bmagraph coefdensity — Regression coefficient density plots after BMA regression

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Methods and formulas	Reference
Also see			

Description

`bmagraph coefdensity` provides posterior density plots for regression coefficients after the `bmaregress` command. This command is useful for exploratory analysis of regression coefficients. For a given predictor, `bmagraph coefdensity` shows the posterior probability of that predictor not being included in a model and, separately, the smooth density of its coefficient conditional on the predictor being included.

Quick start

Plot the analytical posterior density of the coefficient for predictor `x` after a Bayesian model averaging (BMA) regression model with a fixed g

```
bmagraph coefdensity {x}
```

Same as above, but plot the MCMC-sample posterior density instead of the analytical one; `bmacoefsample` must be run first

```
bmaregress, saving(bmamodelmcmc)
bmacoefsample
bmagraph coefdensity {x}, mcmcsample
```

Plot posterior densities of coefficients for predictors `x1` and `x2`, and customize the look of the vertical probability-mass line at zero for the second graph

```
bmagraph coefdensity {x1 x2}, przeroline2opts(lcolor(green))
```

Same as above, but do not show the lines for probability mass at zero

```
bmagraph coefdensity {x1 x2}, noprzerolines
```

Customize the kernel function used and the line pattern for the graph for `{x1}`

```
bmagraph coefdensity {x1 x2}, dens1opts(kernel(gaussian) lpattern(dot))
```

Plot densities for all coefficients on one graph in two rows

```
bmagraph coefdensity _all, combine(rows(2))
```

Plot the MCMC-sample posterior density of the coefficient for predictor `x` after a BMA regression model with a random g

```
bmaregress, saving(bmamodelmcmc2)
bmacoefsample
bmagraph coefdensity {x}
```

Equivalent to the above `bmagraph coefdensity`

```
bmagraph coefdensity {x}, mcmcsample
```

Menu

Statistics > Bayesian model averaging > Coefficient densities

Syntax

Density plot for one coefficient

`bmagraph coefdensity {`*coef*`}` [, *singleopts*]

Density plot for multiple coefficients

`bmagraph coefdensity` *coefspec* [, *multiopts*]

Density plot for all coefficients

`bmagraph coefdensity _all` [, *multiopts*]

coef is an unabbreviated name of the variable or a factor level used in the `bmaregress` model. *coefspec* may be a regression coefficient {*coef*}, a list of coefficients {*coef1*}, {*coef2*}, etc., or, equivalently, {*coef1 coef2* ...}. `_all` refers to all regression coefficients.

singleopts	Description
Main	
`analytic`	plot analytical posterior density; default for fixed g
`mcmcsample`	plot MCMC-sample posterior density; only choice for random g
`name(`*name*`, ...)`	specify name of graph
`saving(`*filename*`, ...)`	save graph in file
[`no`]`przeroline`	plot or hide vertical line for probability mass at zero
`przerolineopt(`*line_options*`)`	affect rendition of vertical line for probability mass at zero
Density options	
densopts	density plot options
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()`, `name()`, and `saving()` documented in [G-3] ***twoway_options***

multiopts	Description
Main	
`analytic`	plot analytical posterior density; default for fixed g
`mcmcsample`	plot MCMC-sample posterior density; only choice for random g
`name(`*namespec*`, ...)`	specify names of graphs
`saving(`*filespec*`, ...)`	save graphs in files
`[no]przerolines`	plot or hide vertical lines for probability mass at zero
`przerolineopts(`*line_options*`)`	affect rendition of all vertical lines for probability mass at zero
`przeroline#opts(`*line_options*`)`	affect rendition of #th vertical line for probability mass at zero
`combine[(`*grcombineopts*`)]`	display plots on one graph
Density options	
`dens#opts(`*densopts*`)`	density options for #th plot
densopts	density options for all plots
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()`, `name()`, and `saving()` documented in [G-3] ***twoway_options***

Options

Main

`analytic` specifies that the density be computed analytically. This is the default for models with a fixed g and is not available for models with a random g. This option may not be specified together with option `mcmcsample`.

`mcmcsample` specifies that the density be estimated from a Markov chain Monte Carlo (MCMC) sample of coefficients. This option uses an MCMC sample generated by the `bmacoefsample` command and may not be specified together with option `analytic`. This is the only choice for models with a random g; that is, option `mcmcsample` is implied with a random g. With a fixed g, if an MCMC sample is not available, option `mcmcsample` is not allowed. You must use `bmacoefsample` to generate an MCMC sample to produce coefficient density graphs based on sample estimates.

`name(`*namespec*`[, replace])` specifies the name of the graph or multiple graphs. See [G-3] ***name_option*** for a single graph. If multiple graphs are produced, then the argument of `name()` is either a list of names or *stub*, in which case graphs are named *stub*1, *stub*2, and so on. With multiple graphs, if `name()` is not specified, `name(Graph__#, replace)` is assumed; thus, the produced graphs may be replaced by subsequent `bmagraph` commands.

The `replace` suboption causes existing graphs with the specified name or names to be replaced.

`saving(`*filespec*`[, replace])` specifies the filename or filenames to use to save the graph or multiple graphs to disk. See [G-3] ***saving_option*** for a single graph. If multiple graphs are produced, then the argument of `saving()` is either a list of filenames or *stub*, in which case graphs are saved with filenames *stub*1, *stub*2, and so on.

The `replace` suboption specifies that the file (or files) may be replaced if it already exists.

`przerolines` and `noprzerolines` show or hide the vertical lines for probability mass at zero. By default, the lines are shown.

`przerolineopts(`*line_options*`)` and `przeroline#opts(`*line_options*`)` affect the rendition of the vertical lines for probability mass at zero; see [G-3] ***line_options***. `przerolineopts()` controls the look of all vertical lines but may be overridden for specific lines by using the respective options `przeroline#opts()`.

`combine`[`(`*grcombineopts*`)`] specifies the display of all plots of coefficients as subgraphs on one graph. By default, a separate graph is produced for each plot when multiple coefficients are specified.

grcombineopts is any of the options documented in [G-2] **graph combine**.

Density options

`dens#opts(`*densopts*`)` specifies density options for the #th density plot.

densopts specify options for the (kernel) density plot; see the options documented in [G-2] **graph twoway kdensity**, except options `horizontal` and `range(`*varname*`)`. When option `analytic` is assumed, the density functions are known; thus, the kernel density estimation is not needed. In that case, *densopts* include only `n()` and *cline_options*, described in [G-2] **graph twoway kdensity**.

Y axis, X axis, Titles, Legend, Overall

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`, `name()`, or `saving()`. These include, for instance, options for titling the graph (see [G-3] ***title_options***).

Remarks and examples

The `bmaregress` command computes and reports only the posterior means and standard deviations of the regression coefficients. But we can use `bmagraph coefdensity` to plot the entire posterior densities for the regression coefficients.

A posterior density for a regression coefficient in a BMA linear regression is a mixture of a discrete and continuous components. A discrete component corresponds to the posterior probability of noninclusion, the probability that the corresponding predictor is not included in a model after observing the data, which is equivalent to the posterior probability that the coefficient is equal to zero. This component is represented by a red vertical line with a probability mass at zero equal to one minus the posterior inclusion probability (PIP). A continuous component corresponds to the continuous density conditional on the predictor being included or, equivalently, on the coefficient not being equal to zero.

For a BMA linear regression with a fixed g, the posterior densities of regression coefficients are known and can be plotted at any prespecified x-axis points; see *Posterior distributions of regression coefficients* in *Methods and formulas* of [BMA] **bmaregress**. We refer to these densities as analytical posterior densities. Alternatively, if an MCMC sample of regression coefficients, as produced by `bmacoefsample`, is available, the posterior densities can be estimated from this sample by using kernel density estimation (see [R] **kdensity**) when you specify the `mcmcsample` option. We refer to these posterior densities as MCMC-sample posterior densities. With a random g, this is the only option because analytical posterior densities are not available. That is, with a random g, you must run the `bmacoefsample` first before you can run `bmagraph coefdensity`.

▷ Example 1: Posterior density plots for BMA linear regression using enumeration

Recall the `performance` dataset (Chatterjee and Hadi 2012, sec. 3.3) analyzed in example 1 of [BMA] **bmaregress**, where the employees' satisfaction with their supervisors, `rating`, is modeled by six potential predictors.

We fit a BMA linear regression for the `rating` outcome using all six other variables as potential predictors. By default, the model space is fully explored using enumeration.

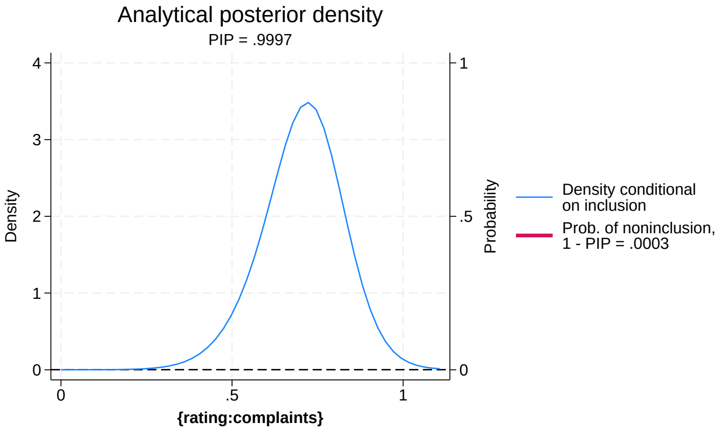
```
. use https://www.stata-press.com/data/r19/performance
(Data on employee satisfaction with supervisor)

. bmaregress rating complaints-advance

Enumerating models ...
Computing model probabilities ...

Bayesian model averaging                   No. of obs         =     30
Linear regression                          No. of predictors  =      6
Model enumeration                                      Groups =      6
                                                       Always =      0
Priors:                                    No. of models      =     64
  Models: Beta-binomial(1, 1)                  For CPMP >= .9 =     10
   Cons.: Noninformative                   Mean model size    =  1.699
   Coef.: Zellner's g
       g: Benchmark, g = 36                Shrinkage, g/(1+g) = 0.9730
  sigma2: Noninformative                   Mean sigma2        = 52.302

------------------------------------------------------------------------------
      rating |      Mean   Std. dev.                            Group      PIP
-------------+----------------------------------------------------------------
  complaints |  .7052859   .1224289                                 1   .99973
    learning |  .0603014   .1285281                                 3   .25249
     advance | -.0167921    .073883                                 6   .13148
  privileges | -.0074174   .0488635                                 2   .10998
      raises |  .0070789   .0670475                                 4   .10642
    critical |  .0009713   .0437848                                 5  .098534
-------------+----------------------------------------------------------------
Always       |
       _cons |   14.8472   7.874219                                 0        1
------------------------------------------------------------------------------
Note: Coefficient posterior means and std. dev. estimated from 64 models.
Note: Default priors are used for models and parameter g.
```

For a fixed *g*, as in our example, the posterior distributions for the regression coefficients can be computed analytically, so we can use `bmagraph coefdensity` directly after `bmaregress`.

Let's look at the distributions of regression coefficients for `complaints` and `learning`. Similarly to other Stata Bayesian commands, we use the curly-braces notation to refer to model parameters—here the regression coefficients.

Let us inspect the analytical marginal posterior density of the coefficient for `complaints`.

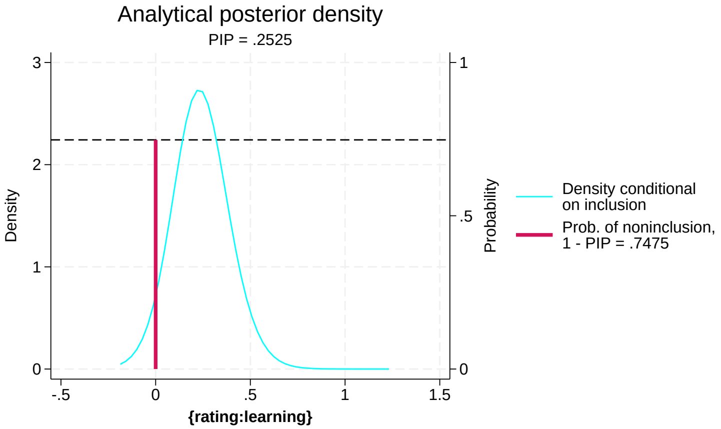
```
. bmagraph coefdensity {complaints}
```



For coefficient `{complaints}` (or using its full name `{rating:complaints}`), the probability of noninclusion is very low, 0.0003, so the red line that represents it is not even visible on the graph. Thus, the posterior density of `{complaints}` is essentially a continuous density, with a mean of roughly 0.7 and with a slightly heavier left tail. Most of the mass of the distribution is between roughly 0.025 and 1.1, away from 0.

Let's plot the analytical marginal posterior density for the `{learning}` coefficient and request a cyan color for the density line:

```
. bmagraph coefdensity {learning}, lcolor(cyan)
```

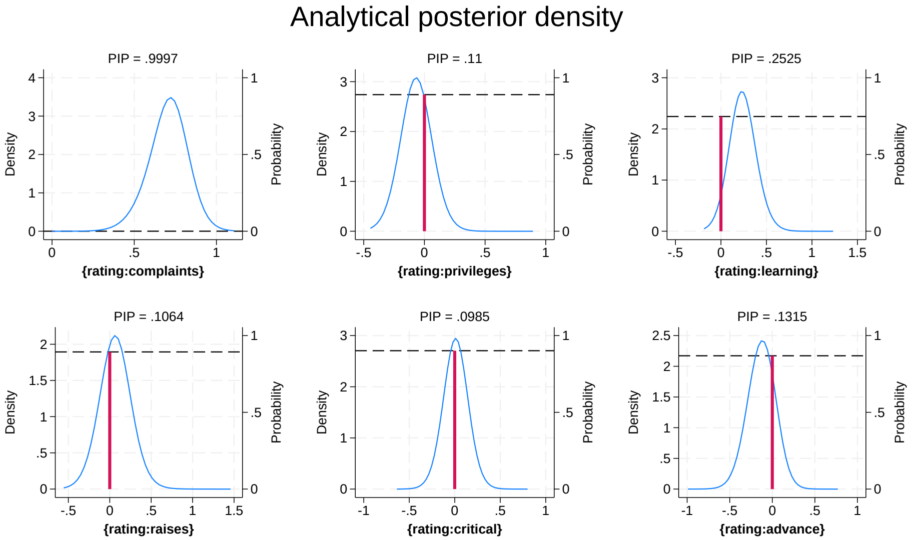


The probability of a noninclusion for `{learning}` is about 0.75, so we see the red vertical line with the horizontal reference line at roughly 0.75. The look of the vertical line can be controlled via the `przerolineopts()` option. Conditional on the inclusion, the continuous density has its mass between roughly -0.2 and 0.7, which includes 0.

The posterior means and standard deviations reported by `bmaregress` are computed with respect to the above mixtures of distributions.

Instead of showing the density of each coefficient separately, we can plot the densities of all coefficients by specifying `_all` and request they be plotted on the same graph using the `combine()` option.

```
. bmagraph coefdensity _all, combine(rows(2))
```



The `rows(2)` suboption of `combine()` specifies that plots be organized in two rows.

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▷ Example 2: Posterior density plots for BMA linear regression using sampling

We refit the same BMA model as in example 1 but now use the `sampling` option to request the MCMC model composition (MC3) algorithm instead of the default model enumeration.

```
. bmaregress rating complaints-advance, sampling rseed(18)
Burn-in ...
Simulation ...
Computing model probabilities ...

Bayesian model averaging                          No. of obs        =     30
Linear regression                                 No. of predictors =      6
MC3 sampling                                                 Groups =      6
                                                             Always =      0
                                                  No. of models     =     32
                                                      For CPMP >= .9 =    10
Priors:                                           Mean model size   =  1.699
  Models: Beta-binomial(1, 1)                     Burn-in           =  2,500
   Cons.: Noninformative                          MCMC sample size  = 10,000
   Coef.: Zellner's g                             Acceptance rate   = 0.2417
       g: Benchmark, g = 36                       Shrinkage, g/(1+g) = 0.9730
  sigma2: Noninformative                          Mean sigma2       = 52.292

Sampling correlation = 0.9990

------------------------------------------------------------------------------
      rating |      Mean   Std. dev.                        Group         PIP
-------------+----------------------------------------------------------------
  complaints |   .705479   .1218881                             1           1
    learning |  .0601919   .1282869                             3      .25234
     advance | -.0167514   .0737415                             6      .13141
  privileges | -.0074265    .048844                             2      .10996
      raises |  .0069949   .0666406                             4      .10629
    critical |  .0009699   .0437742                             5     .098526
-------------+----------------------------------------------------------------
Always       |
       _cons |  14.84478   7.871046                             0           1
------------------------------------------------------------------------------
Note: Coefficient posterior means and std. dev. estimated from 32 models.
Note: Default priors are used for models and parameter g.
```

Although the MC3 sampling is used for the model-space exploration, we can still use `bmagraph coefdensity` directly after `bmaregress` to plot the analytical posterior densities of regression coefficients. This is because we are still assuming a fixed *g* parameter in our model.

Let's compare the analytical and MCMC-sample posterior densities. To obtain the sample estimates, we must first simulate an MCMC sample from the posterior distribution of regression coefficients by using `bmacoefsample`. To use `bmacoefsample`, we first need to save the simulation results produced by `bmaregress`.

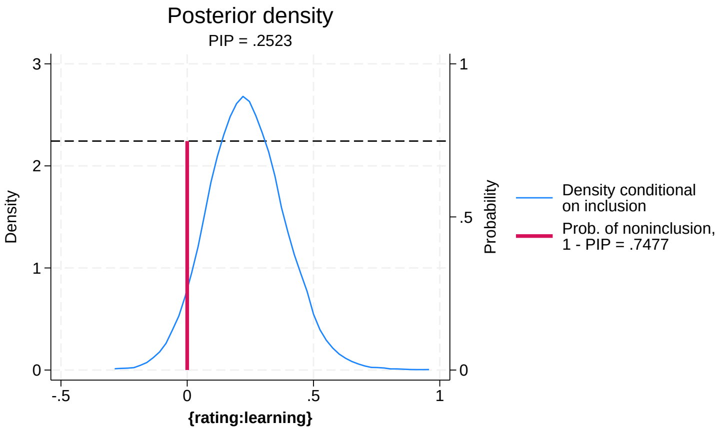
```
. bmaregress, saving(bmaex2, replace)
note: file bmaex2.dta not found; file saved.

. bmacoefsample, rseed(18)

Simulation (10000): ....5000....10000 done
```

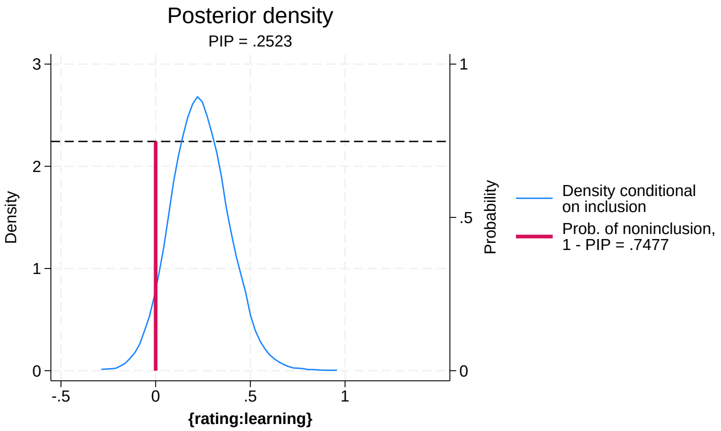
To request the density estimate based on the MCMC sample, we specify the `mcmcsample` option. We plot the MCMC-sample posterior density estimate for the `{learning}` coefficient.

```
. bmagraph coefdensity {learning}, mcmcsample
```



To more easily compare the plot above with the one in example 1, we rescale the x axis to have the same range.

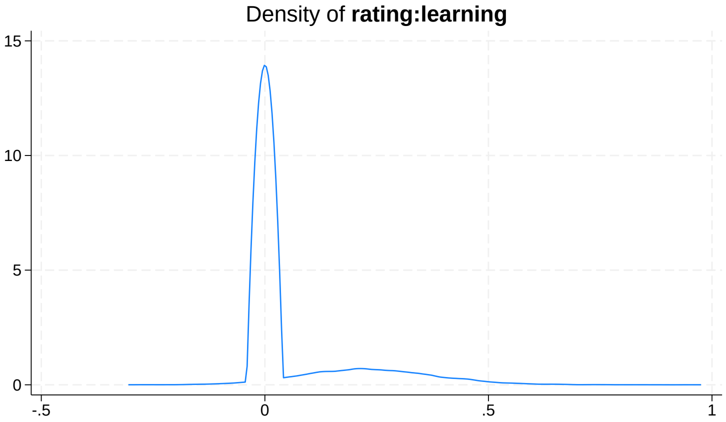
```
. bmagraph coefdensity {learning}, mcmcsample xscale(range(-.5 1.5))
```



The plot is similar to that in example 1.

The marginal density of the `learning` coefficient can also be estimated using the `bayesgraph kdensity` command (see [BAYES] **bayesgraph**). This command, however, incorporates the mass at zero and shows the distribution mixture as one smooth curve, which may not be of practical use in the context of BMA models.

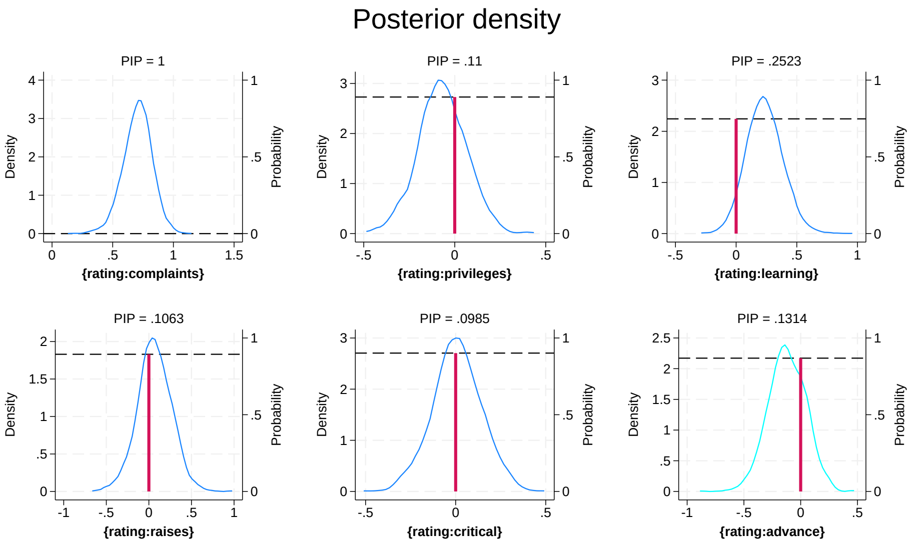
```
. bayesgraph kdensity {learning}
```



Notice how the density curve shrinks toward 0 given the relatively large probability mass (1 − PIP = 0.7477) at that point.

For comparison with the density plots in example 1, we will plot MCMC-sample densities for all coefficients in our model. To demonstrate, we also use `dens6opts(lcolor(cyan))` to specify a cyan color for the density on the sixth plot corresponding to `{rating:advance}`.

```
. bmagraph coefdensity _all, mcmcsample combine(rows(2)) dens6opts(lcolor(cyan))
```



If adequate exploration of the model space by `bmaregress` occurred and a sufficiently large MCMC sample is generated by `bmacoefsample`, the analytical and MCMC-sample posterior densities are expected to be similar. This is the case in our examples (after we adjust for the scales of the x axes).

With a random g, the analytical posterior densities are not available, and the MCMC sampling is needed to approximate these distributions. In that case, the `bmacoefsample` command must be run first to obtain posterior samples of regression coefficients, as we showed above. `bmagraph coefdensity` can then be used to plot an MCMC-sample posterior density, except we do not need to specify the `mcmcsample` option—it is implied with a random g.

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Methods and formulas

Continuing with the notation in *Methods and formulas* of [BMA] **bmaregress**, we consider a predictor X_k for $1 \le k \le p$. Let β_k be the regression coefficient associated with predictor X_k.

The posterior distribution of β_k has a mixed structure, which consists of a continuous portion (a mixture of location-scale t-distributions) and a discrete portion (point mass at 0),

$$p(\beta_k|\mathbf{y}) = (1 - \mathrm{PIP}_k)\, \boldsymbol{\delta}_0 + \mathrm{PIP}_k\, \mathbf{f}_k$$

where $\boldsymbol{\delta}_0$ denotes the point mass at 0 and $\mathbf{f}_k$ is defined by (10) in *Posterior distributions of regression coefficients* in *Methods and formulas* of [BMA] **bmaregress** for models with a fixed g (option `analytic`). When the `mcmcsample` option is assumed, either by default for models with a random g or if specified for models with a fixed g, $\mathbf{f}_k$ is computed using the `kdensity` (see [R] **kdensity**) command based on the coefficient sample generated by `bmacoefsample`.

The vertical line for the probability mass at 0 corresponds to $1 - \mathrm{PIP}_k$, where PIP_k is the PIP of X_k computed as

$$\mathrm{PIP}_k = \sum_{j \in J} I(X_k \in M_j) P(M_j|\mathbf{y})$$

and J indexes a subspace of the model space visited by `bmaregress`. Also see *Posterior inclusion probability* in *Methods and formulas* of [BMA] **bmaregress**.

In the above formula, for models with a fixed g parameter, $P(M_j|\mathbf{y})$ is either $P_a(M_j|\mathbf{y})$ (option `analytic`) or $P_f(M_j|\mathbf{y})$ (option `mcmcsample`). For models with a random g parameter, $P(M_j|\mathbf{y})$ is $P_f(M_j|\mathbf{y})$. These quantities are defined, respectively, by (7) and (8) in *Posterior model probability* in *Methods and formulas* of [BMA] **bmaregress**.

Reference

Chatterjee, S., and A. S. Hadi. 2012. *Regression Analysis by Example*. 5th ed. New York: Wiley.

Also see

[BMA] **bmagraph** — Graphical 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**

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