mecloglog — Multilevel mixed-effects complementary log–log regression

Description

mecloglog fits mixed-effects models for binary or binomial responses. The conditional distribution of the response given the random effects is assumed to be Bernoulli, with probability of success determined by the inverse complementary log–log function.

Quick start

Two-level complementary log–log model of $y$ on $x$ with random intercepts by $\text{lev2}$

```
mecloglog y x || lev2:
```

Add binary variable $a$ and random coefficients for $a$

```
mecloglog y x a || lev2: a
```

As above, but allow the random effects to be correlated

```
mecloglog y x a || lev2: a, covariance(unstructured)
```

Three-level random-intercept model of $y$ on $x$ with $\text{lev2}$ nested within $\text{lev3}$

```
mecloglog y x || lev3: || lev2:
```

Crossed-effects model of $y$ on $x$ with two-way crossed random effects by factors $a$ and $b$

```
mecloglog y x || _all:R.a || b:
```

Menu

Statistics > Multilevel mixed-effects models > Complementary log–log regression
Syntax

mecloglog  depvar  fe_equation  [  ||  re_equation  ]  [  ||  re_equation  ...  ]  [  ,  options  ]

where the syntax of  fe_equation  is

\[  \text{indepvars}  \]  \[  \text{if}  \]  \[  \text{in}  \]  \[  \text{weight}  \]  \[  ,  fe_options  \]

and the syntax of  re_equation  is one of the following:

for random coefficients and intercepts

\[  \text{levelvar: }  \text{varlist}  \]  \[  ,  re_options  \]

for random effects among the values of a factor variable in a crossed-effects model

\[  \text{levelvar: }  \text{R. varname}  \]

\text{levelvar}  \ is a variable identifying the group structure for the random effects at that level or is  _all  representing one group comprising all observations.

<table>
<thead>
<tr>
<th>fe_options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\text{noconstant}</td>
<td>suppress constant term from the fixed-effects equation</td>
</tr>
<tr>
<td>\text{offset(varname)}</td>
<td>include  \text{varname}  in model with coefficient constrained to 1</td>
</tr>
<tr>
<td>\text{asis}</td>
<td>retain perfect predictor variables</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>re_options</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>\text{covariance(vartype)}</td>
<td>variance–covariance structure of the random effects</td>
</tr>
<tr>
<td>\text{noconstant}</td>
<td>suppress constant term from the random-effects equation</td>
</tr>
<tr>
<td>\text{fweight(varname)}</td>
<td>frequency weights at higher levels</td>
</tr>
<tr>
<td>\text{iweight(varname)}</td>
<td>importance weights at higher levels</td>
</tr>
<tr>
<td>\text{pweight(varname)}</td>
<td>sampling weights at higher levels</td>
</tr>
</tbody>
</table>
### mecloglog — Multilevel mixed-effects complementary log–log regression

#### options

<table>
<thead>
<tr>
<th>Model</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>`binomial(varname</td>
<td>#)`</td>
</tr>
<tr>
<td><code>constraints(constraints)</code></td>
<td>apply specified linear constraints</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>SE/R robust</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>vce(vcetype)</code></td>
<td><code>vcetype</code> may be oim, opg, robust, or cluster clustvar</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Reporting</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>level(#)</code></td>
<td>set confidence level; default is level(95)</td>
</tr>
<tr>
<td><code>eform</code></td>
<td>report exponentiated coefficients</td>
</tr>
<tr>
<td><code>nocnsreport</code></td>
<td>do not display constraints</td>
</tr>
<tr>
<td><code>notable</code></td>
<td>suppress coefficient table</td>
</tr>
<tr>
<td><code>noheader</code></td>
<td>suppress output header</td>
</tr>
<tr>
<td><code>nogroup</code></td>
<td>suppress table summarizing groups</td>
</tr>
<tr>
<td><code>display_options</code></td>
<td>control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Integration</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>intmethod(intmethod)</code></td>
<td>integration method</td>
</tr>
<tr>
<td><code>intpoints(#)</code></td>
<td>set the number of integration (quadrature) points for all levels; default is intpoints(7)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Maximization</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>maximize_options</code></td>
<td>control the maximization process; seldom used</td>
</tr>
<tr>
<td><code>startvalues(svmethod)</code></td>
<td>method for obtaining starting values</td>
</tr>
<tr>
<td><code>startgrid[ gridspec ]</code></td>
<td>perform a grid search to improve starting values</td>
</tr>
<tr>
<td><code>noestimate</code></td>
<td>do not fit the model; show starting values instead</td>
</tr>
<tr>
<td><code>dnumerical</code></td>
<td>use numerical derivative techniques</td>
</tr>
<tr>
<td><code>collinear</code></td>
<td>keep collinear variables</td>
</tr>
<tr>
<td><code>coeflegend</code></td>
<td>display legend instead of statistics</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>vartype</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>independent</code></td>
<td>one unique variance parameter per random effect and all covariances 0; the default unless the R. notation is used</td>
</tr>
<tr>
<td><code>exchangeable</code></td>
<td>equal variances for random effects and one common pairwise covariance</td>
</tr>
<tr>
<td><code>identity</code></td>
<td>equal variances for random effects and all covariances 0; the default if the R. notation is used</td>
</tr>
<tr>
<td><code>unstructured</code></td>
<td>all variances and covariances to be distinctly estimated</td>
</tr>
<tr>
<td><code>fixed(matname)</code></td>
<td>user-selected variances and covariances constrained to specified values; the remaining variances and covariances unrestricted</td>
</tr>
<tr>
<td><code>pattern(matname)</code></td>
<td>user-selected variances and covariances constrained to be equal; the remaining variances and covariances unrestricted</td>
</tr>
</tbody>
</table>
### Model

**noconstant** suppresses the constant (intercept) term and may be specified for the fixed-effects equation and for any of or all the random-effects equations.

**offset**(_varname_) specifies that _varname_ be included in the fixed-effects portion of the model with the coefficient constrained to be 1.

**asis** forces retention of perfect predictor variables and their associated, perfectly predicted observations and may produce instabilities in maximization; see [R] _probit_.

**covariance**(_vartype_) specifies the structure of the covariance matrix for the random effects and may be specified for each random-effects equation. _vartype_ is one of the following: independent, exchangeable, identity, unstructured, fixed(_matname_), or pattern(_matname_).

**covariance**(_independent_) covariance structure allows for a distinct variance for each random effect within a random-effects equation and assumes that all covariances are 0. The default is covariance(_independent_) unless a crossed random-effects model is fit, in which case the default is covariance(_identity_).

**covariance**(_exchangeable_) structure specifies one common variance for all random effects and one common pairwise covariance.

**covariance**(_identity_) is short for “multiple of the identity”; that is, all variances are equal and all covariances are 0.

**covariance**(_unstructured_) allows for all variances and covariances to be distinct. If an equation consists of _p_ random-effects terms, the unstructured covariance matrix will have _p_( _p_ + 1)/2 unique parameters.

**covariance**(_fixed(_matname_)) and **covariance**(_pattern(_matname_)) covariance structures provide a convenient way to impose constraints on variances and covariances of random effects. Each specification requires a _matname_ that defines the restrictions placed on variances and
covariances. Only elements in the lower triangle of *matname* are used, and row and column names of *matname* are ignored. A missing value in *matname* means that a given element is unrestricted.

In a **fixed**(*matname*) covariance structure, (co)variance (*i, j*) is constrained to equal the value specified in the *i, j*th entry of *matname*. In a **pattern**(*matname*) covariance structure, (co)variances (*i, j*) and (*k, l*) are constrained to be equal if *matname*[i,j] = *matname*[k,l].

**fweight**(*varname*) specifies frequency weights at higher levels in a multilevel model, whereas frequency weights at the first level (the observation level) are specified in the usual manner, for example, [fw=fwtvar1]. *varname* can be any valid Stata variable name, and you can specify **fweight()** at levels two and higher of a multilevel model. For example, in the two-level model

```
. mecmcmd fixed_portion [fw = wt1] || school: ... , fweight(wt2) ...
```

the variable wt1 would hold the first-level (the observation-level) frequency weights, and wt2 would hold the second-level (the school-level) frequency weights.

**iweight**(*varname*) specifies importance weights at higher levels in a multilevel model, whereas importance weights at the first level (the observation level) are specified in the usual manner, for example, [iw=iwtvar1]. *varname* can be any valid Stata variable name, and you can specify **iweight()** at levels two and higher of a multilevel model. For example, in the two-level model

```
. mecmcmd fixed_portion [iw = wt1] || school: ... , iweight(wt2) ...
```

the variable wt1 would hold the first-level (the observation-level) importance weights, and wt2 would hold the second-level (the school-level) importance weights.

**pweight**(*varname*) specifies sampling weights at higher levels in a multilevel model, whereas sampling weights at the first level (the observation level) are specified in the usual manner, for example, [pw=pwtvar1]. *varname* can be any valid Stata variable name, and you can specify **pweight()** at levels two and higher of a multilevel model. For example, in the two-level model

```
. mecmcmd fixed_portion [pw = wt1] || school: ... , pweight(wt2) ...
```

variable wt1 would hold the first-level (the observation-level) sampling weights, and wt2 would hold the second-level (the school-level) sampling weights.

**binomial**(varname | #) specifies that the data are in binomial form; that is, *depvar* records the number of successes from a series of binomial trials. This number of trials is given either as *varname*, which allows this number to vary over the observations, or as the constant #. If **binomial()** is not specified (the default), *depvar* is treated as Bernoulli, with any nonzero, nonmissing values indicating positive responses.

**constraints**(constraints); see [R] Estimation options.

**vce**(vcetype) specifies the type of standard error reported, which includes types that are derived from asymptotic theory (oim, opg), that are robust to some kinds of misspecification (robust), and that allow for intragroup correlation (cluster clustvar); see [R] vce_option. If **vce**(robust) is specified, robust variances are clustered at the highest level in the multilevel model.

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

**eform** reports exponentiated coefficients and corresponding standard errors and confidence intervals. This option may be specified either at estimation or upon replay.

**nocnsreport**; see [R] Estimation options.
notable suppresses the estimation table, either at estimation or upon replay.
noheader suppresses the output header, either at estimation or upon replay.
nogroup suppresses the display of group summary information (number of groups, average group size, minimum, and maximum) from the output header.

display_options: noci, nopvalues, noomitted, vsquish, noemptycells, baselevels, allbaselevels, noflabel, fwrap(#), fwrapon(style), cformat(\%fmt), pformat(\%fmt), sformat(\%fmt), and nolstretch; see [R] Estimation options.

Integration
intmethod(intmethod) specifies the integration method to be used for the random-effects model. mvaghermite performs mean–variance adaptive Gauss–Hermite quadrature; mcaghermite performs mode-curvature adaptive Gauss–Hermite quadrature; ghermite performs nonadaptive Gauss–Hermite quadrature; and laplace performs the Laplacian approximation, equivalent to mode-curvature adaptive Gaussian quadrature with one integration point.

The default integration method is mvaghermite unless a crossed random-effects model is fit, in which case the default integration method is laplace. The Laplacian approximation has been known to produce biased parameter estimates; however, the bias tends to be more prominent in the estimates of the variance components rather than in the estimates of the fixed effects.

For crossed random-effects models, estimation with more than one quadrature point may be prohibitively intensive even for a small number of levels. For this reason, the integration method defaults to the Laplacian approximation. You may override this behavior by specifying a different integration method.

intpoints(#) sets the number of integration points for quadrature. The default is intpoints(7), which means that seven quadrature points are used for each level of random effects. This option is not allowed with intmethod(laplace).

The more integration points, the more accurate the approximation to the log likelihood. However, computation time increases as a function of the number of quadrature points raised to a power equaling the dimension of the random-effects specification. In crossed random-effects models and in models with many levels or many random coefficients, this increase can be substantial.

Maximization
maximize_options: difficult, technique(algorithm_spec), iterate(#), [no]log, trace, gradient, showstep, hessian, showtolerance, tolerance(#), ltolerance(#), nrtolerance(#), nonrtolerance, and from(init_specs); see [R] Maximize. Those that require special mention for mecloglog are listed below.

from() accepts a properly labeled vector of initial values or a list of coefficient names with values. A list of values is not allowed.

The following options are available with mecloglog but are not shown in the dialog box:
startvalues(svmethod), startgrid[ gridspec ], noestimate, and dnumerical; see [ME] meglm.
collinear, coeflegend; see [R] Estimation options.
Remarks and examples

Mixed-effects complementary log–log (cloglog) regression is cloglog regression containing both fixed effects and random effects. In longitudinal data and panel data, random effects are useful for modeling intracluster correlation; that is, observations in the same cluster are correlated because they share common cluster-level random effects.

mecloglog allows for many levels of random effects. However, for simplicity, we here consider the two-level model, where for a series of \( M \) independent clusters, and conditional on a set of fixed effects \( x_{ij} \) and a set of random effects \( u_j \),

\[
\Pr(y_{ij} = 1|x_{ij}, u_j) = H(x_{ij}\beta + z_{ij}u_j) \tag{1}
\]

for \( j = 1, \ldots, M \) clusters, with cluster \( j \) consisting of \( i = 1, \ldots, n_j \) observations. The responses are the binary-valued \( y_{ij} \), and we follow the standard Stata convention of treating \( y_{ij} = 1 \) if \( \text{depvar}_{ij} \neq 0 \) and treating \( y_{ij} = 0 \) otherwise. The \( 1 \times p \) row vector \( x_{ij} \) are the covariates for the fixed effects, analogous to the covariates you would find in a standard cloglog regression model, with regression coefficients (fixed effects) \( \beta \). For notational convenience here and throughout this manual entry, we suppress the dependence of \( y_{ij} \) on \( x_{ij} \).

The \( 1 \times q \) vector \( z_{ij} \) are the covariates corresponding to the random effects and can be used to represent both random intercepts and random coefficients. For example, in a random-intercept model, \( z_{ij} \) is simply the scalar 1. The random effects \( u_j \) are \( M \) realizations from a multivariate normal distribution with mean 0 and \( q \times q \) variance matrix \( \Sigma \). The random effects are not directly estimated as model parameters but are instead summarized according to the unique elements of \( \Sigma \), known as variance components. One special case of (1) places \( z_{ij} = x_{ij} \), so that all covariate effects are essentially random and distributed as multivariate normal with mean \( \beta \) and variance \( \Sigma \).

Finally, because this is cloglog regression, \( H(\cdot) \) is the inverse of the complementary log–log function that maps the linear predictor to the probability of a success \( (y_{ij} = 1) \) with \( H(v) = 1 - \exp\{-\exp(v)\} \).

Model (1) may also be stated in terms of a latent linear response, where only \( y_{ij} = I(y_{ij}^* > 0) \) is observed for the latent

\[
y_{ij}^* = x_{ij}\beta + z_{ij}u_j + \epsilon_{ij}
\]

The errors \( \epsilon_{ij} \) are independent and identically extreme-value (Gumbel) distributed with the mean equal to Euler’s constant and variance \( \sigma^2 = \pi^2/6 \), independently of \( u_j \). This nonsymmetric error distribution is an alternative to the symmetric error distribution underlying logistic and probit analysis and is usually used when the positive (or negative) outcome is rare.

Below we present two short examples of mixed-effects cloglog regression; refer to \[\text{ME} \] me and \[\text{ME} \] meglm for examples of other random-effects models. A two-level cloglog model can also be fit using xtcloglog with the re option; see \[\text{XT} \] xtcloglog. In the absence of random effects, mixed-effects cloglog regression reduces to standard cloglog regression; see \[\text{R} \] clog.

Example 1: Two-level random-intercept model

In example 1 of \[\text{XT} \] xtcloglog, we analyze unionization of women in the United States over the period 1970–1988. The women are identified by the variable idcode. Here we refit that model with mecloglog. Because the original example used 12 integration points by default, we request 12 integration points as well.

```
. use https://www.stata-press.com/data/r17/union
(NLS Women 14-24 in 1968)
```
Fitting fixed-effects model:
Iteration 0:  log likelihood = -14237.139
Iteration 1:  log likelihood = -13546.159
Iteration 2:  log likelihood = -13540.611
Iteration 3:  log likelihood = -13540.607
Iteration 4:  log likelihood = -13540.607
Refining starting values:
Grid node 0:  log likelihood = -11104.448
Fitting full model:
Iteration 0:  log likelihood = -11104.448
Iteration 1:  log likelihood = -10617.891
Iteration 2:  log likelihood = -10537.919
Iteration 3:  log likelihood = -10535.946
Iteration 4:  log likelihood = -10535.941
Iteration 5:  log likelihood = -10535.941

Mixed-effects cloglog regression
Number of obs = 26,200
Group variable: idcode  Number of groups = 4,434
Obs per group:
    min =  1
    avg =  5.9
    max =  12
Integration method: mvaghermite  Integration pts. = 12
Wald chi2(6) =  248.12
Log likelihood = -10535.941  Prob > chi2 =  0.0000

                      Coefficient  Std. err.      z    P>|z|     [95% conf. interval]
union
  age        0.0128542     0.0119441    1.08  0.282    -0.0105559   0.0362642
  grade      0.0699965     0.0138551    5.05  0.000     0.0428409   0.0971522
  not_smsa   -0.1982009     0.0649258   -3.05  0.002    -0.3254531   -0.0709487
  1.south    -2.049901      0.4892644   -4.19  0.000    -3.008842   -1.090961
  year       -0.0006158     0.0123999   -0.05  0.960    -0.0249191   0.0236875
south#c.year 1           0.0164457     0.0060685    2.71  0.007     0.0045516   0.0283399
  _cons     -3.277375      0.6610552   -4.96  0.000    -4.573021   -1.981731
idcode
  var(_cons)  3.489803       0.1630921   20.92  0.000      3.184351    3.824555

LR test vs. cloglog model:  chibar2(01) = 6009.33  Prob >= chibar2 = 0.0000

The estimates are practically the same. xtcloglog reports the estimated variance component as a standard deviation, \( \hat{\sigma}_u = 1.86 \). mecloglog reports \( \hat{\sigma}_u^2 = 3.49 \), the square root of which is 1.87. We find that age and education each have a positive effect on union membership, although the former is not statistically significant. Women who live outside of metropolitan areas are less likely to unionize. The estimated variance of the random intercept at the individual level, \( \hat{\sigma}^2 \), is 3.49 with standard error 0.16. The reported likelihood-ratio test shows that there is enough variability between women to favor a mixed-effects cloglog regression over an ordinary cloglog regression; see Distribution theory for likelihood-ratio test in [ME] me for a discussion of likelihood-ratio testing of variance components.
Example 2: Three-level random-intercept model

Rabe-Hesketh, Touloupolou, and Murray (2001) analyzed data from a study that measured the cognitive ability of patients with schizophrenia compared with their relatives and control subjects. Cognitive ability was measured as the successful completion of the “Tower of London”, a computerized task, measured at three levels of difficulty. For all but one of the 226 subjects, there were three measurements (one for each difficulty level). Because patients’ relatives were also tested, a family identifier, family, was also recorded.

We fit a cloglog model with response dttlm, the indicator of cognitive function, and with covariates difficulty and a set of indicator variables for group, with the controls (group==1) being the base category. We also allow for random effects due to families and due to subjects within families. The first is a random intercept (constant only) at the family level, and the second is a random intercept at the subject level. The order in which these are specified (from left to right) is significant—mecloglog assumes that subject is nested within family. The equations are separated by ||.
After adjusting for the random-effects structure, the probability of successful completion of the Tower of London decreases dramatically as the level of difficulty increases. Also, schizophrenics (group==3) tended not to perform as well as the control subjects.

The above extends to models with more than two levels of nesting by adding more random-effects equations, each separated by `||`. 

\[ \text{Grouping information} \]

<table>
<thead>
<tr>
<th>Group variable</th>
<th>No. of groups</th>
<th>Observations per group</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Minimum</td>
</tr>
<tr>
<td>family</td>
<td>118</td>
<td>2</td>
</tr>
<tr>
<td>subject</td>
<td>226</td>
<td>2</td>
</tr>
</tbody>
</table>

Integration method: mvaghermite
Integration pts. = 7
Wald chi2(3) = 83.32
Log likelihood = -305.26516
Prob > chi2 = 0.0000

| dtlm | Coefficient | Std. err. | z    | P>|z| | [95% conf. interval] |
|------|-------------|-----------|------|------|----------------------|
| difficulty | -1.342844 | .1501508 | -8.94 | 0.000 | -1.637135 -1.048554 |
| group | | | | | |
| 2 | -.1331007 | .269389 | -0.49 | 0.621 | -.6610935 .3948922 |
| 3 | -.7714314 | .309799 | -2.49 | 0.013 | -.1378452 -.164411 |
| _cons | -1.6718 | .2290352 | -7.30 | 0.000 | -2.120695 -1.222905 |

| family | var(_cons) | .2353453 | .2924064 | .0206122 | 2.687117 |
| family>subject | var(_cons) | .7737687 | .4260653 | .2629714 | 2.276742 |

LR test vs. cloglog model: chi2(2) = 16.61
Prob > chi2 = 0.0002
Note: LR test is conservative and provided only for reference.
Stored results

mecloglog stores the following in e():

Scalars
- e(N) number of observations
- e(k) number of parameters
- e(k_dv) number of dependent variables
- e(k_eq) number of equations in e(b)
- e(k_eq_model) number of equations in overall model test
- e(k_f) number of fixed-effects parameters
- e(k_r) number of random-effects parameters
- e(k_rs) number of variances
- e(k_rc) number of covariances
- e(df_m) model degrees of freedom
- e(ll) log likelihood
- e(N_clust) number of clusters
- e(chi2) \( \chi^2 \)
- e(p) \( p \)-value for model test
- e(ll_c) log likelihood, comparison model
- e(chi2_c) \( \chi^2 \), comparison test
- e(df_c) degrees of freedom, comparison test
- e(p_c) \( p \)-value for comparison test
- e(rank) rank of e(V)
- e(ic) number of iterations
- e(rc) return code
- e(converged) 1 if converged, 0 otherwise

Macros
- e(cmd) meglm
- e(cmd2) mecloglog
- e(cmdline) command as typed
- e(depvar) name of dependent variable
- e(wtype) weight type
- e(wexp) weight expression (first-level weights)
- e(fweight) fweight variable for kth highest level, if specified
- e(iweight) iweight variable for kth highest level, if specified
- e(pweight) pweight variable for kth highest level, if specified
- e(covariates) list of covariates
- e(ivars) grouping variables
- e(model) cloglog
- e(title) title in estimation output
- e(link) cloglog
- e(family) bernoulli or binomial
- e(clustvar) name of cluster variable
- e(offset) offset
- e(binomial) binomial number of trials
- e(intmethod) integration method
- e(n_quad) number of integration points
- e(chi2type) Wald: type of model \( \chi^2 \)
- e(vce) vcetype specified in vce()
- e(vcetype) title used to label Std. err.
- e(opt) type of optimization
- e(which) max or min: whether optimizer is to perform maximization or minimization
- e(ml_method) type of ml method
- e(user) name of likelihood-evaluator program
- e(technique) maximization technique
- e(datasignature) the checksum
- e(datasignaturevars) variables used in calculation of checksum
- e(properties) b V
- e(estat_cmd) program used to implement estat
- e(predict) program used to implement predict
- e(marginsnotok) predictions disallowed by margins
- e(marginswtype) weight type for margins
mecloglog — Multilevel mixed-effects complementary log–log regression

- `e(marginswexp)` weight expression for margins
- `e(asbalanced)` factor variables fvset as asbalanced
- `e(asobserved)` factor variables fvset as asobserved

Matrices
- `e(b)` coefficient vector
- `e(Cns)` constraints matrix
- `e(ilog)` iteration log (up to 20 iterations)
- `e(gradient)` gradient vector
- `e(N_g)` group counts
- `e(g_min)` group-size minimums
- `e(g_avg)` group-size averages
- `e(g_max)` group-size maximums
- `e(V)` variance–covariance matrix of the estimators
- `e(V_modelbased)` model-based variance

Functions
- `e(sample)` marks estimation sample

In addition to the above, the following is stored in `r()`:

Matrices
- `r(table)` matrix containing the coefficients with their standard errors, test statistics, p-values, and confidence intervals

Note that results stored in `r()` are updated when the command is replayed and will be replaced when any r-class command is run after the estimation command.

Methods and formulas

mecloglog is a convenience command for meglm with a cloglog link and a bernoulli or binomial family; see [ME] meglm.

Model (1) assumes Bernoulli data, a special case of the binomial. Because binomial data are also supported by mecloglog (option binomial()), the methods presented below are in terms of the more general binomial mixed-effects model.

For a two-level binomial model, consider the response $y_{ij}$ as the number of successes from a series of $r_{ij}$ Bernoulli trials (replications). For cluster $j$, $j = 1, \ldots, M$, the conditional distribution of $y_j = (y_{j1}, \ldots, y_{jn_j})'$, given a set of cluster-level random effects $u_j$, is

$$f(y_j | u_j) = \prod_{i=1}^{n_j} \left( \frac{r_{ij}}{y_{ij}} \right) \left\{ H(\eta_{ij}) \right\}^{y_{ij}} \left\{ 1 - H(\eta_{ij}) \right\}^{r_{ij} - y_{ij}}$$

$$= \exp \left( \sum_{i=1}^{n_j} \left[ y_{ij} \log \left\{ H(\eta_{ij}) \right\} - (r_{ij} - y_{ij}) \exp(\eta_{ij}) + \log \left( \frac{r_{ij}}{y_{ij}} \right) \right] \right)$$

for $\eta_{ij} = x_{ij} \beta + z_{ij} u_j + \text{offset}_{ij}$ and $H(v) = 1 - \exp\{-\exp(v)\}$.

Defining $r_j = (r_{j1}, \ldots, r_{jn_j})'$ and

$$c(y_j, r_j) = \sum_{i=1}^{n_j} \log \left( \frac{r_{ij}}{y_{ij}} \right)$$

where $c(y_j, r_j)$ does not depend on the model parameters, we can express the above compactly in matrix notation,

$$f(y_j | u_j) = \exp \left[ y_j' \log \left\{ H(\eta_j) \right\} - (r_j - y_j)' \exp(\eta_j) + c(y_j, r_j) \right]$$
where $\eta_j$ is formed by stacking the row vectors $\eta_{ij}$. We extend the definitions of the functions $H(\cdot)$, \log(\cdot), and $\exp(\cdot)$ to be vector functions where necessary.

Because the prior distribution of $u_j$ is multivariate normal with mean 0 and $q \times q$ variance matrix $\Sigma$, the likelihood contribution for the $j$th cluster is obtained by integrating $u_j$ out of the joint density $f(y_j, u_j)$,

$$L_j(\beta, \Sigma) = (2\pi)^{-q/2} |\Sigma|^{-1/2} \int f(y_j | u_j) \exp \left( -u_j' \Sigma^{-1} u_j / 2 \right) du_j$$

(2)

where

$$h(\beta, \Sigma, u_j) = y_j' \log \left( H(\eta_j) \right) - (r_j - y_j)' \exp(\eta_j) - u_j' \Sigma^{-1} u_j / 2$$

and for convenience, in the arguments of $h(\cdot)$ we suppress the dependence on the observable data $(y_j, r_j, X_j, Z_j)$.

The integration in (2) has no closed form and thus must be approximated; see Methods and formulas in [ME] meglm for details.

mecloglog supports multilevel weights and survey data; see Methods and formulas in [ME] meglm for details.

Reference


Also see

[ME] mecllog postestimation — Postestimation tools for mecloglog

[ME] meologit — Multilevel mixed-effects logistic regression

[ME] meprobit — Multilevel mixed-effects probit regression

[ME] me — Introduction to multilevel mixed-effects models

[BAYES] bayes: mecloglog — Bayesian multilevel complementary log–log regression

[SEM] Intro 5 — Tour of models (Multilevel mixed-effects models)

[SVY] svy estimation — Estimation commands for survey data

[XT] xtcloglog — Random-effects and population-averaged cloglog models

[U] 20 Estimation and postestimation commands