

[Description](#)
[Options](#)
[References](#)[Quick start](#)
[Remarks and examples](#)
[Also see](#)[Menu](#)
[Stored results](#)[Syntax](#)
[Methods and formulas](#)

Description

`bmastats lps` computes and optionally stores in a new variable the log predictive-score (LPS) for observations after the `bmaregress` command. LPS is used to assess the predictive performance of Bayesian model averaging (BMA) models.

Quick start

Compute and summarize LPS for all observations

```
bmastats lps
```

Same as above, but use a known variance to compute and report the entropy

```
bmastats lps, sigma2(0.1)
```

Compute LPS for the first 12 observations, and store them in `newvar`

```
bmastats lps in 1/12, generate(newvar)
```

Compute LPS for previously stored `bma1` and `bma2` estimation results, and store respective LPS in variables `newvar1` and `newvar2`

```
bmastats lps bma1 bma2, generate(newvar*)
```

Display multiple estimation results compactly in one table

```
bmastats lps bma1 bma2, compact
```

After fitting `bmaregress` using a training sample, `sample == 1`, compute LPS for out-of-sample observations—test sample `sample == 2`—to compare out-of-sample predictive performance of two BMA models with estimation results stored in `bma1` and `bma2`

```
bmastats lps bma1 bma2 if sample == 2
```

Menu

Statistics > Bayesian model averaging > Log predictive-score

Syntax

Summarize LPS for current estimation results

```
bmastats lps [if] [in] [, sigma2(#) generate(newvar [, double])]
```

Summarize LPS for multiple estimation results

```
bmastats lps namelist [if] [in] [, sigma2(# [# [...] ])]  
generate(newvarspec [, double]) compact]
```

namelist includes names of previously stored estimation results after `bmaregress`. The current (active) results are the default.

newvarspec is a *newvar* for a single estimation result or *newvarlist* or *stub** for multiple estimation results.

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

Options

Main

`sigma2(# [# [...]])` specifies the variance to be used to compute the entropy. With out-of-sample observations, the posterior mean estimate of the error variance from `bmaregress` is used. With multiple estimation results, you can specify just one variance value to be used for all estimation results or specific values for each result. A missing value (.) in place of a `#` means that the default variance estimate is to be used for the corresponding estimation result. This option is useful to compute the entropy more precisely when the variance is known, such as during simulation studies.

`generate(newvarspec [, double])` specifies the name (or names) of new variables to store the LPS values. A new variable name is specified with one estimation result. A list of new variable names or *stub** is specified with multiple estimation results.

`double` specifies that the new variables be stored as double. If the `double` suboption is not specified, the variables are stored using the current type as set by `set type` (see [D] `generate`), which is `float` by default.

`compact` specifies that multiple estimation results be displayed in a compact form. By default, a separate header and table are displayed for each estimation result. If option `compact` is specified, the results are displayed in one table with a common header. If the variances differ across multiple estimation results, the variance and entropy are not reported in the header. This option requires at least two estimation results.

Remarks and examples

To evaluate the predictive performance of a model, one needs a measure that summarizes the quality of predictions (Piironen and Vehtari 2017). Good (1952) suggests that such a measure be defined based on the posterior predictive distribution. The LPS is defined as the negative of the log of the posterior predictive density evaluated at an observation. The LPS for out-of-sample observations can be used to evaluate the predictive performance of models. Fernández, Ley, and Steel (2001b) were among the first to use the LPS to evaluate the predictive performance of BMA. And Ley and Steel (2012) compared a variety of *g*-priors for the linear BMA using the LPS.

As pointed out in [Fernández, Ley, and Steel \(2001a\)](#), the LPS is related to the Kullback–Leibler divergence between the actual sampling density and the out-of-sample predictive density. In theory, the expected LPS is bounded from below by the entropy of the sampling density, but in practice, this may not always hold because the entropy itself is being estimated. The closer the expected value is to the entropy, the more accurate the prediction. For the normal linear model, the entropy is given by $0.5\{\log(2\pi\sigma^2) + 1\}$, where σ^2 is the error variance.

`bmastats lps` reports the mean, minimum, and maximum of LPS for each specified estimation result. By default, the command reports the LPS summaries computed using the current dataset that includes in-sample observations, which were used during estimation and are identified by `e(sample) == 1`, for the current or active estimation results. These summaries are useful when comparing multiple models. By themselves, their values are not directly interpretable, unless the entropy is known or can be estimated reliably. In this case, the closer the mean LPS is to the entropy, the better the model fit. For instance, if you are using `bmastats lps` with a simulated dataset, you can specify the known error variance in the `sigma2()` option, and the corresponding entropy value will be reported. You can compare this value with the mean LPS to check model fit. When `bmastats lps` is used with only out-of-sample observations, observations not used to fit the model for which `e(sample) == 0`, the command uses the posterior mean estimate of the error variance from the fitted `bmaregress` model to estimate and report the entropy. You can then compare the out-of-sample mean LPS with the estimated entropy to check the out-of-sample model fit, assuming that the entropy estimate is a reliable estimate of the entropy of the true model. The entropy estimate is not reported when `bmastats lps` is used with in-sample observations.

You can use the `generate()` option to store observation-specific LPS values in a new variable. This is equivalent to using `bmapredict, lps`; see [\[BMA\] bmapredict](#). With multiple estimation results, you must specify the same number of new variable names or one variable stub in `generate()`.

With multiple estimation results, `bmastats lps` displays a separate table for each result. You can use the `compact` option to display the results in one table, which is more convenient for comparison.

Below, we demonstrate a more common usage of `bmastats lps` for comparing out-of-sample predictive performance of multiple BMA models.

► Example 1: Prediction of systolic blood pressure

Consider the `chd` dataset from [Hastie, Tibshirani, and Friedman \(2009\)](#), which is a subset of the coronary heart disease dataset used in [Rossouw et al. \(1983\)](#). It contains information about potential heart disease factors such as age, adiposity, `sbp` (systolic blood pressure), tobacco (consumption of), `ldl` (low density lipoprotein), and others.

```
. use https://www.stata-press.com/data/r19/chd
(Coronary risk factor data from rural communities)

. describe
Contains data from https://www.stata-press.com/data/r19/chd.dta
Observations:          462          Coronary risk factor data from
                                rural communities
Variables:             10          7 Mar 2025 09:19
                                (_dta has notes)
```

Variable name	Storage type	Display format	Value label	Variable label
<code>sbp</code>	<code>int</code>	<code>%8.0g</code>		Systolic blood pressure
<code>tobacco</code>	<code>float</code>	<code>%6.2f</code>		Yearly tobacco use (kg)
<code>ldl</code>	<code>float</code>	<code>%6.2f</code>		Low-density lipoprotein (LDL)
<code>adiposity</code>	<code>float</code>	<code>%6.2f</code>		Body adiposity index
<code>famhist</code>	<code>byte</code>	<code>%9.0g</code>	<code>noyes</code>	Family history of ischaemic heart disease
<code>typea</code>	<code>byte</code>	<code>%8.0g</code>		Type A personality score
<code>obesity</code>	<code>float</code>	<code>%6.2f</code>		Obesity (body mass index)
<code>alcohol</code>	<code>float</code>	<code>%7.2f</code>		Alcohol use (grams/day)
<code>age</code>	<code>byte</code>	<code>%8.0g</code>		Age (years)
<code>chd</code>	<code>byte</code>	<code>%8.0g</code>	<code>noyes</code>	Diagnosed with CHD

Sorted by:

We wish to use BMA to build a prediction model for systolic blood pressure using all other available factors, tobacco through age, as predictors. We consider the log-transformed `sbp` variable, `lsbp`, to make its distribution closer to normal. We also split the sample into five groups to have training and test subsamples to evaluate the predictive performance of a model. Because the sample is split randomly, we specify a random-number seed with `splitsample` for reproducibility.

```
. splitsample, generate(sample) nsplit(5) rseed(100)
. generate double lsbp = log(sbp)
```

We will use the first four subsamples as our training data to fit a model. And we will check the model's performance using the fifth, test, subsample. To demonstrate, we fit the `bmaregress` command using the default settings.

```
. bmaregress lsbp tobacco-age if sample != 5
Enumerating models ...
Computing model probabilities ...

Bayesian model averaging          No. of obs      =    370
Linear regression                 No. of predictors =     8
Model enumeration                  Groups          =     8
                                   Always             =     0

Priors:                            No. of models   =   256
  Models: Beta-binomial(1, 1)      For CPMP >= .9 =     7
  Cons.: Noninformative           Mean model size =  2.132
  Coef.: Zellner's g
    g: Benchmark, g = 370         Shrinkage, g/(1+g) = 0.9973
  sigma2: Noninformative          Mean sigma2      =  0.015
```

lsbp	Mean	Std. dev.	Group	PIP
age	.0020223	.0008055	8	.93569
adiposity	.0042121	.0016916	3	.92348
obesity	.0004441	.001573	6	.10111
typea	-.0000344	.0002133	5	.047293
alcohol	9.80e-06	.0000733	7	.03971
tobacco	-.0000101	.0002961	1	.028973
ldl	-9.92e-06	.0005911	2	.02786
famhist	.0000648	.0022977	4	.027833
Always				
_cons	4.71339	.0366564	0	1

Note: Coefficient posterior means and std. dev. estimated from 256 models.

Note: Default priors are used for models and parameter g .

With a small number of predictors, the model space is explored fully by model enumeration. The default fixed benchmark g -prior is used, which results in a negligible shrinkage factor of almost 1. The posterior mean size of the models is 2.1, and all potential predictors have PIPs greater than 2%.

We use the `bmastats lps` command to evaluate the prediction performance of the fit model on the test sample by using the condition `if sample == 5`.

```
. bmastats lps if sample == 5
Log predictive-score (LPS)
Number of observations =      92
Posterior mean sigma2  = .015329
Entropy                = -.670055
```

	Mean	Minimum	Maximum
LPS	-.5183101	-1.169732	4.861686

Note: Using analytical PMPs.

The command reports the number of predicted observations, the estimated entropy, and the variance estimate used to compute the entropy in the header. The output table reports the mean, minimum, and maximum LPS values.

The mean LPS of -0.52 is, as expected, greater than the entropy estimate, -0.67 . The closer it is to the entropy, the better the predictive performance. The actual LPS values cannot be interpreted, but we can use them to compare the predictive performances among several BMA models.

Based on their PIPs above 90%, age and adiposity appear to be the more important predictors of the elevated blood pressure (at least based on our training sample). We may ask what would be the performance of the model using only these two predictors?

To fit just one model of interest using `bmaregress`, we can specify all predictors of interest as one always-included group as follows. (In this case, the results from `bmaregress` will be similar to those from `regress`; see [\[R\] regress](#).)

```
. bmaregress lsbp (age adiposity, always) if sample != 5
Enumerating models ...
Computing model probabilities ...
Bayesian model averaging          No. of obs      =    370
Linear regression                 No. of predictors =     2
Model enumeration                  Groups          =     0
                                   Always            =     2
Priors:                           No. of models    =     1
  Models: Beta-binomial(1, 1)      For CPMP >= .9 =     1
  Cons.: Noninformative           Mean model size =   2.000
  Coef.: Zellner's g
    g: Benchmark, g = 370          Shrinkage, g/(1+g) = 0.9973
  sigma2: Noninformative          Mean sigma2       =   0.015
```

lsbp	Mean	Std. dev.	Group	PIP
Always				
age	.002073	.0005608	0	1
adiposity	.0044281	.0010493	0	1
_cons	4.715601	.0236217	0	1

Note: Coefficient posterior means and std. dev. estimated from 1 model.

Note: Default priors are used for models and parameter g .

`bmaregress` visits only one model: `regress lsbp age adiposity`. In this case, the prior model probability has no effect on the BMA results, and `bmaregress` is equivalent to fitting a Bayesian linear model with Zellner's g -prior on regression coefficients with $g = 370$ and Jeffreys prior for the error variance parameter; see [\[BAYES\] bayes: regress](#) or [\[BAYES\] bayesmh](#).

Let's calculate the mean LPS score for this model on the test sample.

```
. bmastats lps if sample == 5
Log predictive-score (LPS)
Number of observations =    92
Posterior mean sigma2  = .015277
Entropy                = -.67177
```

	Mean	Minimum	Maximum
LPS	-.5173158	-1.171843	4.890529

Note: Using analytical PMPs.

The mean LPS score of -0.52 is about the same as that of the full BMA regression, which suggests a similar predictive performance for the two models.

We can also investigate the impact of a particular factor on the prediction performance of our BMA model. For instance, in the first model, the tobacco usage term had a PIP of about 3%. We may investigate further whether the tobacco usage indeed has a relatively low impact on systolic blood pressure. To do this, we can fit BMA to all predictors except tobacco and compare its predictive performance to the full model.

```
. bmaregress lsbp ldl-age if sample != 5
Enumerating models ...
Computing model probabilities ...
Bayesian model averaging          No. of obs      =    370
Linear regression                 No. of predictors =     7
Model enumeration                  Groups =       7
                                   Always =       0
Priors:                            No. of models   =   128
  Models: Beta-binomial(1, 1)      For CPMP >= .9 =     6
  Cons.: Noninformative           Mean model size =  2.150
  Coef.: Zellner's g              Shrinkage, g/(1+g) = 0.9973
    g: Benchmark, g = 370         Mean sigma2      =  0.015
  sigma2: Noninformative
```

lsbp	Mean	Std. dev.	Group	PIP
age	.0020391	.0007811	7	.94501
adiposity	.0041866	.0016762	2	.92399
obesity	.0004608	.0015953	5	.10886
typea	-.0000412	.0002329	4	.056801
alcohol	.0000118	.0000802	6	.04785
ldl	-.0000121	.0006497	1	.033757
famhist	.0000758	.0025216	3	.03369
Always				
_cons	4.713174	.0370391	0	1

Note: Coefficient posterior means and std. dev. estimated from 128 models.

Note: Default priors are used for models and parameter g .

```
. bmastats lps if sample == 5
Log predictive-score (LPS)
Number of observations =      92
Posterior mean sigma2 = .015323
Entropy                = -.670276
```

	Mean	Minimum	Maximum
LPS	-.5186576	-1.169858	4.855259

Note: Using analytical PMPs.

The mean LPS score of -0.52 is again close to that of the full model. This suggests that excluding the tobacco predictor does not diminish the predictive performance of the model. It does not appear to be a strong predictor in this dataset.

To more easily compare the LPS from the above models, we could have stored the estimation results from each model first and then specified these results with `bmastats lps`. To store the estimation results, we must use the `saving()` option with `bmaregress`. For instance,

```
. quietly bmaregress lsbp tobacco-age if sample != 5, saving(bma1)
. estimates store bma1
. quietly bmaregress lsbp (age adiposity, always) if sample != 5, saving(bma2)
. estimates store bma2
. quietly bmaregress lsbp ldl-age if sample != 5
. bmastats lps bma1 bma2 . if sample == 5, compact
Log predictive-score (LPS)
Number of observations = 92
```

LPS	Mean	Minimum	Maximum
bma1	-.5183101	-1.169732	4.861686
bma2	-.5173158	-1.171843	4.890529
Active	-.5186576	-1.169858	4.855259

Notes: Using analytical PMPs.
Result **Active** has the smallest mean LPS.

We also specified the `compact` option to display the results in one table with a common header. Because the variance estimates differ between the estimation results, the variance and entropy are not shown in the header. (You can see them if you do not specify `compact`.) If the variances were the same, the variance and the entropy would have been displayed.

Remember to remove the generated datasets if they are no longer needed.

```
. erase bma1.dta
. erase bma2.dta
```



In addition to the regression-function specification, in BMA, it is also important to evaluate the effect of different prior specifications on the results. Depending on how much information there is in the data about the data-generating process, different prior specifications may lead to different conclusions. We explore this in [example 2](#).

► Example 2: Comparing different g -priors using cross-validation

For some data, the performance of linear BMA may depend strongly on the choice of the prior for regression coefficients ([Fernández, Ley, and Steel 2001a](#)). The classical Zellner's g -prior is commonly used in BMA for regression coefficients. The g parameter of this prior can be fixed or random. For a [random \$g\$](#) , a hyperprior for g must be specified. With a variety of prior choices available for g , the BMA specification can be challenging. As an objective criterion for choosing a prior, we can use a model's predictive performance on the data not used for fitting the model. In this example, we show how we can use cross-validation of log predictive-score to compare different choices of priors.

Let's continue with the analysis of the `chd` dataset from [example 1](#). Here we will compare five different priors for g : two fixed and three random. The two fixed priors are the default benchmark, `bench`, and empirical Bayes local, `eb1`. The former uses a constant g -value for all models, whereas the latter uses a model-specific g . The three random priors are the benchmark beta-shrinkage, `betabench(1)`; hyper- g/n , `hypergn(3)`; and robust, `robust`; see [Priors for parameter \$g\$ in *Methods and formulas* of \[BMA\] `bmaregress`](#) for details.

In [example 1](#), we randomly split our sample into five subsamples. For cross-validation, we will treat each of five subsamples as a test sample and fit each of five models to the remaining four subsamples, which will give us 25 results. For each model i and test sample j , we will save the mean LPS in a 5-by-5 matrix.

To avoid manually fitting 25 models, we will automate this task by writing a simple program later. But first, let's go over one step of this automation manually. We will use a robust prior for g and, as in [example 1](#), withhold the fifth sample for testing.

We use the `gprior(robust)` option to specify the robust g -prior and, because this is a random prior, use the `rseed()` option for reproducibility.

```
. bmaregress lsbp tobacco-age if sample != 5, gprior(robust) rseed(18)
Burn-in ...
Simulation ...
Computing model probabilities ...
Bayesian model averaging                No. of obs      =    370
Linear regression                      No. of predictors =     8
MC3 and adaptive MH sampling              Groups =     8
                                         Always =     0
                                         No. of models  =    78
                                         For CPMP >= .9 =     9
Priors:                                Mean model size =  2.366
  Models: Beta-binomial(1, 1)          Burn-in        =  2,500
  Cons.: Noninformative                MCMC sample size = 10,000
  Coef.: Zellner's g                   Acceptance rate =  0.3419
    g: Robust                           Mean sigma2     =  0.015
  sigma2: Noninformative
Sampling correlation = 0.9974
```

lsbp	Mean	Std. dev.	Group	PIP
age	.0020676	.0007043	8	.9688
adiposity	.0041715	.0015489	3	.9442
obesity	.0004562	.0015458	6	.1378
typea	-.0000531	.0002624	5	.0739
ldl	-.0000286	.0009378	2	.0716
alcohol	.0000163	.0000937	7	.0665
famhist	.0001123	.0032103	4	.0555
tobacco	-.000021	.0003703	1	.0474
Always				
_cons	4.713145	.0364241	0	1

Note: Coefficient posterior means and std. dev. estimated from 78 models.

Note: Default prior is used for models.

	Mean	Std. dev.	MCSE	Median	Equal-tailed [95% cred. interval]	
g	325.2053	671.8658	18.0907	185.5779	82.95733	1396
Shrinkage	.9945226	.0029212	.000183	.9946403	.9880892	.9992842

The results are somewhat similar to those from the first model in [example 1](#), except g is now random and Markov chain Monte Carlo (MCMC) sampling is used to estimate its posterior distribution.

```
. bmastats lps if sample == 5
Log predictive-score (LPS)
Number of observations =      92
Posterior mean sigma2  =  .015309
Entropy                = -.670731
```

	Mean	Minimum	Maximum
LPS	-.5191868	-1.170108	4.839892

```
Note: Using frequency PMPs.
. return list
scalars:
      r(N) = 92
      r(sigma2) = .0153086079526961
      r(entropy) = -.6707314655467329
macros:
      r(pmptype) : "frequency"
matrices:
      r(summary) : 1 x 3
. matrix list r(summary)
r(summary)[1,3]
      Mean      Minimum      Maximum
LPS  -.51918683  -1.1701082   4.839892
. display el(r(summary),1,1)
-.51918683
```

After running `bmastats lps`, we use `return list` to display the stored results. The LPS summary is stored in the `r(summary)` matrix. We can access its first element, the mean LPS, by using the `el()` Stata matrix function.

Let's now automate the above in a program.

```
. program bma_cv
1.     args matlps i gprior extraopts
2.     forvalues j = 1/5 {
3.         bmaregress lsbp tobacco-age if sample != 'j', ///
>         gprior('gprior') 'extraopts'
4.         bmastats lps if sample == 'j'
5.         matrix 'matlps'['i','j'] = el(r(summary),1,1)
6.     }
7. end
```

The `bma_cv` program takes four arguments: a matrix name `matlps` to store the mean LPS values, the matrix row index `i`, the prior specification `gprior`, and any additional options `extraopts` for `bmaregress`, such as `rseed()` for the random g -priors. We then perform cross-validation by looping over the five subsamples and withholding each one of them for testing. For each prior i , we save the mean LPS for each cross-validation sample j in row ' i ' and column ' j ' of the specified matrix '`matlps`'.

We create a 5-by-5 matrix `lpscvmat` to store the mean LPS values and call the `bma_cv` program for each prior specification. Because the last three priors are random and thus use MCMC sampling to estimate the results, the program may take a few moments longer to run compared with the one for the fixed priors.

```
. matrix lpscvmat = J(5, 5, .)
. quietly bma_cv lpscvmat 1 "bench"
. quietly bma_cv lpscvmat 2 "ebl"
. quietly bma_cv lpscvmat 3 "betabench 1" "rseed(18)"
. quietly bma_cv lpscvmat 4 "hypergn 3" "rseed(18)"
. quietly bma_cv lpscvmat 5 "robust" "rseed(18)"
. matrix rownames lpscvmat = "bench" "ebl" "betabench 1" "hypergn 3" "robust"
. matrix colnames lpscvmat = "CV1" "CV2" "CV3" "CV4" "CV5"
. matlist lpscvmat
```

	CV1	CV2	CV3	CV4	CV5
bench	-.57771455	-.6311993	-.6583148	-.7233847	-.5183101
ebl	-.5778856	-.6339036	-.6623052	-.7182023	-.5224309
betabench 1	-.5774324	-.6320177	-.6591742	-.7232513	-.5199717
hypergn 3	-.5774459	-.6322509	-.6600753	-.7212745	-.5203261
robust	-.5758851	-.6344241	-.6594026	-.7210064	-.5191868

Smaller mean LPS scores indicate better predictive performance. All mean LPSs are rather similar, which suggests a similar predictive performance for the models with considered priors (assuming a similar variability between LPSs).

We can use a Mata matrix function, `colmin()`, to compute the smallest mean LPS value among all models for each cross-validated sample.

```
. mata: colmin(st_matrix("lpscvmat"))
```

	1	2	3	4
1	-.5778855962	-.6344241355	-.6623052219	-.723384674
	5			
1	-.5224308762			

The second model, `ebl`, has the lowest mean LPS for the majority of models.

Let's fit a model using the ebl g -prior to the entire dataset.

```
. bmaregress lsbp tobacco-age, gprior(ebl)
Enumerating models ...
Computing model probabilities ...
Bayesian model averaging
Linear regression
Model enumeration
No. of obs = 462
No. of predictors = 8
Groups = 8
Always = 0
Priors:
Models: Beta-binomial(1, 1)
Cons.: Noninformative
Coef.: Zellner's g
g: Empirical Bayes (local)
sigma2: Noninformative
No. of models = 256
For CPMP >= .9 = 46
Mean model size = 3.516
Shrinkage, g/(1+g) = 0.9660
Mean sigma2 = 0.016
```

lsbp	Mean	Std. dev.	Group	PIP
age	.0026375	.0006026	8	.99981
adiposity	.0024261	.0016807	3	.7727
alcohol	.0003029	.0003148	7	.58378
obesity	.0014017	.0021937	6	.40683
tobacco	.0001807	.0007427	1	.2009
typea	-.0000758	.0003079	5	.19862
famhist	-.0005746	.0052701	4	.17773
ldl	-8.63e-06	.0013313	2	.17572
Always				
_cons	4.706904	.0433882	0	1

Note: Coefficient posterior means and std. dev. estimated from 256 models.

Note: Default prior is used for models.

Using the full dataset and the ebl prior, age is still a highly important predictor with a PIP of close to 1. The PIP of 0.77 for adiposity is now smaller, but the PIPs of 0.58 and 0.41 for alcohol and obesity, respectively, are now noticeably higher. The other predictors have slightly higher PIPs too, but they are still somewhat weak predictors relative to the other four.

If we run models using the other considered priors, we will find that our conclusions about the relative importance of predictors are almost the same. Of course, the PIP estimates themselves will be different because different priors impose different levels of shrinkage for the coefficients.

Beware that the results will also change if you use a different random-number seed. But for stable datasets and models, changing the random-number seed should not affect the conclusions.



Stored results

`bmastats lps` stores the following in `r()` with one estimation result:

Scalars

<code>r(N)</code>	number of observations
<code>r(sigma2)</code>	variance used to compute entropy
<code>r(entropy)</code>	entropy estimate

Macros

<code>r(name)</code>	name of the estimation result (if any specified)
<code>r(pmptype)</code>	analytical or frequency

Matrices

<code>r(summary)</code>	summary matrix with mean, minimum, and maximum LPS
-------------------------	--

`bmastats lps` stores the following in `r()` for each `#th` estimation result:

Scalars

<code>r(N#)</code>	number of observations
<code>r(sigma2_#)</code>	variance used to compute entropy
<code>r(entropy#)</code>	entropy estimate

Macros

<code>r(name#)</code>	name of the <code>#th</code> estimation result
<code>r(pmptype#)</code>	analytical or frequency

Matrices

<code>r(summary#)</code>	summary matrix with mean, minimum, and maximum LPS
--------------------------	--

`bmastats lps, compact` stores the following in `r()` with multiple estimation results:

Macros

<code>r(names)</code>	names of estimation results
<code>r(pmptypes)</code>	type of PMP for each model: analytical or frequency

Matrices

<code>r(N)</code>	numbers of observations
<code>r(sigma2)</code>	variances used to compute entropy
<code>r(entropy)</code>	entropy estimates
<code>r(summary)</code>	summary matrix with mean, minimum, and maximum LPS for all estimation results

Methods and formulas

Let y^* be a new observation of the outcome and \mathbf{x}^* be a p -vector of new values for the predictors, and let $\mathbf{z}^* = \mathbf{x}^* - \bar{\mathbf{x}}$, where $\bar{\mathbf{x}}' = \mathbf{1}'\mathbf{X}/n$ is a $p \times 1$ vector of predictor means. Let \mathbf{y} be an n -vector of observed outcome values. LPS for y^* is defined as

$$\text{LPS}_{y^*} = -\log\{f(y^*|\mathbf{y}, \mathbf{z}^*)\}$$

For a BMA linear model with a Zellner's g -prior for the regression coefficients and fixed g , $f(y^*|\mathbf{y}, \mathbf{z}^*)$ is a 2^p mixture of t distributions. In this case, LPS can be calculated exactly, if we enumerate the entire model space (Fernández, Ley, and Steel 2001a),

$$\text{LPS}_{y^*} = -\log\left\{\sum_{j=1}^{2^p} P_a(M_j|\mathbf{y})f(y^*|M_j, \mathbf{y}, \mathbf{z}_j^*)\right\}$$

where $P_a(M_j|\mathbf{y})$'s are the analytical PMPs defined by (7) in *Posterior model probability* in *Methods and formulas* of [BMA] **bmaregress** and $f(y^*|M_j, \mathbf{y}, \mathbf{z}_j^*)$ is the conditional posterior predictive distribution, which is a t -distribution with $(n-1)$ degrees of freedom and location and scale given by (5) and (6) in *Conditional posterior predictive distribution* in *Methods and formulas* of [BMA] **bmaregress** with $q = 1$.

With fixed g and when model sampling is used, such as when **bmaregress**'s sampling option is specified, the above formula is computed with respect to the set $J \subset \{1, 2, \dots, 2^p\}$ of distinct models visited by the MCMC sampler.

With random g , we have an MCMC sample $\{g_t, m_t\}$ of size T from the joint g and model posterior distribution. Then, $f(y^*|\mathbf{y}, \mathbf{z}^*)$ in the definition of LPS is replaced with the following frequency-based MCMC estimator,

$$\hat{f}(y^*|\mathbf{y}, \mathbf{z}^*) = \frac{1}{T} \sum_{t=1}^T f(y^*|g_t, m_t, \mathbf{y}, \mathbf{z}^*)$$

where $f(y^*|g_t, m_t, \mathbf{y}, \mathbf{z}^*)$ is the density of the location-scale t distribution with the respective mean and scale given by (5) and (6) in *Conditional posterior predictive distribution* in *Methods and formulas* of [BMA] **bmaregress** with $q = 1$ and j substituted for t . The **bmastats lps** command thus computes the following frequency-based LPS estimator:

$$\widehat{\text{LPS}}_{y^*} = -\log\{\hat{f}(y^*|\mathbf{y}, \mathbf{z}^*)\}$$

Fernández, Ley, and Steel (2001b) and Ley and Steel (2012) suggest exploring the summary statistics of LPS such as the mean, minimum, and maximum to evaluate the quality of the predictions.

The entropy of a continuous distribution with density $f(x)$ is defined to be $-E[\log\{f(x)\}]$. For a normal distribution with mean μ and variance σ^2 , the entropy is

$$\frac{1}{2}\{1 + \log(2\pi\sigma^2)\}$$

bmastats lps reports the estimated entropy with σ^2 in the above replaced by the estimated posterior mean variance as described by (13) and (14) in *Posterior inclusion probability* in *Methods and formulas* of [BMA] **bmaregress**.

References

- Fernández, C., E. Ley, and M. F. J. Steel. 2001a. Benchmark priors for Bayesian model averaging. *Journal of Econometrics* 100: 381–427. [https://doi.org/10.1016/S0304-4076\(00\)00076-2](https://doi.org/10.1016/S0304-4076(00)00076-2).
- . 2001b. Model uncertainty in cross-country growth regressions. *Journal of Applied Econometrics* 16: 563–576. <https://doi.org/10.1002/jae.623>.
- Good, I. J. 1952. Rational decisions. *Journal of the Royal Statistical Society, B ser.*, 14: 107–114. <https://doi.org/10.1111/j.2517-6161.1952.tb00104.x>.
- Hastie, T. J., R. J. Tibshirani, and J. H. Friedman. 2009. *The Elements of Statistical Learning: Data Mining, Inference, and Prediction*. 2nd ed. New York: Springer. <https://doi.org/10.1007/978-0-387-84858-7>.
- Ley, E., and M. F. J. Steel. 2012. Mixtures of g -priors for Bayesian model averaging with economic applications. *Journal of Econometrics* 171: 251–266. <https://doi.org/10.1016/j.jeconom.2012.06.009>.
- Piironen, J., and A. Vehtari. 2017. Comparison of Bayesian predictive methods for model selection. *Statistics and Computing* 27: 711–735. <https://doi.org/10.1007/s11222-016-9649-y>.
- Rossouw, J. J., J. E. du Plessis, J. P. Benadé, A. J. S. Jordaan, P. C. J. Kotzé, J. P. Jooste, and P. L. Ferreira. 1983. Coronary risk factor screening in three rural communities. The CORIS baseline study. *South African Medical Journal* 64: 430–436. https://doi.org/10.10520/AJA20785135_9894.

Also see

- [BMA] **bmastats** — Summary for models and predictors after BMA regression
- [BMA] **bmaregress** — Bayesian model averaging for linear regression
- [BMA] **BMA postestimation** — Postestimation tools for Bayesian model averaging
- [BMA] **Glossary**

Stata, Stata Press, and Mata are registered trademarks of StataCorp LLC. Stata and Stata Press are registered trademarks with the World Intellectual Property Organization of the United Nations. StataNow and NetCourseNow are trademarks of StataCorp LLC. Other brand and product names are registered trademarks or trademarks of their respective companies. Copyright © 1985–2025 StataCorp LLC, College Station, TX, USA. All rights reserved.

For suggested citations, see the FAQ on [citing Stata documentation](#).

