Package ‘BMS’

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Author Martin Feldkircher and Stefan Zeugner
Maintainer Stefan Zeugner <bms@zeugner.eu>
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Description Bayesian model averaging for linear models with a wide choice of (customizable) priors. Built-in priors include coefficient priors (fixed, flexible and hyper-g priors), 5 kinds of model priors, moreover model sampling by enumeration or various MCMC approaches. Post-processing functions allow for inferring posterior inclusion and model probabilities, various moments, coefficient and predictive densities. Plotting functions available for posterior model size, MCMC convergence, predictive and coefficient densities, best models representation, BMA comparison.
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BMS-package ................................................................. 2
as.zlm ........................................................................... 4
beta.draws.bma .............................................................. 5
bin2hex .......................................................................... 6
bma-class ................................................................. 7
bms ........................................................................ 9
c.bma ........................................................................ 15
coef.bma ................................................................. 16
<table>
<thead>
<tr>
<th>Function</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>datafls</td>
<td>19</td>
</tr>
<tr>
<td>density.bma</td>
<td>21</td>
</tr>
<tr>
<td>f21hyper</td>
<td>23</td>
</tr>
<tr>
<td>fullmodel.ssq</td>
<td>25</td>
</tr>
<tr>
<td>gdensity</td>
<td>26</td>
</tr>
<tr>
<td>gprior-class</td>
<td>28</td>
</tr>
<tr>
<td>image.bma</td>
<td>29</td>
</tr>
<tr>
<td>is.bma</td>
<td>31</td>
</tr>
<tr>
<td>lps.bma</td>
<td>31</td>
</tr>
<tr>
<td>mprior-class</td>
<td>33</td>
</tr>
<tr>
<td>plot.bma</td>
<td>34</td>
</tr>
<tr>
<td>plot.pred.dense</td>
<td>35</td>
</tr>
<tr>
<td>plotConv</td>
<td>36</td>
</tr>
<tr>
<td>plotComp</td>
<td>37</td>
</tr>
<tr>
<td>plotModels.size</td>
<td>39</td>
</tr>
<tr>
<td>pmp.bma</td>
<td>40</td>
</tr>
<tr>
<td>pmpmodel</td>
<td>42</td>
</tr>
<tr>
<td>post.var</td>
<td>44</td>
</tr>
<tr>
<td>pred.dense</td>
<td>45</td>
</tr>
<tr>
<td>predict.bma</td>
<td>47</td>
</tr>
<tr>
<td>predict.zlm</td>
<td>49</td>
</tr>
<tr>
<td>print.bma</td>
<td>50</td>
</tr>
<tr>
<td>print.topmod</td>
<td>51</td>
</tr>
<tr>
<td>quantile.pred.dense</td>
<td>52</td>
</tr>
<tr>
<td>summary.bma</td>
<td>54</td>
</tr>
<tr>
<td>summary.zlm</td>
<td>56</td>
</tr>
<tr>
<td>topmod</td>
<td>57</td>
</tr>
<tr>
<td>topmod-class</td>
<td>60</td>
</tr>
<tr>
<td>topmodels.bma</td>
<td>62</td>
</tr>
<tr>
<td>variable.names.bma</td>
<td>63</td>
</tr>
<tr>
<td>variable.names.zlm</td>
<td>64</td>
</tr>
<tr>
<td>zlm</td>
<td>65</td>
</tr>
<tr>
<td>zlm-class</td>
<td>67</td>
</tr>
<tr>
<td>[.bma</td>
<td>68</td>
</tr>
</tbody>
</table>

**Index**

*a.bma* 70

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**Description**

This package enables Bayesian Model Averaging over the classical normal-conjugate model with many prior options and posterior statistics.
Details

Package: BMS
Type: Package
Version: 0.3.4
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License: Artistic 2.0

The most important function is `bms` to perform bayesian model sampling for Bayesian model Averaging or Bayesian Model Selection. It basically offers to sample data according to different g-priors and model priors, and leaves the choice of different samplers (MCMC samplers, full or partial enumeration, and interaction samplers). The results provide analysis into models according to MCMC frequencies, and according to the posterior likelihood of the best nmodel models (cf. `bms`).

The functions `coef.bma` and `summary.bma` summarize the most important results.

The plotting functions `plot.bma, image.bma, density.bma, pred.density, and gdensity` are the most important plotting functions (inter alia). Most of them also produce numerical output.

Moreover there are other functions for posterior results, such as `beta.draws.bma, pmp.bma, pmpmodel, post.var, post.pr2` and `topmodels.bma`, while `c.bma` helps to combine and parallelize sampling chains.

The function `zlm` estimates a Bayesian linear regression under Zellner’s g prior, i.e. estimating a particular model without taking model uncertainty into account. The function `as.zlm` may be used for model selection.

Finally, the small-scale functions `f21hyper, hex2bin` and `fullmodel.ssq` provide addidtional utilities, as well as bma- and zlm-specific methods for `variable.names, deviance, vcov, etc.`

Consider the function `topmod` for more advanced programming tasks, as well as the possibility to customize coefficient priors (`gprior-class`) and model priors (`mprior-class`).

Author(s)

Martin Feldkircher and Stefan Zeugner
Maintainer: Stefan Zeugner <bms@zeugner.eu>

References


See Also

http://bms.zeugner.eu
Examples

data(datafls)
mfls = bms(X.data=datafls,burn=1000,iter=9000,nmodel=100)
info.bma(mfls)
coef(mfls)
coef(mfls,exact=TRUE,std.coefs=TRUE)
mfls[3]$topmod
image(mfls[1:20],FALSE)
plotModelsize(mfls,exact=TRUE)
density(mfls,"Spanish")

Description

Extracts a model out of a bma object’s saved models and converts it to a \texttt{zlm} linear model

Usage

\texttt{as.zlm(bmao, model = 1)}

Arguments

- \texttt{bmao} A bma object, e.g. resulting from a call to \texttt{bms}
- \texttt{model} The model index, in one of the following forms:
  - An integer, denoting the rank of the model (1 for best, 2 for second-best, ...)
  - A numeric or logical vector of length K describing which covariates are contained in the model
  - A hexcode character describing which covariates are contained in the model

Details

A bma object stores several 'best' models it encounters (cf. argument \texttt{nmodel} in \texttt{bms}). \texttt{as.zlm} extracts a single model and converts it to an object of class \texttt{zlm}, which represents a linear model estimated under Zellner’s g prior.

The utility \texttt{model.frame} allows to transform a \texttt{zlm} model into an OLS model of class \texttt{lm}.

Value

- a list of class \texttt{zlm}

Author(s)

Stefan Zeugner
beta.draws.bma

See Also

bms for creating bma objects, zlm for creating zlm objects, topmodels.bma and pmp.bma for displaying the topmodels in a bma object
Check http://bms.zeugner.eu for additional help.

Examples

data(datafls)

mm=bms(datafls[,1:6],mcmc="enumeration") # do a small BMA chain
topmodels.bma(mm)[,1:5] #display the best 5 models

m2a=as.zlm(mm,4) #extract the fourth best model
summary(m2a)

# Bayesian Model Selection:
# transform the best model into an OLS model:
lm(model.frame(as.zlm(mm)))

# extract the model only containing the 5th regressor
m2b=as.zlm(mm,c(0,0,0,0,1))

# extract the model only containing the 5th regressor in hexcode
print(bin2hex(c(0,0,0,0,1)))
m2c=as.zlm(mm,"01")

beta.draws.bma

Coefficients of the Best Models

Description

Returns a matrix whose columns are the (expected value or standard deviations of) coefficients for the best models in a bma object.

Usage

beta.draws.bma(bmao, stdev=FALSE)

Arguments

bmao a 'bma' object (as e.g. resulting from bms)
stdev if stdev=FALSE then beta.draws.bma returns the (conditional) posterior expected values of the coefficients (i.e. 'Bayesian coefficients'). If stdev=TRUE it returns their posterior standard deviations.
Each column presents the coefficients for the model indicated by its column name. The zero coefficients are the excluded covariates per model. Note that the coefficients returned are only those of the best (100) models encountered by the bma object (cf. argument nmodels of bms). For aggregate coefficients please refer to coef.bma.

Note

Note that the elements of beta.draws.bma(bmao) correspond to bmao$topmood$betas()

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

bms for creating bms objects, coef.bma for aggregate coefficients

Check http://bms.zeugner.eu for additional help.

Examples

```r
#sample a bma object:
data(datafls)
mm=bms(datafls,burn=500,iter=5000,nmodel=20)

#coefficients for all
beta.draws.bma(mm)

#standard deviations for the fourth- to eight best models
beta.draws.bma(mm[4:8],TRUE);
```

---

### bin2hex

**Converting Binary Code to and from Hexadecimal Code**

**Description**

A simple-to-use function for converting a logical ('binary') vector into hex code and reverse.

**Usage**

- `bin2hex(binvec)`
- `hex2bin(hexcode)`
Arguments

binvec  a logical vector (alternatively a vector coercible into logical)
hexcode a single-element character denoting an integer in hexcode (admissible character: 0 to 9, a to f)

Details

The argument is an integer in binary form (such as "101"), provided as a logical (c(T,F,T)) or numeric vector (c(1,0,1)).
bin2hex then returns a character denoting this number in hexcode (in this case "5").
The function hex2bin does the reverse operation, e.g. hex2bin("5") gives (c(1,0,1)).

Value

bin2hex returns a single element character; hex2bin returns a numeric vector equivalent to a logical vector

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

hex2bin for converting hexcode into binary vectors, format.hexmode for a related R function.
Check http://bms.zeugner.eu for additional help.

Examples

bin2hex(c(TRUE,FALSE,TRUE,FALSE,TRUE,TRUE))
bin2hex(c(1,0,1,0,1,1))
hex2bin("b8a")
bin2hex(hex2bin("b8a"))
Slots

.S3Class: Object of class "list", elements are:

  info: An object of class "list" holding aggregate statistics: iter is the number of iterations, burn the number of burn-ins.

  The following have to be divided by cumsumweights to get posterior expected values:

  inccount are the posterior inclusion probabilities, bQmo and bRmo the first and second moment of coefficients, add.otherstats other statistics of interest (typically the moments of the shrinkage factor), msize is the post. expected model size, k.vec the posterior model size distribution, pos.sign the unconditional pos. probability of positive coefficients, corr.pmp is the correlation between the best models' MCMC frequencies and their marg. likelihoods.

  timed is the time that was needed for MCMC sampling, cons is the posterior expected value of the constant. k and N are the maximum number of covariates and the sample size, respectively.

  arguments: An object of class "list" holding the evaluated function arguments provided to bms

  topmod: An object of class topmod containing the best drawn models. see topmod for more details

  start.pos: the positions of the starting model. If bmao is a bma object this corresponds to covariates bmao$reg.names[bmao$start.pos]. If bmao is a chain that resulted from several starting models (cf. c.bma, then start.pos is a list detailing all of them.

  gprior.info: a list of class gprior-class, detailing information on the g-prior: gtype corresponds to argument g above, is.constant is FALSE if gtype is either "hyper" or "EBL", return.g.stats corresponds to argument g.stats above, shrinkage.moments contains the first and second moments of the shrinkage factor (only if return.g.stats==TRUE), g details the fixed g (if is.constant==TRUE), hyper.parameter corresponds to the hyper-g parameter a as in Liang et al. (2008).

  mprior.info: a list of class mprior-class, detailing information on the model prior: origargs lists the original arguments to mprior and mprior.size above; mp.msize denotes the prior mode size; mp.Kdist is a (K+1) vector with the prior model size distribution from 0 to K

  X.data: Object of class "data.frame" or class "matrix", matrix: corresponds to argument X.data in bms, possibly cleaned for NAs

  reg.names: Vector of class "character": the covariate names to be used for X.data in bms

  bms.call: Object of class "call": the original call to the bms function

Methods

  summary.bma, print.bma, coef.bma, density.bma, image.bma, plot.bma

Author(s)

  Martin Feldkircher and Stefan Zeugner

References

  http://bms.zeugner.eu
See Also

bms for creating bma objects,
or topmod for the topmod object

Examples

```r
data(datafls)
mm=bms(datafls)
#show posterior model size
print(mm$info$msize/mm$info$cumsumweights)
#is the same number as in
summary(mm)
```

**bms**  
*Bayesian Model Sampling and Averaging*

Description

Given data and prior information, this function samples all possible model combinations via MC3 or enumeration and returns aggregate results.

Usage

```r
bms(X.data, burn = 1000, iter = NA, nmodel = 500, mcmc = "bd",
g = "UIP", mprior = "random", mprior.size = NA, user.int = TRUE,
start.value = NA, g.stats = TRUE,
logfile = FALSE, logstep = 10000, force.full.ols = FALSE,
fixed.reg = numeric(0), data = NULL, randomizeTimer = TRUE)
```

Arguments

- **X.data**  
a data frame or a matrix, with the dependent variable in the first column, followed by the covariates. Alternatively, `X.data` can also be provided as a *formula*. In that case, it may advisable to provide the data in argument `data`). Note that `bms` automatically estimates a constant, therefore including constant terms is not necessary.

- **burn**  
The (positive integer) number of burn-in draws for the MC3 sampler, defaults to 1000. (Not taken into account if `mcmc="enumerate"`)

- **iter**  
If `mcmc` is set to an MC3 sampler, then this is the number of iteration draws to be sampled (ex burn-ins), default 3000 draws. If `mcmc="enumerate"`, then `iter` is the number of models to be sampled, starting from 0 (defaults to $2^K - 1$) - cf. `start.value`.

- **nmodel**  
the number of best models for which information is stored (default 500). Best models are used for convergence analysis between likelihoods and MCMC frequencies, as well as likelihood-based inference. Note that a very high value for `nmodel` slows down the sampler significantly. Set `nmodel=0` to speed up sampling (if best model information is not needed).
mcmc

A character denoting the model sampler to be used. 
The MC3 sampler mcmc="bd" corresponds to a birth/death MCMC algorithm. mcmc="rev.jump" enacts a reversible jump algorithm adding a "swap" step to the birth / death steps from "bd". Alternatively, the entire model space may be fully enumerated by setting mcmc="enumerate" which will iterate all possible regressor combinations (Note: consider that this means $2^K$ iterations, where $K$ is the number of covariates.) Default is full enumeration (mcmc="enumerate") with less than 15 covariates, and the birth-death MC3 sampler (mcmc="bd") with 15 covariates or more. Cf. section 'Details' for more options.

g

The hyperparameter on Zellner's g-prior for the regression coefficients.
g="UIP" corresponds to $g = N$, the number of observations (default); g="BRIC" corresponds to the benchmark prior suggested by Fernandez, Ley and Steel (2001), i.e $g = \max(N, K^2)$, where $K$ is the total number of covariates; g="RIC" sets $g = K^2$ and conforms to the risk inflation criterion by George and Foster (1994) g="HQ" sets $g = \log(N^3)$ and asymptotically mimics the Hannan-Quinn criterion with $C_{HQ} = 3$ (cf. Fernandez, Ley and Steel, 2001, p.395) g="EBL" estimates a local empirical Bayes g-parameter (as in Liang et al. (2008)); g="hyper" takes the 'hyper-g' prior distribution (as in Liang et al., 2008) with the default hyper-parameter $a$ set such that the prior expected shrinkage factor conforms to 'UIP'; This hyperparameter $a$ can be adjusted (between $2 < a <= 4$) by setting g="hyper=2.9", for instance. Alternatively, g="hyper=UIP" sets the prior expected value of the shrinkage factor equal to that of UIP (default), g="hyper=BRIC" sets it according to BRIC cf section 'Details' for more on the hyper-g prior

mprior

A character denoting the model prior choice, defaulting to "random": mprior="fixed" denotes fixed common prior inclusion probabilities for each regressor as e.g. in Sala-i-Martin, Doppelhofer, and Miller(2004) - for their fine-tuning, cf. mprior.size. Preferable to mcmc="random" if strong prior information on model size exists; mprior="random" (default) triggers the 'random theta' prior by Ley and Steel (2008), who suggest a binomial-beta hyperprior on the a priori inclusion probability; mprior="uniform" employs the uniform model prior; mprior="customk" allows for custom model size priors (cf. mprior.size); mprior="pip" allows for custom prior inclusion probabilities (cf. mprior.size); Note that the prior on models with more than N-3 regressors is automatically zero: these models will not be sampled.

mprior.size

If mprior is "fixed" or "random", mprior.size is a scalar that denotes the prior expected value of the model size prior (default K/2). If mprior="customk" then a custom model size prior can be provided as a K+1 vector detailing the priors from model size 0 to K (e.g. rep(1,K+1) for the uniform model prior); if mprior="pip", then custom prior inclusion probabilities can be provided as a vector of size K, with elements in the interval (0,1)

user.int

'interactive mode': print out results to console after ending the routine and plots
start.value specifies the starting model of the iteration chain. For instance a specific model by the corresponding column indices (e.g. starting.model=numeric(K) starts from the null model including solely a constant term) or start.value=c(3,6) for a starting model only including covariates 3 and 6.

If start.model is set to an integer (e.g. start.model=15) then that number of covariates (here: 15 covariates) is randomly chosen and the starting model is identified by those regressors with an OLS t-statistic>0.2.

The default value start.value=NA corresponds to start.value=min(ncol(X.data),nrow(X.data)-3).

Note that start.value=0 or start.value=NULL starts from the null model. If mcmc="enumerate" then start.value is the index to start the iteration (default: 0, the null model). Any number between 0 and $K^2 - 1$ is admissible.

g.stats TRUE if statistics on the shrinkage factor $g/(1+g)$ should be collected, defaulting to TRUE (Note: set g.stats=FALSE for faster iteration.)

logfile setting logfile=TRUE produces a logfile named "test.log" in your current working directory, in order to keep track of the sampling procedure. logfile equal to some filepath (like logfile="subfolder/log.txt") puts the logfile into that specified position. (default: logfile=FALSE). Note that logfile="" implies log printouts on the console.

logstep specifies at which number of posterior draws information is written to the log file; default: 10 000 iterations

force.full.ols default FALSE. If force.full.ols=TRUE, the OLS estimation part of the sampling procedure relies on slower matrix inversion, instead of streamlined routines. force.full.ols=TRUE can slow down sampling but may deal better with highly collinear data

fixed.reg indices or variable names of X.data that are fixed regressors to be always included in every sampled model. Note: the parameter mprior.size refers to prior model size including these fixed regressors.

data an optional data.frame (or one that can be coerced to that class such as a matrix: cf. lm) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which bms is called.

randomizeTimer default TRUE makes a call to set.seed in order to generate random numbers for the MCMC sampler. In laymen’s terms: If set to default FALSE, then there the sampler will always parse to exactly the same random numbers.

Details

Ad mcmc:

Interaction sampler: adding an ".int" to an MC3 sampler (e.g. "mcmc="bd.int") provides for special treatment of interaction terms. Interaction terms will only be sampled along with their component variables: In the column names of X.data, interaction terms need to be denominated by names consisting of the base terms separated by # (e.g. an interaction term of base variables "A", "B" and "C" needs column name "A#B#C"). Then variable "A#B#C" will only be included in a model if all of the component variables ("A", "B", and "C") are included.

The MC3 samplers "bd", "rev.jump", "bd.int" and "rev.jump.int", iterate away from a starting model by adding, dropping or swapping (only in the case of rev.jump) covariates.
In an MCMC fashion, they thus randomly draw a candidate model and then move to it in case its marginal likelihood (marg. lik.) is superior to the marg. lik. of the current model.

In case the candidate’s marg. lik is inferior, it is randomly accepted or rejected according to a probability formed by the ratio of candidate marg. lik over current marg. lik. Over time, the sampler should thus converge to a sensible distribution. For aggregate results based on these MC3 frequencies, the first few iterations are typically disregarded (the ‘burn-ins’).

Ad g and the hyper-g prior: The hyper-g prior introduced by Liang et al. (2008) puts a prior distribution on the shrinkage factor \( g/(1 + g) \), namely a Beta distribution Beta(1, 1/2 – 1) that is governed by the parameter \( a \). \( a = 4 \) means a uniform prior distribution of the shrinkage factor, while \( a > 2 \) close to 2 concentrates the prior shrinkage factor close to one. The prior expected value is \( E(g/(1 + g)) = 2/a \). In this sense \( g\text{Hyper} = \text{UIP} \) and \( g\text{Hyper} = \text{BRIC} \) set the prior expected shrinkage such that it conforms to a fixed UIP-\( g \) (eqng=N) or BRIC-\( g \) (\( g = \max(K^2, N) \)).

Value

A list of class bma, that may be displayed using e.g. summary.bma or coef.bma. The list contains the following elements:

- **info** a list of aggregate statistics: iter is the number of iterations, burn the number of burn-ins. The following have to be divided by cumsumweights to get posterior expected values: incount are the posterior inclusion probabilities, b1mo and b2mo the first and second moment of coefficients, add.otherstats other statistics of interest (typically the moments of the shrinkage factor), msize is the post. expected model size, k.vec the posterior model size distribution, pos.sign the unconditional post. probability of positive coefficients, corr.pmp is the correlation between the best models’ MCMC frequencies and their marg. likelihoods. timed is the time that was needed for MCMC sampling, cons is the posterior expected value of the constant. K and N are the maximum number of covariates and the sample size, respectively.

- **arguments** a list of the evaluated function arguments provided to bms (see above)

- **topmod** a ’topmod’ object containing the best drawn models. see topmod for more details

- **start.pos** the positions of the starting model. If bmao is a ’bma’ object this corresponds to covariates bmao$reg.names[bmao$start.pos]. If bmao is a chain that resulted from several starting models (cf. c.bma, then start.pos is a list detailing all of them.

- **gprior.info** a list of class gprior-class, detailing information on the g-prior: gtype corresponds to argument g above, is.constant is FALSE if gtype is either ”hyper” or ”EBL”, return.g.stats corresponds to argument g.stats above, shrinkage.moments contains the first and second moments of the shrinkage factor (only if return.g.stats==TRUE), g details the fixed g (if is.constant==TRUE), hyper.parameter corresponds to the hyper-g parameter \( a \) as in Liang et al. (2008)

- **mprior.info** a list of class mprior-class, detailing information on the model prior: origargs lists the original arguments to mprior and mprior.size above; mp.msize denotes the prior mode size; mp.Kdist is a (K+1) vector with the prior model size distribution from 0 to K
The models analyzed are Bayesian normal-gamma conjugate models with improper constant and variance priors akin to Fernandez, Ley and Steel (2001): A model $M$ can be described as follows, with $\epsilon \sim N(0, \sigma^2 I)$:

$$f(\beta|\sigma, M, g) \sim N(0, g\sigma^2 (X'X)^{-1})$$

Moreover, the (improper) prior on the constant $f(\alpha)$ is put proportional to 1. Similarly, the variance prior $f(\sigma)$ is proportional to $1/\sigma$.

Note

There are several ways to speed-up sampling: nmodel=10 saves only the ten best models, at most a marginal improvement. nmodels=0 does not save the best (500) models, however then posterior convergence and likelihood-based inference are not possible.

g.stats=FALSE saves some time by not retaining the shrinkage factors for the MC3 chain (and the best models). force.fullobject=TRUE in contrast, slows sampling down significantly if mcmc="enumerate".

Author(s)

Martin Feldkircher and Stefan Zeugner

References


Ley, E. and M. Steel (2008): On the Effect of Prior Assumptions in Bayesian Model Averaging with Applications to Growth Regressions. working paper


See Also

ccoef, plotModels, and density for some operations on the resulting 'bma' object,
cbma for integrating separate MC3 chains and splitting of sampling over several runs.
Check http://bms.zeugner.eu for additional help.

Examples

data(datafls)
# estimating a standard MC3 chain with 1000 burn-ins and 2000 iterations and uniform model priors
bma1 = bms(datafls, burn=1000, iter=2000, mprior="uniform")

## standard coefficients based on exact likelihoods of the 100 best models:
coef(bma1, exact=TRUE, std.coefs=TRUE)

# suppressing user-interactive output, using a customized starting value, and not saving the best
# models for only 19 observations (but 41 covariates)
bma2 = bms(datafls[20:39,], burn=1000, iter=2000, nmodel=0, start.value=c(1,4,7,30),
  user.int=FALSE)
coef(bma2)

## MC3 chain with a hyper-g prior (custom coefficient a=2.1), saving only the 20 best models,
# ... and an alternative sampling procedure; putting a log entry to console every 1000th step
bma3 = bms(datafls, burn=1000, iter=5000, nmodel=20, g="hyper=2.1", mcmc="rev.jump",
  logfile="", logstep=1000)
image(bma3) # showing the coefficient signs of the 20 best models

# enumerating with 10 covariates (= 1024 models), keeping the shrinkage factors
# ... of the best 200 models
bma4 = bms(datafls[,1:11], mcmc="enumerate", nmodel=200, g.stats=TRUE)

# another enumeration example: with less than 15 covariates, enumeration is the default
# ... of the best 200 models
data(attitude)
bma4b = bms(attitude)
bma4c = bms(rating ~ complaints + privileges + raises, data = attitude)

# using an interaction sampler for two interaction terms
dataint=datafls
dataint=cbind(datafls, datafls$LifeExp, datafls$Abslat/1000,
datafls$Protestants, datafls$Brit, datafls$Muslim)
names(dataint)[ncol(dataint)-1]="LifeExp#Abslat"
names(dataint)[ncol(dataint)]="Protestants#Brit#Muslim"
bma5 = bms(X.data=dataint, burn=1000, iter=9000, start.value=0, mcmc="bd.int")
density(bma5, reg="English") # plot posterior density for covariate "English"

# a matrix as X.data argument
bms(matrix(rnorm(1000), 100, 10))

# keeping a set of fixed regressors:
bms(datafls, mprior.size=7, fixed.reg = c("PrScEnroll", "LifeExp", "GDP60"))
# Note that mprior.size=7 means prior model size of 3 fixed to 4 'uncertain' regressors

## c.bma

### Concatenate bma objects

**Description**

Combines bma objects (resulting from `bms`). Can be used to split estimation over several machines, or combine the MCMC results obtained from different starting points.

**Usage**

```r
c(bma, ...)  
## S3 method for class 'bma'
c(..., recursive = FALSE)
```

**Arguments**

- `...` At least two 'bma' objects (cf. `bms`)
- `recursive` retained for compatibility with `c` method

**Details**

Aggregates the information obtained from several chains. The result is a 'bma' object (cf. 'Values' in `bms`) that can be used just as a standard 'bma' object.

Note that `combine_chains` helps in particular to parallelize the enumeration of the total model space: A model with $K$ regressors has $2^K$ potential covariate combinations. With $K$ large (more than 25), this can be pretty time intensive. With the `bms` arguments `start.value` and `iter`, sampling can be done in steps: cf. example 'enumeration' below.

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

- `bms` for creating bma objects
- Check [http://bms.zuegner.eu](http://bms.zuegner.eu) for additional help.
Examples

data(datafls)

# MCMC case
model1 = bms(datafls, burn=1000, iter=4000, mcmc="bd", start.value=c(20, 30, 35))
model2 = bms(datafls, burn=1500, iter=7000, mcmc="bd", start.value=c(1, 10, 15))

model_all = c(model1, model2)
coef(model_all)
plot(model_all)

# splitting enumeration

# standard case with 12 covariates (4096 different combinations):
enum0 = bms(datafls[,1:13], mcmc="enumerate")

# now split the task:
# enum1 does everything from model zero (the first model) to model 1999
enum1 = bms(datafls[,1:13], mcmc="enumerate", start.value=0, iter=1999)

# enum2 does models from index 2000 to the index 3000 (in total 1001 models)
enum2 = bms(datafls[,1:13], mcmc="enumerate", start.value=2000, iter=1000)

# enum3 does models from index 3001 to the end
enum3 = bms(datafls[,1:13], mcmc="enumerate", start.value=3001)

enum_combi = c(enum1, enum2, enum3)
coef(enum_combi)
coef(enum0)

# both enum_combi and enum0 have exactly the same results
# (one difference: enum_combi has more 'top models' (1500 instead of 500))

---

**coef.bma**  
*Posterior Inclusion Probabilities and Coefficients from a 'bma' Object*

**Description**

Returns a matrix with aggregate covariate-specific Bayesian model Averaging: posterior inclusion probabilities (PIP), post. expected values and standard deviations of coefficients, as well as sign probabilities.

**Usage**

```r
## S3 method for class 'bma'
coef(object, exact = FALSE, order.by.pip = TRUE, include.constant = FALSE,
```
incl.possign = TRUE, std.coefs = FALSE, condi.coef = FALSE, ...)

# equivalent:
estimates.bma(object, exact = FALSE, order.by.pip = TRUE, include.constant = FALSE,
incl.possign = TRUE, std.coefs = FALSE, condi.coef = FALSE)

## Arguments

- **object**: a 'bma' object (cf. `bms`)
- **exact**: if exact=FALSE, then PIPs, coefficients, etc. will be based on aggregate information from the sampling chain with posterior model distributions based on MCMC frequencies (except in case of enumeration - cf. 'Details'); if exact=TRUE, estimates will be based on the `nmodel` best models encountered by the sampling chain, with the posterior model distribution based on their exact marginal likelihoods - cf. 'Details' below.
- **order.by.pip**: order.by.pip=TRUE orders the resulting matrix according to posterior inclusion probabilities, order.by.pip=FALSE ranks them according to the original data (order of the covariates as in provided in `x.data` to `bms`), default TRUE
- **include.constant**: If include.constant=TRUE then the resulting matrix includes the expected value of the constant in its last row. Default FALSE
- **incl.possign**: If incl.possign=FALSE, then the sign probabilities column (cf. 'Values' below) is omitted from the result. Default TRUE
- **std.coefs**: If std.coefs=TRUE then the expected values and standard deviations are returned in standardized form, i.e. as if the original data all had mean zero and variance 1. If std.coefs=FALSE (default) then both expected values and standard deviations are returned 'as is'.
- **condi.coef**: If condi.coef=FALSE (default) then coefficients \( \beta_i \) and standard deviations are unconditional posterior expected values, as in standard model averaging; if condi.coef=FALSE then they are given as conditional on inclusion (equivalent to \( \beta_i / \text{PIP}_i \)).

... further arguments for other `coef` methods

## Details

More on the argument `exact`:
In case the argument `exact`=TRUE, the PIPs, coefficient statistics and conditional sign probabilities are computed on the basis of the (500) best models the sampling chain encountered (cf. argument `nmodel` in `bms`). Here, the weights for Bayesian model averaging (BMA) are the posterior marginal likelihoods of these best models.
In case `exact`=FALSE, then these statistics are based on all accepted models (except burn-ins): If `mcmc`="enumerate" then this are simply all models of the traversed model space, with their marginal likelihoods providing the weights for BMA.
If, however, the bma object `bmao` was based on an MCMC sampler (e.g. when `bms` argument `mcmc`="bd"), then BMA statistics are computed differently: In contrast to above, the weights for BMA are MCMC frequencies, i.e. how often the respective models were encountered by the MCMC sampler. (cf. a comparison of MCMC frequencies and marginal likelihoods for the best models via the function `pmp.bma`.)
Value

A matrix with five columns (or four if incl.pos.sign=FALSE)

Column 'PIP'  Posterior inclusion probabilities $p(\gamma|i \in \gamma,Y)/\sum p(\gamma|Y)$

Column 'Post Mean'

posterior expected value of coefficients, unconditional $E(\beta|Y) = \sum p(\gamma|Y)E(\beta|\gamma,Y)$, where $E(\beta|\gamma,i \notin \gamma,Y) = 0$ if condi.coef=FALSE, or conditional on inclusion $(E(\beta|Y)/\sum p(\gamma|Y,i \in \gamma))$ if condi.coef=TRUE

Column 'Post SD'

posterior standard deviation of coefficients, unconditional or conditional on inclusion, depending on condi.coef

Column 'Cond.Pos.Sign'

The ratio of how often the coefficients’ expected values were positive conditional on inclusion. (over all visited models in case exact=FALSE, over the best models in case exact=TRUE)

Column 'Idx'

the original order of covariates as the were used for sampling. (if included, the constant has index 0)

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also


Examples

```r
#sample, with keeping the best 200 models:
data(datafls)
mm=bms(datafls,burn=1000,iter=5000,nmodel=200)

#standard BMA PIPs and coefficients from the MCMC sampling chain, based on
# ...how frequently the models were drawn
coeff(mm)

#standardized coefficients, ordered by index
coeff(mm, std.coefs=TRUE, order.by.pip=FALSE)

#coefficients conditional on inclusion:
coeff(mm, condi.coef=TRUE)

#same as
eststs=coeff(mm, condi.coef=FALSE)
eststs[,2]/eststs[,1]

#PIPs, coefficients, and signs based on the best 200 models
estmates.bma(mm, exact=TRUE)
```

datafls

#... and based on the 50 best models
coeff(mm[1:50], exact=TRUE)

---

datafls

**FLS (2001) growth data**

**Description**


**Usage**

data(datafls)

**Format**

A data frame with 72 observations on the following 42 variables.

- `y` numeric: Economic growth 1960-1992 as from the Penn World Tables Rev 6.0
- `abslat` numeric: Absolute latitude
- `spanish` numeric: Spanish colony dummy
- `french` numeric: French colony dummy
- `brit` numeric: British colony dummy
- `wardummy` numeric: War dummy
- `latamerica` numeric: Latin America dummy
- `subsahara` numeric: Sub-Sahara dummy
- `outwaror` numeric: Outward Orientation
- `area` numeric: Area surface
- `prscenroll` numeric: Primary school enrolment
- `lifeexp` numeric: Life expectancy
- `gdp60` numeric: Initial GDP in 1960
- `mining` numeric: Fraction of GDP in mining
- `ecoorg` numeric: Degree of capitalism
- `yrsopen` numeric: Number of years having an open economy
- `age` numeric: Age
- `buddha` numeric: Fraction Buddhist
- `catholic` numeric: Fraction Catholic
Confucian numeric: Fraction Confucian
Ethnol numeric: Ethnolinguistic fractionalization
Hindu numeric: Fraction Hindu
Jewish numeric: Fraction Jewish
Muslim numeric: Fraction Muslim
PrExports numeric: Primary exports 1970
Protestants numeric: Fraction Protestants
RuleofLaw numeric: Rule of law
Popg numeric: Population growth
WorkPop numeric: workers per inhabitant
LabForce numeric: Size of labor force
HighEnroll numeric: Higher education enrolment
PubEdupct numeric: Public education share
RevnCoup numeric: Revolutions and coups
PolRights numeric: Political rights
CivilLib numeric: Civil liberties
English numeric: Fraction speaking English
Foreign numeric: Fraction speaking foreign language
RFEXDist numeric: Exchange rate distortions
EquipInv numeric: Equipment investment
NequipInv numeric: Non-equipment investment
stdBMP numeric: stand. dev. of black market premium
BlMktPm numeric: black market premium

Source

References

Examples
data(datafls)
## maybe str(datafls) ; plot(datafls) ...
**density.bma**

### Coefficient Marginal Posterior Densities

**Description**

Calculates the mixture marginal posterior densities for the coefficients from a BMA object and plots them.

**Usage**

```r
## S3 method for class 'bma'
density(x, reg = NULL, addons = "lmsz", std.coefs = FALSE,
        n = 300, plot = TRUE, hnbsteps = 30, addons.lwd = 1.5, ...)
```

```r
## S3 method for class 'zlm'
density(x, reg = NULL, addons = "lmsz", std.coefs = FALSE,
        n = 300, plot = TRUE, hnbsteps = 30, addons.lwd = 1.5, ...)
```

**Arguments**

- `x`: A bma object (see `bms`) or a zlm object.
- `reg`: A scalar integer or character detailing which covariate’s coefficient should be plotted. If `reg=NULL` (default), then all regressors are plotted one after the other, waiting for user interaction.
- `addons`: character. Specifies which additional information should be added to the plot via low-level commands (see 'Details' below).
- `std.coefs`: logical. If TRUE then the posterior density is estimated for standardized coefficients (representing the case where all variables have mean zero and standard deviation 1) - default is FALSE.
- `n`: numeric. the number of equally spaced points at which the density is to be estimated.
- `plot`: logical. If TRUE (default), the density is plotted; if FALSE then density.bma only returns the estimated posterior densities without plotting.
- `hnbsteps`: even integer, default 30. The number of numerical integration steps to be used in case of a hyper-g prior (cf. argument `g` in `bms`). Increase this number to increase accuracy.
- `addons.lwd`: scalar, default 1.5. Line width to be used for the low-level plotting commands specified by addons. Cf. argument `lwd` in `par`
- `...`: Additional arguments for `plot.default` with sensible defaults
Details

The argument addons specifies what additional information should be added to the plot(s) via the low-level commands \texttt{lines} and \texttt{legend}:

- "e" for the posterior expected value (EV) of coefficients conditional on inclusion (see argument exact=\texttt{TRUE} in \texttt{coef.bma}),
- "s" for 2 times posterior standard deviation (SD) bounds,
- "m" for the posterior median,
- "b" for posterior expected values of the individual models whom the density is averaged over,
- "E" for posterior EV under MCMC frequencies (see argument exact=\texttt{FALSE} in \texttt{coef.bma}),
- "S" for the corresponding SD bounds (MCMC),
- "p" for plotting the Posterior Inclusion Probability above the density plot,
- "l" for including a \texttt{legend}, "z" for a zero line, "g" for adding a \texttt{grid}

Any combination of these letters will give the desired result. Use addons="" for not using any of these.
In case of \texttt{density.zlm}, only the letters e, s, l, z, and g will have an effect.

Value

The function returns a list containing objects of the class \texttt{density} detailing the marginal posterior densities for each coefficient provided in \texttt{reg}.
In case of \texttt{density.zlm}, simple marginal posterior coefficient densities are computed, while \texttt{density.bma} calculates there mixtures over models according to posterior model probabilities.
These densities contain only the density points apart from the origin. (see 'Note' below)
As long as plot=\texttt{TRUE}, the densities are plotted too. Note that (for \texttt{density.bma}) if the posterior inclusion probability of a covariate is zero, then it will not be plotted, and the returned density will be \texttt{list(x=numeric(n),y=numeric(n))}.

Note

The computed marginal posterior densities from \texttt{density.bma} are a Bayesian Model Averaging mixture of the marginal posterior densities of the individual models. The accuracy of the result therefore depends on the number of 'best' models contained in \texttt{x} (cf. argument nmodel in \texttt{bms}).

The marginal posterior density can be interpreted as 'conditional on inclusion': If the posterior inclusion probability of a variable is smaller than one, then some of its posterior density is Dirac at zero. Therefore the integral of the returned density vector adds up to the posterior inclusion probability, i.e. the probability that the coefficient is not zero.

Correspondingly, the posterior EV and SD specified by addons="es" are based on 'best' model likelihoods ('exact') and are conditional on inclusion. They correspond to the results from command \texttt{coef.bma(x, exact=TRUE, condi.coef=TRUE, order.by.pip=FALSE)} (cf. the example below).

The low-level commands enacted by the argument addons rely on colors of the \texttt{palette}: color 2 for "e" and "s", color 3 for "m", color 8 for "b", color 4 for "E" and "S". The default colors may be changed by a call to \texttt{palette}.

Up to BMS version 0.3.0, \texttt{density.bma} may only cope with built-in \texttt{gpriors}, not with any user-defined priors.
f21hyper

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

quantile.coef.density for extracting quantiles, coef.bma for similar concepts, bms for creating bma objects

Check http://bms.zeugner.eu for additional help.

Examples

data(datafls)
mm=bms(datafls)

density(mm,reg="SubSahara")
density(mm,reg=7,addons="1bz")
density(mm,1:9)
density(mm,reg=2,addons="zgSE",addons.lwd=2, std.coefs=TRUE)

# plot the posterior density only for the very best model
density(mm[1],reg=1,addons="esz")

#using the calculated density for other purposes...

dd=density(mm,reg="SubSahara")
plot(dd)

dd_list=density(mm,reg=1:3,plot=FALSE,n=400)
plot(dd_list[[1]])

#Note that the shown density is only the part that is not zero

dd=density(mm,reg="Abslat",addons="esl")
pip_Abslat=sum(dd$y)*diff(dd$x)[1]

#this pip and the EV conform to what is done by the following command
coef(mm,exact=TRUE,condi.coef=TRUE)["Abslat",]

---

f21hyper  

**Gaussian Hypergeometric Function** \( F(a,b,c,z) \)

Description

Computes the value of a Gaussian hypergeometric function \( F(a, b, c, z) \) for \(-1 \leq z \leq 1\) and \( a, b, c \geq 0 \)
Usage

\texttt{f21hyper(a, b, c, z)}

Arguments

\begin{itemize}
  \item \texttt{a}: The parameter \texttt{a} of the Gaussian hypergeometric function, must be a positive scalar here.
  \item \texttt{b}: The parameter \texttt{b} of the Gaussian hypergeometric function, must be a positive scalar here.
  \item \texttt{c}: The parameter \texttt{c} of the Gaussian hypergeometric function, must be a positive scalar here.
  \item \texttt{z}: The parameter \texttt{z} of the Gaussian hypergeometric function, must be between \(-1\) and \(1\) here.
\end{itemize}

Details

The function \texttt{f21hyper} complements the analysis of the 'hyper-g prior' introduced by Liang et al. (2008).
For parameter values, compare cf. \url{http://en.wikipedia.org/wiki/Hypergeometric_function#The_series_2F1}.

Value

The value of the Gaussian hypergeometric function \(F(a, b, c, z)\)

Note

This function is a simple wrapper function of sped-up code that is intended for sporadic application by the user; it is neither efficient nor general; for a more general version cf. the package 'hypergeo'.

Author(s)

Martin Feldkircher and Stefan Zeugner

References

\url{http://en.wikipedia.org/wiki/Hypergeometric_function#The_series_2F1}

See Also

package hypergeo for a more proficient implementation.
Check \url{http://bms.zeugner.eu} for additional help.
Examples

```r
f21hyper(30,1,20,.8) #returns about 165.8197
f21hyper(30,10,20,0) #returns one
f21hyper(10,15,20,-0.1) # returns about 0.4872972
```

---

**fullmodel.ssq**

*OLS Statistics for the Full Model Including All Potential Covariates*

---

**Description**

A utility function for reference: Returns a list with R2 and sum of squares for the OLS model encompassing all potential covariates that are included in a bma object.

**Usage**

```r
fullmodel.ssq(yX.data)
```

**Arguments**

- `yX.data`: a bma object (cf. `bms`) - alternatively a `data.frame` or `matrix` whose first column is the dependent variable

**Value**

Returns a list with some basic OLS statistics

- `R2`: The R-squared of the full model
- `yMy`: The sum of squares of residuals of the full model
- `ypy`: The explained sum of squares of the full model
- `yty`: The sum of squares of the (demeaned) dependent variable
- `Fstat`: The F-statistic of the full model

**Note**

This function is just for quick comparison; for proper OLS estimation consider `lm`

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

- `bms` for creating bma objects, `lm` for OLS estimation
- Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.
**Examples**

data(datafls)
mm=bms(datafls)

fullmodel.ssq(mm)

#equivalent:
fullmodel.ssq(mm$X.data)

gdensity

---

**gdensity**

*Posterior Density of the Shrinkage Factor*

**Description**

Calculates the mixture marginal posterior density for the shrinkage factor \(g/(1+g)\) from a BMA object under the hyper-g prior and plots it.

**Usage**

```r
 gdensity(x, n = 512, plot = TRUE, addons = "zles", addons.lwd = 1.5, ...) 
```

**Arguments**

- `x`: A bma object (see `bms`).
- `n`: The integer number of equally spaced points at which the density is to be estimated. See 'Details' below.
- `addons`: character, defaulting to "zles". Specifies which additional information should be added to the plot via low-level commands (see 'Details' below).
- `plot`: logical. If `TRUE` (default), the density is plotted; if `FALSE` then `gdensity` only returns the estimated posterior density without plotting.
- `addons.lwd`: scalar, default 1.5. Line width to be used for the low-level plotting commands specified by `addons`. Cf. argument `lwd` in `par`.
- `...`: Additional arguments for `plot.default` with sensible defaults.

**Details**

The function `gdensity` estimates and plots the posterior density for the shrinkage factor \(g/(1 + g)\). This is evidently only possible if the shrinkage factor if not fixed, i.e. if the bma object `x` was estimated with a hyper-g prior - cf. argument `g` in `bms`.

The density is based only on the best models retained in the bma object `x`, cf. argument `nmodel` in `bms`.

A note on argument `n`: The points at which the density is estimated start at \(\max(0, E - 5 \times SD)\), where `E` and `SD` are the expected value and standard deviation of the shrinkage factor, respectively. For plotting the entire domain \((0, 1)\) use `xlim=c(0,1)` as an argument for `gdensity`. 

---

**Posterior Density of the Shrinkage Factor**

Calculates the mixture marginal posterior density for the shrinkage factor \(g/(1+g)\) from a BMA object under the hyper-g prior and plots it.
The argument `addons` specifies what additional information should be added to the plot(s) via the low-level commands `lines` and `legend`:
- "e" for the posterior expected value (EV) of the shrinkage factor,
- "s" for 2 times posterior standard deviation (SD) bounds,
- "m" for the posterior median,
- "f" for posterior expected values of the individual models whom the density is averaged over,
- "z" for a zero line, "1" for including a `legend`

The following two are only possible if the bma object collected statistics on shrinkage, cf. argument `g.stats` in `bms`:
- "E" for posterior expected value under MCMC frequencies (see argument `exact` in `coefNbma`),
- "S" for the corresponding 2 times standard deviation bounds (MCMC),

Any combination of these letters will give the desired result. Use `addons=""` for not using any of these.

**Value**

`gdensity` returns an object of the class `density` detailing the posterior mixture density of the shrinkage factor.

**Note**

The computed marginal posterior density is a Bayesian Model Averaging mixture of the marginal posterior densities of the shrinkage factor under individual models. The accuracy of the result therefore depends on the number of 'best' models contained in x (cf. argument `nmodel` in `bms`).

Correspondingly, the posterior EV and SD specified by `addons="es"` are based on 'best' model likelihoods ('exact') and are conditional on inclusion.

The low-level commands enacted by the argument `addons` rely on colors of the `palette`: color 2 for "e" and "s", color 3 for "m", color 8 for "f", color 4 for "E" and "S". The default colors may be changed by a call to `palette`.

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

`densityNbma` for computing coefficient densities, `bms` for creating bma objects, `density` for the general method

Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

**Examples**

```r
data(datafls)
mm=bms(datafls,g="hyper=UIP")
gdensity(mm) # default plotting```
# the grey bars represent expected shrinkage factors of the individual models
gdensity(mm,addons="l2fes")

# plotting the median 'm' and the posterior mean and bounds based on MCMC results:
gdensity(mm,addons="zSEm",addons.lwd=2)

# plot the posterior shrinkage density only for the very best model
gdensity(mm[1],addons="esz")

# using the calculated density for other purposes...
dd=gdensity(mm,plot=FALSE)
plot(dd)

gprior-class  

Class "gprior"

Description

An object pertaining to a coefficient prior

Objects from the Class

A gprior object holds descriptions and subfunctions pertaining to coefficient priors. Functions such as bms or zlm rely on this class to 'convert' the output of OLS results into posterior expressions for a Bayesian Linear Model. Post-processing functions such as density.bma also resort to gprior objects.

There are currently three coefficient prior structures built into the BMS package, generated by the following functions (cf. Feldkircher and Zeugner, 2009):
gprior.constg.init: creates a Zellner's g-prior object with constant g.
gprior.eblocal.init: creates an Empirical Bayes Zellner's g-prior.
gprior.hyperg.init: creates a hyper g-prior with a Beta-prior on the shrinkage parameter.

The following describes the necessary slots

Slots

gtype: A string with a human-readable identifier of the prior.
is.constant: Boolean whether the gprior relies on a constant scalar g (that is not dependent on a model)
return.g.stats: Boolean for whether to collect posterior statistics on shrinkage.
g: Should hold the value of g when is.constant==TRUE.
lprobcalc: A list with a least two sub-functions:
  just.loglik(ymy, k, ...): returns scalar posterior log-likelihood based on residual sum of squares ymy and number of parameters k
  lprob.all(ymy, k, bhat, diag.inverse, ...): Takes output from an OLS model (bhat: OLS coefficients, diag.inverse: diagonal of the matrix inv(t(X)*X)), and returns a list with log-likelihood and posterior moments.
Methods

As for now, there are no methods defined with class "gprior" in the signature.

Author(s)

Martin Feldkircher and Stefan Zeugner

References


See Also

bms and zlm for creating bma or zlm objects.
Check the appendix of vignette(BMS) for a more detailed description of built-in priors.
Check http://bms.zeugner.eu/custompriors.php for examples.

Examples

data(datafls)
mm1=bms(datafls[,1:10], g="EBL")
gg=mm1$gprior.info # is the g-prior object, augmented with some posterior statistics

mm2=bms(datafls[,1:10], g=gg) #produces the same result

mm3=bms(datafls[,1:10], g=BMS:::gprior.eblocal.init)
#this passes BMS's internal Empirical Bayes g-prior object as the coefficient prior
# - any other object might be used as well

---

Image bma

Plot Signs of Best Models

Description

Plots a grid with signs and inclusion of coefficients vs. posterior model probabilities for the best models in a 'bma' object.

Usage

### S3 method for class 'bma'

image(x, yprop2pip = FALSE, order.by.pip = TRUE,

    do.par = TRUE, do.grid = TRUE, do.axis = TRUE, cex.axis = 1, ...)

---
Arguments

- **x**: a list of class bma (cf. bms for further details)
- **yprop2pip**: if yprop2pip=TRUE then the grid lines on the vertical axis are scaled according to the coefficients' inclusion probabilities. If yprop2pip=FALSE (default) then the grid lines on the vertical axis are equidistant.
- **order.by.pip**: with order.by.pip=TRUE (default), coefficients are sorted according to their posterior inclusion probabilities along the vertical axis. If order.by.pip=FALSE they are ordered as they were provided to bms.
- **do.par**: Defaults to do.par=TRUE, which adjusts par()$mar for optimal positioning. Set do.par=FALSE for customizing par yourself.
- **do.grid**: do.grid=TRUE (default) plots grid lines among the chart's boxes, akin to the low level command grid. do.grid=FALSE omits the grid lines.
- **do.axis**: do.axis=TRUE (default) plots axis tick marks and labels (cf. axis). do.axis=FALSE omits them.
- **cex.axis**: font size for the axes (cf. axis), defaults to 1
- **...**: Parameters to be passed on to image.default.

Details

Under default settings, blue corresponds to positive sign, red to a negative sign, white to non-inclusion.

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

coe bma for the coefficients in matrix form, bms for creating 'bma' objects.

Check http://bms.zeugner.eu for additional help.

Examples

data(datafls)

model=bms(datafls,nmodel=200)

#plot all models
image(model,order.by.pip=FALSE)
image(model,order.by.pip=TRUE,cex.axis=.8)

#plot best 7 models, with other colors
image(model[1:7],yprop2pip=TRUE,col=c("black","lightgrey"))
is.bma

Tests for a 'bma' Object

Description
tests for objects of class "bma"

Usage
is.bma(bmao)

Arguments
bmao a 'bma' object: see 'value'

Value
Returns TRUE if bmao is of class 'bma', FALSE otherwise.

Author(s)
Martin Feldkircher and Stefan Zeugner

See Also
'Output' in bms for the structure of a 'bma' object
Check http://bms.zeugner.eu for additional help.

Examples
data(datafls)
m=bms(datafls,burn=1000, iter=4000)
is.bma(m)

lps.bma

Log Predictive Score

Description
Computes the Log Predictive Score to evaluate a forecast based on a bma object

Usage
lps.bma(object, realized.y, newdata = NULL)
Arguments

object       an object of class `pred.density`, or class `bma` (cf. `bms`), or class `zlm`
realized.y   a vector with realized values of the dependent variables to be plotted in addition
to the predictive density, must have its length conforming to `newdata`
newdata      Needs to be provided if `object` is not of class `pred.density`: a data.frame,
             matrix or vector containing variables with which to predict.

Details

The log predictive score is an indicator for the likelihood of several forecasts.
It is defined as minus the arithmetic mean of the logarithms of the point densities for `realized.y`
given `newdata`.
Note that in most cases is more efficient to first compute the predictive density object via a call to
`pred.density` and only then pass the result on to `lps.bma`.

Value

A scalar denoting the log predictive score

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

`pred.density` for constructing predictive densities, `bms` for creating `bma` objects, `density.bma` for plotting coefficient densities

Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

Examples

```r
data(datafls)
mm=bms(datafls, user.int=FALSE,nmodel=100)

#LPS for actual values under the used data (static forecast)
lps.bma(mm, realized.y=datafls[,1], newdata=datafls[,-1])

#the same result via predicitve.density
pd=pred.density(mm, newdata=datafls[,-1])
lps.bma(pd,realized.y=datafls[,1])

# similarly for a linear model (not BMA)
zz = zlm(datafls)
lps.bma(zz, realized.y=datafls[,1], newdata=datafls[,-1])
```
Class "mprior"

Description

An object pertaining to a BMA model prior

Objects from the Class

An mprior object holds descriptions and subfunctions pertaining to model priors. The BMA functions bms and post-processing functions rely on this class. There are currently five model prior structures built into the BMS package, generated by the following functions (cf. the appendix of vignette(BMS)):

- mprior.uniform.init: creates a uniform model prior object.
- mprior.fixedt.init: creates the popular binomial model prior object with common inclusion probabilities.
- mprior.randomt.init: creates a beta-binomial model prior object.
- mprior.pip.init: creates a binomial model prior object that allows for defining individual prior inclusion probabilities.
- mprior.customk.init: creates a model prior object that allows for defining a custom prior for each model parameter size.

The following describes the necessary slots:

Slots

- mp.mode: A string with a human-readable identifier of the prior.
- mp.msize: A scalar holding the prior model size
- mp.Kdist: A vector holding the prior probabilities for each parameter size, from 0 to K. (Not necessary for bms, but for some post-processing functions.)
- pmp(ki, moldraw, ...): A sub-function returning log-prior model probability depending on moldraw (a logical/numeric indicating the positions of regressors included in the model) and model size k (equivalent to sum(moldraw)).

Methods

As for now, there are no methods defined with class "mprior" in the signature.

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

bms for creating bma objects.
Check the appendix of vignette(BMS) for a more detailed description of built-in priors.
Check http://bms.zeugner.eu/custompriors.php for examples.
plot.bma

Plot Posterior Model Size and Model Probabilities

Description

Produces a combined plot: upper row shows prior and posterior model size distribution, lower row shows posterior model probabilities for the best models

Usage

```r
## S3 method for class 'bma'
plot(x, ...)
```

Arguments

- `x`: an object of class 'bma'
- `...`: additional arguments for `matplot`

Value

Combines the plotting functions `plotModels` and `plotConv`

Note

The upper plot shows the prior and posterior distribution of model sizes (`plotModels`). The lower plot is an indicator of how well the bma object has converged (`plotConv`).

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

- `plotModels` and `plotConv`
- Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

Examples

```r
data(datafls)
mm=bms(datafls, user.int=FALSE)

plot(mm)
```
plot.pred.density

Predictive Densities for bma Objects

Description

Plots predictive densities for conditional forecasts of class 'pred.density'

Usage

```r
## S3 method for class 'pred.density':
## S3 method for class 'pred.density'
plot(x, predict_index = NULL, addons = "eslz", realized.y = NULL,
     addons.lwd = 1.5, ...)
```

Arguments

- `x`  
an object of class `pred.density`
- `predict_index`  
  An integer vector detailing which forecasted observations (corresponding to the argument `newdata` in `pred.density`) should be plotted. Or the observation names to be plotted (as in `rownames(newdata)`).
- `addons`  
  character, defaulting to "eslz". Specifies which additional information should be added to the plot via low-level commands (see 'Details' below).
- `realized.y`  
  A vector with realized values of the dependent variables to be plotted in addition to the predictive density, must have its length conforming to `predict_index` (or `newdata`)
- `addons.lwd`  
  Line width to be used for the low-level plotting commands specified by `addons`. Cf. argument `lwd` in `par`.
- `...`  
  arguments to be passed on to `plotNdensity`.

Details

The argument `addons` specifies what additional information should be added to the plot(s) via the low-level commands `lines` and `legend`:
- "e" for the posterior expected value (EV) of the prediction,
- "s" for 2 times its posterior standard deviation ('standard errors'),
- "z" for a zero line, "l" for including a `legend`

Any combination of these letters will give the desired result. Use `addons=""` for not using any of these.

Author(s)

Martin Feldkircher and Stefan Zeugner
See Also

`pred_density` for constructing predictive densities, `bms` for creating `bma` objects, `density.bma` for plotting coefficient densities.

Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

Examples

```r
data(datafls)
mm=bms(datafls, user.int=FALSE)

#predictive density for two 'new' data points
pd=pred_density(mm, newdata=datafls[1:2,])

#plot the density for the second forecast observation
plot(pd,2)

#plot the density with realized dep. variable, and no standard errors
plot(pd, 1, realized.y=0, addons="lseg")
```

---

```r
plotComp
```

---

**plotComp**

*Compare Two or More bma Objects*

**Description**

Plots a comparison of posterior inclusion probabilities, coefficients or their standard deviation between various `bma` objects.

**Usage**

```r
plotComp(..., varNr = NULL, comp = "PIP", exact = FALSE,
          include.legend = TRUE, add.grid = TRUE, do.par = TRUE, cex.xaxis = 0.8)
```

**Arguments**

- `...`: one or more objects of class `bma` to be compared. `plotComp` passes on any other parameters in `...` to `matplot`.
- `varNr`: optionally, covariate indices to be included in the plot, can be either integer vector or character vector - see examples.
- `comp`: a character denoting what should be compared: `comp="PIP"` (default) for posterior inclusion probabilities, `comp="Post Mean"` for coefficients, `comp="Post SD"` for their standard deviations, `comp="Std Mean"` or standardized coefficients, or `comp="Std SD"` for standardized standard deviations.
plotConv

exact if FALSE, the statistics to be compared are based on aggregate bma statistics, if TRUE, they are based solely on the best models retained in the bma objects
include.legend whether to include a default legend in the plot (custom legends can be added with the command legend)
add.grid whether to add a grid to the plot
do.par whether to adjust par("mar") in order to fit in the tick labels on the x-axis
cex.xaxis font size scaling parameter for the x-axis - cf. argument cex.axis in par

Author(s)
Martin Feldkircher and Stefan Zeugner

See Also

ccoef.bma for the underlying function
Check http://bms.zeugner.eu for additional help.

Examples

## sample two simple bma objects
data(datafls)
mm1=bms(datafls[,1:15])
mm2=bms(datafls[,1:15])

#compare PIPs
plotComp(mm1,mm2)

#compare standardized coefficeitns
plotComp(mm1,mm2,comp="Std Mean")

#...based on the likeklhoods of best models
plotComp(mm1,mm2,comp="Std Mean",exact=TRUE)

#plot only PIPs for first four covariates
plotComp(mm1,mm2,varNr=1:4, col=c("black","red"))

#plot only coefficients for covariates 'GDP60' and 'LifeExp'
plotComp(mm1,mm2,varNr=c("GDP60", "LifeExp"),comp="Post Mean")

plotConv

*Plot Convergence of BMA Sampler*

Description

Plots the posterior model probabilties based on 1) marginal likelihoods and 2) MCMC frequencies for the best models in a 'bma' object and details the sampler's convergence by their correlation
Usage

    plotConv(bmao, include.legend = TRUE, add.grid=TRUE, ...)

Arguments

    bmao            an object of class 'bma' - see bms
    include.legend  whether to include a legend in the plot
    add.grid        whether to include a grid in the plot
    ...             other parameters for matplot

Details

A call to bms with a MCMC sampler (e.g. bms(datafls, mcmc="bd", nmodel=100) uses a Metropolis-Hastings algorithm to sample through the model space: the frequency of how often models are drawn converges to the distribution of their posterior marginal likelihoods. While sampling, each 'bma' object stores the best models encountered by its sampling chain with their marginal likelihood and their MCMC frequencies. plotConv compares the MCMC frequencies to marginal likelihoods, and thus visualizes how well the sampler has converged.

Note

    plotConv is also used by plot.bma

Author(s)

    Martin Feldkircher and Stefan Zeugner

See Also

    pmp.bma for posterior model probabilities based on the two concepts, bms for creating objects of class 'bma'

    Check http://bms.zeugner.eu for additional help.

Examples

    data(datafls)
    mm=bms(datafls[,1:12],user.int=FALSE)
    plotConv(mm)

    #is similar to
    matplot(pmp.bma(mm),type="l")
**plotModelsize**  
*Plot Model Size Distribution*

**Description**

Plots posterior and prior model size distribution

**Usage**

```r
gplotModelsize(bmao, exact = FALSE, ksubset = NULL, include.legend = TRUE, do.grid = TRUE, ...)
```

**Arguments**

- `bmao`: a 'bma' object (cf. `bms`)
- `exact`: if TRUE, then the posterior model distribution is based on the best models of `bmao` and their marginal likelihoods; if FALSE (default) then the distribution is based on all encountered models and their MCMC frequencies (cf. 'Details' in `coefNbma`)
- `ksubset`: integer vector detailing for which model sizes the plot should be done
- `include.legend`: if TRUE, a small legend is included via the low-level command `legend`
- `do.grid`: if TRUE, a grid is added to the plot (with a simple `grid()`).
- `...`: parameters passed on to `matplot` with sensible defaults

**Value**

As a default, `plotModelsize` plots the posterior model size distribution as a blue line, and the prior model distribution as a dashed red line.
In addition, it returns a list with the following elements:

- `mean`: The posterior expected value of model size
- `var`: The variance of the posterior model size distribution
- `dens`: A vector detailing the posterior model size distribution from model size 0 (the first element) to `K` (the last element)

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

See also `bms`, `image.bma`, `density.bma`, `plotConv`
Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.
Examples

data(datafls)
mm=bms(datafls,burn=1500, iter=5000, nmodel=200, mprior="fixed", mprior.size=6)

#plot Nb.1 based on aggregate results
postdist= plotModels(mm)

#plot based only on 30 best models
plotModels(mm[1:30], exact=TRUE, include.legend=FALSE)

#plot based on all best models, but showing distribution only for model sizes 1 to 20
plotModels(mm, exact=TRUE, ksubset=1:20)

# create a plot similar to plot Nb. 1
plot(postdist$dens,type="l")
lines(mm$mprior.info$mp.Kdist)


def pmp bma

Description

Returns the posterior model probabilities for the best models encountered by a 'bma' object

Usage

pmp.bma(bmao, oldstyle = FALSE)

Arguments

bmao A bma object (see argument nmodel in bms), alternatively an object of class topmod

oldstyle For normal use, leave this at FALSE. It is an argument for compatibility with older BMS versions - see section 'Notes'

Details

A call to bms with an MCMC sampler (e.g. bms(datafls, mcmc="bd", nmodel=100) uses a Metropolis-Hastings algorithm to sample through the model space - and the frequency of how often models are drawn converges to the distribution of their posterior marginal likelihoods. While sampling, each 'bma' object stores the best models encountered by its sampling chain with their marginal likelihood and their MCMC frequencies.

pmp.bma then allows for comparing the posterior model probabilities (PMPs) for the two different methods, similar to plotConv. It calculates the PMPs based on marginal likelihoods (first column) and the PMPs based on MCMC frequencies (second column) for the best x models stored in the bma object.
The correlation of the two columns is an indicator of how well the MCMC sampler has converged to the actual PMP distribution - it is therefore also given in the output of `summary.bma`. The second column is slightly different in case the `bms` argument `mcmc` was set to `mcmc="enumeration"`. In this case, the second column is also based on marginal likelihoods. The correlation between the two columns is therefore one.

**Value**

the result is a matrix, its row names describe the model binaries
There are two columns in the matrix:

- **PMP (Exact)** posterior model probabilities based on the posterior likelihoods of the best models in `bma`
- **PMP (MCMC)** posterior model probabilities of the best models in `bma` based on their MCMC frequencies, relative to all models encountered by `bma` - see 'Details'

**Note**

The second column thus shows the PMPs of the best models relative to all models the call to `bms` has sampled through (therefore typically the second column adds up to less than one). The first column relates to the likelihoods of the best models, therefore it would add up to 1. In order estimate for their marginal likelihoods with respect to the other models (the ones not retained in the best models), these PMP adding up to one are multiplied with the sum of PMP of the best models according to MCMC frequencies. Therefore, the two columns have the same column sum.

CAUTION: In package versions up to `BMS 0.2.5`, the first column was indeed set always equal to one. This behaviour can still be mimicked by setting `oldstyle=TRUE`.

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

- `plotConv` for plotting `pmp.bma`, `pmpmodel` to obtain the PMP for any individual model, `bms` for sampling `bma` objects
- Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

**Examples**

```r
## sample BMA for growth dataset, MCMC sampler
data(datafls)
m=bms(datafls[,1:10],rmodel=20, mcmc="bd")

## model likelihoods and MCMC frequencies of best 20 models
print(m$topmod)
pmp.bma(m)

#first column: posterior model prob based on model likelihoods,
# relative to best models in 'mm'
```

```
#second column: posterior model prob based MCMC frequencies,
# relative to all models encountered by 'mm'

cor(pmp.bma(mm)[,1],pmp.bma(mm)[,2])

#correlation between the two shows how well the sampler converged
summary(mm)["Corr PMP"]

#plot the two model probabilities
plotConv(mm)

#equivalent to the following chart
plot(pmp.bma(mm)[,2], type="s")
lines(pmp.bma(mm)[,1],col=2)

#moreover, note how the first column is constructed
liks=exp(mm$tpsl$lik())
liks/sum(liks)
pmp.bma(mm)[,1] #these two are equivalent

#the example above does not converge well,
#too few iterations and best models
mm=bms(datafls[,1:10],burn=2000,iter=5000,nmodel=200)

# in case the sampler has been 'enumeration' instead of MCMC,
# then both matrix columns are of course equivalent
co(pmp.bma(mm)[,1],pmp.bma(mm)[,2])
colSums(pmp.bma(mm))

---

**Description**

Returns the posterior model probability for any model based on bma results
**pmpmodel**

**Usage**

```r
pmpmodel(bmao, model = numeric(0), exact = TRUE)
```

**Arguments**

- `bmao`: A `bma` object as created by `bms`.
- `model`: A model index - either variable names, or a logical with model binaries, or the model hexcode (cf. `hex2bin`), or a numeric with positions of the variables to be included.
- `exact`: If `TRUE`, then the resulting PMP is based on analytical model likelihoods (works for any model). If `FALSE`, the resulting PMP is derived from MCMC frequencies (works only for the null and full model, as well as for models contained in `bmao`'s `topmod` object. If `bmao` is based on enumeration (cf. argument `mcmc` in `bms`), then `exact` does not matter.

**Details**

If the model as provided in `model` is the null or the full model, or is contained in `bmao`'s `topmod` object (cf. argument `nmodel` in `bms`), then the result is the same as in `pmp.bma`.

If not and `exact=TRUE`, then `pmpmodel` estimates the model based on comparing its marginal likelihood (times model prior) to the likelihoods in the `topmod` object and multiplying by their sum of PMP according to MCMC frequencies.

**Value**

A scalar with (an estimate of) the posterior model probability for `model`.

**Author(s)**

Stefan Zeugner

**See Also**

- `pmp.bma` and `topmodels.bma` for similar functions
- Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

**Examples**

```r
# sample BMA for growth dataset, enumeration sampler
data(datafls)
nm=bms(datafls[,1:10],nmodel=5)

# show the best 5 models:
pmp.bma(nm)
# first column: posterior model prob based on model likelihoods,
```
#second column: posterior model prob based MCMC frequencies,

### Different ways to get the same result: #######

#PMP of 2nd-best model (hex-code representation)
```r
pmpmodel(mm,"00c")
```

#PMP of 2nd-best model (binary representation)
```r
incls=as.logical(beta.draws.bma(mm)[,2])
pmpmodel(mm,incls)
```

#PMP of 2nd-best model (via variable names)
```r
#names of regressors in model "00c":
#names(datafls[,2:10])
incls
pmpmodel(mm,c("SubSahara", "LatAmerica"))
```

#PMP of 2nd-best model (via positions)
```r
pmpmodel(mm,c(6,7))
```

#####PMP of another model #######
```r
pmpmodel(mm,1:5)
```

---

**post.var**

*Posterior Variance and Deviance*

**Description**

Returns posterior residual variance, deviance, or pseudo R-squared, according to the chosen prior structure

**Usage**

```r
post.var(object, exact = FALSE)
post.pr2(object, exact = FALSE)
# S3 method for class 'bma'
deviance(object, exact = FALSE, ...)
# S3 method for class 'zlm'
deviance(object, ...)
```

**Arguments**

- `object` A bma object (as produced by `bms`) or a zlm object.
- `exact` When exact=FALSE, then deviance will be based on MCMC frequencies, if exact=TRUE then it will be based on analytical posterior model probabilities - cf. argument exact in `coef.bma`.
- `...` further arguments passed to or from other methods
**Details**

post.var: Posterior residual variance as according to the prior definitions contained in object
post.pr2: A pseudo-R-squared corresponding to unity minus posterior variance over dependent variance.
deviance.bma: returns the deviance of a bma model as returned from bms.
deviance.zlm: returns the deviance of a zlm model.

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

bms for creating bma objects and priors, zlm object.
Check http://bms.zeugner.eu for additional help.

**Examples**

data(datafls)

mm=bms(datafls[,1:10])
deviance(mm)/nrow(datafls) # is equivalent to post.var(mm)

post.pr2(mm) # is equivalent to
1 - post.var(mm) / ( var(datafls[,1])*(1-1/nrow(datafls)) )

---

**pred.density**  
*Predictive Densities for bma Objects*

**Description**
Predictive densities for conditional forecasts

**Usage**

pred.density(object, newdata = NULL, n = 300, hnbsteps = 30, ...)

**Arguments**

- **object**: a bma object - see bms, alternatively a zlm object
- **newdata**: A data.frame, matrix or vector containing variables with which to predict.
- **n**: The integer number of equally spaced points at which the density is to be estimated.
pred.density

**hnbsteps**

The number of numerical integration steps to be used in case of a hyper-\(g\) prior (cf. argument \(g\) in \texttt{bms}). Increase this number to increase accuracy. Must be an even integer.

... arguments to be passed on to \texttt{plot.density}.

**Details**

The predictive density is a mixture density based on the \(n\) models best models in a \texttt{bma} object (cf. \texttt{nmodel} in \texttt{bms}). The number of 'best models' to retain is therefore vital and should be set quite high for accuracy.

**Value**

\texttt{pred.density} returns a list of class \texttt{pred.density} with the following elements:

- \texttt{densities()} a list whose elements each contain the estimated density for each forecasted observation
- \texttt{fit} a vector with the expected values of the predictions (the 'point forecasts')
- \texttt{std.err} a vector with the standard deviations of the predictions (the 'standard errors')
- \texttt{dyf(realized.y, predict_index=NULL)} Returns the densities of realized response variables provided in \texttt{realized.y}. If \texttt{realized.y} is a matrix, then each row corresponds to a forecast observation in \texttt{newdata} if not left empty, \texttt{predict.index} specifies to which observations in \texttt{newdata} the \texttt{realized.y} should apply
- \texttt{lps(realized.y, predict_index=NULL)} Computes the log predictive score for the response variable provided in \texttt{realized.y} (cf. \texttt{lps.bma}) - Note that the LPS equals minus the mean of the logarithmized results from \texttt{dyf}
- \texttt{plot((x, predict_index = NULL, addons = "eslz", realized.y = NULL, addons.lwd = 1.5, ...)} the same as \texttt{plot.pred.density}
- \texttt{n} The number of equally spaced points for which the density (under \texttt{densities()}) was computed.
- \texttt{nmodel} The number of best models predictive densities are based upon.
- \texttt{call} the call that created this \texttt{pred.density} object

**Note**

In \texttt{BMS} version 0.3.0, \texttt{pred.density} may only cope with built-in \texttt{gprior}s, not with any user-defined priors.

**Author(s)**

Martin Feldkircher and Stefan Zeugner
predict.bma

Predict Method for bma Objects

Description

Expected value of prediction based on 'bma' object

Usage

## S3 method for class 'bma'
predict(object, newdata = NULL, exact = FALSE, topmodels = NULL, ...)

See Also

predict.bma for simple point forecasts, plot.pred.density for plotting predictive densities, lps.bma for calculating the log predictive score independently, quantile.pred.density for extracting quantiles

Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.

Examples

data(datafls)
mm=bms(datafls,user.int=FALSE)

#predictive density for two 'new' data points
pd=pred.density(mm,newdata=datafls[1:2,])

#fitted values based on best models, same as predict(mm, exact=TRUE)
pd$fitted

#plot the density for the first forecast observation
plot(pd,1)

# the same plot 'naked'
plot(pd$density()[[1]])

#predict density for the first forecast observation if the dep. variable is 0
pd$dyf(0,1)

#predict densities for both forecasts for the realizations 0 and 0.5
pd$dyf(rbind(c(0,.5),c(0,.5)))

# calc. Log Predictive Score if both forecasts are realized at 0:
lps.bma(pd,c(0,0))
Arguments

object       a bma object - see bms
newdata     An optional data.frame, matrix or vector containing variables with which to pre-
dict. If omitted, then (the expected values of) the fitted values are returned.
exact       If FALSE (default), then prediction is based on all models (i.e. on their MCMC
frequencies in case the bms parameter mcmc was set to an mcmc sampler.
If TRUE, then prediction is based on analytical likelihoods of the best models
retained in object - cf. bms parameter nmodel.
topmodels   index of the models with whom to predict: for instance, topmodels=1 predicts
based solely on the best model, whereas topmodels=1:5 predicts based on a
combination of the five best models.
Note that setting topmodels triggers exact=TRUE.

... further arguments passed to or from other methods.

Value

A vector with (expected values of) fitted values.

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

coeff.bma for obtaining coefficients, bms for creating bma objects, predict.lm for a comparable
function

Check http://bms.zeugner.eu for additional help.

Examples

data(datafls)
mm=bms(datafls,user.int=FALSE)
predict(mm) #fitted values based on MCMC frequencies
predict(mm, exact=TRUE) #fitted values based on best models

predict(mm, newdata=1:41) #prediction based on MCMC frequencies
predict(mm, newdata=datafls[1,], exact=TRUE) #prediction based on a data.frame

# the following two are equivalent:
predict(mm, topmodels=1:10)
predict(mm[1:10], exact=TRUE)
**predict.zlm** *Predict Method for zlm Linear Model*

---

**Description**

Expected value (and standard errors) of predictions based on 'zlm' linear Bayesian model under Zellner's g prior.

**Usage**

```r
## S3 method for class 'zlm':
## S3 method for class 'zlm'
predict(object, newdata = NULL, se.fit = FALSE, ...)
```

**Arguments**

- `object`: a zlm linear model object - see `zlm`
- `newdata`: An optional data.frame, matrix or vector containing variables with which to predict. If omitted, then (the expected values of) the fitted values are returned.
- `se.fit`: A switch indicating if the standard deviations for the predicted variables are required.
- `...`: further arguments passed to or from other methods.

**Value**

A vector with (expected values of) fitted values. If `se.fit` is `TRUE`, then the output is a list with the following elements:

- `fit`: a vector with the expected values of fitted values
- `std.err`: a vector with the standard deviations of fitted values
- `se.fit`: a vector with the standard errors without the residual scale akin to `se.fit` in `predict.lm`
- `residual.scale`: The part from the standard deviations that involves the identity matrix. Note that `sqrt(se.fit^2+residual.scale^2)` yields `std.err`.

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

- `bms` for creating zlm objects, `predict.lm` for a comparable function, `predict.bma` for predicting with bma objects
- Check [http://bms.zuegner.eu](http://bms.zuegner.eu) for additional help.
Examples

data(datafls)
mm=lm(datafls,g="EBL")

predict(mm) # fitted values
predict(mm, newdata=1:41) # prediction based on a 'new data point'

# prediction based on a 'new data point', with 'standard errors'
predict(mm, newdata=datafls[,1], se.fit=TRUE)

print.bma

Printing bma Objects

Description

Print method for objects of class 'bma'

Usage

## S3 method for class 'bma'
print(x, ...)

Arguments

x a bma object - see bms
...

additional arguments to print

Value

prints calls to coef.bma(x) and summary.bma(x)

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

coeff.bma and summary.bma for the underlying functions, bms for creating bma objects, print

Check http://bms.zeugner.eu for additional help.
print.topmod

Examples

data(datafls)
mm=bms(datafls, user.int=FALSE)
print(mm)

## similar:
coef(mm)
summary(mm)

print.topmod Printing topmod Objects

Description

Print method for objects of class 'topmod', typically the best models stored in a 'bma' object

Usage

## S3 method for class 'topmod'
print(x, ...)

Arguments

x an object of class 'topmod' - see topmod
...
additional arguments passed to link{print}

Details

See pmp.bma for an explanation of likelihood vs. MCMC frequency concepts

Value

if x contains more than one model, then the function returns a 2-column matrix:

<table>
<thead>
<tr>
<th>Row Names</th>
<th>show the model binaries in hexcode (cf. topmodels.bma)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Column 'Marg. Log.Lik'</td>
<td>shows the marginal log-likelihoods of the models in x</td>
</tr>
<tr>
<td>Column 'MCMC Freq'</td>
<td>shows the MCMC frequencies of the models in x</td>
</tr>
</tbody>
</table>

if x contains only one model, then more detailed information is shown for this model:

<table>
<thead>
<tr>
<th>first line</th>
<th>'Model Index' provides the model binary in hexcode, 'Marg.Log.Lik' its marginal log likelihood, 'Sampled Freq.' how often it was accepted (function ncount() in topmod)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Estimates</td>
<td>first column: covariate indices included in the model, second column: posterior expected value of the coefficients, third column: their posterior standard deviations (excluded if no coefficients were stored in the topmod object - cf. argument bbeta in topmod)</td>
</tr>
</tbody>
</table>
quantile.pred.density

Included Covariates
the model binary
Additional Statistics
any custom additional statistics saved with the model

Author(s)
Martin Feldkircher and Stefan Zeugner

See Also
topmod for creating topmod objects, bms for their typical use, pmp.bma for comparing posterior model probabilities
Check http://bms.zeugner.eu for additional help.

Examples

# do some small-scale BMA for demonstration
data(datafls)
mm=bms(datafls[,1:10],nmodel=20)

# print info on the best 20 models
print(mm$topmod)
print(mm$topmod,digits=10)

# equivalent:
cbind(mm$topmod$lik(),mm$topmod$ncount())

# now print info only for the second-best model:
print(mm$topmod[2])

# compare 'Included Covariates' to:
topmodels.bma(mm[2])

# and to
as.vector(mm$topmod[2]$bool_binary())

quantile.pred.density  Extract Quantiles from 'density' Objects

Description
Quantiles for objects of class "density", "pred.dense" or "coef.density"
Usage

```r
## S3 method for class 'pred.density'
quantile(x, probs = seq(.25,.75,.25), names = TRUE, ...)

## S3 method for class 'coef.density'
quantile(x, probs = seq(.25,.75,.25), names = TRUE, ...)

## S3 method for class 'density'
quantile(x, probs = seq(.25,.75,.25), names = TRUE, normalize = TRUE, ...)
```

Arguments

- `x`: a object of class `pred_density`, `coef_density`, `density`, or a list of densities.
- `probs`: numeric vector of probabilities with values in [0,1] - elements very close to the boundaries return `Inf` or `-Inf`
- `names`: logical; if TRUE, the result has a names attribute, resp. a `rownames` and `colnames` attributes. Set to FALSE for speedup with many probs.
- `normalize`: logical; if TRUE then the values in x$y are multiplied with a factor such that their integral is equal to one.
- `...`: further arguments passed to or from other methods.

Details

The methods `quantile_coef_density` and `quantile_pred_density` both apply `quantile_density` to densities nested with object of class `coef_density` or `pred_density`. The function `quantile_density` applies generically to the built-in class `density` (as least for versions where there is no such method in the pre-configured packages). Note that `quantile_density` relies on trapezoidal integration in order to compute the cumulative densities necessary for the calculation of quantiles.

Value

If `x` is of class `density` (or a list with exactly one element), a vector with quantiles.
If `x` is a list of densities with more than one element (e.g. as resulting from `pred_density` or `coef_density`), then the output is a matrix of quantiles, with each matrix row corresponding to the respective density.

Author(s)

Stefan Zeugner

See Also

- `quantile.default` for a comparable function, `pred_density` and `density.bma` for the BMA-specific objects.
- Check [http://bms.zuegner.eu](http://bms.zuegner.eu) for additional help.
Examples

```r
data(datafls)
mm = bms(datafls[1:70,], user.int=FALSE)

#predict last two observations with preceding 70 obs:
pmm = pred.density(mm, newdata=datafls[71:72,], plot=FALSE)
#'standard error' quantiles
quantile(pmm, c(.05, .95))

#Posterior density for Coefficient of "GDP60"
cmm = density(mm, reg="GDP60", plot=FALSE)
quantile(cmm, probs=c(.05, .95))

#application to generic density:
dd1 = density(rnorm(1000))
quantile(dd1)

#application to list of densities:
quantile.density( list(density(rnorm(1000)), density(rnorm(1000))) )
```

---

**summary.bma**  
*Summary Statistics for a 'bma' Object*

**Description**

Returns a vector with summary statistics for a 'bma' object

**Usage**

```r
## S3 method for class 'bma'
summary(object,...)
```

```r
## or
info.bma(object,...)
```

**Arguments**

- **object**  
a list/object of class 'bma' that typically results from the function bms (see bms for details)
- **...**  
further arguments passed to or from other methods

**Details**

info.bma is equivalent to summary.bma, its argument bmao conforms to the argument object
**Value**

A character vector summarizing the results of a call to `bms`

- **Mean no. of Regressors**: the posterior mean of model size
- **Draws**: the number of iterations (ex burn-ins)
- **Burnins**: the number of burn-in iterations
- **Time**: the time spent on iterating through the model space
- **No. of models visited**: the number of times a model was accepted (including burn-ins)
- **Modelspace**: the total model space $2^K$
- **Percentage visited**: No. of models visited/Modelspace*100
- **Percentage Topmodels**: number of times the best models were drawn in percent of Draws
- **Corr. PMP**: the correlation between the MCMC frequencies of the best models (the number of times they were drawn) and their marginal likelihoods.
- **No. Obs.**: Number of observations
- **Model Prior**: a character conforming to the argument `mprior` of `bms`, and the expected prior model size
- **g-prior**: a character corresponding to argument `g` of function `bms`
- **Shrinkage-Stats**: Posterior expected value und standard deviation (if applicable) of the shrinkage factor. Only included if argument `g.stats` of function `bms` was set to TRUE

**Note**

All of the above statistics can also be directly extracted from the bma object (`bmao`). Therefore `summary.bma` only returns a character vector.

**Author(s)**

Martin Feldkircher and Stefan Zeugner

**See Also**

- `bms` and `c.bma` for functions creating bma objects, `print.bma` makes use of `summary.bma`.
- Check [http://bms.zuegner.eu](http://bms.zuegner.eu) for additional help.

**Examples**

```r
data(datafls)
m_fixed=bms(datafls,burn=1000,iter=3000,user.int=FALSE,)
summary(m_fixed)
```
m_ebl=bms(datafls,burn=1000,iter=3000,user.int=FALSE, g="EBL",g.stats=TRUE)
info.bma(m_ebl)

summary.zlm  Summarizing Linear Models under Zellner's g

Description

summary method for class "zlm"

Usage

## S3 method for class 'zlm'
summary(object, printout = TRUE, ...)

Arguments

object       an object of class zlm: see "Examples" below
printout     If TRUE (default, then information is printed to console in a neat form
...          further arguments passed to or from other methods

Details

summary.zlm prints out coefficients expected values and their standard deviations, as well as in-
formation on the gprior and the log marginal likelihood. However, it invisibly returns a list with
elements as described below:

Value

A list with the following elements

residuals    The expected value of residuals from the model
coefficients The posterior expected values of coefficients (including the intercept)
coef.sd      Posterior standard deviations of the coefficients (the intercept SD is NA, since an
             improper prior was used)
gprior       The g prior as it has been submitted to object
E.shrinkage  the shrinkage factor $g/(1 + g)$, respectively its posterior expected value in case
             of a hyper-g prior
SD.shrinkage (Optionally) the shrinkage factor’s posterior standard deviation (in case of a
             hyper-g prior)
log.lik      The log marginal likelihood of the model

Author(s)

Stefan Zeugner
See Also

zlm for creating zlm objects, link{summary.lm} for a similar function on OLS models

See also http://bms.zeugner.eu for additional help.

Examples

data(datafls)

# simple example
foo = zlm(datafls)
summary(foo)

sfoo = summary(foo, printout=FALSE)
print(sfoo$E.shrinkage)

---

topmod

Topmodel Object

Description

Create or use an updateable list keeping the best x models it encounters (for advanced users)

Usage

topmod(nbmodels, nmaxregressors = NA, bbeta = FALSE, lengthfixedvec = 0,
likks = numeric(0), ncounts = numeric(0), modelbinaries = matrix(0, 0, 0),
betas = matrix(0, 0, 0), betas2 = matrix(0, 0, 0), fixed_vector = matrix(0, 0, 0))

is.topmod(tmo)

Arguments

nbmodels The maximum number of models to be retained by the topmod object
nmaxregressors The maximum number of covariates the models in the topmod object are allowed to have
bbeta if bbeta=TRUE, then first and second moments of model coefficients are stored in addition to basic model statistics (Note: if bbeta<0 then only the first moments are saved)
lengthfixedvec The length of an optional fixed vector adhering to each model (for instance R-squared, etc). If lengthfixedvec=0 then no additional fixed vector will be stored.
likks optional vector of log-likelihoods to initialize topmod object with (length must be <= nbmodels) - see example below
ncounts
optional vector of MCMC frequencies to initialize topmod object with (same length as \texttt{lik}s) - see example below

modelbinaries
optional matrix whose columns detail model binaries to initialize topmod object with (same \texttt{nb columns as \texttt{lik}s, nb rows as \texttt{nmaxregressors}) - see example below

betas
optional matrix whose columns are coefficients to initialize topmod object with (same dimensions as \texttt{modelbinaries}) - see example below

betas2
 optional matrix whose columns are coefficients’ second moments to initialize topmod object with (same dimensions as \texttt{modelbinaries}) - see example below

fixed_vector
optional matrix whose columns are a fixed vector initialize topmod object with (same \texttt{ncol as \texttt{modelbinaries}) - see example below

tmo
A 'topmod' object, as e.g. created by topmod, or as element of the result of \textit{bms}

Details

A 'topmod' object (as created by \texttt{topmod}) holds three basic vectors: \texttt{lik} (for the (log) likelihood of models or similar), \texttt{bool()} for a hexcode presentation of the model binaries (cf. \texttt{bin2hex}) and \texttt{ncount()} for the times the models have been drawn.

All these vectors are sorted descendently by \texttt{lik}, and are of the same length. The maximum length is limited by the argument \texttt{nbmodels}.

If \texttt{tmo} is a topmod object, then a call to \texttt{tmo$addmodel} (e.g. \texttt{tmo$addmodel(\texttt{mylik}=4, \texttt{vec01}=c(T,F,F,T)}) updates the object \texttt{tmo} by a model represented by \texttt{vec01} (here the one including the first and fourth regressor) and the marginal (log) likelihood \texttt{lik} (here: 4).

If this model is already part of \texttt{tmo}, then its respective \texttt{ncount} entry is incremented by one; else it is inserted into a position according to the ranking of \texttt{lik}.

In addition, there is the possibility to save (the first moments of) coefficients of a model (\texttt{betas}) and their second moments (\texttt{betas2}), as well as an arbitrary vector of statistics per model (\texttt{fixed_vector}).

\texttt{is.topmod} returns \texttt{TRUE} if the argument is of class 'topmod'

Value

A call to \texttt{topmod} returns a list of class "topmod" with the following elements:

- \texttt{addmodel(\texttt{mylik}, \texttt{vec01}, \texttt{vbeta}=\texttt{numeric(0)}, \texttt{vbeta2}=\texttt{numeric(0)}, \texttt{fixedvec}=\texttt{numeric(0)})}
  function that adjusts the list of models in the 'topmod' object (see Details).
  \texttt{mylik} is the basic selection criterion (usually log likelihood), \texttt{vec01} is the model binary (logical or numeric) indicating which regressors are included.
  \texttt{vbeta} is a vector of length equal to \texttt{sum(vec01)}, containing only the non-zero coefficients (only accounted for if \texttt{bbeta}!=\texttt{FALSE}). \texttt{vbeta2} is a similar vector of second moments etc. (only accounted for if \texttt{bbeta}==\texttt{TRUE}); \texttt{fixedvec} is an arbitrary vector of length \texttt{length(fixedvec)} (see above)

- \texttt{lik()}  A numeric vector of the best models (log) likelihoods, in decreasing order

- \texttt{bool()}  A character vector of hexmode expressions for the model binaries (cf. \texttt{bin2hex}), sorted by \texttt{lik()}

- \texttt{ncount()}  A numeric vector of MCMC frequencies for the best models (i.e. how often the respective model was introduced by \texttt{addmodel})
nbmodels Returns the argument nbmodel
nregs Returns the argument nmaxregressors
bool_binary() Returns a matrix whose columns present the models conforming to lik() in binary form
betas() a matrix whose columns are the coefficients conforming to bool_binary() (Note that these include zero coefficients due to non-inclusion of covariates); Note: if bbeta=FALSE this returns an empty matrix
betas2() similar to betas, for the second moments of coefficients Note: if bbeta=0, this returns an empty matrix
fixed_vector() The columns of this matrix return the fixed_vector statistics conforming to lik() (see Details); Note: if lengthfixedvec=0 this returns an empty matrix

Note
topmod is rather intended as a building block for programming; it has no direct application for a user of the BMS package.

Author(s)
Martin Feldkircher and Stefan Zeugner

See Also
the object resulting from bms includes an element of class 'topmod'
Check http://bms.zeugner.eu for additional help.

Examples
#standard use
tm=topmod(2,4,TRUE,0) #should keep a maximum two models
tm$addmodel(-2.3,c(1,1,1,1),1:4,5:8) #update with some model
tm$addmodel(-2.2,c(0,1,1,1),1:3,5:7) #add another model
tm$addmodel(-2.2,c(0,1,1,1),1:3,5:7) #add it again -> adjust ncount
tm$addmodel(-2.5,c(1,0,0,1),1:2,5:6) #add another model

#read out
tm$lik()
tm$ncount()
tm$bool_binary()
tm$betas()

is.topmod(tm)

#extract a topmod object only containing the second best model
tm2=tm[2]

#advanced: should return the same result as
## Description
An updateable list keeping the best x models it encounters in any kind of model iteration.

## Objects from the Class
Objects can be created by calls to `topmod`, or indirectly by calls to `bms`.

A `topmod` object (as created by `topmod`) holds three basic vectors: `lik` (for the (log) likelihood of models or similar), `bool()` for a hexcode presentation of the model binaries (cf. `bin2hex`) and `ncount()` for the times the models have been drawn. All these vectors are sorted descendantly by `lik`, and are of the same length. The maximum length is limited by the argument `nbmodels`.

If `tm` is a `topmod` object, then a call to `tm$addmodel` (e.g. `tm$addmodel(mylik=4, vec01=c(T,F,F,T))`) updates the object `tm` by a model represented by `vec01` (here the one including the first and fourth regressor) and the marginal (log) likelihood `lik` (here: 4). If this model is already part of `tm`, then its respective `ncount` entry is incremented by one; else it is inserted into a position according to the ranking of `lik`. In addition, there is the possibility to save (the first moments of) coefficients of a model (`betas`) and their second moments (`betas2`), as well as an arbitrary vector of statistics per model (`fixed_vector`).

## Slots
`.S3Class`: Object of class "list", elements are:

- `addmodel`: function that adjusts the list of models in the `topmod` object (see Details). `mylik` is the basic selection criterion (usually log likelihood), `vec01` is the model binary (logical or numeric) indicating which regressors are included - cf. `topmod`
lik: the function lik() returns a numeric vector of the best models (log) likelihoods, in
decreasing order
bool: the function bool() returns a character vector of hexmode expressions for the model
binaries (cf. bin2hex), sorted by lik()
ncount: the function ncount() returns a numeric vector of MCMC frequencies for the best
models (i.e. how often the respective model was introduced by addmodel)
nbmodels: the function nbmodels() returns the argument nbmodel to function topmod
nregs: the function nregs() returns the argument nmaxregressors to bms
betas_raw: the function betas_raw() returns a vector containing the coefficients in betas
(see below) without the zero entries
betas2_raw: the function betas2_raw() returns a vector containing the coefficient second
moments in betas2 (see below) without the zero entries
kvec_raw: the function kvec_raw() returns a vector with model sizes (integers) for the mod-
els denoted in bool
bool_binary: the function bool_binary() returns a matrix whose columns present the mod-
els conforming to lik() in binary form
betas: the function betas() returns a matrix whose columns are the cofficients conform-
ing to bool_binary() (Note that these include zero coefficients due to non-inclusion of
covariates); Note: may be an empty matrix
betas2: the function betas2() returns a matrix similar to betas(), but with the coefficients
second moments (Note: can be empty)
fixed_vector: the function fixed_vector() returns a matrix whose columns bear the fixed_vector
statistics conforming to lik() (see Details); Note: if lengthfixedvec=0 in topmod this
returns an empty matrix

Methods

print.topmod

Author(s)

Martin Feldkircher and Stefan Zeugner

References

http://bms.zeugner.eu

See Also

topmod to create topmod objects and a more detailed description,
[.topmod for subselections, is.topmod to test for this class

Examples

tm= topmod(2,4,TRUE,0) #should keep a maximum two models
tm$addmodel(-2.3,c(1,1,1),1:4,5:8) #update with some model
tm$addmodel(-2.2,c(0,1,1),1:3,5:7) #add another model
tm$addmodel(-2.2,c(0,1,1),1:3,5:7) #add it again --> adjust ncount
tm$addmodel(-2.5,c(1,0,0,1),1:2,5:6) #add another model
#read out
tm$lik()
tm$ncount()
tm$bool_binary()
tm$betas()

topmodels.bma

\textit{Model Binaries and their Posterior model Probabilities}

\textbf{Description}

Returns a matrix whose columns show which covariates were included in the best models in a 'bma' object. The last two columns detail posterior model probabilities.

\textbf{Usage}

topmodels.bma(bmao)

\textbf{Arguments}

\begin{itemize}
  \item \texttt{bmao} an object of class 'bma' - see \texttt{bms}
\end{itemize}

\textbf{Value}

Each column in the resulting matrix corresponds to one of the 'best' models in \texttt{bmao}: the first column for the best model, the second for the second-best model, etc.

The model binaries have elements 1 if the regressor given by the row name was included in the respective models, and 0 otherwise.

The second-last row shows the model's posterior model probability based on marginal likelihoods (i.e. its marginal likelihood over the sum of likelihoods of all best models).

The last row shows the model's posterior model probability based on MCMC frequencies (i.e. how often the model was accepted vs sum of acceptance of all models).

\textbf{Note}

Note that the column names are hexcode representations of the model binaries (e.g. "03" for \texttt{c(0,0,1,0,0)})

\textbf{Author(s)}

Martin Feldkircher and Stefan Zeugner

\textbf{See Also}

\texttt{topmod} for accessing model binaries, \texttt{pmp.bma} for posterior model probabilities

Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.
variable.names.bma

Examples

data(datafls)
# sample with a limited data set for demonstration
mm=bms(datafls[,1:12],nmodel=20)

# show binaries for all
topmodels.bma(mm)

# show binaries for 2nd and 3rd best model, without the model probs
topmodels.bma(mm[2:3])[1:11,]

# access model binaries directly
mm$topmod$bool_binary()

---

variable.names.bma  Variable names and design matrix

Description

Simple utilities retrieving variable names and design matrix from a bma object

Usage

```r
## S3 method for class 'bma'
variable.names(object,...)
## S3 method for class 'bma'
model.frame(formula,...)
```

Arguments

- **object**: A bma object (as produced by `bms`)
- **formula**: A bma object (as produced by `bms`)
- **...**: further arguments passed to or from other methods

Details

All functions are bma-functions for the generic methods `variable.names`, `deviance`, and `model.frame`.

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

- `bms` for creating bma objects
- Check [http://bms.zeugner.eu](http://bms.zeugner.eu) for additional help.
variable.names.zlm

Examples

data(datafls)
bma_enum=bms(datafls[1:20,1:10])

model.frame(bma_enum) # similar to
bma_enum$X.data

variable.names(bma_enum)[-1] # is equivalent to
bma_enum$reg.names

---

variable.names.zlm Variable names and design matrix

Description

Simple utilities retrieving variable names and design matrix from a bma object

Usage

## S3 method for class 'zlm'
variable.names(object,...)

## S3 method for class 'zlm'
vcov(object, include.const = FALSE, ...)

## S3 method for class 'zlm'
logLik(object, ...)

Arguments

object A bma object (as produced by bms)
include.const Whether the variance-covariance matrix returned by vcov.zlm should also include a line and row for the intercept (which will be NA for most priors)
...
further arguments passed to or from other methods

Details

variable.names.zlm: method variable.names for a zlm model.
vcov.zlm: the posterior variance-covariance matrix of the coefficients of a zlm model - cf. vcov.logLik.zlm: a zlm model's log-likelihood p(y|M) according to the implementation of the respective coefficient prior

Author(s)

Martin Feldkircher and Stefan Zeugner
See Also

zlm for creating zlm objects

Check http://bms.zeugner.eu for additional help.

Examples

data(datafls)

zz=zlm(datafls)
variable.names(zz)
vcov(zz)
logLik(zz)

zlm

Bayesian Linear Model with Zellner’s g

Description

Used to fit the Bayesian normal-conjugate linear model with Zellner’s g prior and mean zero coefficient priors. Provides an object similar to the lm class.

Usage

zlm(formula, data = NULL, subset = NULL, g = "UIP")

Arguments

formula an object of class "formula" (or one that can be coerced to that class), such as a data.frame - cf. lm
data an optional data.frame (or one that can be coerced to that class): cf. lm
subset an optional vector specifying a subset of observations to be used in the fitting process.
g specifies the hyperparameter on Zellner’s g-prior for the regression coefficients. g="UIP" corresponds to \( g = N \), the number of observations (default); g="BRIC" corresponds to the benchmark prior suggested by Fernandez, Ley and Steel (2001), i.e \( g = \max(N, K^2) \), where \( K \) is the total number of covariates; g="EBL" estimates a local empirical Bayes g-parameter (as in Liang et al. (2008)); g="hyper" takes the ‘hyper-g’ prior distribution (as in Liang et al., 2008) with the default hyper-parameter \( a = 3 \). This hyperparameter can be adjusted (between \( 2 < a <= 4 \)) by setting g="hyper=2.9", for instance. Alternatively, g="hyper=UIP" sets the prior expected value of the shrinkage factor equal to that of UIP (above), g="hyper=BRIC" sets it according to BRIC
Details

zlm estimates the coefficients of the following model \( y = \alpha + X\beta + \epsilon \) where \( \epsilon \sim N(0, \sigma^2) \) and \( X \) is the design matrix.

The priors on the intercept \( \alpha \) and the variance \( \sigma \) are improper: \( \alpha \propto 1, \sigma \propto \sigma^{-1} \).

Zellner's g affects the prior on coefficients: \( \beta \sim N(0, \sigma^2 g(X'X)^{-1}) \).

Note that the prior mean of coefficients is set to zero by default and cannot be adjusted. Note moreover that zlm always includes an intercept.

Value

Returns a list of class zlm that contains at least the following elements (cf. lm):

- coefficients: a named vector of posterior coefficient expected values
- residuals: the residuals, that is response minus fitted values
- fitted.values: the fitted mean values
- rank: the numeric rank of the fitted linear model
- df.residual: the residual degrees of freedom
- call: the matched call
- terms: the terms object used
- model: the model frame used
- coef2moments: a named vector of coefficient posterior second moments
- marg.lik: the log marginal likelihood of the model
- gprior.info: a list detailing information on the g-prior, cf. output value gprior.info in bms

Author(s)

Stefan Zeugner

References


See also http://bms.zeugner.eu for additional help.

See Also

The methods summary.zlm and predict.lm provide additional insights into zlm output.

The function as.zlm extracts a single out model of a bma object (as e.g. created through bms).

Moreover, lm for the standard OLS object, bms for the application of zlm in Bayesian model averaging.

Check http://bms.zeugner.eu for additional help.
Examples

data(datafls)

# simple example
foo = zlm(datafls)
summary(foo)

# example with formula and subset
foo2 = zlm(y~GDP60+LifeExp, data=datafls, subset=2:70) # basic model, omitting three countries
summary(foo2)

---

zlm-class

Class "zlm"

Description

A list holding output from the Bayesian Linear Model under Zellner's g prior akin to class 'lm'

Objects from the Class

Objects can be created via calls to zlm, but indirectly also via as.zlm.

zlm estimates a Bayesian Linear Model under Zellner's g prior - its output is very similar to objects of class lm (cf. section 'Value')

Slots

.S3Class: Object of class "list", elements are:

coefficients: A named vector of class "numeric": holds the posterior expected values of 'regression' coefficients. The first element always holds the intercept
residuals: Vector of class "numeric": the residuals, that is the response variable minus fitted values
rank: Scalar integer class "numeric": the number of estimated parameters
fitted.values: The (posterior expected values of the) fitted values
df.residual: Scalar integer of class "numeric": the residual degrees of freedom
call: Object of class "call": the matched call to zlm that created the object
terms: Object of class "formula": the terms object used
model: Object of class "data.frame": the model frame used
coeff2moments: Named vector of class "numeric": coefficient posterior second moments
marg.lik: Scalar integer of class "numeric": the log marginal likelihood of the model
gprior.info: An object of class "list" detailing information on the g-prior, cf. output value gprior.info in bms
Extends

Class "oldClass", directly.

Methods

No methods defined with class "zlm" in the signature.

Author(s)

Martin Feldkircher and Stefan Zeugner

References

http://bms.zeugner.eu

See Also

zlm and as.zlm for creating zlm objects,
density.zlm, predict.zlm and summary.zlm for other posterior results

[.bma] Extract Parts of a topmod Object

Description

returns a bma (or topmod) object whose

Usage

### S3 method for class 'bma'
x[i, ...]

### S3 method for class 'topmod'
x[i, ...]

Arguments

x an object of class 'bma' or of class topmod
i index of the best models to be retained
... arguments such as 'drop' will not have an effect

Details

Both functions are equivalent: they serve to select a subset of the best models in a bma object.
Value

If \( x \) is a topmod object (see topmod), then \( x[i] \) returns a topmod object that only retains the models specified by \( i \).

if \( x \) is an object of class bma (see bms), \( x[i] \) returns a bma object whose topmod object (i.e. \( x\$topmod \) has been adjusted accordingly).

Note

Note that the method parameter drop is of no importance here. Moreover the corresponding assignment operator [<- is of no use.

Author(s)

Martin Feldkircher and Stefan Zeugner

See Also

[ for the default method, bms for crating bma objects

Check http://bms.zeugner.eu for additional help.

Examples

```r
#sample some BMA
data(datafls)
mm=bms(datafls[,1:11])

#plotConv for all models
plotConv(mm)

#plotConv for the best 20 models
plotConv(mm[1:20])

#model binary for the second best model
topmodels.bma(mm[2])

#similar:
as.vector(mm$topmod[2]$bool_binary())

#exactly the same
as.vector(mm[2]$topmod$bool_binary())

#print stats for second best model
print(mm$topmod[2])
```
Index

*Topic **aplot**
density.bma, 21
gdensity, 26
plot.pred.density, 35
plotConv, 37

*Topic **arith**
bin2hex, 6

*Topic **classes**
bma-class, 7
gprior-class, 28
is.bma, 31
mprior-class, 33
topmod-class, 60
zlm-class, 67

*Topic **datasets**
datafls, 19

*Topic **hplot**
image.bma, 29
plot.bma, 34
plotComp, 36
plotModels.size, 39

*Topic **models**
as.zlm, 4
bms, 9
c.bma, 15
coeff.bma, 16
topmod, 57
zlm, 65

*Topic **package**
BMS-package, 2

*Topic **print**
print.bma, 50
print.topmod, 51

*Topic **utilities**
[, bma, 68
beta.draws.bma, 5
density.bma, 21
f2hyper, 23
fullmodel.ssq, 25
gdensity, 26
lps.bma, 31
pmp.bma, 40
pmpmodel, 42
post.var, 44
pred.density, 45
predict.bma, 47
predict.zlm, 49
quantile.pred.density, 52
summary.bma, 54
summary.zlm, 56
topmodels.bma, 62
variable.names.bma, 63
variable.names.zlm, 64
[. , 69
[.bma, 68
[.topmod, 61
[.topmod([.bma), 68

as.zlm, 3, 4, 66–68
axis, 30

beta.draws.bma, 3, 5
bin2hex, 6, 58, 60, 61
bma-class, 7
BMS (BMS-package), 2
bms, 3–9, 15, 17, 18, 21–23, 25–33, 36,
38–41, 43–46, 48–50, 52, 54, 55,
58–64, 66, 67, 69
BMS-package, 2

c, 15
c.bma, 3, 7, 8, 12, 14, 15, 55
coeff, 17
coeff.bma, 3, 6, 8, 12, 14, 16, 22, 23, 27, 30,
37, 39, 44, 48, 50
combine_chains(c.bma), 15

data.frame, 11, 25, 65
datafls, 19
INDEX

density, 22, 27, 53
density.bma, 3, 8, 14, 21, 27, 28, 32, 36, 39, 53
density.zlm, 68
density.zlm(density.bma), 21
deviance, 3, 45, 63
deviance.bma(post.var), 44
deviance.zlm(post.var), 44

estimates.bma(coef.bma), 16

f2lhyper, 3, 23
format.hexmode, 7
formula, 9
fullmodel.ssq, 3, 25
gdensity, 3, 26
gprior-class, 28
grid, 22, 30, 37–39
hex2bin, 3, 7, 43
hex2bin(bin2hex), 6

image.bma, 3, 8, 29, 39
image.default, 30
info.bma(summary.bma), 54
is.bma, 31
is.topmod, 61
is.topmod(topmod), 57

legend, 22, 27, 35, 37–39
lines, 22, 27, 35
list, 53, 56
lm, 4, 11, 25, 65–67
logLik.zlm(variable.names.zlm), 64
lps.bma, 31, 46, 47

matplot, 34, 36, 38, 39
matrix, 11, 25
model.frame, 4, 13, 63
model.frame.bma(variable.names.bma), 63
mprior-class, 33

nmodel, 17

oldClass, 68

palette, 22, 27
par, 21, 26, 30, 35, 37
plot.bma, 3, 8, 34, 38

plot.default, 21, 26
plot.density, 35, 46
plot.pred.density, 35, 46, 47
plotComp, 36
plotConv, 34, 37, 39–41
plotModels.size, 14, 34, 39
pmp.bma, 3, 5, 17, 18, 38, 40, 43, 51, 52, 62
pmpmodel, 3, 41, 42
post.pr2, 3
post.pr2(post.var), 44
post.var, 3, 44
pred.density, 3, 32, 35, 36, 45, 53
pred.density-class(pred.density), 45
predict.bma, 47, 47, 49
predict.lm, 48, 49, 66
predict.zlm, 49, 68
print, 50
print.bma, 3, 50, 55
print.pred.density(pred.density), 45
print.topmod, 51, 61

quantile.coef.density, 23
quantile.coef.density
  (quantile.pred.density), 52
quantile.default, 53
quantile.density
  (quantile.pred.density), 52
quantile.pred.density, 47, 52

set.seed, 11
summary.bma, 3, 8, 12, 41, 50, 54
summary.zlm, 56, 66, 68
terms, 66, 67
topmod, 3, 8, 9, 12, 40, 51, 52, 60–62, 68, 69
topmod-class, 60
topmodels.bma, 3, 5, 43, 51, 62

variable.names, 3, 63, 64
variable.names.bma, 13, 63
variable.names.zlm, 64
vcov, 3, 64
vcov.zlm(variable.names.zlm), 64
zlm, 3–5, 21, 28, 29, 32, 45, 49, 57, 64, 65, 65, 67, 68
zlm-class, 67