant than the standard deviation to heavy tails or outliers, in particular from distributions with heavier tails than the normal or Gaussian. The first measure was named the MAD by Andrews et al. in 1972, but known already to K.F. Gauss in 1816, according to Hampel et al. (1986). For further historical and statistical details, see David (1998).

• `skew(`*varname*`)` and `kurt(`*varname*`)`

`skew()` and `kurt()` put the results of skewness and kurtosis calculations from `summarize` (see [R] **summarize**) into new variables.

Most commonly with such functions, we might wish to analyze variations in spread or shape measures between groups, so that typically the `by()` option will be used to produce values for distinct groups. But then the same MAD or skewness, for example, applies to every value in each group and the variable contains redundant information. In these circumstances, many tasks need use only one such value from each group.

• `tag(`*varlist*`)`

The answer to that need is `tag()`. `tag()` tags just one observation in each distinct group with 1 and all others with 0. Missing is never produced as a result, even for observations excluded by an `if` or `in` condition. This allows the user to be safe with idioms such as `if tag`. (`if tag` is a contraction of `if tag != 0`, which is always the same as `if tag == 1`, which is turn is always the same as `if tag`, when applied to the results of `tag()`.)

As an illustration, suppose we want a plot of group kurtosis versus group skewness. 100,000 values are divided into 100 groups.

```
. egen skew = skew(myvar), by(group)
. egen kurt = kurt(myvar), by(group)
. egen tag = tag(group)
. graph kurt skew if tag
```

This sequence of commands ensures that the graph is based on 100 data points, not 100,000 data points, each 1,000 of which is identical.

Evidently the same approach can be used with any other calculations of group summaries, whether with `egen` functions discussed here or with other Stata commands or programs.

A programming detail is that since groups might be as small as 1 in number, there are two possible approaches, to tag the first or the last in each group. `tag()` tags the first. This should be immaterial, but just in case it is important to you, note that which value is taken as first may not be identical, even with the same data, from application to application, because of the indeterminancy associated with sorting.

• `atan2(`*sinevar cosinevar*`)`

Official Stata already has an `atan()` function (see [U] **16.3.1 Mathematical functions**). `atan()` takes a single argument and returns a result in radians, between $-\pi/2$ and $\pi/2$, namely a range of half the circle. `atan2()` takes two variables as arguments, which we may call a sine variable and a cosine variable, as in

```
. egen atan = atan2(sinevar cosinevar)
```

It returns a result that is by default in degrees and between 0° and 360°. The option `radians` specifies a result in radians.

The choice of default range, 0° to 360° not -180° to 180°, and of default units, degrees not radians, arises from conventions in the statistical analysis of circular data, where these are the standard ways of expressing both data and results (see, for example, Fisher 1993).

- `pc(`*exp*`)` and `prop(`*exp*`)`

  `pc()` and `prop()` produce percents (which sum to 100) and proportions (which sum to 1).

- `rev(`*varname*`)`

  `rev()` is applicable to any variable, but perhaps most likely to be used with some quantitative variable which we want to reverse for some reason, making the first last, and *vice versa*.

Acknowledgments

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gr38	Enhancement to the hilite command

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For the visualization of more-than-two-dimensional data on a two-dimensional computer display, I find crosstabs in which points that satisfy some condition are marked (highlighted) quite useful. Stata provides the `hilite` command for this purpose. In my work, I feel often bothered that `hilite` is able to hilite a single expression only. Trying to get some understanding of three- or higher-dimensional structure is already hard enough for me to want to glance at different plots obtained by subsequent calls of `hilite`; I rather want to look at all these plots at the same time. Of course, printing is sometimes an option. The `forgraph` command (see Weesie 1999) is also sometimes of use.

Frustration with existing constraints often being the source of innovation, I wrote an extension to `hilite`, called `hilite2`, that reduces some of my frustrations; the frustrations that remain may well induce many future submissions to the *Stata Technical Bulletin*. I hope that some readers may feel the same, that is, a minor relief after glancing through this command. As far as I know, `hilite2` is backward compatible with `hilite`.

Syntax

`hilite2` *yvar xvar* [`if` *exp*] [`in` *range*], { `hilite(`*exp-list*`)` | `hivar(`*zvarlist*`)` }

[`miss` { `overlay` | `matrix` } `margin(`#`)` `symbol(`*str*`)` `nolabel`

`saving(`*filename*`)` `title(`*str*`)` `bsize(`#`)` *graph_options*]

Options

`hilite(`*exp-list*`)` specifies a list of expressions, separated by blanks, to be highlighted. The expressions should not contain embedded spaces.

`hivar(`*varlist*`)` specifies a *varlist* so that observations with the same values for variables in *varlist*, are highlighted. The variables may be numeric or string-typed.

`miss` specifies that observations with missing values of the `hivar`-*varlist* should be treated as a separate hilite group.

`overlay` specifies that the highlights for all expressions should be plotted in a single 'overlay' plot. In an overlay plot, at most 6 expressions should be implied by `hilite` or `hivar`.

`matrix` specifies that a matrix plot is produced of separate hilite plots for each explicit or implicit expression. For readability, vertical and horizontal labels are only displayed in the left-most and down-most plots. At most, 49 expressions should be implied by `hilite` or `hivar`.

`margin(#)` specifies the margin for a matrix-style plot.

`symbol(`*str*`)` specifies the symbols used to highlight expressions (see `symbols()` in online help for `graph`). If a matrix plot is produced, *str* should contain at most 2 characters. In an overlay plot, the number of characters in *str* should equal the number of expressions to be highlighted.

`nolabel` specifies that the titles describing the highlighting expressions for `hivar`-induced `hilite` groups ignore value labels. This may be useful if the resulting expressions are too long.

`saving(`*filename*`)` specifies the overlay plot or the matrix plot should be saved in a file named *filename*.

`title(`*str*`)` specifies the title displayed in the combined matrix plot.

`bsize(#)` specifies the plot size of the title describing the `hilite` expression.

graph_options are any of the options allowed with `graph, twoway`; see online help for `graph`. In the case of a matrix plot, these options are applied to each of the two-way scattergrams, not to the combined plot. Even `by()` is permitted but usually leads to an ugly plot.

Examples

First, `hilite2` allows highlighting of multiple sets of points, identified by a sequence of expressions. Expressions should be separated by white space, and thus should not contain embedded blanks. For example,

```
. hilite2 price mpg, hilite(rep78==1|rep78==2 rep78==3 rep78==4 rep78>4)
```

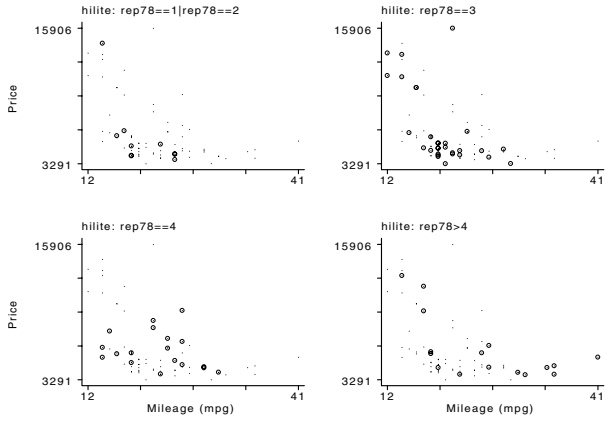

Figure 1. Using `hilite2` with four expressions.

produces Figure 1. (As a technical aside, `hilite2` parses off the option `hilite` using `parsoptp` (see Weesie 1997) and hence expressions may contain parentheses.) I would prefer to actually identify the two sets of points in one graph. This is accomplished with the `overlay` option:

```
hilite2 price mpg, hilite(rep78==1|rep78==2 rep78==3 rep78>3) overlay border xlabel ylabel
```

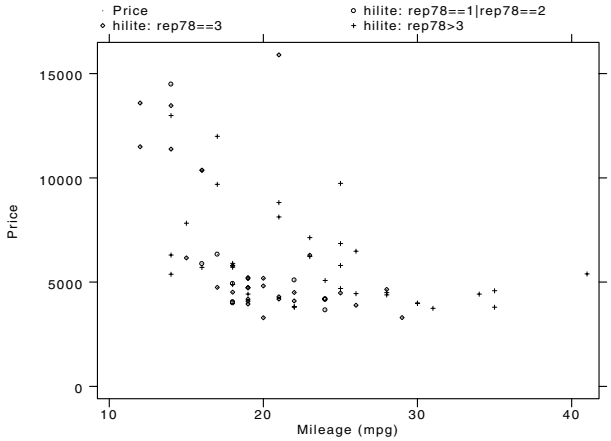

Figure 2. Using the `overlay` option.

Note that `hilite2` allows the specification of the normal options for `twoway` plots. Overlay plots are only possible with a restricted number of marker symbols; Stata currently allows up to six highlighted sets. Note that Stata will display identifying labels above the figure for at most 4 different sets.

Typing a sequence of explicit equations is tedious and often leads to errors. Often, as in the case above, the expressions are very similar. Thus, I added an option `hivar` that accepts a *varlist* and makes an overlay or matrix plot in which groups are highlighted that have the same values for the variables in *varlist*. Two examples

```
. hilite2 price mpg, hivar(rep78)
. hilite2  price mpg, hivar(rep78 foreign) border bsize(200) title(A big plot)
```

are shown in Figures 3 and 4.

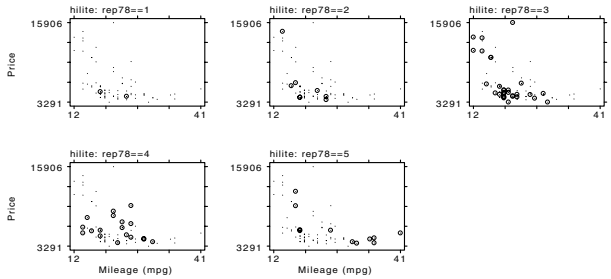

Figure 3.

(*Figure 4 on next page*)

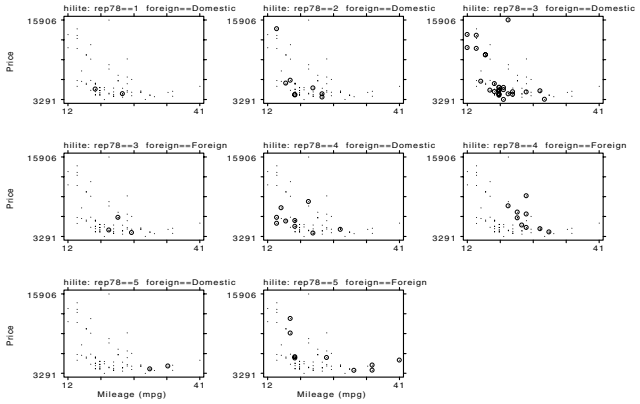

Figure 4.

Note that value labels are used whenever defined to enhance the readability of the plots.

References

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ip28 Automatically sorting by subgroup

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One of the powerful features of Stata is the fairly wide support for subgroup evaluation of commands via a `by` prefix command and a `by` option. Unfortunately, Stata requires the data to be sorted "manually" before invoking the `by` command. The command `bys` is a tiny program that simplifies the `by` command. Formally,

```
. bys varlist1 [(varlist2)] : command
```

is (almost) equivalent to

```
. sort varlist1 varlist2
. by varlist1 : command
```

"Almost" refers to two minor modifications. First, `bys` does not change (Stata's information about) the sorting order if the data are already sorted on at least *varlist1 varlist2*. Second, if `bys` does sort the data, it displays a message.

Examples of sublist sorting

Suppose I want to generate a variable that ranks men and women separately on their income. (For simplicity I ignore ties.) Thus, the richest man and woman should both be given the value 1, the second richest man and woman the value 2, and so on. The following command will do the trick.

```
. bys sex (income): gen rank = _n
```

If I have survival time data with subjects identified with `respnr` and entry times `_t0`, to generate a counter of episodes within subjects, sorted on entry time, we can use

```
. bys respnr (_t0): gen episode = _n
```

Remarks

The `byvar` command in Royston (1995) also automatically performs sorts, but does not permit subsorting. Also it adds a lot of functionality, namely the possibility to save results of analyses on subgroups. This comes at a high price in terms of performance if the added functionality is not needed.

I used a version of `bys` since I started to use Stata, because I never liked to "manually" sort variables. In addition, it was hard to explain to my colleagues and to students of my applied statistics classes why a modern program such as Stata would not sort itself. Recently on the discussion list, Bill Gould described his reason why Stata does not sort automatically: one requires the data to be sorted within the groups formed by the values of a *varlist*. This point is well taken. In an earlier version of `bys`, I dealt with this problem by *only* sorting if the data were not already "sufficiently" sorted, that is, sorted on the specified variables, and, possibly, on additional variables.

Bill suggested the syntax used above in order to specify sorting on *varlist2* within groups formed by *varlist1*. I like this new syntax as it expresses semantics much better than the current implicit approach with `by` and my original `bys`. I therefore modified my code of `bys`.

References

Royston, P. 1995. ip9: Repeat Stata command by variable(s). *Stata Technical Bulletin* 27: 3–5. Reprinted in *Stata Technical Bulletin Reprints* vol. 5, pp. 67–69.

sbe29	Generalized linear models: extensions to the binomial family

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In this article we present a new command for fitting generalized linear models with binary outcomes. The `binreg` command is an extension to the `glm` command that provides some features not available with `glm`. The `binreg` command offers one new link function (log complement) and provides proper range checking for other link functions (identity and log) so that one may obtain estimates with those links.

Using this new command, one may fit a generalized linear model with the binomial family and one of the four links identity, logistic, log, and log complement. Exponentiated coefficients are presented by default for the logistic, log, and log complement links, but the raw coefficients may be obtained using the `coeff` option. The identity link provides only the raw coefficients.

Syntax

`binreg` *depvar* [*varlist*] [*weight*] [`if` *exp*] [`in` *range*] [`, noconstant scale(x2|dev|#)` [`ln`]`offset(`*varname*`)`

`disp(#) coeff` [`or`|`rr`|`hr`|`rd`] `level(#) iterate(#) ltol(#) init(`*varname*`) n(`*varname*|`#)`

`nolog(#)`]

`aweights`, `fweights`, and `iweights` are allowed, see [U] **18.1.6 weight**.

`binreg` shares the features of all estimation commands.

Syntax for predict

`predict` [*type*] *newvarname* [`if` *exp*] [`in` *range*] [`,` *statistic*] [`nooffset`]

where *statistic* is

`mu`	predicted mean of $\widehat{y} = g^{-1}(\mathbf{x}\widehat{\mathcal{B}})$ (the default)
`xb`	linear prediction
`stdp`	standard error of the linear prediction; SE($\mathbf{x}_j\mathbf{b}$)
`deviance`	deviance residual
`pearson`	Pearson residual

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

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

Note that estimates of odds, risk and health ratios are obtained by exponentiating the appropriate coefficients. The option or produces the same results as Stata's logistic command and or coeff yields the same results as the logit command. When no link is specified/implied, or is assumed (logistic link is implied).

Options

noconstant specifies that the linear predictor has no intercept term, thus forcing it through the origin on the scale defined by the link function.

scale(x2|dev|#) overrides the default scale parameter. By default, scale(1) is assumed for discrete distributions (binomial, Poisson, negative binomial) and scale(x2) for continuous distributions (Gaussian, gamma, inverse Gaussian).

scale(x2) specifies the scale parameter be set to the Pearson chi-squared (or generalized chi-squared) statistic divided by the residual degrees of freedom.

scale(dev) sets the scale parameter to the deviance divided by the residual degrees of freedom. This provides an alternative to scale(x2) for continuous distributions and over- or under-dispersed discrete distributions.

scale(#) sets the scale parameter to #.

[ln]offset(*varname*) specifies an offset to be added to the linear predictor. offset() specifies the values directly: $g(E(y)) = xB$+*varname*. lnoffset() specifies exponentiated values: $g(E(y)) = xB$+ln(*varname*).

disp(#) multiplies the variance of y by # and divides the deviance by #. The resulting distributions are members of the quasi-likelihood family.

coeff displays the nonexponentiated coefficients and corresponding standard errors and confidence intervals. This has no effect when the rd option is specified as it is always presenting the nonexponentiated coefficients.

or requests the logit link and results in odds ratios if coeff is not specified.

rr requests the log link and results in risk ratios if coeff is not specified.

hr requests the log complement link and results in health ratios if coeff is not specified.

rd requests the identity link and results in risk differences if coeff is not specified.

level(#) specifies the confidence level, in percent, for confidence intervals of the coefficients.

iterate(#) specifies the maximum number of iterations allowed in estimating the model; iterate(50) is the default.

ltol(#) specifies the convergence criterion for the change in deviance between iterations; ltol(1e-6) is the default.

init(*varname*) specifies varname containing an initial estimate for the mean of *depvar*. This can be useful if you encounter convergence difficulties.

n(*varname*|#) specifies either a constant integer to use as the denominator for the binomial family, or a variable which holds the denominator for each observation. This is useful for grouped data; see [R] **glogit** for a complete description.

nolog(#) suppresses the iteration log.

Options for predict

mu the default, requests the predicted value of y; $\widehat{y} = g^{-1}(\mathbf{x}\widehat{\mathcal{B}})$.

xb calculates the linear prediction.

stdp requests the standard error of the linear predictor.

deviance requests the deviance residuals.

pearson requests Pearson residuals.

nooffset is relevant only if you specified offset() or lnoffset() for glm. It modifies the calculations made by predict so that they ignore the offset variable; the linear prediction is treated as $x_j b$ rather than $x_j b + \text{offset}_j$.

Remarks

Wacholder (1986) suggests methods for estimating risks ratios and risk differences from prospective binomial data. These estimates are obtained by selecting the proper link functions in the generalized linear model framework.

Let π_i be the probability of success for the i observation, $i = 1, \ldots, N$ and $X\beta$ the linear predictor. Then 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 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 it is possible to obtain fitted probabilities outside of 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.

Example

Wacholder (1986) presents an example utilizing data from Wright et al. (1983) of an investigation of the relationship between alcohol consumption and the risk of a low birth weight 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 is illustrated below.

Let's first describe the data and list a few observations.

```
. list, noobs
      cat          d          n        alc        smo        soc
        1         11         84          3          1          1
        2          5         79          2          1          1
        3         11        169          1          1          1
        4          6         28          3          2          1
        5          3         13          2          2          1
        6          1         26          1          2          1
        7          4         22          3          1          2
        8          3         25          2          1          2
        9         12        162          1          1          2
       10          4         17          3          2          2
       11          2          7          2          2          2
       12          6         38          1          2          2
       13          0         14          3          1          3
       14          1         18          2          1          3
       15         12         91          1          1          3
       16          7         19          3          2          3
       17          2         18          2          2          3
       18          8         70          1          2          3
```

Each observation corresponds to one of the 18 covariate structures. The number of low birth babies out of `n` in each category is given by the variable `d`.

We will begin by estimating risk ratios:

(*Example continued on next page*)

```
xi: binreg d I.soc I.alc I.smo, n(n) rr
I.smo                Ismo_1-2     (naturally coded; Ismo_1 omitted)
I.soc                Isoc_1-3     (naturally coded; Isoc_1 omitted)
I.alc                Ialc_1-3     (naturally coded; Ialc_1 omitted)

Iteration 1 : deviance =   14.2879
Iteration 2 : deviance =   13.6070
Iteration 3 : deviance =   13.6050
Iteration 4 : deviance =   13.6050

Residual df  =        12                              No. of obs =        18
Pearson X2   =  11.51517                              Deviance   =  13.60503
Dispersion   =  .9595976                              Dispersion =  1.133752

Binomial (N=n) distribution, log link
------------------------------------------------------------------------------
       d | Risk Ratio   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
  Ismo_2 |   1.648444    .332875      2.475   0.013       1.109657    2.448836
  Isoc_2 |   1.340001   .3127382      1.254   0.210        .848098     2.11721
  Isoc_3 |   1.349487   .3291488      1.229   0.219       .8366715    2.176619
  Ialc_2 |   1.191157   .3265354      0.638   0.523       .6960276    2.038503
  Ialc_3 |   1.974078   .4261751      3.150   0.002       1.293011    3.013884
------------------------------------------------------------------------------
```

By default, the program outputs 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 $\exp(0.6801017) = 1.9740785$. That is, mothers who drink heavily during their pregnancy have approximately twice the risk of delivering low weight babies than mothers who are light drinkers.

The nonexponentiated coefficients can be obtained via the `coeff` option.

```
. xi: binreg d I.smo I.soc I.alc, n(n) rr coeff
I.smo                Ismo_1-2     (naturally coded; Ismo_1 omitted)
I.soc                Isoc_1-3     (naturally coded; Isoc_1 omitted)
I.alc                Ialc_1-3     (naturally coded; Ialc_1 omitted)

Iteration 1 : deviance =   14.2879
Iteration 2 : deviance =   13.6070
Iteration 3 : deviance =   13.6050
Iteration 4 : deviance =   13.6050

Residual df  =        12                              No. of obs =        18
Pearson X2   =  11.51517                              Deviance   =  13.60503
Dispersion   =  .9595976                              Dispersion =  1.133752

Binomial (N=n) distribution, log link
Risk ratio coefficients
------------------------------------------------------------------------------
       d |      Coef.   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
  Ismo_2 |   .4998317   .2019329      2.475   0.013       .1040505    .8956129
  Isoc_2 |   .2926702   .2333866      1.254   0.210      -.1647591    .7500994
  Isoc_3 |   .2997244   .2439066      1.229   0.219      -.1783238    .7777726
  Ialc_2 |   .1749248    .274133      0.638   0.523       -.362366    .7122156
  Ialc_3 |   .6801017   .2158856      3.150   0.002       .2569737     1.10323
   _cons |  -2.764079   .2031606    -13.605   0.000      -3.162266   -2.365891
------------------------------------------------------------------------------
```

Risk differences are obtained using the `rd` option:

```
xi: binreg d I.soc I.alc I.smo, n(n) rd
I.soc                Isoc_1-3     (naturally coded; Isoc_1 omitted)
I.alc                Ialc_1-3     (naturally coded; Ialc_1 omitted)
I.smo                Ismo_1-2     (naturally coded; Ismo_1 omitted)

Iteration 1 : deviance =   18.6728
Iteration 2 : deviance =   14.9436
Iteration 3 : deviance =   14.9185
Iteration 4 : deviance =   14.9176
Iteration 5 : deviance =   14.9176
Iteration 6 : deviance =   14.9176
Iteration 7 : deviance =   14.9176
```

```
Residual df  =        12                              No. of obs =        18
Pearson X2   =  12.60353                             Deviance   =  14.91758
Dispersion   =  1.050294                             Dispersion =  1.243132

Binomial (N=n) distribution, identity link
Risk difference coefficients
------------------------------------------------------------------------------
       d |      Coef.   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
  Ismo_2 |   .0542415   .0270838      2.003   0.045       .0011582    .1073248
  Isoc_2 |   .0263817   .0232124      1.137   0.256      -.0191137    .0718771
  Isoc_3 |   .0365553   .0268668      1.361   0.174      -.0161026    .0892132
  Ialc_2 |   .0122539   .0257713      0.475   0.634      -.0382569    .0627647
  Ialc_3 |   .0801291   .0302878      2.646   0.008        .020766    .1394921
   _cons |    .059028   .0160693      3.673   0.000       .0275327    .0905232
------------------------------------------------------------------------------
```

The risk difference between the heavy drinkers and the light drinkers is simply the value of the coefficient for `Ialc_3` $= 0.0801291$. Note that risk differences are obtained directly from the coefficients estimated using the identity link, thus the `coeff` option has no effect in this case.

Health ratios are obtained using the `hr` option. The health ratios (exponentiated coefficients for the log complement link), are reported directly.

```
xi: binreg d I.soc I.alc I.smo, n(n) hr
.smo                Ismo_1-2     (naturally coded; Ismo_1 omitted)
I.soc                Isoc_1-3     (naturally coded; Isoc_1 omitted)
I.alc                Ialc_1-3     (naturally coded; Ialc_1 omitted)

Iteration 1 : deviance =   21.1523
Iteration 2 : deviance =   15.1647
Iteration 3 : deviance =   15.1320
Iteration 4 : deviance =   15.1311
Iteration 5 : deviance =   15.1311
Iteration 6 : deviance =   15.1311
Iteration 7 : deviance =   15.1311

Residual df  =        12                              No. of obs =        18
Pearson X2   =  12.84204                             Deviance   =  15.13111
Dispersion   =   1.07017                             Dispersion =  1.260925

Binomial (N=n) distribution, log-complement link
------------------------------------------------------------------------------
       d |Health Ratio   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
  Ismo_2 |   .9409983   .0296125     -1.932   0.053       .8847125    1.000865
  Isoc_2 |   .9720541    .024858     -1.108   0.268       .9245342    1.022017
  Isoc_3 |   .9597182   .0290412     -1.359   0.174       .9044535     1.01836
  Ialc_2 |   .9871517   .0278852     -0.458   0.647       .9339831    1.043347
  Ialc_3 |   .9134243   .0325726     -2.539   0.011       .8517631    .9795493
------------------------------------------------------------------------------
```

To see the nonexponentiated coefficients we can specify the `coeff` option.

Saved Results

`binreg` saves the same results in `e()` as `glm`. See [R] **glm** for a listing.

References

Wacholder, S. 1986. Binomial regression in GLIM: estimating risk ratios and risk differences. *American Journal of Epidemiology* 123: 174–184.

Wright, J. T., I. G. Barrison, I. G. Lewis et al. 1983. Alcohol consumption, pregnancy and low birthweight. *Lancet* 1: 663–665.

sg81.2	Multivariable fractional polynomials: update

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A small bug in one of the support routines to `mfracpol` (see Royston and Ambler, 1999) has been found and corrected.

Reference

Royston, P. and G. Ambler. 1999. sg81.1: Multivariable fractional polynomials: update. *Stata Technical Bulletin* 49: 17–23.

sg112.1 | Nonlinear regression models involving power or exponential functions of covariates: update

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The support routine `frac_ext.ado` was inadvertently left out of the distribution for `boxtid` (see Royston and Ambler, 1999). This caused an error in the `init` option. The diskette accompanying this issue of the STB has the complete distribution for `boxtid`.

Reference

Royston, P. and G. Ambler. 1999. sg112: Nonlinear regression models involving power or exponential functions of covariates. *Stata Technical Bulletin* 49: 25–30.

sg113 | Tabulation of modes

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Syntax

`modes` *varname* [*weight*] [`if` *exp*] [`in` *range*] [`, min(#)`]

Description

`modes` tabulates the mode(s) of *varname*, that is, the value(s) of *varname* that occur most frequently. *varname* may be numeric or string.

`fweights` and `aweights` are allowed.

Options

`min(#)` specifies that all values with a frequency of # or more should be shown.

Remarks

The mode may be defined strictly as the most common value of a variable, meaning the value with the highest frequency. Modes may be defined more broadly as common values, as is implied by terms such as bimodal or multimodal. In practice precise work with any broad definition requires a specification, possibly arbitrary, of the minimum acceptable frequency. Even with the strict definition several modes may be identified whenever two or more values occur with the highest observed frequency. Hence the problem of reporting modes is often a problem of tabulating several commonly observed values.

Information on modes is supplied as part of the output of `tabulate` (see [R] **tabulate**). However, with many data sets such output may be so long that a more specialized tool aimed at tabulating only the most common values may be useful.

`modes` by itself tabulates the value or values with the highest frequency. `modes` with the `min( )` option tabulates that value or values with at least the specified minimum frequency.

`modes` is most obviously useful with a discrete or categorical variable. Indeed, it may be applied to both numeric and string variables. Continuous variables may need to be placed in bins or classes first; otherwise with arbitrarily precise measurement each value approaches uniqueness. Alternatively, with a continuous (or nearly continuous) variable it may be much more helpful to inspect a graph of the frequency distribution when looking for modes, such as a histogram or a dotplot or a spike plot (see [G] **graph**). A graph is also likely to be much better for showing local modes; which may be defined as values more common than values just higher or lower, even if they are not especially common, and for showing other fine structure in the frequency distribution. Some form of density estimation (see [R] **kdensity**) may also be useful.

Example

```
. use auto
(1978 Automobile Data)
. modes rep78
Mode of rep78
----------+-----------
Repair    |
Record    |
1978      |  Frequency
----------+-----------
        3 |         30
----------+-----------
```

```
. modes rep78, min(10)
Modes of rep78
----------+-----------
Repair    |
Record    |
1978      |  Frequency
----------+-----------
        3 |          30
        4 |          18
        5 |          11
----------+-----------
```

sg114 | rglm - Robust variance estimates for generalized linear models

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Syntax

`rglm` [*varlist*] [*weight*] [`if` *exp*] [`in` *range*] [`,` `cluster`(*varname*) `mspec` `tdist` `minus`(*#*) *glm-options*]

`fweights`, `iweights` and `aweights` are allowed; see [U] **18.1.6 weight**.

Description

`rglm` fits generalized linear models and calculates a Huber (sandwich) estimate of the variance–covariance matrix of estimates. It can be used alone or called without arguments after a previous call to `glm`. As with other "robust" commands, the units may be considered to fall into clusters.

Options

`cluster`(*varname*) specifies the variable which defines sampling clusters.

`mspec` specifies that full Huber variances be used. These are robust to misspecification of conditional means. If `mspec` is absent, semi-Huber variances are calculated, robust to variance misspecification caused by overdispersion, underdispersion, heteroscedasticity and clustering, but assuming that conditional means are specified correctly by the model. (Except in the case of canonical link functions, where the semi-Huber variance is the full Huber variance. See Section 2.5 of McCullagh and Nelder (1989).)

`tdist` specifies that p values and confidence intervals are to be calculated assuming estimates to have a t distribution with $M - p$ degrees of freedom, where p is the number of model parameters, and M is the number of clusters if `cluster` is specified, or the number of observations (or sum of frequency weights) if `cluster` is not specified.

`minus(#)` specifies the `minus` parameter to pass to `_robust`, to apply a finite-sample adjustment to the Huber covariance matrix. If absent (or negative), it is reset to p (the number of model parameters).

glm-options are any of the options available for `glm`; see [R] **glm**.

If a *varlist* is supplied, then all `glm` options are allowed. If not, then the only `glm` options allowed are `level` and `eform`, and `cluster`, `mspec`, `tdist` and `minus` are ignored.

Methods and Formulas

In a generalized linear model (GLM), we attempt to predict an $(n \times 1)$ outcome variate Y using an $(n \times p)$ matrix X of predictor variates, where n is the number of observations and p is the number of parameters. These parameters form a $(p \times 1)$ vector β. The $(n \times 1)$ vector $\eta = X\beta$, known as the linear predictor, is used to predict Y, which is assumed in the model to have a conditional expectation equal to the $(n \times 1)$ vector μ. The vectors η and μ are assumed in the model to have a relation of the form $\eta_i = g(\mu_i)$, where $g(\cdot)$ is a monotonically increasing function, referred to as the link function. The conditional variance of y_i, given X, is assumed in the model to be proportional to a variance function $V(\mu_i)$. The choice of link function $g(\cdot)$ and variance function $V(\cdot)$ distinguishes one GLM from another. We will assume frequency weights (`fweights`) f_i and non-frequency weights (`iweights`) w_i, both defaulting to ones if not specified. (In fact, only one kind of weight may be specified, but that is a very minor defect of Stata, not a mathematical requirement.)

The fitting of a GLM involves finding values of β which give a zero value simultaneously for the p sums of scores $\sum_{i=1}^{n} f_i \psi_{ij}$, for j from 1 to p. The $(n \times p)$ matrix Ψ is defined such that $\psi_{ij} = w_i x_{ij} S_i$, where the S_i are in turn defined by

$$S_i = S(y_i, \eta_i) = \frac{d\mu_i}{d\eta_i} \left[V(\mu_i)\right]^{-1} (\mu_i - y_i) \tag{1}$$

In the model, S_i is interpreted as the derivative, with respect to η_i, of the ith squared deviance residual, which is proportional to the conditional log likelihood of y_i given the row matrix X_i. ψ_{ij} is the corresponding derivative with respect to β_j. (See [R] **glm** or McCullagh and Nelder 1989.)

The derivative of the jth sum of scores with respect to the kth parameter β_k is equal to $\sum_{i=1}^{n} f_i w_i x_{ij} x_{ik} H_i$, where H_i is the ith Hessian function

$$\begin{aligned}
H_i =& \frac{dS_i}{d\eta_i} \\
=& \left[V(\mu_i)\right]^{-1} \left(\frac{d\mu_i}{d\eta_i}\right)^2 + (\mu_i - y_i) \frac{d}{d\eta_i} \left\{ \left[V(\mu_i)\right]^{-1} \frac{d\mu_i}{d\eta_i} \right\} \\
=& \left[V(\mu_i)\right]^{-1} \left(\frac{d\mu_i}{d\eta_i}\right)^2 + \left[V(\mu_i)\right]^{-1} \frac{d^2\mu_i}{d\eta_i^2} (\mu_i - y_i) - \left[V(\mu_i)\right]^{-2} \frac{dV(\mu_i)}{d\mu_i} \left(\frac{d\mu_i}{d\eta_i}\right)^2 (\mu_i - y_i) \\
=& \left[V(\mu_i)\right]^{-1} \left[\left(\frac{d\mu_i}{d\eta_i}\right)^2 + \frac{d^2\mu_i}{d\eta_i^2} (\mu_i - y_i) - \frac{dV(\mu_i)}{d\mu_i} \frac{d\mu_i}{d\eta_i} S_i \right]
\end{aligned} \tag{2}$$

To estimate the dispersion matrix of the parameters β_j, we proceed as follows, using the principles of Huber (1967). Define the $(p \times p)$ matrix $D = \sum_{i=1}^{n} f_i w_i H_i X_i^T X_i$. The variance expression depends on whether or not clusters are specified. If there are no clusters, then the estimated dispersion matrix is

$$\frac{\sum_{i=1}^{n} f_i}{\sum_{i=1}^{n} f_i - k_{\text{minus}}} \left(\Psi D^{-1}\right)^T F \left(\Psi D^{-1}\right) \tag{3}$$

where k_{minus} is the value given by the `minus` option, and F is the $(n \times n)$ diagonal matrix of the frequency weights, f_i. If there are clusters, we denote by M the number of these clusters and define Ψ^* as the $(M \times p)$ matrix with one row per cluster, equal to the sum of the rows of Ψ corresponding to observations in that cluster, and estimate the dispersion matrix as

$$\frac{n}{n - k_{\text{minus}}} \left(\Psi^* D^{-1}\right)^T \left(\Psi^* D^{-1}\right) \tag{4}$$

(It does not make sense to have both clusters and `fweights`, because $f_i > 1$ implies that the ith observation represents multiple clusters.)

To calculate the Hessian in the general case by (2), we must know the variance function with its first derivative, and the inverse link function with its first two derivatives. The available variance functions have names corresponding to distributional families, whose variances are proportional to the respective functions, and their formula and derivatives are as follows:

Family name	$V(\mu)$	$dV(\mu)/d\mu$
Gaussian (normal)	1	0
Gamma	μ^2	2μ
Inverse Gaussian	μ^3	$3\mu^2$
Bernoulli	$\mu(1-\mu)$	$1-2\mu$
Poisson	μ	1
Negative binomial (shape parameter $= k$)	$\mu + k\mu^2$	$1 + 2k\mu$

The case of fitting a binomial model with totals m_i to the y_i is handled by `rglm` as equivalent to fitting a Bernoulli model to the proportions y_i/m_i and multiplying the `iweights` by the m_i. (That is to say, we substitute y_i/m_i for y_i, and $w_i m_i$ for w_i, in the formula above.) In the case of the negative binomial distribution, the shape parameter k is defined according to the conventions of the Stata manuals and the innards of `glm.ado`, in which k is the reciprocal of the parameter of the same name defined in McCullagh and Nelder (1989). I do not know how this confusing state of affairs came about.

The available forms for a link function $\eta = g(\mu)$ also have names. The following table gives their formula and inverses, with their first and second derivatives. The derivatives are expressed in a computationally convenient form. In the case of the probit link, $\Phi(\cdot)$ is the standard Gaussian cumulative distribution function, and $\phi(\cdot)$ is its derivative, the standard Gaussian probability density function.

Link function	$g(\mu)$	$g^{-1}(\eta)$	$d\mu/d\eta$	$d^2\mu/d\eta^2$
Identity	μ	η	1	0
Log	$\ln\mu$	e^η	μ	μ
Logit	$\ln[\mu/(1-\mu)]$	$e^\eta/(1+e^\eta)$	$\mu(1-\mu)$	$\mu(1-\mu)(1-2\mu)$
Probit	$\Phi^{-1}(\mu)$	$\Phi(\eta)$	$\phi(\eta)$	$-\eta\phi(\eta)$
Complementary log-log	$\log[-\log(1-\mu)]$	$1-e^{-e^\eta}$	$(\mu-1)\log(1-\mu)$	$[1+\log(1-\mu)]d\mu/d\eta$
Odds power q	$[\mu/(1-\mu)]^q$	$\eta^{1/q}/(1+\eta^{1/q})$	$1/q\mu^{1-q}(1-\mu)^{1+q}$	$\mu^{-q}(1-\mu)^q(1-2\mu-q)d\mu/d\eta$
Power q	μ^q	$\eta^{1/q}$	$q^{-1}\mu^{1-q}$	$(1-q)q^{-1}\mu^{-q}d\mu/d\eta$
Negative binomial (shape parameter$=k$)	$\ln[k\mu/(k\mu+1)]$	$k^{-1}e^\eta/(1-e^\eta)$	$\mu+k\mu^2$	$(1+2k\mu)d\mu/d\eta$

The negative binomial link function defined here is the correct version, consistent with the notation of the Stata manuals and with `glm.ado`. (The definition in [R] **glm** is a misprint.)

The calculation of the Hessian is greatly simplified if we can ignore the second term of the second line of (2), in which case we have

$$H_i = [V(\mu_i)]^{-1}\left(\frac{d\mu_i}{d\eta_i}\right)^2 \tag{5}$$

and we need only know the variance function and the first derivative of the inverse link. This equality holds, in the expectation, if the model is indeed a correct specification of the conditional mean of Y given X, so that $E(\mu_i - y_i) = 0$ for each individual i. It also holds if the link function is the canonical link for the variance function. In this case, the variance function is proportional to the first derivative of the inverse link, and their ratio is a constant function of η, so the second term of the second line in (2) is zero. (See Section 2.5 of McCullagh and Nelder 1989.) The variances calculated using the formula (5) are known as semi-Huber variances, whereas the variances calculated using formula (2) are known as full Huber variances. The semi-Huber variances (given by default) are robust to heteroscedasticity, overdispersion, underdispersion and clustering. The full Huber variances (obtained by the `mspec` option) are robust to all of these, and also to mis-specification of the conditional expectation. So, for instance, if we are fitting the parameters of a straight line, using a link function non-canonical for the chosen variance function, and the true relationship is slightly curved, then the parameters are estimates of the straight line giving the best fit to that curve, and the full Huber variances are consistent estimators of the true variance, in the population from which the rows of X and Y are jointly sampled. (I have not had time to do much research on how important the difference between semi-Huber and full Huber variances is in practice.)

Example 1

I often use `rglm` for carrying out unequal-variance t tests on logs, using the `eform` option to get confidence intervals (CIs) for the two group geometric means and their ratio. For instance, in the case of the auto data, we might decide (after looking at stem-and-leaf plots) that `mpg` (miles per gallon) was distributed lognormally rather than normally. The calculation of the geometric means and their ratio is carried out by Stata as follows:

```
. * Geometric averages and their ratio *
. gen logmpg=log(mpg)
. gen byte us=!foreign
. * Stem and leaf plots *
. 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
. stem logmpg
Stem-and-leaf plot for logmpg
logmpg rounded to nearest multiple of .01
plot in units of .01
  24* | 88
  25* |
  26* | 444444
  27* | 117777
  28* | 3333999999999
  29* | 44444444
  30* | 0004444499999
  31* | 4448888
  32* | 22222666
  33* | 3337
  34* | 003
  35* | 366
  36* |
  37* | 1
. * Geometric averages *
. rglm logmpg foreign us,tdist eform noconst
GLM with semi-Huber standard errors
Gaussian (normal) distribution, identity link
Number of observations: 74
------------------------------------------------------------------------------
             |             Semi-Huber
      logmpg |     e^coef   Std. Err.       t     P>|t|       [95% Conf. Interval]
-------------+----------------------------------------------------------------
     foreign |   23.96499   1.333711     57.079   0.000       21.44846    26.77678
          us |   19.30189   .6250385     91.414   0.000       18.09527    20.58898
------------------------------------------------------------------------------
. * Ratio between geometric averages *
. rglm logmpg foreign,tdist eform
GLM with semi-Huber standard errors
Gaussian (normal) distribution, identity link
Number of observations: 74
------------------------------------------------------------------------------
             |             Semi-Huber
      logmpg |     e^coef   Std. Err.       t     P>|t|       [95% Conf. Interval]
-------------+----------------------------------------------------------------
     foreign |   1.241587   .0799433      3.361   0.001       1.092027    1.411631
------------------------------------------------------------------------------
```

We find that foreign cars traveled at a geometric average of 23.96 mpg, whereas US cars traveled at a geometric average of 19.30 mpg. The foreign/US ratio was 1.24 (95% CI, 1.09 to 1.41), so foreign cars, on average, were 9% to 41% more efficient than US cars.

Example 2

We might also do a probit analysis to find a way of guessing whether a car is foreign, based on knowledge of its fuel efficiency and weight. The probit link is non-canonical for the Bernoulli variance function, so the full Huber variance will in general be different from the semi-Huber variance. Here, the analysis is carried out in three ways: using `glm`, using `rglm` with semi-Huber variances, and using `rglm` with full Huber variances. The results are as follows:

```
. * Non-robust using glm *
. glm foreign mpg weight,family(bernoulli) link(probit)
Iteration 1 : deviance =   58.5137
Iteration 2 : deviance =   54.3546
Iteration 3 : deviance =   53.7194
Iteration 4 : deviance =   53.6887
Iteration 5 : deviance =   53.6884
Iteration 6 : deviance =   53.6884
Iteration 7 : deviance =   53.6884
Residual df  =        71                                No. of obs =        74
Pearson X2   =  51.28325                                Deviance   =  53.68838
Dispersion   =  .7222992                                Dispersion =  .7561743
Bernoulli distribution, probit link
------------------------------------------------------------------------------
 foreign |      Coef.   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
     mpg |  -.1039505    .054209     -1.918   0.055      -.2101981    .0022972
  weight |  -.0023355    .000557     -4.193   0.000      -.0034273   -.0012438
   _cons |   8.275465   2.578791      3.209   0.001       3.221128     13.3298
------------------------------------------------------------------------------

. * Robust using rglm *
. rglm foreign mpg weight,family(bernoulli) link(probit)
GLM with semi-Huber standard errors
Bernoulli distribution, probit link
Number of observations: 74
------------------------------------------------------------------------------
         |             Semi-Huber
 foreign |      Coef.   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
     mpg |  -.1039505   .0690653     -1.505   0.132       -.239316     .031415
  weight |  -.0023355    .000497     -4.699   0.000      -.0033097   -.0013614
   _cons |   8.275465   2.751861      3.007   0.003       2.881916    13.66901
------------------------------------------------------------------------------

. * Robust using rglm with mis-specification correction *
. rglm foreign mpg weight,family(bernoulli) link(probit) mspec
GLM with full Huber standard errors
Bernoulli distribution, probit link
Number of observations: 74
------------------------------------------------------------------------------
         |                Huber
 foreign |      Coef.   Std. Err.       z     P>|z|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
     mpg |  -.1039505    .060185     -1.727   0.084      -.2219109      .01401
  weight |  -.0023355   .0005003     -4.669   0.000       -.003316   -.0013551
   _cons |   8.275465   2.574692      3.214   0.001       3.229161    13.32177
------------------------------------------------------------------------------
```

Note that the parameter estimates are the same with all three methods, but the confidence limits are slightly different. All three methods find that the data are (just) compatible with the hypothesis that the coefficient of `mpg` is zero. (That is to say, the hypothesis that, once you know the weight of a car, you can hazard a guess as to whether or not it is American, and be as likely to be right as you would have been if you also knew its fuel efficiency.)

Example 3

This example is based on Stata's housing data. Here, the data points are states of the USA, and we want to predict median rent from `pcturban` (percent urban) and `hsngval` (median housing value). This example compares the output from `rglm, tdist` with those from `regress` and `regress, robust`. Note that the two robust methods produce the same result (as they should), but the nonrobust method gives the same estimates and very different CIs.

```
. * Regression analysis *
. * Non-robust *
. regr rent hsngval pcturban
  Source |       SS       df       MS              Number of obs =      50
---------+------------------------------           F(  2,    47) =   47.54
   Model |  40983.5269     2  20491.7635            Prob > F      =  0.0000
Residual |  20259.5931    47  431.055172            R-squared     =  0.6692
---------+------------------------------           Adj R-squared =  0.6551
   Total |    61243.12    49  1249.85959            Root MSE      =  20.762
```

```
------------------------------------------------------------------------------
    rent |      Coef.   Std. Err.       t     P>|t|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
 hsngval |   .0015205   .0002276      6.681   0.000       .0010627    .0019784
pcturban |   .5248216   .2490782      2.107   0.040       .0237408    1.025902
   _cons |   125.9033   14.18537      8.876   0.000       97.36603    154.4406
------------------------------------------------------------------------------

. * Robust using regress *
. regr rent hsngval pcturban,robust
Regression with robust standard errors                Number of obs =      50
                                                      F(  2,    47) =   34.47
                                                      Prob > F      =  0.0000
                                                      R-squared     =  0.6692
                                                      Root MSE      =  20.762
------------------------------------------------------------------------------
             |               Robust
    rent |      Coef.   Std. Err.       t     P>|t|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
 hsngval |   .0015205   .0004654      3.267   0.002       .0005842    .0024568
pcturban |   .5248216    .309813      1.694   0.097      -.0984417    1.148085
   _cons |   125.9033   12.60741      9.986   0.000       100.5405    151.2662
------------------------------------------------------------------------------

. * Robust using rglm *
. rglm rent hsngval pcturban,tdist mspec
GLM with full Huber standard errors
Gaussian (normal) distribution, identity link
Number of observations: 50
------------------------------------------------------------------------------
             |                Huber
    rent |      Coef.   Std. Err.       t     P>|t|       [95% Conf. Interval]
---------+--------------------------------------------------------------------
 hsngval |   .0015205   .0004654      3.267   0.002       .0005842    .0024568
pcturban |   .5248216    .309813      1.694   0.097      -.0984417    1.148085
   _cons |   125.9033   12.60741      9.986   0.000       100.5405    151.2662
------------------------------------------------------------------------------
```

Validation

A program as comprehensive as `rglm` requires more validation than three examples. Accordingly, an intensive validation was carried out, using the auto data. `rglm` was tested using all six available variance functions, with one y variate for each (`rep78` for the three discrete families, `mpg` for the three continuous families). Each family was tested with one canonical and one non-canonical link, except the binomial family, which was tested with its canonical logit link and all the non-canonical links for which the Binomial family is obligatory. (So every family and link was tested, and every family was tested with a canonical and a non-canonical link.) For each combination of family and link, three models were fitted. These had parameters as follows:

Model 1. One parameter, corresponding to the grand mean.

Model 2. Two groups (US and foreign cars), with parameters corresponding to two group means.

Model 3. Two parameters (an intercept and the slope of a quantitative covariate).

The quantitative covariate in Model 3 was always `gratio` for identity links and `weight` for non-identity links. (This was done because when `mpg` and `rep78` were plotted against `weight` and `gratio`, the relationships involving `gratio` looked more linear.) The models fitted for each distributional family are summarized below.

Family	Y-variate	Canonical link	Covariate for canonical link	Non-canonical link(s)	Covariate for non-canonical link(s)
gaussian	mpg	identity	gratio	log	weight
gamma	mpg	power -1	weight	identity	gratio
igaussian	mpg	power -2	weight	identity	gratio
binomial	rep78	logit	weight	probit,cloglog,opower 2	weight
poisson	rep78	log	weight	identity	gratio
nbinomial	rep78	nbinomial	weight	identity	gratio

For each of the 42 models fitted, the dispersion was estimated in five different ways. These were the orthodox (Nelder) method given as default by `glm`, semi-Huber and full Huber variances without clustering, and semi-Huber and full Huber variances with clustering by `manuf`. Each parameter of each model therefore had five alternative standard errors (SEs).

In theory, some of these distinct SEs were expected to be equal. In the case of Model 1, there was no possibility for heteroscedasticity, overdispersion, underdispersion or misspecification (as there is a single constant X variate of ones), so all three unclustered SEs were expected to be equal, and both the clustered SEs were expected to be equal. In Model 2, there was a possibility of heteroscedasticity (because of unequal group variances), and sometimes overdispersion and underdispersion, but no possibility of misspecification (because the predicted value of each individual is its group mean). The semi-Huber SE was therefore expected to be equal to the corresponding full Huber SE in each clustering class, although the orthodox, unclustered Huber and clustered Huber SEs were expected to be different. In Model 3, there was a possibility of heteroscedasticity, overdispersion, underdispersion and misspecification, so all five SEs were expected to be different. Therefore, if `rglm` is working correctly, then we expect the SEs of Model 1 parameters to fall into two pre-defined equivalence groups (clustered and unclustered), the SEs of Model 2 parameters to fall into three pre-defined equivalence groups (orthodox, clustered Huber and unclustered Huber), and the SEs of Model 3 parameters to fall into five pre-defined equivalence groups of one each. SEs in the same equivalence group should be equal (or different only to the extent compatible with floating point calculation error), whereas SEs for the same model in different equivalence groups should be different.

As it happened, no two SEs in the same equivalence class were different by a ratio of more than 1.0001 (that is to say, the largest SE in an equivalence class was never more than 0.01% greater than the smallest SE in the same equivalence class). There was a lot more variation between equivalence classes for the same parameter of the same model. No two SEs in different equivalence classes for the same parameter of the same model differed by a ratio of less than 1.0020. That is to say, for any two SEs in different equivalence classes for the same parameter of the same model, the larger was always greater than the smaller by more than 0.2%, and usually the variation was much greater.

Figure 1 shows standard errors plotted on a binary log scale for all parameters of all models fitted. In the left-hand plot, the data points are SE equivalence classes (more than one for each parameter of each model), and the largest SE in the equivalence class is plotted against the smallest SE in the equivalence class. Note that all points are on the line of equality. In the right-hand plot, the data points are model parameters (one for each parameter of each model), and the largest SE for the parameter is plotted against the smallest SE calculated for that parameter. Note that the data points are visibly above the line of equality, although usually not so far above it as to indicate that the different SE calculation formulae give results in different binary orders of magnitude. So, unlike Example 3, these *ad hoc* examples do not truly demonstrate the advantages of Huber variances, although they do demonstrate that the SEs calculated by `rglm` using different methods are equal when they are supposed to be.

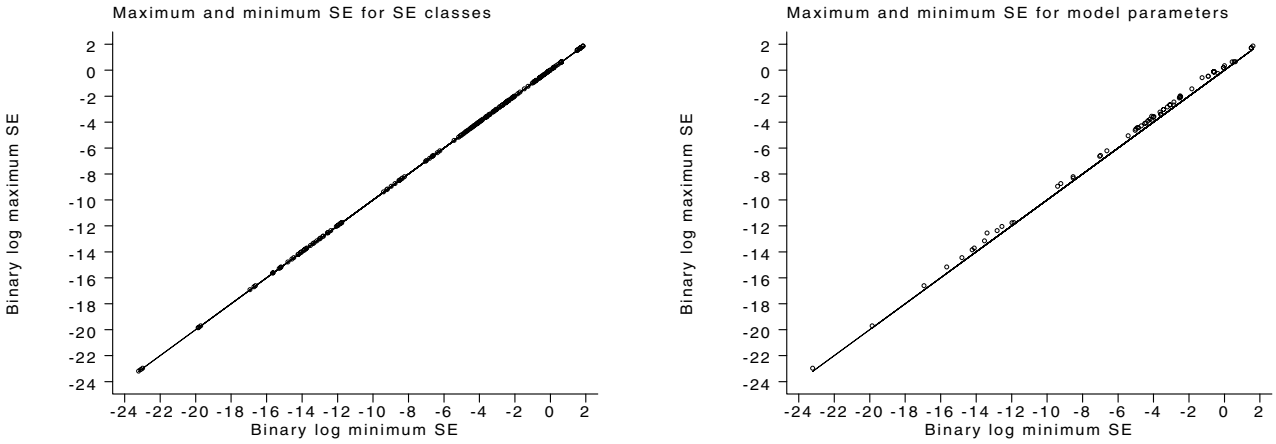

Figure 1. The results of the validation study for `rglm`.

Acknowledgment

This program was based on a previous version called `hglm`, which calculated only semi-Huber variances, and was kindly supplied to the author by David Clayton of MRC in Cambridge, England. The present author cleaned out some bugs, and added the options `mspec`, `tdist` and `minus`.

References

Huber, P. J. 1967. The behaviour of maximum likelihood estimates under non-standard conditions. In *Proceedings of the Fifth Berkeley Symposium in Mathematical Statistics and Probability*. Berkeley, CA: University of California Press, 221–233.

McCullagh, P. and J. A. Nelder. 1989. *Generalized Linear Models*. *2d ed.* London: Chapman and Hall.

stata53	censored option added to sts graph command

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`sts graph` has been modified so that tick marks indicating the number of censored observations may be placed on graphs of Kaplan–Meier survivor functions and Nelson–Aalen cumulative hazard functions.

The new option `censored()` does this; all other options remain unchanged.

Syntax

`sts graph` now has syntax

`sts graph` [`if` *exp*] [`in` *range*] [`, by(`*varlist*`) strata(`*varlist*`) adjustfor(`*varlist*`) nolabel failure gwood na cna level(#) lost enter separate tmin(#) tmax(#) xasis yasis noborder noshow noorigin atrisk censored(single | number | multiple)` *graph_options*]

Options

The `censored()` option is new. See [R] **sts graph** for a description of the other options.

`censored(single|number|multiple)` specifies that tick marks be placed on the graph to indicate the censored observations.

`censored(single)` places one tick at each censoring time regardless of the number of censorings at that time.

`censored(number)` places one tick at each censoring time and displays the number of censorings above the tick.

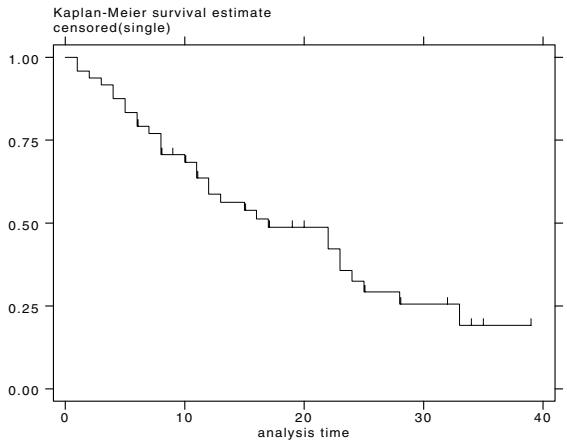
`censored(multiple)` places multiple ticks for multiple censorings at the same time. If three observations are censored at time 5, then three ticks are placed around time 5. `censored(multiple)` is intended for use when there are few censored observations; if there are too many, the graph can look bad and in such cases we recommend that `censored(number)` be used.

`censored()` is not allowed with options `lost`, `enter` or `atrisk`.

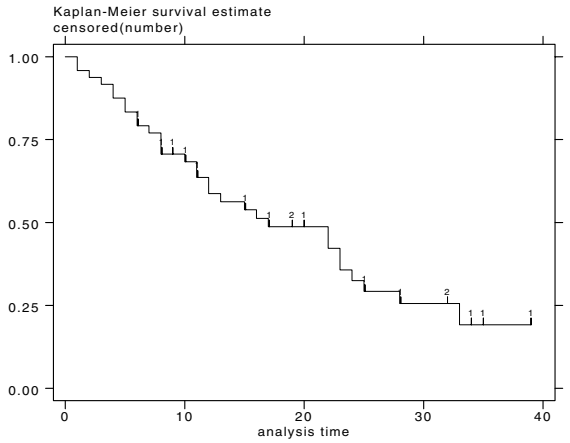
Example

Using the cancer data distributed with Stata, we will plot the Kaplan–Meier estimated survivor function using each of the three censoring options:

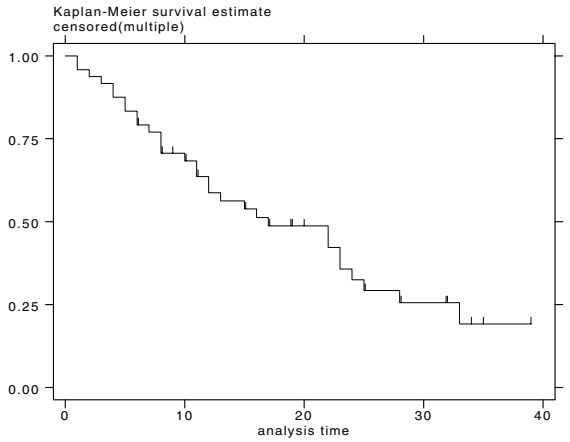
```
. use cancer.dta
(Patient Survival in Drug Trial)
. stset studytim, failure(died)
(output omitted)
. sts graph, censored(single) t1("censored(single)")
```



```
. sts graph, censored(number) t1("censored(number)")
```

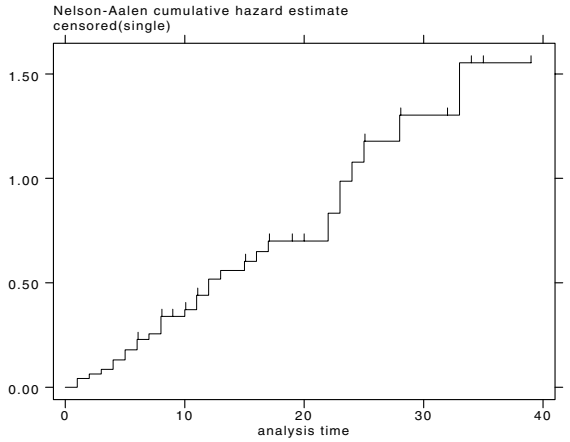



```
. sts graph, censored(multiple) t1("censored(multiple)")
```

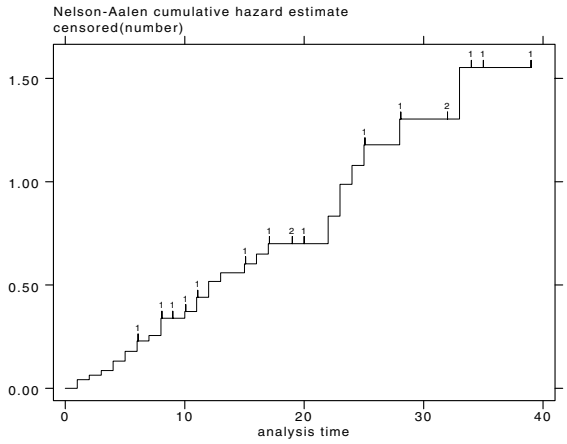


Similarly, the new option can be used when plotting the estimated Nelson–Aalen cumulative hazard function.

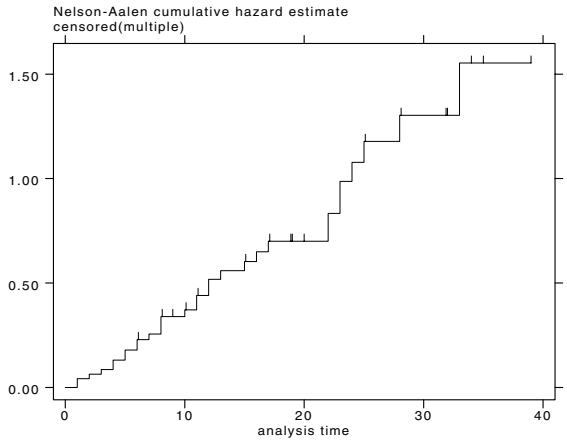
```
. sts graph, na censored(single) t1("censored(single)")
```



```
. sts graph, na censored(number) t1("censored(number)")
```




```
. sts graph, na censored(multiple) t1("censored(multiple)")
```



sxd1.1 Update to random allocation of treatments to blocks

Philip Ryan, University of Adelaide, Australia, pryan@medicine.adelaide.edu.au

In Ryan (1998) I published a program `ralloc` that randomly allocates treatments in blocks. I have updated the program in the following ways:

1. There is a new option `tr#lab(`*string*`)` (where # can be 1, 2, 3, or 4) allowing user-specified treatment names. The defaults remain `A`, `B`, `C`, and `D`.

2. There is a new option `shape({ long | wide })` allowing the randomization schedule to be saved in wide or long forms. In long form each observation is a treatment allocation, while in wide form each observation is a block (see the example below). Further, Stata's `reshape` parameters are set so that one can easily switch between long and wide forms.

3. As a consequence of the above, the old variable called *Order* produced by `ralloc` is replaced by a new *SeqInBlk* (sequence within block) variable.

4. There are new choices of 1 or 2 in the `osize(#)` option. Previously, this option, which sets the number of different block sizes, took arguments 3, 4, 5, 6, or 7. This was really because my own work placed a premium on concealing the allocation sequence, rather than minimizing the chance of imbalance. For smaller studies, the latter may be more important, so a constant minimum block size (equal to the number of treatments) can now be specified by `osize(1)`. The value 2 was included for good measure.

5. Modification of, and addition to, the saved notes.

Note that `ralloc` is still written in Stata 5; the only change required to make it Stata 6 would be to modify the `syntax` statement, but I felt that some people may have used it to generate randomization schedules under Stata 5, still only have Stata 5, and would like the continuing facility to be able to reproduce their schedule, say for auditing purposes.

Example

To illustrate the new `shape` option, we have

```
. ralloc blknum blksiz Rx, ns(494) osiz(2) eq ntreat(2) sav(mywide) shape(wide)
>   tr1lab(Placebo) tr2lab(Active)
Frequency of block sizes:
 block size |      Freq.     Percent        Cum.
------------+-----------------------------------
          2 |         81       49.39       49.39
          4 |         83       50.61      100.00
------------+-----------------------------------
      Total |        164      100.00

  Randomisation data is saved to mywide.dta and is now in memory.
  Issue the notes command to review your protocol.

. list in 1/7
       blknum     blksiz        Rx1        Rx2        Rx3        Rx4
  1.        1          2     Active    Placebo          .          .
  2.        2          4    Placebo    Placebo     Active     Active
  3.        3          4     Active    Placebo     Active    Placebo
  4.        4          4     Active     Active    Placebo    Placebo
  5.        5          4    Placebo    Placebo     Active     Active
  6.        6          2    Placebo     Active          .          .
  7.        7          4    Placebo     Active    Placebo     Active
```

If we now use `reshape` we have

```
. reshape long
(note:  j = 1 2 3 4)
Data                               wide   ->  long
-----------------------------------------------------------------------------
Number of obs.                      164   ->     656
Number of variables                   6   ->       4
j variable (4 values)                     ->   SeqInBlk
xij variables:
                        Rx1 Rx2 ... Rx4   ->   Rx
-----------------------------------------------------------------------------
```

To illustrate the new *SeqInBlk* variable, we have

```
. sort blknum SeqInBlk
. drop if Rx == .
(162 observations deleted)
. list in 1/10
       blknum   SeqInBlk     blksiz         Rx
  1.        1          1          2     Active
  2.        1          2          2    Placebo
  3.        2          1          4    Placebo
  4.        2          2          4    Placebo
  5.        2          3          4     Active
  6.        2          4          4     Active
  7.        3          1          4     Active
  8.        3          2          4    Placebo
  9.        3          3          4     Active
 10.        3          4          4    Placebo
```

Reference

Ryan, P. 1998. sxd1: Random allocation of treatments in blocks. *Stata Technical Bulletin* 41: 43–46. Reprinted in *Stata Technical Bulletin Reprints* vol. 7, pp. 297–300.

STB categories and insert codes

Inserts in the STB are presently categorized as follows:

General Categories:

an	announcements	*ip*	instruction on programming
cc	communications & letters	*os*	operating system, hardware, & interprogram communication
dm	data management		
dt	datasets	*qs*	questions and suggestions
gr	graphics	*tt*	teaching
in	instruction	*zz*	not elsewhere classified

Statistical Categories:

sbe	biostatistics & epidemiology	*ssa*	survival analysis
sed	exploratory data analysis	*ssi*	simulation & random numbers
sg	general statistics	*sss*	social science & psychometrics
smv	multivariate analysis	*sts*	time-series, econometrics
snp	nonparametric methods	*svy*	survey sampling
sqc	quality control	*sxd*	experimental design
sqv	analysis of qualitative variables	*szz*	not elsewhere classified
srd	robust methods & statistical diagnostics		

In addition, we have granted one other prefix, *stata*, to the manufacturers of Stata for their exclusive use.

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The Stata Technical Bulletin (STB) is a journal that is intended to provide a forum for Stata users of all disciplines and levels of sophistication. The STB contains articles written by StataCorp, Stata users, and others.

Articles include new Stata commands (ado-files), programming tutorials, illustrations of data analysis techniques, discussions on teaching statistics, debates on appropriate statistical techniques, reports on other programs, and interesting datasets, announcements, questions, and suggestions.

A submission to the STB consists of

1. An insert (article) describing the purpose of the submission. The STB is produced using plain TEX so submissions using TEX (or LATEX) are the easiest for the editor to handle, but any word processor is appropriate. If you are not using TEX and your insert contains a significant amount of mathematics, please FAX (409–845–3144) a copy of the insert so we can see the intended appearance of the text.

2. Any ado-files, `.exe` files, or other software that accompanies the submission.

3. A help file for each ado-file included in the submission. See any recent STB diskette for the structure a help file. If you have questions, fill in as much of the information as possible and we will take care of the details.

4. A do-file that replicates the examples in your text. Also include the datasets used in the example. This allows us to verify that the software works as described and allows users to replicate the examples as a way of learning how to use the software.

5. Files containing the graphs to be included in the insert. If you have used STAGE to edit the graphs in your submission, be sure to include the `.gph` files. Do not add titles (e.g., "Figure 1: ...") to your graphs as we will have to strip them off.

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```

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