Package ‘abc’

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Description The package implements several ABC algorithms for
performing parameter estimation, model selection, and goodness-of-fit.
Cross-validation tools are also available for measuring the
accuracy of ABC estimates, and to calculate the
misclassification probabilities of different models.
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Parameter estimation with Approximate Bayesian Computation (ABC)

Description

This function performs multivariate parameter estimation based on summary statistics using an ABC algorithm. The algorithms implemented are rejection sampling, and local linear or non-linear (neural network) regression. A conditional heteroscedastic model is available for the latter two algorithms.

Usage

```r
abc(target, param, sumstat, tol, method, hcorr = TRUE, transf = "none", logit.bounds, subset = NULL, kernel = "epanechnikov", numnet = 10, sizenet = 5, lambda = c(0.0001, 0.001, 0.01), trace = FALSE, maxit = 500, ...)
```

Arguments

- `target`: a vector of the observed summary statistics.
- `param`: a vector, matrix or data frame of the simulated parameter values, i.e. the dependent variable(s) when method is "loclinear", "neuralnet" or "ridge".
- `sumstat`: a vector, matrix or data frame of the simulated summary statistics, i.e. the independent variables when method is "loclinear", "neuralnet" or "ridge".
- `tol`: tolerance, the required proportion of points accepted nearest the target values.
- `method`: a character string indicating the type of ABC algorithm to be applied. Possible values are "rejection", "loclinear", "neuralnet" and "ridge". See also Details.
- `hcorr`: logical, the conditional heteroscedastic model is applied if TRUE (default).
- `transf`: a vector of character strings indicating the kind of transformation to be applied to the parameter values. The possible values are "log", "logit", and "none" (default), when no is transformation applied. See also Details.
- `logit.bounds`: a matrix of bounds if `transf` is "logit". The matrix has as many lines as parameters (including the ones that are not "logit" transformed) and 2 columns. First column is the minimum bound and second column is the maximum bound.
- `subset`: a logical expression indicating elements or rows to keep. Missing values in `param` and/or `sumstat` are taken as FALSE.
kernel: a character string specifying the kernel to be used when method is "loclinear", "neuralnet" or "ridge". Defaults to "epanechnikov". See density for details.

numnet: the number of neural networks when method is "neuralnet". Defaults to 10. It indicates the number of times the function nnet is called.

sizenet: the number of units in the hidden layer. Defaults to 5. Can be zero if there are no skip-layer units. See nnet for more details.

lambda: a numeric vector or a single value indicating the weight decay when method is "neuralnet". See nnet for more details. By default, 0.0001, 0.001, or 0.01 is randomly chosen for each of the networks.

trace: logical, if TRUE switches on tracing the optimization of nnet. Applies only when method is "neuralnet".

maxit: numeric, the maximum number of iterations. Defaults to 500. Applies only when method is "neuralnet". See also nnet.

Details

These ABC algorithms generate random samples from the posterior distributions of one or more parameters of interest, $\theta_1, \theta_2, \ldots, \theta_n$. To apply any of these algorithms, (i) data sets have to be simulated based on random draws from the prior distributions of the $\theta_i$’s, (ii) from these data sets, a set of summary statistics have to be calculated, $S(y)$, (iii) the same summary statistics have to be calculated from the observed data, $S(y_0)$, and (iv) a tolerance rate must be chosen (tol). See cvTabc for a cross-validation tool that may help in choosing the tolerance rate.

When method is "rejection", the simple rejection algorithm is used. Parameter values are accepted if the Euclidean distance between $S(y)$ and $S(y_0)$ is sufficiently small. The percentage of accepted simulations is determined by tol. When method is "loclinear", a local linear regression method corrects for the imperfect match between $S(y)$ and $S(y_0)$. The accepted parameter values are weighted by a smooth function (kernel) of the distance between $S(y)$ and $S(y_0)$, and corrected according to a linear transform: $\theta^* = \theta - b(S(y) - S(y_0))$. $\theta^*$’s represent samples form the posterior distribution. This method calls the function lsfit from the stats library. When using the "loclinear" method, a warning about the collinearity of the design matrix of the regression might be issued. In that situation, we recommend to rather use the related "ridge" method that performs local-linear ridge regression and deals with the collinearity issue. The non-linear regression correction method ("neuralnet") uses a non-linear regression to minimize the departure from non-linearity using the function nnet. The posterior samples of parameters based on the rejection algorithm are returned as well, even when one of the regression algorithms is used.

Several additional arguments can be specified when method is "neuralnet". The method is based on the function nnet from the library nnet, which fits single-hidden-layer neural networks. numnet defines the number of neural networks, thus the function nnet is called numnet number of times. Predictions from different neural networks can be rather different, so the median of the predictions from all neural networks is used to provide a global prediction. The choice of the number of neural networks is a trade-off between speed and accuracy. The default is set to 10 networks. The number of units in the hidden layer can be specified via sizenet. Selecting the number of hidden units is similar to selecting the independent variables in a linear or non-linear regression. Thus, it corresponds to the complexity of the network. There is several rule of thumb to choose the number
of hidden units, but they are often unreliable. Generally speaking, the optimal choice of \texttt{sizenet} depends on the dimensionality, thus the number of statistics in \texttt{sumstat}. It can be zero when there are no skip-layer units. See also \texttt{nnet} for more details. The method "neuralnet" is recommended when dealing with a large number of summary statistics.

If \texttt{method} is "loclinear", "neuralnet" or "ridge", a correction for heteroscedasticity is applied by default (\texttt{hcorr = TRUE}).

Parameters maybe transformed priori to estimation. The type of transformation is defined by \texttt{transf}. The length of \texttt{transf} is normally the same as the number of parameters. If only one value is given, that same transformation is applied to all parameters and the user is warned. When a parameter transformation used, the parameters are back-transformed to their original scale after the regression estimation. No transformations can be applied when \texttt{method} is "rejection".

Using names for the parameters and summary statistics is strongly recommended. Names can be supplied as \texttt{names} or \texttt{colnames} to \texttt{param} and \texttt{sumstat} (and \texttt{target}). If no names are supplied, \texttt{P1}, \texttt{P2}, … is assigned to parameters and \texttt{S1}, \texttt{S2}, … to summary statistics and the user is warned.

**Value**

The returned value is an object of class "abc", containing the following components:

- \texttt{adj.values} The regression adjusted values, when \texttt{method} is "loclinear", "neuralnet" or "ridge".
- \texttt{unadj.values} The unadjusted values that correspond to "rejection" method.
- \texttt{ss} The summary statistics for the accepted simulations.
- \texttt{weights} The regression weights, when \texttt{method} is "loclinear", "neuralnet" or "ridge".
- \texttt{residuals} The residuals from the regression when \texttt{method} is "loclinear", "neuralnet" or "ridge". These are the "raw" residuals from \texttt{lsfit} or \texttt{nnet}, respectively, thus they are not on the original scale of the parameter(s).
- \texttt{dist} The Euclidean distances for the accepted simulations.
- \texttt{call} The original call.
- \texttt{na.action} A logical vector indicating the elements or rows that were excluded, including both \texttt{NA}/\texttt{NaN}'s and elements/rows selected by \texttt{subset}.
- \texttt{region} A logical expression indicting the elements or rows that were accepted.
- \texttt{transf} The parameter transformations that have been used.
- \texttt{logit.bounds} The bounds, if transformation was "logit".
- \texttt{kernel} The kernel used.
- \texttt{method} Character string indicating the method, i.e. "rejection", "loclinear", or "neuralnet".
- \texttt{lambda} A numeric vector of length \texttt{numnet}. The actual values of the decay parameters used in each of the neural networks, when \texttt{method} is "neuralnet". These values are selected randomly from the supplied vector of values.
- \texttt{numparam} Number of parameters used.
- \texttt{numstat} Number of summary statistics used.
The sum of the AIC of the `numparam` regression. Returned only if `method` is "loclinear". It is used for selecting informative summary statistics.

*bic*

The same but with the BIC.

*names*

A list with two elements: `parameter.names` and `statistics.names`. Both contain a vector of character strings with the parameter and statistics names, respectively.

**Author(s)**

Katalin Csillery, Olivier Francois and Michael Blum with some initial code from Mark Beaumont ([http://www.rubic.rdg.ac.uk/~mab](http://www.rubic.rdg.ac.uk/~mab)).

**References**


**See Also**

`summary.abc`, `hist.abc`, `plot.abc`, `lsfit`, `nnet`, `cv.abc`

**Examples**

data(musigma2)
?musigma2

```r
## The rejection algorithm
##
## rej <- abc(target=stat.obs, param=par.sim, sumstat=stat.sim, tol=.1, method = "rejection")

## ABC with local linear regression correction without/with correction
## for heteroscedasticity
##
## lin <- abc(target=stat.obs, param=par.sim, sumstat=stat.sim, tol=.1, hcorr = FALSE, method = "loclinear", transf=c("none","log"))
## linhc <- abc(target=stat.obs, param=par.sim, sumstat=stat.sim, tol=.1, method = "loclinear", transf=c("none","log"))

## posterior summaries
##
## linsum <- summary(linhc, intvl = .9)
```
linsum
## compare with the rejection sampling
summary(linhc, unadj = TRUE, intvl = .9)

## posterior histograms
##
hist(linhc, breaks=30, caption=c(expression(mu),
expression(sigma^2)))

## or send histograms to a pdf file
hist(linhc, file="linhc", breaks=30, caption=c(expression(mu),
expression(sigma^2)))

## diagnostic plots: compare the 2 'abc' objects: "loclinear",
## "loclinear" with correction for heteroscedasticity
##
plot(lin, param=par.sim)
plot(linhc, param=par.sim)

## example illustrates how to add "true" parameter values to a plot
##
postmod <- c(post.mu[match(max(post.mu[,2]), post.mu[,2]),1],
post.sigma2[match(max(post.sigma2[,2]), post.sigma2[,2]),1])

plot(linhc, param=par.sim, true=postmod)

## artificial example to show how to use the logit tranformations
##
myd <- data.frame(par1=runif(1000,-1,1),par2=rnorm(1000),par3=runif(1000,0,2))
mys <- myp+rnorm(1000,sd=.1)
myt <- c(0,0,1.5)
lin2 <- abc(target=myt, param=myd, sumstat=mys, tol=.1, method =
"loclinear", transf=c("logit","none","logit"),logit.bounds = rbind(c(-1,
1), c(NA, NA), c(0, 2)))
summary(lin2)

---

**cv4abc**

Cross validation for Approximate Bayesian Computation (ABC)

**Description**

This function performs a leave-one-out cross validation for ABC via subsequent calls to the function `abc`. A potential use of this function is to evaluate the effect of the choice of the tolerance rate on the quality of the estimation with ABC.

**Usage**

```
cv4abc(param, sumstat, abc.out = NULL, nval, tols, statistic = "median",
prior.range = NULL, method, hcorr = TRUE, transf = "none", logit.bounds =
c(0,0), subset = NULL, kernel = "epanechnikov", numnet = 10, sizenet =
S, lambda = c(0.0001,0.001,0.01), trace = FALSE, maxit = 500, ...)
```
Arguments

param a vector, matrix or data frame of the simulated parameter values.

sumstat a vector, matrix or data frame of the simulated summary statistics.

abc.out an object of class "abc", optional. If supplied, all arguments passed to abc are extracted from this object, except for sumstat, param, and tol, which always have to be supplied as arguments.

nval size of the cross-validation sample.

tols a single tolerance rate or a vector of tolerance rates.

statistic a character string specifying the statistic to calculate a point estimate from the posterior distribution of the parameter(s). Possible values are "median" (default), "mean", or "mode".

prior.range a range to truncate the prior range.

method a character string indicating the type of ABC algorithm to be applied. Possible values are "rejection", "loclinear", and "neuralnet". See also abc.

hcorr logical, if TRUE (default) the conditional heteroscedastic model is applied.

transf a vector of character strings indicating the kind of transformation to be applied to the parameter values. The possible values are "log", "logit", and "none" (default), when no is transformation applied. See also abc.

logit.bounds a vector of bounds if transf is "logit". These bounds are applied to all parameters that are to be logit transformed.

subset a logical expression indicating elements or rows to keep. Missing values in param and/or sumstat are taken as FALSE.

kernel a character string specifying the kernel to be used when method is "loclinear" or "neuralnet". Defaults to "epanechnikov". See density for details.

numnet the number of neural networks when method is "neuralnet". Defaults to 10. It indicates the number of times the function nnet is called.

sizenet the number of units in the hidden layer. Defaults to 5. Can be zero if there are no skip-layer units. See nnet for more details.

lambda a numeric vector or a single value indicating the weight decay when method is "neuralnet". See nnet for more details. By default, 0.0001, 0.001, or 0.01 is randomly chosen for each of the networks.

trace logical, TRUE switches on tracing the optimization of nnet. Applies only when method is "neuralnet".

maxit numeric, the maximum number of iterations. Defaults to 500. Applies only when method is "neuralnet". See also nnet.

... other arguments passed to nnet.

Details

A simulation is selected repeatedly to be a validation simulation, while the other simulations are used as training simulations. Each time the function abc is called to estimate the parameter(s). A total of nval1 validation simulations are selected.
The arguments of the function `abc` can be supplied in two ways. First, simply give them as arguments when calling this function, in which case `abc.out` can be `NULL`. Second, via an existing object of class "abc", here `abc.out`. WARNING: when `abc.out` is supplied, the same `sumstat` and `param` objects have to be used as in the original call to `abc`. Column names of `sumstat` and `param` are checked for match.

See `summary.cv4abc` for calculating the prediction error from an object of class "cv4abc".

Value

An object of class "cv4abc", which is a list with the following elements

- `call`: The original calls to `abc` for each tolerance rates.
- `cvsamples`: Numeric vector of length `nval`, indicating which rows of the `param` and `sumstat` matrices were used as validation values.
- `tols`: The tolerance rates.
- `true`: The parameter values that served as validation values.
- `estim`: The estimated parameter values.
- `names`: A list with two elements: `parameter.names` and `statistics.names`. Both contain a vector of character strings with the parameter and statistics names, respectively.
- `seed`: The value of `.Random.seed` when `cv4abc` is called.

See Also

- `abc`, `plot.cv4abc`, `summary.cv4abc`

Examples

data(musigma2)
```r
## this data set contains five R objects, see ?musigma2 for
do# details

## cv4abc() calls abc(). Here we show two ways for the supplying
## arguments of abc(). 1st way: passing arguments directly. In this
## example only 'param', 'sumstat', 'tol', and 'method', while default
## values are used for the other arguments.
## Number of eval. should be much more greater in realistic settings
cv.rej <- cv4abc(param=par.sim, sumstat=stat.sim, nval=5,
tols=c(.1,.2,.3), method="rejection")

## 2nd way: first creating an object of class 'abc', and then using it
## to pass its arguments to abc().
## lin <- abc(target=stat.obs, param=par.sim, sumstat=stat.sim, tol=.2,
## method="loclinear", transf=c("none","log"))
cv.lin <- cv4abc(param=par.sim, sumstat=stat.sim, abc.out=lin, nval=5,
tols=c(.1,.2,.3))
```

## using the plot method. Different tolerance levels are plotted with
## cv4postpr

Leave-one-out cross validation for model selection ABC

### Description

This function performs a leave-one-out cross validation for model selection with ABC via subsequent calls to the function `postpr`.

### Usage

```r
cv4postpr(index, sumstat, postpr.out = NULL, nval, tols, method, 
subset = NULL, kernel = "epanechnikov", numnet = 10, sizenet = 5, lambda 
= c(0.0001, 0.001, 0.01), trace = FALSE, maxit = 500, ...)
```

### Arguments

- **index**: a vector of model indices. It can be character or numeric and will be coerced to factor. It must have the same length as the number of rows in `sumstat` to indicate which row of `sumstat` belong to which model.
- **sumstat**: a vector, matrix or data frame of the simulated summary statistics.
- **postpr.out**: an object of class "postpr", optional. If supplied, all arguments passed to `postpr` are extracted from this object, except for `sumstat`, `index`, and `tols`, which always have to be supplied as arguments.
- **nval**: the size of the cross-validation sample for each model.
- **tols**: a single tolerance rate or a vector of tolerance rates.
- **method**: a character string indicating the type of simulation required. Possible values are "rejection", "mnlogistic", "neuralnet". See `postpr` for details.
subset  a logical expression indicating elements or rows to keep. Missing values in
index and/or sumstat are taken as FALSE.
kernel  a character string specifying the kernel to be used when method is "loclinear"
or "neuralnet". Defaults to "epanechnikov". See density for details.
numnet  the number of neural networks when method is "neuralnet". Defaults to 10. It
indicates the number of times the function nnet is called.
sizenet  the number of units in the hidden layer. Defaults to 5. Can be zero if there are
no skip-layer units. See nnet for more details.
lambda  a numeric vector or a single value indicating the weight decay when method is
"neuralnet". See nnet for more details. By default, 0.0001, 0.001, or 0.01 is
randomly chosen for each of the networks.
trace  logical, TRUE switches on tracing the optimization of nnet. Applies only when
method is "neuralnet".
maxit  numeric, the maximum number of iterations. Defaults to 500. Applies only
when method is "neuralnet". See also nnet.

Details

For each model, a simulation is selected repeatedly to be a validation simulation, while the other
simulations are used as training simulations. Each time the function postpr is called to estimate
the parameter(s).

Ideally, we want nval to be equal to the number of simulations for each model, however, this might
take too much time. Users are warned not to choose a too large number of simulations (especially
when the neural networks are used). Beware that the actual number of cross-validation estimation
steps that need to be performed is nval*the number of models.

The arguments for the function postpr can be supplied in two ways. First, simply give them as
arguments when calling this function, in which case postpr.out can be NULL. Second, via an
existing object of class "postpr", here postpr.out. WARNING: when postpr.out is supplied,
the same sumstat and param objects have to be used as in the original call to postpr. Column
names of sumstat and param are checked for match.

See summary.cv4postpr for calculating the prediction error from an object of class "cv4postpr"
and plot.cv4postpr for visualizing the misclassification of the models using barplots.

Value

An object of class "cv4postpr", which is a list with the following elements

call  The original calls to postpr for each tolerance rates.
cvsamples Numeric vector of length nval*the number of models, indicating which rows of
sumstat were used as validation values.
tols  The tolerance rates.
true  The true models.
estim  The estimated model probabilities.
method  The method used.
expected.deviance

names A list of two elements: model contains the model names, and statistics.names the names of the summary statistics.

seed The value of .Random.seed when cv4postpr is called.

See Also

cv4postpr, summary.cv4postpr, plot.cv4postpr

Examples

data(human)
#Reduce the sample size of the simulations to reduce the running time.
#Do not do that with your own data!
ss<-c(1:1000,5000:51000,100001:101000)
cv.modsel <- cv4postpr(models[ss], stat.3pops.sim[ss,], nval=5, tols=c(.05,.1), method="rejection")
summary(cv.modsel)
plot(cv.modsel, names.arg=c("Bottleneck", "Constant", "Exponential"))

expected.deviance  Expected deviance

Description

Model selection criterion based on posterior predictive distributions and approximations of the expected deviance.

Usage

expected.deviance(target, postsumstat, kernel = "gaussian", subset=NULL, print=TRUE)

Arguments

target a vector of the observed summary statistics.

postsumstat a vector, matrix or data frame of summary statistics simulated a posteriori.

kernel a character string specifying the kernel to be used when. Defaults to "gaussian". See density for details.

subset a logical expression indicating elements or rows to keep. Missing values in postsumstat are taken as FALSE.

print prints out what percent of the distances have been zero.
Details
This function implements an approximation for the expected deviance based on simulation performed a posteriori. Thus, after the posterior distribution of parameters or the posterior model probabilities have been determined, users need to re-simulate data using the posterior. The Monte-Carlo estimate of the expected deviance is computed from the simulated data as follows: 

\[ D = -\frac{2}{n} \sum_{j=1}^{n} \log(K_\epsilon(\| s^j - s_0 \|)) \]

where \( n \) is number of simulations, \( K \) is the statistical kernel, \( \epsilon \) is the error, i.e. difference between the observed and simulated summary statistics below which simulations were accepted in the original call to `postpr`, the \( s^j \)'s are the summary statistics obtained from the posterior predictive simulations, and \( s_0 \) are the observed values of the summary statistics. The expected deviance averaged over the posterior distribution to compute a deviance information criterion (DIC).

Value
A list with the following components:

- `expected.deviance`  
  The approximate expected deviance.
- `dist`  
  The Euclidean distances for summary statistics simulated a posteriori.

References

Examples
```r
## Function definitions
skewness <- function(x) {
  sk <- mean((x-mean(x))^3)/(sd(x)^3)
  return(sk)
}
kurtosis <- function(x) {
  k <- mean((x-mean(x))^4)/(sd(x)^4) - 3
  return(k)
}

## Observed summary statistics
obs.sumstat <- c(2.084821, 3.110915, -0.7831861, 0.1440266)

## Model 1 (Gaussian)
## ##############################
## Simulate data
theta <- rnorm(10000, 2, 10)
zeta <- 1/exp(10000, 1)
param <- cbind(theta, zeta)
y <- matrix(rnorm(200000, rep(theta, each = 20), sd = rep(sqrt(zeta), each = 20)), nrow = 20, ncol = 10000)

## Calculate summary statistics
s <- cbind(apply(y, 2, mean), apply(y, 2, sd), apply(y, 2, skewness),
```

expected.deviance
apply(y, 2, kurtosis))

## ABC inference
gaus <- abc(target=obs.sumstat, param = param, sumstat=s, tol=.1, hcorr = FALSE, method = "loclinear")
param.post <- gaus$adj.values

## Posterior predictive simulations
postpred.gaus <- matrix(rnorm(20000, rep(param.post[,1], each = 20), sd = rep(sqrt(param.post[,2]), each = 20)), nrow = 20, ncol = 1000)
statpost.gaus <- cbind(apply(postpred.gaus, 2, mean),apply(postpred.gaus, 2, sd),apply(postpred.gaus, 2, skewness),apply(postpred.gaus, 2, kurtosis))

# Computation of the expected deviance
expected.deviance(obs.sumstat, statpost.gaus)$expected.deviance

## Modele 2 (Laplace)
## ##################
## Simulate data
zeta <- rexp(10000)
param <- cbind(theta, zeta)
y <- matrix(theta + sample(c(-1,1),200000, replace = TRUE)*rexp(200000, rep(zeta, each = 20)), nrow = 20, ncol = 10000)

## Calculate summary statistics
s <- cbind(apply(y, 2, mean), apply(y, 2, sd), apply(y, 2, skewness), apply(y, 2, kurtosis))

## ABC inference
lapl <- abc(target=obs.sumstat, param = param, sumstat=s, tol=.1, hcorr = FALSE, method = "loclinear")
param.post <- lapl$adj.values

## Posterior predictive simulations
postpred.lapl <- matrix(param.post[,1] + sample(c(-1,1),20000, replace = TRUE)*rexp(20000, rep(param.post[,2], each = 20)), nrow = 20, ncol = 1000)
statpost.lapl <- cbind(apply(postpred.lapl, 2, mean),apply(postpred.lapl, 2, sd),apply(postpred.lapl, 2, skewness),apply(postpred.lapl, 2, kurtosis))

## Computation of the expected deviance
expected.deviance(obs.sumstat, statpost.lapl)$expected.deviance
expected.deviance(obs.sumstat, statpost.lapl, kernel = "epanechnikov")$expected.deviance
gfit  

Goodness of fit

Description

Perform a test for goodness-of-fit.

Usage

gfit(target, sumstat, nb.replicate, tol=.01, statistic=mean, subset=NULL, trace=FALSE)

Arguments

target  
a data frame or vector of the observed summary statistic.

sumstat  
a vector, matrix or data frame of the simulated summary statistics.

nb.replicate  
number of replicates used to estimate the null distribution of the goodness-of-fit statistic.

tol  
a tolerance rate. Defaults to 0.01

statistic  
define the goodness-of-fit statistic. Typical values are median (default), mean, or max. When using median for instance, the g.o.f. statistic is the median of the distance between observed and accepted summary statistics.

subset  
optional. A logical expression indicating elements or rows to keep. Missing values in sumstat are taken as FALSE.

trace  
a boolean indicating if a trace should be displayed when calling the function. Default to FALSE.

Details

The null distribution is estimated using already performed simulations contained in sumstat as pseudo-observed datasets. For each pseudo-observed dataset, the rejection algorithm is performed to obtain a value of the goodness-of-fit statistic. A better estimate of the P-value is obtained for larger nb.replicate but the running time of the function is increased.

Value

An object of class "gfit", which is a list with the following elements

dist.obs  
the value of the goodness-of-fit statistic for the data.

dist.sim  
a vector of size nb.replicate. It is a sample of the null distribution of the test statistic.

Author(s)

Louisiane Lemaire and Michael Blum.
### gfitpca

**Goodness of fit with principal component analysis**

**Description**

Perform a priori goodness of fit using the two first components obtained with PCA.

**Usage**

```r
gfitpca(target, sumstat, index, cprob=0.1, xlim=NULL, ylim=NULL, ...)```

**Arguments**

- `target`: a data frame or vector of the observed summary statistic.
- `sumstat`: a matrix or data frame of the simulated summary statistics.
- `index`: a vector of models names. It must be character and have the same length as the number of row in `sumstat` to indicate which row belong to which model.
- `cprob`: `cprob` is the proportion of points outside the displayed envelope. Default to 0.1 which corresponds to a 90% envelope.
- `xlim, ylim`: optional, numeric vectors of length 2, giving the x and y coordinates ranges.
- `...`: other parameters passed to `plot`.

**Examples**

```r
## human demographic history
data(human)

## Perform a test of goodness-of-fit.
## The data are the European data and we test the fit of the bottleneck model (good fit) and of the constant-size population model (poor fit)
## Use larger values of `nb.replicate` (e.g. 1000)
## for real applications
res.gfit.bott=gfit(target=stat.voight["italian"], sumstat=stat.3pops.sim[models="bott"], statistic=mean, nb.replicate=10)
res.gfit.const=gfit(target=stat.voight["italian"], sumstat=stat.3pops.sim[models="const"], statistic=mean, nb.replicate=10)

## Plot the distribution of the null statistic and indicate where is the observed value.
plot(res.gfit.bott, main="Histogram under H0")
## Call the function `summary`
## It computes the P-value, call `summary` on the vector `dist.sim` and returns the value of the observed statistic
summary(res.gfit.bott)
```
Details

The function performs PCA using the a priori simulated summary statistics. It displays envelopes containing 1-hprob percent of the simulations. The projection of the observed summary statistics is displayed in order to check if they are contained or not in the envelopes. If the projection lies outside the envelope of a given model, it is an indication of poor fit.

Author(s)

Louisiane Lemaire and Michael Blum

See Also

abc.plot.gfit, summary.gfit, gfit

Examples

```r
## human demographic history
data(human)
## five R objects are loaded. See ?human and vignette("abc") for details.

## Perform a priori goodness of fit for 3 different demographic models
## The envelopes containing 90% of the simulations are displayed.
## For the European data, a reasonable fit is only provided by the
## bottleneck model.
## The number of simulations is reduced to improve speed (do not do that
## with your own data)
index<-c(1:5000,5001:55000,100001:105000)
gfitpca(target=stat.voight["italian",], sumstat=stat.3pops.sim[index,],
index=models[index], cprob=0.1)
```

---

hist.abc  Posterior histograms

Description

Histograms of posterior samples from objects of class "abc".

Usage

```r
## S3 method for class 'abc'
hist(x, unadj = FALSE, true = NULL, file = NULL,
postscript = FALSE, onefile = TRUE, ask =
!is.null(deviceIsInteractive()), col.hist = "grey", col.true = "red",
caption = NULL, ...)
```
Arguments

- **x**
  - an object of class "abc".

- **unadj**
  - logical, if TRUE the unadjusted values are plotted even if method is "loclinear" or "neuralnet".

- **true**
  - the true parameter value(s), if known. Vertical bar(s) are drawn at the true value(s). If more than one parameters were estimated, a vector of the true values have to be supplied.

- **file**
  - a character string giving the name of the file. See **postscript** for details on accepted file names. If NULL (the default) histograms are printed to the null device (e.g. X11). If not NULL histograms are printed on a pdf device. See also **postscript**.

- **postscript**
  - logical; if FALSE (default) histograms are printed on a pdf device, if TRUE on a postscript device.

- **onefile**
  - logical, if TRUE (the default) allow multiple figures in one file. If FALSE, generate a file name containing the page number for each page. See **postscript** for further details.

- **ask**
  - logical; if TRUE (the default), the user is asked before each plot, see **par(ask=.)**.

- **col.hist**
  - the colour of the histograms.

- **col.true**
  - the colour of the vertical bar at the true value.

- **caption**
  - captions to appear above the histogram(s); character vector of valid graphics annotations, see **as.graphicsAnnot** for details. When NULL (default), parnames are used, which are extracted from x (see **abc**). Can be set to NA to suppress all captions.

- **...**
  - other parameters passed to hist.

Value

A list of length equal to the number of parameters, the elements of which are objects of class "histogram". See **hist** for details.

See Also

**abc, plot.abc**

Examples

```r
### see ?abc for examples
```
human

A set of R objects containing observed data from three human populations, and simulated data under three different demographic models. The data set is used to illustrate model selection and parameter inference in an ABC framework (see the package’s vignette for more details).

Description
data(human) loads in four R objects: stat.voight is a data frame with 3 rows and 3 columns and contains the observed summary statistics for three human populations, stat.3pops.sim is also a data frame with 150,000 rows and 3 columns and contains the simulated summary statistics, models is a vector of character strings of length 150,000 and contains the model indices, par.italy.sim is a data frame with 50,000 rows and 4 columns and contains the parameter values that were used to simulate data under a population bottleneck model. The corresponding summary statistics can be subsetted from the stat.3pops.sim object as subset(stat.3pops.sim, subset=models=="bott").

Usage
data(human)

Format

The stat.voight data frame contains the following columns:

- **pi** The mean nucleotide diversity over 50 loci in 3 human populations, Hausa, Italian, and Chinese.
- **TajD.m** The mean of Tajima’s D statistic over 50 loci in 3 human populations, Hausa, Italian, and Chinese.
- **TajD.v** The variance of Tajima’s D statistic over 50 loci in 3 human populations, Hausa, Italian, and Chinese.

Each row represents a simulation. Under each model 50,000 simulations were performed. Row names indicate the type of demographic model.

The stat.3pops.sim data frame contains the following columns:

- **pi** The mean of nucleotide diversity over 50 simulated loci under 3 demographic scenarios: constant size population, population bottleneck, and population expansion.
- **TajD.m** The mean of Tajima’s D statistic over 50 simulated loci under 3 demographic scenarios: constant size population, population bottleneck, and population expansion.
- **TajD.v** The variance of Tajima’s D statistic over 50 simulated loci under 3 demographic scenarios: constant size population, population bottleneck, and population expansion.

Each row represents a simulation. Under each model 50,000 simulations were performed. Row names indicate the type of demographic model.

The par.italy.sim data frame contains the following columns:

- **Ne** The effective population size.
**Details**

Data is provided to estimate the posterior probabilities of classical demographic scenarios in three human populations: Hausa, Italian, and Chinese. These three populations represent the three continents: Africa, Europe, Asia, respectively. `par.italy.sim` may then be used to estimate the ancestral population size of the European population assuming a bottleneck model.

It is generally believed that African human populations are expanding, while human populations from outside of Africa have gone through a population bottleneck. Tajima’s D statistic has been classically used to detect changes in historical population size. A negative Tajima’s D signifies an excess of low frequency polymorphisms, indicating population size expansion. While a positive Tajima’s D indicates low levels of both low and high frequency polymorphisms, thus a sign of a population bottleneck. In constant size populations, Tajima’s D is expected to be zero.

With the help of the human data one can reach these expected conclusions for the three human population samples, in accordance with the conclusions of Voight et al. (2005) (where the observed statistics was taken from), but using ABC.

**Source**

The observed statistics were taken from Voight et al. 2005 (Table 1.). Also, the same input parameters were used as in Voight et al. 2005 to simulate data under the three demographic models. Simulations were performed using the software ms and the summary statistics were calculated using `sample_stats` (Hudson 1983).

**References**


**See Also**

`ppc`
musigma2  

A set of objects used to estimate the population mean and variance in a Gaussian model with ABC.

Description

musigma2 loads in five R objects: par.sim is a data frame and contains the parameter values of the simulated data sets, stat is a data frame and contains the simulated summary statistics, stat.obs is a data frame and contains the observed summary statistics, post.mu and post.sigma2 are data frames and contain the true posterior distributions for the two parameters of interest, \( \mu \) and \( \sigma^2 \), respectively.

Usage

data(musigma2)

Format

The par.sim data frame contains the following columns:

- mu  The population mean.
- sigma2  The population variance.

The stat.sim and stat.obs data frames contain the following columns:

- mean  The sample mean.
- var  The logarithm of the sample variance.

The post.mu and post.sigma2 data frames contain the following columns:

- x  the coordinates of the points where the density is estimated.
- y  the posterior density values.

Details

The prior of \( \sigma^2 \) is an inverse \( \chi^2 \) distribution with one degree of freedom. The prior of \( \mu \) is a normal distribution with variance of \( \sigma^2 \). For this simple example, the closed form of the posterior distribution is available.

Source

The observed statistics are the mean and variance of the sepal of Iris setosa, estimated from part of the iris data.

The data were collected by Anderson, Edgar.

References

plot.abc

Diagnostic plots for ABC

Description

A plotting utility for quick visualization of the quality of an ABC analysis from an object of class "abc" generated with methods "loclinear" or "neuralnet" (see abc for details). Four plots are currently available: a density plot of the prior distribution, a density plot of the posterior distribution, a scatter plot of the Euclidean distances as a function of the parameter values, and a Normal Q-Q plot of the residuals from the regression.

Usage

## S3 method for class 'abc'
plot(x, param, subsample = 1000, true = NULL, file = NULL, postscript = FALSE, onefile = TRUE, ask = !is.null(deviceIsInteractive()), ...)

Arguments

x an object of class "abc" generated with methods "loclinear" or "neuralnet" (see abc for details).

param a vector or matrix of parameter values from the simulations that were used in the original call to abc.

subsample the number of rows (simulations) to be plotted. Rows are randomly selected from param.

true a vector of true parameter values, if known. Vertical lines are drawn at these values.

file a character string giving the name of the file. See postscript for details on accepted file names. If NULL (the default) plots are printed to the null device (e.g. X11). If not NULL plots are printed on a pdf device. See also postscript.

postscript logical; if FALSE (default) plots are printed on a pdf device, if TRUE on a postscript device.

onefile logical, if TRUE (the default) allow multiple figures in one file. If FALSE, generate a file name containing the page number for each page. See postscript for further details.

ask logical; if TRUE (the default), the user is asked before each plot, see par(ask=.).

... other parameters passed to plot.
Details

In order to use this function, one of the regression correction methods had to be used in the original call to \texttt{abc}, i.e. "loclinear" or "neuralnet" (see \texttt{abc} for details). Four plots are printed for each parameter. (i) A density plot of the prior distribution. (ii) A density plot of the posterior distribution using the regression correction (red thick lines) and, for reference, using the simple rejection method (black fine lines). The prior distribution (in the posterior distributions’ range) is also displayed (dashed lines). (iii) A scatter plot of the log Euclidean distances as a function of the true parameter values. Points corresponding to the accepted simulations are displayed in red. (iv) A Normal Q-Q plot of the residuals from the regression, thus from \texttt{lsfit} when method was "loclinear", and from \texttt{nnet} when method was "neuralnet" in the original \texttt{abc}.

For plots (i) and (iii) not the whole data but a subsample is used, the size of which can be is given by \texttt{subsample}. This is to avoid plots that may take too much time to print.

If a parameter transformation was applied in the original call to \texttt{abc}, the same transformations are applied to the parameters for plotting (on plots (i)-(iii)).

See Also

\texttt{abc, hist.abc, summary.abc}

Examples

\begin{verbatim}
## see ?abc for examples
\end{verbatim}

\begin{verbatim}
plot.cv4abc
\end{verbatim}

\textit{Cross-validation plots for ABC}

Description

Plotting method for cross-validation ABC objects. Helps to visually evaluate the quality of the estimation and/or the effect of the tolerance level.

Usage

\begin{verbatim}
## S3 method for class 'cv4abc'
plot(x, exclude = NULL, log = NULL, file = NULL, postscript = FALSE, onefile = TRUE, ask =
!is.null(deviceIsInteractive()), caption = NULL, ...)  
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{x} an object of class "cv4abc".
\item \texttt{exclude} a vector of row indices indicating which rows should be excluded from plotting. Useful when the prior distribution has a long tail.
\item \texttt{log} character vector of the same length as the number of parameters in the "cv4abc" object. Allows plotting on a log scale. Possible values are "" (normal scale) and "xy" (log scale for both the x and y axis). "x" and "y" are possible as well, but not of any interest here. Negative values are set to NA and there is a warning.
\end{itemize}
plot.cv4postpr

file
postscript
onename
ask
caption
...

Details

Different tolerance levels are plotted with `heat.colors`. Thus, the colors correspond to different levels of the tolerance rate in an increasing order from red to yellow.

See Also

cv4abc, abc

Examples

## see ?cv4abc for examples

<table>
<thead>
<tr>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Displays a barplot of either the proportion of simulations classified to any of the models or the mean misclassification probabilities of models for all tolerance levels in the &quot;cv4postpr&quot; object.</td>
</tr>
</tbody>
</table>

Usage

## S3 method for class 'cv4postpr'
plot(x, probs = FALSE, file = NULL, postscript = FALSE, onename = TRUE, ask = !is.null(deviceIsInteractive()), caption = NULL, ...)
Arguments

x  an object of class "cv4postpr".
probs logical, if TRUE the mean posterior model probabilities are plotted. If FALSE the frequencies of the simulations classified to the different models (default).
file a character string giving the name of the file. See postscript for details on accepted file names. If NULL (the default) plots are printed to the null device (e.g. X11). If not NULL plots are printed on a pdf device. See also postscript.
postcode logical; if FALSE (default) plots are printed on a pdf device, if TRUE on a postscript device.
onfile logical, if TRUE (the default) allow multiple figures in one file. If FALSE, generate a file name containing the page number for each page. See postscript for further details.
ask logical; if TRUE (the default), the user is asked before each plot, see par(ask=.).
caption captions to appear above the plot(s); character vector of valid graphics annotations, see as.graphicsAnnot. Can be set to "" or NA to suppress all captions.
... other parameters passed to barplot.

Details

Model are distinguished with different intensities of the gray colour. The first model in alphabetic order has the darkest colour. If the classification of models is perfect (so that the frequency (or probability) of each model is zero for all but the correct model) each bar has a single colour of its corresponding model.

See Also

cv4postpr, summary.cv4postpr

Examples

## see ?cv4postpr for examples

plot.gfit Goodness-of-fit plot for ABC

Description

Plotting method for goodness-of-fit ABC objects.

Usage

## S3 method for class 'gfit'
plot(x, breaks="Freedman-Diaconis", main, ...)
Arguments

- **x**: an object of class "gfit".
- **breaks**: number of cells for the histogram. Defaults to "Freedman-Diaconis".
- **main**: title for the plot
- **...**: other parameters passed to `plot`.

Details

Plot the distribution of the statistic under the null hypothesis and indicate where is the observed value.

See Also

gfit, abc, summary.gfit, hist

Examples

```r
## see ?gfit for examples
```

---

**postpr**

*Estimating posterior model probabilities*

Description

Model selection with Approximate Bayesian Computation (ABC).

Usage

```r
postpr(target, index, sumstat, tol, subset = NULL, method, corr=TRUE, 
kernel="epanechnikov", numnet = 10, sizenet = 5, lambda = 
c(0.0001,0.001,0.01), trace = TRUE, maxit = 500, ...)
```

Arguments

- **target**: a vector of the observed summary statistics.
- **index**: a vector of model indices. It can be character or numeric and will be coerced to factor. It must have the same length as `sumstat` to indicate which row of `sumstat` belong to which model.
- **sumstat**: a vector, matrix or data frame of the simulated summary statistics.
- **tol**: numeric, the required proportion of points nearest the target values (tolerance), or a vector of the desired tolerance values. If a vector is given
- **subset**: a logical expression indicating elements or rows to keep. Missing values in `index` and/or `sumstat` are taken as FALSE.
- **method**: a character string indicating the type of simulation required. Possible values are "rejection", "mnlogistic", "neuralnet". See Details.
correction, if TRUE (default) posterior model probabilities are corrected for the number of simulations performed for each model. If equal number of simulations are available for all models, corr has no effect.

kernel a character string specifying the kernel to be used when method is "mnlogistic" or "neuralnet". Defaults to "epanechnikov". See density for details.

numnet the number of neural networks when method is "neuralnet". It corresponds to the number of times the function nnet is called.

correction has no effect.

numnet the number of neural networks when method is "neuralnet". It corresponds to the number of times the function nnet is called.

Details

The function computes the posterior model probabilities. Simulations have to be performed with at least two distinct models. When method is "rejection", the posterior probability of a given model is approximated by the proportion of accepted simulations given this model. This approximation holds when the different models are a priori equally likely, and the same number of simulations is performed for each model. When method is "mnlogistic" the posterior model probabilities are estimated using a multinomial logistic regression as implemented in the function multinom from the package nnet. When method is "neuralnet", neural networks are used to predict the probabilities of models based on the observed statistics using nnet. This method can be useful if many summary statistics are used.

Names for the summary statistics are strongly recommended. Names can be supplied as colnames to sumstat (and target). If no names are supplied S1, S2, ... to summary statistics will be assigned to parameters and the user will be warned.

Value

An object of class "postpr", containing the following components:

- pred a vector of model probabilities when method is "mnlogistic" or "neuralnet".
- values the vector of model indices in the accepted region using the rejection method.
- weights vector of regression weights when method is "mnlogistic" or "neuralnet".
- ss summary statistics in the accepted region.
- call the original call.
- na.action a logical vector indicating the elements or rows that were excluded, including both NA/NaN's and elements/rows selected by subset.
- method a character string indicating the method used, i.e. "rejection", "mnlogistic" or "neuralnet".
logical, if TRUE the posterior model probabilities are corrected for the number of simulations performed for each model.

- **nmodels**: the number of simulations performed for each model a priori.

- **models**: a character vector of model names (a priori).

- **numstat**: the number of summary statistics used.

- **names**: a list of two elements: model contains the model names, and statistics.names the names of the summary statistics.

**Author(s)**

Katalin Csillery, Olivier Francois and Michael Blum with some initial code from Mark Beaumont (http://www.rubic.rdg.ac.uk/~mab/).

**References**


**See Also**

`summary.postpr`

**Examples**

```r
## an artifical example
ss <- cbind(runif(1000), rt(1000, df=20))
postpr(target=c(3), index=c(rep("norm", 500), rep("t", 500)),
sumstat=ss[,1], tol=.1, method="rejection")

## human demographic history
data(human)
## five R objects are loaded. See ?human and vignette("abc") for details.

## illustrate the informativeness of two summary statistics: mean and
## variance of Tajima's D
par(mfcol = c(1,3))
boxplot(stat.3pops.sim[, "pi"]~models, main="Mean nucleotide diversity")
boxplot(stat.3pops.sim[, "TajD.m"]~models, main="Mean Tajima's D")
boxplot(stat.3pops.sim[, "TajD.v"]~models, main="Var in Tajima's D")

## model selection with ABC for the European population

modsel.it <- postpr(stat.voight["italian"], models, stat.3pops.sim, tol=.05, method="mnlogistic")
summary(modsel.it)

## In Europe, the most supported model
## is a population bottleneck
```
## Description

data(ppc) loads in the data frame post.bott, which contains the summary statistics calculated from data simulated a posteriori under the bottleneck model (see data(human) and the package’s vignette for more details).

## Usage

data(ppc)

## Format

The post.bott data frame contains the following columns:

- **pi** The mean nucleotide diversity over 50 loci.
- **TajD.m** The mean of Tajima’s D statistic over 50 loci.
- **TajD.v** The variance of Tajima’s D statistic over 50 loci.

Each row represents a simulation. 1000 simulations were performed under the bottleneck model.

## See Also

- **human**
Summary of posterior samples generated by ABC algorithms

Description

Calculates simple summaries of posterior samples: the minimum and maximum, the weighted mean, median, mode, and credible intervals.

Usage

```r
# S3 method for class 'abc'SUM
summary(object, unadj = FALSE, intvl = .95, print = TRUE,
digits = max(3, getOption("digits")-3), ...)
```

Arguments

- `object`: an object of class "abc".
- `unadj`: logical, if TRUE it forces to plot the unadjusted values when method is "loclinear" or "neuralnet".
- `intvl`: size of the symmetric credible interval.
- `print`: logical, if TRUE prints messages. Mainly for internal use.
- `digits`: the digits to be rounded to. Can be a vector of the same length as the number of parameters, when each parameter is rounded to its corresponding digits.
- `...`: other arguments passed to `density`.

Details

If method is "rejection" in the original call to `abc`, posterior means, medians, modes and percentiles defined by `intvl`, 95 by default (credible intervals) are calculated. If a regression correction was used (i.e. method is "loclinear" or "neuralnet" in the original call to `abc`) the weighted posterior means, medians, modes and percentiles are calculated.

To calculate the mode, parameters are passed on from `density.default`. Note that the posterior mode can be rather different depending on the parameters to estimate the density.

Value

The returned value is an object of class "table". The rows are,

<table>
<thead>
<tr>
<th>Min.</th>
<th>minimum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lower perc.</td>
<td>lower percentile</td>
</tr>
<tr>
<td>Median</td>
<td>or weighted median</td>
</tr>
<tr>
<td>Mean</td>
<td>or weighted mean</td>
</tr>
<tr>
<td>Mode</td>
<td>or weighted mode</td>
</tr>
<tr>
<td>Upper perc.</td>
<td>upper percentile</td>
</tr>
<tr>
<td>Max.</td>
<td>maximum</td>
</tr>
</tbody>
</table>
See Also

\texttt{abc, hist.abc, plot.abc}

Examples

\texttt{## see \texttt{?abc} for examples}

\begin{verbatim}
summary.cv4abc
\end{verbatim}

\textit{Calculates the cross-validation prediction error}

Description

This function calculates the prediction error from an object of class "cv4abc" for each parameter and tolerance level.

Usage

\texttt{## S3 method for class 'cv4abc'
summary(object, print = TRUE, digits = max(3,
getOption("digits")-3), ...)}

Arguments

\begin{verbatim}
object an object of class "abc".
print logical, if \texttt{TRUE} prints messages. Mainly for internal use.
digits the digits to be rounded to. Can be a vector of the same length as the number of
parameters, when each parameter is rounded to its corresponding digits.
... other arguments passed to \texttt{density}.
\end{verbatim}

Details

The prediction error is calculated as \( \sum_{nval} \frac{((\theta^\star - \theta)^2)}{\text{Var}(\theta)} \), where \( \theta \) is the true parameter value, \( \theta^\star \) is the predicted parameter value, and \( nval \) is the number of points where true and predicted values are compared.

Value

The returned value is an object of class "table", where the columns correspond to the parameters and the rows to the different tolerance levels.

See Also

\texttt{cv4abc, plot.cv4abc}

Examples

\texttt{## see \texttt{?cv4abc} for examples}
**summary.cv4postpr**

Confusion matrix and misclassification probabilities of models

**Description**

This function calculates the confusion matrix and the mean misclassification probabilities of models from an object of class "cv4postpr".

**Usage**

```r
## S3 method for class 'cv4postpr'
summary(object, probs = TRUE, print = TRUE, digits =
max(3, getOption("digits")-3), ...)
```

**Arguments**

- `object`: an object of class "cv4postpr".
- `probs`: logical, if TRUE (default), mean posterior model probabilities are returned.
- `print`: logical, if TRUE prints the mean models probabilities.
- `digits`: the digits to be rounded to.
- `...`: other arguments.

**Value**

If `probs=FALSE` a matrix with the frequencies of the simulations classified to the different models (the confusion matrix). If `probs=TRUE`, a list with two components:

- `conf.matrix`: The confusion matrix.
- `probs`: The mean model misclassification probabilities.

**See Also**

- `cv4postpr`, `plot.cv4postpr`

**Examples**

```r
## see ?cv4postpr for examples
```
summary.gfit  
Calculates the p-value of the goodness-of-fit test.

Description

This function calculates the p-value of the goodness-of-fit test from an object of class "gfit".

Usage

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

Arguments

- `object` - an object of class "gfit".
- `...` - other parameters passed to `summary`.

Details

It computes the P-value, call `summary` on the vector of statistics simulated under the null and returns the value of the observed statistic.

Value

A list of the following elements

- `pvalue` - P-value for goodness-of-fit.
- `s.dist.sim` - the result of a call to the function `summary`. Provides a summary of the distribution of the goodness-of-fit statistic simulated under the null.
- `dist.obs` - the observed value goodness-of-fit statistic.

See Also

- `gfit`, `abc`, `plot.gfit`

Examples

```r
## see ?gfit for examples
```
**summary.postpr**

*Posterior model probabilities and Bayes factors*

**Description**

This function extracts the posterior model probabilities and calculates the Bayes factors from an object of class "postpr".

**Usage**

```r
## S3 method for class 'postpr'
summary(object, rejection = TRUE, print = TRUE, digits = max(3, getOption("digits")-3), ...)
```

**Arguments**

- `object`: an object of class "postpr".
- `rejection`: logical, if method is "mnlogistic" or "neuralnet", should the approximate model probabilities based on the rejection method returned.
- `print`: logical, if TRUE prints the mean models probabilities.
- `digits`: the digits to be rounded to.
- `...`: other arguments.

**Value**

A list with the following components if method="rejection":

- **Prob**: an object of class table of the posterior model probabilities.
- **BayesF**: an object of class table with the Bayes factors between pairs of models.

A list with the following components if method is "mnlogistic" or "neuralnet" and rejection is TRUE:

- **rejection**: a list with the same components as above
- **mnlogistic**: a list with the same components as above

**See Also**

- `postpr`

**Examples**

```r
## see ?postpr for examples
```
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