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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, hyper-g and empirical 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. Also includes Bayesian normal-conjugate linear model with Zellner's g prior, and assorted methods.

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as.zlm

Extract a Model from a bma Object

Description

Extracts a model out of a bma object's saved models and converts it to a [zlm](#) linear model

Usage

```
as.zlm(bmao, model = 1)
```

Arguments

| | |
|-------|--|
| bmao | A bma object, e.g. resulting from a call to bms |
| 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 `nmodel` in [bms](#)). `as.zlm` extracts a single model and converts it to an object of class `zlm`, which represents a linear model estimated under Zellner's g prior.

The utility `model.frame` allows to transform a `zlm` model into an OLS model of class `lm`.

Value

a list of class `zlm`

Author(s)

Stefan Zeugner

See Also

[bms](#) for creating bma objects, [zlm](#) for creating `zlm` objects, [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 | <i>Coefficients of the Best Models</i> |
|----------------|--|

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. |

Value

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\$topmod\$betas()

See Also

[bms](#) for creating bms objects, [coef.bma](#) for aggregate coefficients

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

Examples

```
#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);
```

bma-class

Class "bma"

Description

A list holding results from a BMA iteration chain

Objects from the Class

Objects can be created via calls to [bms](#), but indirectly also via [c.bma](#)

A bma object is a list whose elements hold information on input and output for a Bayesian Model Averaging iteration chain, such as from a call to [bms](#):

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

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

Description

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

Usage

```
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)
)
```

Arguments

| | |
|---------------------|--|
| <code>X.data</code> | a data frame or a matrix, with the dependent variable in the first column, followed by the covariates (alternatively, <code>X.data</code> can also be provided as a formula). Note that <code>bms</code> automatically estimates a constant, therefore including constant terms is not necessary. |
| <code>burn</code> | The (positive integer) number of burn-in draws for the MC3 sampler, defaults to 1000. (Not taken into account if <code>mcmc="enumerate"</code>) |
| <code>iter</code> | If <code>mcmc</code> is set to an MC3 sampler, then this is the number of iteration draws to be sampled (ex burn-ins), default 3000 draws. If <code>mcmc="enumerate"</code> , then <code>iter</code> is the number of models to be sampled, starting from 0 (defaults to $2^K - 1$) - cf. <code>start.value</code> . |
| <code>nmodel</code> | 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 <code>nmodel</code> slows down the sampler significantly. Set <code>nmodel=0</code> to speed up sampling (if best model information is not needed). |

| | |
|-------------|---|
| mcmc | <p>a character denoting the model sampler to be used.</p> <p>The MC3 sampler <code>mcmc="bd"</code> corresponds to a birth/death MCMC algorithm. <code>mcmc="rev.jump"</code> enacts a reversible jump algorithm adding a "swap" step to the birth / death steps from "bd".</p> <p>Alternatively, the entire model space may be fully enumerated by setting <code>mcmc="enumerate"</code> which will iterate all possible regressor combinations (Note: consider that this means 2^K iterations, where K is the number of covariates.)</p> <p>Default is full enumeration (<code>mcmc="enumerate"</code>) with less than 15 covariates, and the birth-death MC3 sampler (<code>mcmc="bd"</code>) with 15 covariates or more. Cf. section 'Details' for more options.</p> |
| g | <p>the hyperparameter on Zellner's g-prior for the regression coefficients.</p> <p><code>g="UIP"</code> corresponds to $g = N$, the number of observations (default);</p> <p><code>g="BRIC"</code> 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;</p> <p><code>g="RIC"</code> sets $g = K^2$ and conforms to the risk inflation criterion by George and Foster (1994)</p> <p><code>g="HQ"</code> sets $g = \log(N)^3$ and asymptotically mimics the Hannan-Quinn criterion with $C_{HQ} = 3$ (cf. Fernandez, Ley and Steel, 2001, p.395)</p> <p><code>g="EBL"</code> estimates a local empirical Bayes g-parameter (as in Liang et al. (2008));</p> <p><code>g="hyper"</code> 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';</p> <p>This hyperparameter a can be adjusted (between $2 < a \leq 4$) by setting <code>g="hyper=2.9"</code>, for instance.</p> <p>Alternatively, <code>g="hyper=UIP"</code> sets the prior expected value of the shrinkage factor equal to that of UIP (default), <code>g="hyper=BRIC"</code> sets it according to BRIC</p> <p>cf section 'Details' for more on the hyper-g prior</p> |
| mprior | <p>a character denoting the model prior choice, defaulting to "random":</p> <p><code>mprior="fixed"</code> 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. <code>mprior.size</code>. Preferable to <code>mcmc="random"</code> if strong prior information on model size exists;</p> <p><code>mprior="random"</code> (default) triggers the 'random theta' prior by Ley and Steel (2008), who suggest a binomial-beta hyperprior on the a priori inclusion probability;</p> <p><code>mprior="uniform"</code> employs the uniform model prior;</p> <p><code>mprior="customk"</code> allows for custom model size priors (cf. <code>mprior.size</code>);</p> <p><code>mprior="pip"</code> allows for custom prior inclusion probabilities (cf. <code>mprior.size</code>);</p> <p>Note that the prior on models with more than N-3 regressors is automatically zero: these models will not be sampled.</p> |
| mprior.size | <p>if <code>mprior</code> is "fixed" or "random", <code>mprior.size</code> is a scalar that denotes the prior expected value of the model size prior (default K/2).</p> <p>If <code>mprior="customk"</code> 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. <code>rep(1,K+1)</code> for the uniform model prior);</p> <p>if <code>mprior="pip"</code>, then custom prior inclusion probabilities can be provided as a vector of size K, with elements in the interval (0,1)</p> |
| user.int | 'interactive mode': print out results to console after ending the routine and plots |

| | |
|-----------------------------|--|
| | a chart (default TRUE). |
| <code>start.value</code> | <p>specifies the starting model of the iteration chain. For instance a specific model by the corresponding column indices (e.g. <code>starting.model=numeric(K)</code> starts from the null model including solely a constant term) or <code>start.value=c(3,6)</code> for a starting model only including covariates 3 and 6.</p> <p>If <code>start.model</code> is set to an integer (e.g. <code>start.model=15</code>) 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.</p> <p>The default value <code>start.value=NA</code> corresponds to <code>start.value=min(ncol(X.data), nrow(X.data)-3)</code>.</p> <p>Note that <code>start.value=0</code> or <code>start.value=NULL</code> starts from the null model.</p> <p>If <code>mcmc="enumerate"</code> then <code>start.value</code> is the index to start the iteration (default: 0, the null model). Any number between 0 and $K^2 - 1$ is admissible.</p> |
| <code>g.stats</code> | TRUE if statistics on the shrinkage factor $g/(1+g)$ should be collected, defaulting to TRUE (Note: set <code>g.stats=FALSE</code> for faster iteration.) |
| <code>logfile</code> | setting <code>logfile=TRUE</code> produces a logfile named "test.log" in your current working directory, in order to keep track of the sampling procedure. <code>logfile</code> equal to some filepath (like <code>logfile="subfolder/log.txt"</code>) puts the logfile into that specified position. (default: <code>logfile=FALSE</code>). Note that <code>logfile=""</code> implies log printouts on the console. |
| <code>logstep</code> | specifies at which number of posterior draws information is written to the log file; default: 10 000 iterations |
| <code>force.full.ols</code> | default FALSE. If <code>force.full.ols=TRUE</code> , the OLS estimation part of the sampling procedure relies on slower matrix inversion, instead of streamlined routines. <code>force.full.ols=TRUE</code> can slow down sampling but may deal better with highly collinear data |
| <code>fixed.reg</code> | indices or variable names of <code>X.data</code> that are fixed regressors to be always included in every sampled model. Note: the parameter <code>mprior.size</code> refers to prior model size including these fixed regressors. |

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 $g = \text{"hyper=UIP"}$ and $g = \text{"hyper=BRIC"}$ 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:

| | |
|--------------------------|--|
| <code>info</code> | a list of aggregate statistics: <code>iter</code> is the number of iterations, <code>burn</code> the number of burn-ins. The following have to be divided by <code>cumsumweights</code> to get posterior expected values: <code>inccount</code> are the posterior inclusion probabilities, <code>b1mo</code> and <code>b2mo</code> the first and second moment of coefficients, <code>add.otherstats</code> other statistics of interest (typically the moments of the shrinkage factor), <code>msize</code> is the post. expected model size, <code>k.vec</code> the posterior model size distribution, <code>pos.sign</code> the unconditional post. probability of positive coefficients, <code>corr.pmp</code> is the correlation between the best models' MCMC frequencies and their marg. likelihoods. <code>timed</code> is the time that was needed for MCMC sampling, <code>cons</code> is the posterior expected value of the constant. <code>K</code> and <code>N</code> are the maximum number of covariates and the sample size, respectively. |
| <code>arguments</code> | a list of the evaluated function arguments provided to <code>bms</code> (see above) |
| <code>topmod</code> | a 'topmod' object containing the best drawn models. see <code>topmod</code> for more details |
| <code>start.pos</code> | the positions of the starting model. If <code>bmao</code> is a 'bma' object this corresponds to covariates <code>bmao\$reg.names[bmao\$start.pos]</code> . If <code>bmao</code> is a chain that resulted from several starting models (cf. <code>c.bma</code> , then <code>start.pos</code> is a list detailing all of them. |
| <code>gprior.info</code> | a list of class <code>gprior-class</code> , detailing information on the g -prior: <code>gtype</code> corresponds to argument <code>g</code> above, <code>is.constant</code> is FALSE if <code>gtype</code> is either "hyper" or "EBL", <code>return.g.stats</code> corresponds to argument <code>g.stats</code> above, <code>shrinkage.moments</code> contains the first and second moments of the shrinkage factor (only if <code>return.g.stats==TRUE</code>), <code>g</code> details the fixed g (if <code>is.constant==TRUE</code>), <code>hyper.parameter</code> corresponds to the hyper- g parameter a as in Liang et al. (2008) |
| <code>mprior.info</code> | a list of class <code>mprior-class</code> , detailing information on the model prior: <code>origargs</code> lists the original arguments to <code>mprior</code> and <code>mprior.size</code> above; <code>mp.msize</code> denotes the prior mode size; <code>mp.Kdist</code> is a $(K+1)$ vector with the prior model size distribution from 0 to K |
| <code>X.data</code> | <code>data.frame</code> or matrix: corresponds to argument <code>X.data</code> above, possibly cleaned for NAs |
| <code>reg.names</code> | character vector: the covariate names to be used for <code>X.data</code> (corresponds to <code>variable.names.bma</code>) |
| <code>bms.call</code> | the original call to the <code>bms</code> function |

Theoretical background

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 $\epsilon \sim N(0, \sigma^2 I)$:

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

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. the best models, but not their coefficients, which renders the use of `image.bma` and the parameter `exact=TRUE` in functions such as `coef.bma` infeasible. `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, Paul Hofmarcher, and Stefan Zeugner

References

- <http://bms.zeugner.eu>: BMS package homepage with help and tutorials
- Feldkircher, M. and S. Zeugner (2015): Bayesian Model Averaging Employing Fixed and Flexible Priors: The BMS Package for R, *Journal of Statistical Software* 68(4).
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- Liang, F., Paulo, R., Molina, G., Clyde, M. A., and Berger, J. O. (2008). Mixtures of g Priors for Bayesian Variable Selection. *Journal of the American Statistical Association* 103, 410-423.
- Sala-i-Martin, X. and G. Doppelhofer and R.I. Miller (2004): Determinants of long-term growth: a Bayesian averaging of classical estimates (BACE) approach. *American Economic Review* 94(4), 813–835

See Also

`coef.bma`, `plotModelsize` and `density.bma` for some operations on the resulting 'bma' object, `c.bma` 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)

#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

```
## 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.

See Also

[bms](#) for creating bma objects

Check <http://bms.zeugner.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 differnt 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))

```

datafls

FLS (2001) growth data

Description

The economic growth data set from Fernandez, Ley and Steel, Journal of Applied Econometrics 2001

Usage

```
datafls
```

Format

A data frame with 53940 rows and 10 variables: 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
PublEduPct numeric: Public education share
RevnCoup numeric: Revolutions and coups
PolRights numeric: Political rights
CivlLib 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

Fernandez, C., Ley, E., and Steel, M. F. (2001b). Model Uncertainty in Cross-Country Growth Regressions. *Journal of Applied Econometrics*, 16:563-576. Data set from https://warwick.ac.uk/fac/sci/statistics/staff/academic-research/steel/steel_homepage/software.

A working paper version of Fernandez, Ley and Steel (2001) is available via https://econpapers.repec.org/article/jaejapmet/v_3a16_3ay_3a2001_3ai_3a5_3ap_3a563-576.htm.

density.bma

*Coefficient Marginal Posterior Densities***Description**

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

Usage

```
## S3 method for class 'bma'
density(
  x,
  reg = NULL,
  addons = "lemsz",
  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 `lines` and `legend`:

"e" for the posterior expected value (EV) of coefficients conditional on inclusion (see argument `exact=TRUE` in `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=FALSE` in `coef.bma`),

"S" for the corresponding SD bounds (MCMC),

"p" for plotting the Posterior Inclusion Probability above the density plot,

"l" for including a `legend`, "z" for a zero line, "g" for adding a `grid`

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

In case of `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 `density` detailing the marginal posterior densities for each coefficient provided in `reg`.

In case of `density.zlm`, simple marginal posterior coefficient densities are computed, while `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=TRUE`, the densities are plotted too. Note that (for `density.bma`) if the posterior inclusion probability of a covariate is zero, then it will not be plotted, and the returned density will be `list(x=numeric(n),y=numeric(n))`.

Note

The computed marginal posterior densities from `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 `x` (cf. argument `nmodel` in `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 `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 `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 `palette`.

Up to BMS version 0.3.0, `density.bma` may only cope with built-in gpriors, not with any user-defined priors.

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="lbz")
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="es1")
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",]
```

estimates.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

```

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

## 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,
  ...
)

```

Arguments

| | |
|-------------------------------|---|
| <code>exact</code> | if <code>exact=FALSE</code> , 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 <code>exact=TRUE</code> , estimates will be based on the <code>nmodel</code> best models encountered by the sampling chain, with the posterior model distribution based on their <i>exact</i> marginal likelihoods - cf. 'Details' below. |
| <code>order.by.pip</code> | <code>order.by.pip=TRUE</code> orders the resulting matrix according to posterior inclusion probabilities, <code>order.by.pip=FALSE</code> ranks them according to the original data (order of the covariates as in provided in <code>X.data</code> to <code>bms</code>), default <code>TRUE</code> |
| <code>include.constant</code> | If <code>include.constant=TRUE</code> then the resulting matrix includes the expected value of the constant in its last row. Default <code>FALSE</code> |
| <code>incl.possign</code> | If <code>incl.possign=FALSE</code> , then the sign probabilities column (cf. 'Values' below) is omitted from the result. Default <code>TRUE</code> |
| <code>std.coefs</code> | If <code>std.coefs=TRUE</code> 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 <code>std.coefs=FALSE</code> (default) then both expected values and standard deviations are returned 'as is'. |
| <code>condi.coef</code> | If <code>condi.coef=FALSE</code> (default) then coefficients β_i and standard deviations are unconditional posterior expected values, as in standard model averaging; if <code>condi.coef=TRUE</code> then they are given as conditional on inclusion (equivalent to β_i/PIP_i). |
| <code>object, bmao</code> | a 'bma' object (cf. <code>bms</code>) |

... 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.possign=FALSE`)

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

Column 'Post Mean'

posterior expected value of coefficients, unconditional $E(\beta|Y) = \sum p(\gamma|Y)E(\beta|\gamma, Y)$, where $E(\beta_i|\gamma, i \notin \gamma, Y) = 0$ 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 they were used for sampling. (if included, the constant has index 0)

See Also

`bms` for creating `bma` objects, `pmp.bma` for comparing MCMC frequencies and marginal likelihoods.

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

Examples

```
#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
coef(mm)

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

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

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

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

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

```

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

```
f21hyper(a, b, c, z)
```

Arguments

| | |
|---|---|
| a | The parameter a of the Gaussian hypergeometric function, must be a positive scalar here |
| b | The parameter b of the Gaussian hypergeometric function, must be a positive scalar here |
| c | The parameter c of the Gaussian hypergeometric function, must be a positive scalar here |
| z | The parameter z of the Gaussian hypergeometric function, must be between -1 and 1 here |

Details

The function f21hyper complements the analysis of the 'hyper-g prior' introduced by Liang et al. (2008).

For parameter values, compare cf. https://en.wikipedia.org/wiki/Hypergeometric_function.

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'

References

Liang F., Paulo R., Molina G., Clyde M., Berger J.(2008): Mixtures of g-priors for Bayesian variable selection. J. Am. Statist. Assoc. 103, p. 410-423

https://en.wikipedia.org/wiki/Hypergeometric_function

See Also

package hypergeo for a more proficient implementation.

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

Examples

```
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

```
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](#)

See Also

[bms](#) for creating bma objects, [lm](#) for OLS estimation

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

Examples

```
data(datafls)
mm=bms(datafls)

fullmodel.ssq(mm)

#equivalent:
fullmodel.ssq(datafls)
```

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

```
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 |
| plot | logical. If TRUE (default), the density is plotted; if FALSE then <code>gdensity</code> only returns the estimated posterior density without plotting. |
| addons | character, defaulting to "zles". Specifies which additional information should be added to the plot via low-level commands (see 'Details' below). |
| addons.lwd | scalar, default 1.5. Line width to be used for the low-level plotting commands specified by addons. Cf. argument <code>lwd</code> in par |
| ... | Additional arguments for <code>plot.default</code> 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 is 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 $\max(0, E - 5 * SD)$, 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`.

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, "l" 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 [coef.bma](#)),

"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`.

See Also

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

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

Examples

```
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="lzfes")

# #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

Author(s)

Martin Feldkircher and Stefan Zeugner

References

Feldkircher, M. and S. Zeugner (2009): Benchmark Priors Revisited: On Adaptive Shrinkage and the Supermodel Effect in Bayesian Model Averaging, IMF Working Paper 09/202.

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
```

hex2bin

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

```
hex2bin(hexcode)
```

```
bin2hex(binvec)
```

Arguments

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

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

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"))
```

 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 <code>par()</code> \$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.

See Also

[coef.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"))

```

info.bma

*Summary Statistics for a 'bma' Object***Description**

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

Usage

```
info.bma(bmao)

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

Arguments

| | |
|--------|--|
| bmao | same as object |
| object | a list/object of class 'bma' that typically results from the function <code>bms</code> (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

`list(list("2^K"))`

the total model space 2^K

Percentage visited

$\text{No. of models visited} / \text{Modelspace} * 100$

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.

See Also

[bms](#) and [c.bma](#) for functions creating bma objects, `print.bma` makes use of `summary.bma`.

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

Examples

```
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)
```

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.

See Also

'Output' in [bms](#) for the structure of a 'bma' object

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

Examples

```
data(datafls)
mm=bms(datafls,burn=1000, iter=4000)
is.bma(mm)
```

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

See Also

[pred.density](#) for constructing predictive densities, [bms](#) for creating bma objects, [density.bma](#) for plotting coefficient densities

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

Examples

```

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 predicitive.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])

```

mprior-class

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:

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

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

Arguments

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

Value

combines the plotting functions `plotModelsize` and `plotConv`

Note

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

See Also

`plotModelsize` and `plotConv`

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

Examples

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


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

```
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 |
| 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 |

See Also

[coef.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 coefficients
plotComp(mm1,mm2,comp="Std Mean")

#...based on the likelihoods 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 probabilities 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](#)

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

```
plotModelsize(
  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 coef.bma) |
| 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 <code>grid()</code>). |
| ... | 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) |

See Also

See also [bms](#), [image.bma](#), [density.bma](#), [plotConv](#)

Check <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= plotModelsize(mm)

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

#plot based on all best models, but showing distribution only for model sizes 1 to 20
plotModelsize(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)
```

pmp.bma

*Posterior Model Probabilities***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 bmao |
| PMP (MCMC) | posterior model probabilities of the best models in bmao based on their MCMC frequencies, relative to all models encountered by bmao - 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`.

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> for additional help.

Examples

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

## mmodel likelihoods and MCMC frequencies of best 20 models
print(mm$topmod)

pmp.bma(mm)
#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'

#consequently, first column adds up to one
#second column shows how much of the sampled model space is
# contained in the best models
colSums(pmp.bma(mm))

#correlation between the two shows how well the sampler converged
cor(pmp.bma(mm)[,1],pmp.bma(mm)[,2])

#is the same as given in summary.bma
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$top$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
# this is already better, but also not good
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
mm=bms(datafls[,1:10],nmodel=512,mcmc="enumeration")
cor(pmp.bma(mm)[,1],pmp.bma(mm)[,2])
colSums(pmp.bma(mm))

```

pmpmodel

Posterior Model Probability for any Model

Description

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

Usage

```
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 the resulting PMP is derived from MCMC frequencies (works only for the null and fullmodel, 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`

See Also

`pmp.bma` for similar functions

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

Examples

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

#show the best 5 models:
pmp.bma(mm)
#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)
pmpmodel(mm,"00c")

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

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

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

####PMP of another model #####
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

```
post.var(object, exact = FALSE, ...)
```

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.

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. |
| hnbsteps | 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. Must be an even integer. |
| ... | arguments to be passed on to plot.density . |

Details

The predictive density is a mixture density based on the `nmodels` best models in a bma object (cf. `nmodel` in [bms](#)).

The number of 'best models' to retain is therefore vital and should be set quite high for accuracy.

Value

`pred.density` returns a list of class `pred.density` with the following elements

| | |
|--|---|
| <code>densities()</code> | a list whose elements each contain the estimated density for each forecasted observation |
| <code>fit</code> | a vector with the expected values of the predictions (the 'point forecasts') |
| <code>std.err</code> | a vector with the standard deviations of the predictions (the 'standard errors') |
| <code>dyf(realized.y, predict_index=NULL)</code> | Returns the densities of realized response variables provided in <code>realized.y</code> . If <code>realized.y</code> is a matrix, then each row corresponds to a forecast observation in <code>newdata</code> if not left empty, <code>predict_index</code> specifies to which observations in <code>newdata</code> the <code>realized.y</code> should apply |
| <code>lps(realized.y, predict_index=NULL)</code> | Computes the log predictive score for the response variable provided in <code>realized.y</code> (cf. lps.bma) - Note that the LPS equals minus the mean of the logarithmized results from <code>dyf</code> |

```
plot((x, predict_index = NULL, addons = "eslz", realized.y = NULL,
      addons.lwd = 1.5, ...))
      the same as plot.pred.density
```

n The number of equally spaced points for which the density (under densities()) was computed.

nmodel The number of best models predictive densities are based upon.

call the call that created this pred.density object

Note

In BMS version 0.3.0, pred.density may only cope with built-in gpriors, not with any user-defined priors.

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> for additional help.

Examples

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

#predictive densityfor 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$fit

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

# the same plot ' naked'
plot(pd$densities()[[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))
```

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, ...)
```

Arguments

| | |
|-----------|---|
| object | a bma object - see bms |
| 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. |
| 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.

See Also

[coef.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 MCM 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

```

## 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 <code>se.fit</code> in predict.lm |
| residual.scale | The part from the standard deviations that involves the identity matrix. Note that $\sqrt{\text{se.fit}^2 + \text{residual.scale}^2}$ yields <code>std.err</code> . |

See Also

[bms](#) for creating zlm objects, [predict.lm](#) for a comparable function, [predict.bma](#) for predicting with bma objects

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

Examples

```

data(datafls)
mm=zlm(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.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:

```

Row Names      show the model binaries in hexcode
Column 'Marg.Log.Lik'
                 shows the marginal log-likelihoods of the models in x
Column 'MCMC Freq'
                 shows the MCMC frequencies of the models in x

```

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

```

first line     '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)

```

Estimates 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`)

Included Covariates
 the model binary

Additional Statistics
 any custom additional statistics saved with the model

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.density

Extract Quantiles from 'density' Objects

Description

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

Usage

```
## S3 method for class 'density'
quantile(x, probs = seq(0.25, 0.75, 0.25), names = TRUE, normalize = TRUE, ...)

## S3 method for class 'coef.density'
quantile(x, probs = seq(0.25, 0.75, 0.25), names = TRUE, ...)

## S3 method for class 'pred.density'
quantile(x, probs = seq(0.25, 0.75, 0.25), names = TRUE, ...)
```

Arguments

| | |
|-----------|---|
| x | a object of class <code>pred.density</code> , <code>coef.density</code> , <code>density</code> , 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.zeugner.eu> for additional help.

Examples

```

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)

## Not run:
#application to list of densities:
quantile.density( list(density(rnorm(1000)), density(rnorm(1000))) )

## End(Not run)

```

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 information 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

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

```

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. |
| liks | 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 liks) - see example below |
| modelbinaries | optional matrix whose columns detail model binaries to initialize topmod object with (same nb columns as liks, nb rows as nmaxregressors) - see example below |
| betas | optional matrix whose columns are coefficients to initialize topmod object with (same dimensions as modelbinaries) - see example below |
| betas2 | optional matrix whose columns are coefficients' second moments to initialize topmod object with (same dimensions as modelbinaries) - see example below |
| fixed_vector | optional matrix whose columns are a fixed vector initialize topmod object with (same ncol as modelbinaries) - see example below |

Details

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 `tmo` is a `topmod` object, then a call to `tmo$addmodel` (e.g. `tmo$addmodel(mylik=4, vec01=c(T,F,F,T))`) updates the object `tmo` 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 `tmo`, 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`).

`is.topmod` returns `TRUE` if the argument is of class `'topmod'`

Value

a call to `topmod` returns a list of class "topmod" with the following elements:

| | |
|---|---|
| <code>addmodel(mylik, vec01, vbeta=numeric(0), vbeta2=numeric(0), fixedvec=numeric(0))</code> | function that adjusts the list of models in the <code>'topmod'</code> object (see Details). <code>mylik</code> is the basic selection criterion (usually log likelihood), <code>vec01</code> is the model binary (logical or numeric) indicating which regressors are included. <code>vbeta</code> is a vector of length equal to <code>sum(vec01)</code> , containing only the non-zero coefficients (only accounted for if <code>bbeta!=FALSE</code>). <code>vbeta2</code> is a similar vector of second moments etc. (only accounted for if <code>bbeta=TRUE</code>); <code>fixedvec</code> is an arbitrary vector of length <code>lengthfixedvec</code> (see above) |
| <code>lik()</code> | A numeric vector of the best models (log) likelihoods, in decreasing order |
| <code>bool()</code> | A character vector of hexmode expressions for the model binaries (cf. <code>bin2hex</code>), sorted by <code>lik()</code> |
| <code>ncount()</code> | A numeric vector of MCMC frequencies for the best models (i.e. how often the respective model was introduced by <code>addmodel</code>) |
| <code>nbmodels</code> | Returns the argument <code>nbmodel</code> |
| <code>nregs</code> | Returns the argument <code>nmaxregressors</code> |
| <code>bool_binary()</code> | Returns a matrix whose columns present the models conforming to <code>lik()</code> in binary form |
| <code>betas()</code> | a matrix whose columns are the coefficients conforming to <code>bool_binary()</code> (Note that these include zero coefficients due to non-inclusion of covariates); Note: if <code>bbeta=FALSE</code> this returns an empty matrix |
| <code>betas2()</code> | similar to <code>betas</code> , for the second moments of coefficients Note: if <code>bbeta<=0</code> , this returns an empty matrix |
| <code>fixed_vector()</code> | The columns of this matrix return the <code>fixed_vector</code> statistics conforming to <code>lik()</code> (see Details); Note: if <code>lengthfixedvec=0</code> 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.

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 oobject only containing the second best model
tm2=tm[2]

#advanced: should return the same result as
#initialize
tm2= topmod(2,4,TRUE,0, likes = c(-2.2,-2.3), ncounts = c(2,1),
           modelbinaries = cbind(c(0,1,1,1),c(1,1,1,1)), betas = cbind(0:3,1:4),
           betas2 = cbind(c(0,5:7),5:8))

#update
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()
```

topmod-class

Class "topmod"

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 `tmo` is a topmod object, then a call to `tmo$addmodel` (e.g. `tmo$addmodel(mylik=4,vec01=c(T,F,F,T))`) updates the object `tmo` 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 `tmo`, 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`).

Author(s)

Martin Feldkircher and Stefan Zeugner

References

<http://bms.zeugner.eu>

See Also

[topmod](#) to create topmod objects and a more detailed description, [is.topmod](#) to test for this class

Examples

```
tm= topmod(2,4,TRUE,0) #should keep a maximum two models
tm$addmodel(-2.3,c(1,1,1,1),1:4,5:8) #update with some model
tm$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()
```

topmodels.bma

Model Binaries and their Posterior model Probabilities

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.

Usage

```
topmodels.bma(bmao)
```

Arguments

bmao an object of class 'bma' - see [bma-class](#)

Details

Each bma class (the result of bms) contains 'top models', the x models with the best analytical likelihood that bms had encountered while sampling

See [pmp.bma](#) for an explanation of likelihood vs. MCMC frequency concepts

Value

Each column in the resulting matrix corresponds to one of the 'best' models in 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) Note that the column names are hexcode representations of the model binaries (e.g. "03" for c(0,0,0,1,0,0))

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

```
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

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

Arguments

object 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](#).

See Also

[bms](#) for creating bma objects

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

Examples

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

model.frame(bma_enum) # similar to
bma_enum$arguments$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, ...)
```

Arguments

| | |
|--------|--|
| object | A bma object (as produced by bms) |
| ... | 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

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 <code>data.frame</code> - cf. <code>lm</code> |
| data | an optional <code>data.frame</code> (or one that can be coerced to that class): cf. <code>lm</code> |
| 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. <code>g="UIP"</code> corresponds to $g = N$, the number of observations (default); <code>g="BRIC"</code> 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; <code>g="EBL"</code> estimates a local empirical Bayes g-parameter (as in Liang et al. (2008)); <code>g="hyper"</code> 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 $2 < a \leq 4$) by setting <code>g="hyper=2.9"</code> , for instance. Alternatively, <code>g="hyper=UIP"</code> sets the prior expected value of the shrinkage factor equal to that of UIP (above), <code>g="hyper=BRIC"</code> 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 α and the variance σ 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 <code>gprior.info</code> in bms |

Author(s)

Stefan Zeugner

References

The representation follows Fernandez, C. E. Ley and M. Steel (2001): Benchmark priors for Bayesian model averaging. *Journal of Econometrics* 100(2), 381–427

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')

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

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