bayes: menbreg — Bayesian multilevel negative binomial regression

Description

bayes: menbreg fits a Bayesian multilevel negative binomial regression to a nonnegative count outcome; see [BAYES] bayes and [ME] menbreg for details.

Quick start

Bayesian two-level negative binomial regression of y on x1 and x2 with random intercepts by id, using default normal priors for regression coefficients and log-overdispersion parameter and default inverse-gamma prior for the variance of random intercepts

```
bayes: menbreg y x1 x2 || id:
```

Use a standard deviation of 10 instead of 100 for the default normal priors

```
bayes, normalprior(10): menbreg y x1 x2 || id:
```

Use uniform priors for the slopes and a normal prior for the intercept

```
bayes, prior({y: x1 x2}, uniform(-10,10)) ///
prior({y:_cons}, normal(0,10)): menbreg y x1 x2 || id:
```

Save simulation results to simdata.dta, and use a random-number seed for reproducibility

```
bayes, saving(simdata) rseed(123): menbreg y x1 x2 || id:
```

Specify 20,000 MCMC samples, set length of the burn-in period to 5,000, and request that a dot be displayed every 500 simulations

```
bayes, mcmcsize(20000) burnin(5000) dots(500): menbreg y x1 x2 || id:
```

In the above, request that the 90% HPD credible interval be displayed instead of the default 95% equal-tailed credible interval

```
bayes, clevel(90) hpd
```

Display incidence-rate ratios instead of coefficients

```
bayes: menbreg y x1 x2 || id: , irr
```

Display incidence-rate ratios on replay

```
bayes, irr
```

Also see Quick start in [BAYES] bayes and Quick start in [ME] menbreg.

Menu

Statistics > Multilevel mixed-effects models > Bayesian regression > Negative binomial regression
Syntax

```
bayes [ , bayesopts ] : menbreg depvar fe_equation
      [ || re_equation ] [ || re_equation . . . ] [ , options ]
```

where the syntax of `fe_equation` is

```
[indepvars] [ if ] [ in ] [ weight ] [ , fe_options ]
```

and the syntax of `re_equation` is one of the following:

- for random coefficients and intercepts
  
  `levelvar: [ varlist ] [ , re_options ]`

- for random effects among the values of a factor variable
  
  `levelvar: R.varname`

`levelvar` either is a variable identifying the group structure for the random effects at that level or is `_all`, representing one group comprising all observations.

### `fe_options`

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>suppress constant term from the fixed-effects equation</td>
</tr>
<tr>
<td>include In(varname_o) in model with coefficient constrained to 1</td>
</tr>
<tr>
<td>include varname_o in model with coefficient constrained to 1</td>
</tr>
</tbody>
</table>

### `re_options`

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>variance–covariance structure of the random effects; only structures</td>
</tr>
<tr>
<td>independent, identity, and unstructured supported</td>
</tr>
<tr>
<td>suppress constant term from the random-effects equation</td>
</tr>
</tbody>
</table>

### `options`

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>parameterization of the conditional overdispersion; dispersion may be mean</td>
</tr>
<tr>
<td>(default) or constant</td>
</tr>
</tbody>
</table>

### Reporting

- report incidence-rate ratios
- suppress coefficient table
- suppress output header
- suppress table summarizing groups
- control spacing, line width, and base and empty cells
- set credible level; default is `level(95)`
**bayes: menbreg** — Bayesian multilevel negative binomial regression

indepvars may contain factor variables; see [U] 11.4.3 Factor variables.
depvar, indepvars, and varlist may contain time-series operators; see [U] 11.4.4 Time-series varlists.
fweights are allowed; see [U] 11.1.6 weight.
bayes: menbreg, level() is equivalent to bayes, clevel(): menbreg.
For a detailed description of options, see Options in [ME] menbreg.

**bayesopts**

<table>
<thead>
<tr>
<th>Description</th>
<th>Options</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Priors</strong></td>
<td></td>
</tr>
<tr>
<td>*normalprior(#)</td>
<td>specify standard deviation of default normal priors for regression coefficients and log-overdispersion parameter; default is normalprior(100)</td>
</tr>
<tr>
<td>*igammaprior(# #)</td>
<td>specify shape and scale of default inverse-gamma prior for variance components; default is igammaprior(0.01 0.01)</td>
</tr>
<tr>
<td>*iwishartprior(# [..])</td>
<td>specify degrees of freedom and, optionally, scale matrix of default inverse-Wishart prior for unstructured random-effects covariance</td>
</tr>
<tr>
<td>prior(priorspec)</td>
<td>prior for model parameters; this option may be repeated</td>
</tr>
<tr>
<td>dryrun</td>
<td>show model summary without estimation</td>
</tr>
<tr>
<td><strong>Simulation</strong></td>
<td></td>
</tr>
<tr>
<td>nchains(#)</td>
<td>number of chains; default is to simulate one chain</td>
</tr>
<tr>
<td>mcmcsize(#)</td>
<td>MCMC sample size; default is mcmcsize(10000)</td>
</tr>
<tr>
<td>burnin(#)</td>
<td>burn-in period; default is burnin(2500)</td>
</tr>
<tr>
<td>thinning(#)</td>
<td>thinning interval; default is thinning(1)</td>
</tr>
<tr>
<td>rseed(#)</td>
<td>random-number seed</td>
</tr>
<tr>
<td>exclude(paramref)</td>
<td>specify model parameters to be excluded from the simulation results</td>
</tr>
<tr>
<td>restubs(restub1 restub2 ...)</td>
<td>specify stubs for random-effects parameters for all levels</td>
</tr>
<tr>
<td><strong>Blocking</strong></td>
<td></td>
</tr>
<tr>
<td>*blocksize(#)</td>
<td>maximum block size; default is blocksize(50)</td>
</tr>
<tr>
<td>block(paramref[, blockopts])</td>
<td>specify a block of model parameters; this option may be repeated display block summary</td>
</tr>
<tr>
<td>*noblocking</td>
<td>do not block parameters by default</td>
</tr>
<tr>
<td><strong>Initialization</strong></td>
<td></td>
</tr>
<tr>
<td>initial(initspec)</td>
<td>specify initial values for model parameters with a single chain</td>
</tr>
<tr>
<td>init#(initspec)</td>
<td>specify initial values for #th chain; requires nchains()</td>
</tr>
<tr>
<td>initall(initspec)</td>
<td>specify initial values for all chains; requires nchains()</td>
</tr>
<tr>
<td>nomleinitial</td>
<td>suppress the use of maximum likelihood estimates as starting values</td>
</tr>
<tr>
<td>initrandom</td>
<td>specify random initial values</td>
</tr>
<tr>
<td>initsummary</td>
<td>display initial values used for simulation</td>
</tr>
<tr>
<td>*noisily</td>
<td>display output from the estimation command during initialization</td>
</tr>
<tr>
<td><strong>Adaptation</strong></td>
<td></td>
</tr>
<tr>
<td>adaptation(adaptopts)</td>
<td>control the adaptive MCMC procedure</td>
</tr>
<tr>
<td>scale(#)</td>
<td>initial multiplier for scale factor; default is scale(2.38)</td>
</tr>
<tr>
<td>covariance(cov)</td>
<td>initial proposal covariance; default is the identity matrix</td>
</tr>
</tbody>
</table>
Reporting

clevel(#) set credible interval level; default is clevel(95)

hpd display HPD credible intervals instead of the default equal-tailed credible intervals

irr report incidence-rate ratios

eform[(string)] report exponentiated coefficients and, optionally, label as string

remargl compute log marginal-likelihood

batch(#) specify length of block for batch-means calculations; default is batch(0)

saving(filename, replace) save simulation results to filename.dta

nomodelsummary suppress model summary

omesummary suppress multilevel-structure summary

chainsdetail display detailed simulation summary for each chain

[no] dots suppress dots or display dots every 100 iterations and iteration numbers every 1,000 iterations; default is dots

dots(#, every(#)) display dots as simulation is performed

[no] show(paramref) specify model parameters to be excluded from or included in the output

showeffects[(reref)] specify that all or a subset of random-effects parameters be included in the output

melabel display estimation table using the same row labels as membreg

nogroup suppress table summarizing groups

notable suppress estimation table

noheader suppress output header

title(string) display string as title above the table of parameter estimates

display_options control spacing, line width, and base and empty cells

Advanced

search(search_options) control the search for feasible initial values

corrlag(#) specify maximum autocorrelation lag; default varies

corrtol(#) specify autocorrelation tolerance; default is corrtol(0.01)

*Starred options are specific to the bayes prefix; other options are common between bayes and bayesmh.
Options prior() and block() may be repeated.
priorspec and paramref are defined in [BAYES] bayesmh.
paramref may contain factor variables; see [U] 11.4.3 Factor variables.

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

Model parameters are regression coefficients {depvar:indepvars}, log-overdispersion parameter {lnalpha} with mean dispersion or {lndelta} with constant dispersion, random effects {rename}, and either variance components {rename:sigma2} or, if option covariance(unstructured) is specified, matrix parameter {restub:Sigma,matrix}; see Likelihood model in [BAYES] bayes for how renames and restub are defined.
Use the dryrun option to see the definitions of model parameters prior to estimation.
For a detailed description of bayesopts, see Options in [BAYES] bayes.

Remarks and examples stata.com

For a general introduction to Bayesian analysis, see [BAYES] Intro. For a general introduction to Bayesian estimation using an adaptive Metropolis–Hastings algorithm, see [BAYES] bayesmh. For remarks and examples specific to the bayes prefix, see [BAYES] bayes. For details about the estimation command, see [ME] membreg.
For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] bayes. For multilevel examples, see *Multilevel models* in [BAYES] bayes.

**Stored results**

See *Stored results* in [BAYES] bayes.

**Methods and formulas**

See *Methods and formulas* in [BAYES] bayesmh.

**Also see**

[BAYES] bayes — Bayesian regression models using the bayes prefix

[ME] membreg — Multilevel mixed-effects negative binomial regression

[BAYES] Bayesian postestimation — Postestimation tools for bayesmh and the bayes prefix

[BAYES] Bayesian estimation — Bayesian estimation commands

[BAYES] Bayesian commands — Introduction to commands for Bayesian analysis

[BAYES] Intro — Introduction to Bayesian analysis

[BAYES] Glossary