bayes: mprobit — Bayesian multinomial probit regression

Description

`bayes: mprobit` fits a Bayesian multinomial probit regression to a categorical outcome; see [BAYES] **bayes** and [R] **mprobit** for details.

Quick start

Bayesian multinomial probit regression of `y` on `x1` and `x2`, using default normal priors for regression coefficients

```
bayes: mprobit y x1 x2
```

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

```
bayes, normalprior(10): mprobit y x1 x2
```

Use uniform priors for the slopes and a normal prior for the intercept for the category 2

```
bayes, prior({2: x1 x2}, uniform(-10,10)) ///
prior({2:_cons}, normal(0,10)): mprobit y x1 x2
```

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

```
bayes, saving(simdata) rseed(123): mprobit y x1 x2
```

Specify 20,000 Markov chain Monte Carlo (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): mprobit y x1 x2
```

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

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

Also see *Quick start* in [BAYES] **bayes** and *Quick start* in [R] **mprobit**.

Menu

Statistics > Categorical outcomes > Bayesian regression >Multinomial probit regression

Syntax

```
bayes [ , bayesopts ] : mprobit depvar [ indepvars ] [ if ] [ in ] [ weight ] [ , options ]
```

options	Description
Model	
noconstant	suppress constant term
baseoutcome(#)	value of *depvar* that will be the base outcome
probitparam	use the probit variance parameterization
Reporting	
display_options	control spacing, line width, and base and empty cells
level(#)	set credible level; default is level(95)

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

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

bayes: mprobit, level() is equivalent to bayes, clevel(): mprobit.

For a detailed description of *options*, see *Options* in **[R] mprobit**.

bayesopts	Description
Priors	
* normalprior(#)	specify standard deviation of default normal priors for regression coefficients; default is normalprior(100)
prior(*priorspec*)	prior for model parameters; this option may be repeated
dryrun	show model summary without estimation
Simulation	
nchains(#)	number of chains; default is to simulate one chain
mcmcsize(#)	MCMC sample size; default is mcmcsize(10000)
burnin(#)	burn-in period; default is burnin(2500)
thinning(#)	thinning interval; default is thinning(1)
rseed(#)	random-number seed
exclude(*paramref*)	specify model parameters to be excluded from the simulation results
Blocking	
* blocksize(#)	maximum block size; default is blocksize(50)
block(*paramref* [, *blockopts*])	specify a block of model parameters; this option may be repeated
blocksummary	display block summary
* noblocking	do not block parameters by default
Initialization	
initial(*initspec*)	specify initial values for model parameters with a single chain
init#(*initspec*)	specify initial values for #th chain; requires nchains()
initall(*initspec*)	specify initial values for all chains; requires nchains()
nomleinitial	suppress the use of maximum likelihood estimates as starting values
initrandom	specify random initial values
initsummary	display initial values used for simulation
* noisily	display output from the estimation command during initialization

Adaptation	
`adaptation(`*adaptopts*`)`	control the adaptive MCMC procedure
`scale(`#`)`	initial multiplier for scale factor; default is `scale(2.38)`
`covariance(`*cov*`)`	initial proposal covariance; default is the identity matrix
Reporting	
`clevel(`#`)`	set credible interval level; default is `clevel(95)`
`hpd`	display HPD credible intervals instead of the default equal-tailed credible intervals
`eform[ (`*string*`) ]`	report exponentiated coefficients and, optionally, label as *string*
`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
`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 `nodots`
`dots(`#`[ , every(`#`) ])`	display dots as simulation is performed
`[no]show(`*paramref*`)`	specify model parameters to be excluded from or included in the output
`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**.

`collect` is allowed; see **[U] 11.1.10 Prefix commands**.

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

Model parameters are regression coefficients {*outcome*$_1$:*indepvars*}, {*outcome*$_2$:*indepvars*}, and so on, where *outcome*$_\#$'s are the values of the dependent variable or the value labels of the dependent variable if they exist. 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

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 [R] **mprobit**.

For a simple example of the `bayes` prefix, see *Introductory example* in [BAYES] **bayes**. Also see *Multinomial logistic regression* 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

[R] **mprobit** — Multinomial probit regression

[BAYES] **Bayesian postestimation** — Postestimation tools after Bayesian estimation

[BAYES] **Bayesian estimation** — Bayesian estimation commands

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

[BAYES] **Intro** — Introduction to Bayesian analysis

[BAYES] **Glossary**