### Package ‘bacon’

**Type** Package

**Title** Controlling bias and inflation in association studies using the empirical null distribution

**Version** 1.32.0

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**Description** Bacon can be used to remove inflation and bias often observed in epigenome- and transcriptome-wide association studies. To this end bacon constructs an empirical null distribution using a Gibbs Sampling algorithm by fitting a three-component normal mixture on z-scores.

**License** GPL (>= 2)

**Encoding** UTF-8

**Depends** R (>= 3.3), methods, stats, ggplot2, graphics, BiocParallel, ellipse

**Suggests** BiocStyle, knitr, rmarkdown, testthat, roxygen2

**biocViews** ImmunoOncology, StatisticalMethod, Bayesian, Regression, GenomeWideAssociation, Transcriptomics, RNASeq, MethylationArray, BatchEffect, MultipleComparison

**RoxygenNote** 7.3.1

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**VignetteBuilder** knitr

**NeedsCompilation** yes

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Gibbs Sampler Algorithm to fit a three component normal mixture to z-scores

usage

\texttt{bacon(}
\texttt{  teststatistics = NULL,}
\texttt{  effectsizes = NULL,}
\texttt{  standarderrors = NULL,}
\texttt{  niter = 5000L,}
\texttt{  nburnin = 2000L,}
\texttt{  nbins = 1000,}
\texttt{  trim = 0.999,}
\texttt{  level = 0.05,}
\texttt{  na.exclude = FALSE,}
\texttt{  verbose = FALSE,}
\texttt{  priors = list(sigma = list(alpha = 1.28, beta = 0.36), mu = list(lambda = c(0, 3, -3), tau = c(1000, 100, 100)), epsilon = list(gamma = c(90, 5, 5))),}
\texttt{  globalSeed = 42,}
\texttt{  parallelSeed = 42}
\texttt{)}
**Arguments**

- `teststatistics`: numeric vector or matrix of test-statistics
- `effectsizes`: numeric vector or matrix of effect-sizes
- `standarderrors`: numeric vector or matrix of standard errors
- `niter`: number of iterations
- `nburnin`: length of the burnin period
- `nbins`: default 1000 else bin test-statistics
- `trim`: default 0.999 trimming test-statistics
- `level`: significance level used to determine prop. null for starting values
- `na.exclude`: see ?na.exclude
- `verbose`: default FALSE
- `priors`: list of parameters for the prior distributions
- `globalSeed`: default 42 global seed. If set to NULL, randomization will occur for sequential and parallel bacon calls
- `parallelSeed`: default 42 BiocParallel RNGseed. If input statistics are a matrix and globalSeed=NULL, setting parallelSeed=NULL will allow randomization across parallel processes within a bacon call and across separate calls to bacon.

**Value**

Object of class-Bacon

**Author(s)**

mvaniterson

**References**

Implementation is based on a version from Zhihui Liu [https://macsphere.mcmaster.ca/handle/11375/9368](https://macsphere.mcmaster.ca/handle/11375/9368)

**Examples**

```r
##simulate some test-statistic from a normal mixture
##and run bacon
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
bc <- bacon(y)
##extract all estimated mixture parameters
estimates(bc)
##extract inflation
inflation(bc)
##extract bias
bias(bc)
##extract bias and inflation corrected test-statistics
head(tstat(bc))
```
Bacon-class

An S4 class container for storing Gibbs Sampler input and output

Description

An S4 class container for storing Gibbs Sampler input and output

Slots

teststatistics numeric vector or matrix of test-statistics
effectsizes numeric vector or matrix of effect-sizes
standarderrors numeric vector or matrix of standard errors
traces array of Gibbs Sampler traces
estimates vector or matrix of parameter estimates
priors list of parameters of for the prior distributions
niter number of iterations
nburnin length of the burnin period
bias

Method to extract the estimated bias from the 'bacon'-object

Description
Method to extract the estimated bias from the 'bacon'-object

Usage
bias(object)

## S4 method for signature 'Bacon'
bias(object)

Arguments
object 'bacon'-object

Value
vector or matrix of inflation

See Also
bacon

Examples
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
##nbins = 100 to speed up the calculations
bc <- bacon(y, nbins=100)
bias(bc)

dnormmix
density of a k-component normal mixture

Description
density of a k-component normal mixture

Usage
dnormmix(x, theta)
Arguments
  x       x like dnorm(x, ... 
theta    parameters of the mixture proportion, mean and sd

Details
  details follow

Value
  density of a k-component normal mixture

Author(s)
  mvaniterson

Examples
  n <- 2000
  theta <- c(0.8, 0, 1, 0, 4, 1)
  x <- rnormmix(n, theta)
  hist(x, freq=FALSE, n=100)
  curve(dnormmix(x, theta), add=TRUE, lwd=2)

---

es  Method to extract inflation- and bias-corrected effect-sizes

Description
  Method to extract inflation- and bias-corrected effect-sizes

Usage
  es(object, corrected = TRUE)

## S4 method for signature 'Bacon'
  es(object, corrected = TRUE)

Arguments
  object       'bacon'-object
  corrected    optional return uncorrected

Value
  vector or matrix of effect-sizes
estimates

See Also

bacon

Examples

```r
es <- replicate(6, rnormmix(2000, c(0.9, 0, 1, 0, 4, 1)))
se <- replicate(6, 0.8*sqrt(4/rchisq(2000,df=4)))
bc <- bacon(NULL, es, se)
head(es(bc))
```

estimates

Method to extract the estimated parameters from the 'bacon'-object

Description

Method to extract the estimated parameters from the 'bacon'-object

Usage

```r
estimates(object)
```

## S4 method for signature 'Bacon'
estimates(object)

Arguments

object 'bacon'-object

Value

vector or matrix of estimates

See Also

bacon

Examples

```r
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
##nbins = 100 to speed up the calculations
bc <- bacon(y, nbins=100)
estimates(bc)
```
Method to plot mixture fit

**Description**

Method to plot mixture fit

**Usage**

```r
fit(object, index = 1, ...)  
```  
```r  
## S4 method for signature 'Bacon'  
fit(object, index, col = "grey75", border = "grey75", ...)  
```  
**Arguments**

- `object`: 'bacon'-object
- `index`: if multiple sets of test statistics were provided
- `...`: additional plotting parameters
- `col`: line color default 'grey75'
- `border`: border color 'grey75'

**Value**

plot of the Gibbs Sampler mixture fit

**See Also**

- `bacon`

**Examples**

```r
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))  
#nbins = 100 to speed up the calculations  
bc <- bacon(y, nbins=100)  
fit(bc)
```
inflation

Method to extract the estimated inflation from the 'bacon'-object

Description
Method to extract the estimated inflation from the 'bacon'-object

Usage
inflation(object)

## S4 method for signature 'Bacon'
inflation(object)

Arguments
object 'bacon'-object

Value
vector or matrix of inflation

See Also
bacon

Examples
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
##nbins = 100 to speed up the calculations
bc <- bacon(y, nbins=100)
inflation(bc)

meta fixed meta-analysis

Description
Perform fixed meta-analysis using inflation and bias corrected effect-sizes and standard errors

Usage
meta(object, corrected = TRUE, ...)

## S4 method for signature 'Bacon'
meta(object, corrected = TRUE, ...)

Examples
plot.Bacon-method

Arguments

object 'bacon'-object
corrected optional return uncorrected
... additional arguments

Details

TODO maybe add idea’s from http://www.netstorm.be/home/meta_analysis#metaAnalysisU

Value

object of class 'bacon' with added fixed-effect meta-analysis test-statistics, effect-sizes and standard-errors

See Also

bacon

Examples

es <- replicate(6, rnormmix(2000, c(0.9, 0, 1, 0, 4, 1)))
se <- replicate(6, 0.8*sqrt(4/rchisq(2000,df=4)))
bc <- bacon(NULL, es, se)
mbc <- meta(bc)

plot.Bacon-method plot hist or qq

Description

simple ggplot2 plotting function for 'bacon'-object

Usage

## S4 method for signature 'Bacon'
plot(x, y, type = c("hist", "qq"))

Arguments

x 'bacon'-object
y NULL
type hist or qq

Value

either qq-plot of P-values or histogram of Test-statistics
Description

plot normal mixtures

Usage

plotnormmix(x, theta, ...)

Arguments

x  vector of test statistics
theta  parameters describing the mixture components
...  arguments passed to hist

Details

details follow

Value

return plot with histogram of the data and mixture and individual components

Author(s)

mvaniterson

Examples

n <- 2000
theta <- c(0.8, 0, 1, 0, 4, 1)
x <- rnormmix(n, theta)
plotnormmix(x, theta)
**Description**

Method to plot posterior distribution

**Usage**

```r
posteriors(
  object,
  thetas = c("sigma.0", "p.0"),
  index = 1,
  alphas = c(0.95, 0.9, 0.75),
  xlab = "",
  ylab = "",
  ...
)
```

## S4 method for signature 'Bacon'

```r
posteriors(
  object,
  thetas = c("sigma.0", "p.0"),
  index = 1,
  alphas = c(0.95, 0.9, 0.75),
  xlab = "",
  ylab = "",
  ...
)
```

**Arguments**

- **object** 'bacon'-object
- **thetas** which thetas to plot
- **index** if multiple sets of test-statsistics where provided
- **alphas** significance level confidence ellipses
- **xlab** optional xlab
- **ylab** optional ylab
- **...** additional plotting parameters

**Value**

plot of the Gibbs Sampler posterior probabilities
Method to extract inflation- and bias-corrected $P$-values

**Description**

Method to extract inflation- and bias-corrected $P$-values

**Usage**

```r
pval(object, corrected = TRUE)
```

## S4 method for signature 'Bacon'

```r
pval(object, corrected = TRUE)
```

**Arguments**

- `object`: 'bacon'-object
- `corrected`: optional return uncorrected

**Value**

vector or matrix of $P$-values

**See Also**

`bacon`

**Examples**

```r
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
#nbins = 100 to speed up the calculations
bc <- bacon(y, nbins=100)
posterior(bc)
```

```r
head(pval(bc))
```
rnormmix  sample from a normal mixture

Description
sample from a normal mixture

Usage
rnormmix(n, theta, shuffle = TRUE)

Arguments
n        size
theta    parameters
shuffle  shuffle return vectors or keep nulls and alternative ordered (null, alts)

Details
details follow

Value
n samples from a normal mixture with parameters theta

Author(s)
mvaniterson

Examples
n <- 2000
theta <- c(0.8, 0, 1, 0, 4, 1)
x <- rnormmix(n, theta)

se  Method to extract inflation- and bias-corrected standard errors

Description
Method to extract inflation- and bias-corrected standard errors
**Usage**

```
se(object, corrected = TRUE)
```

```R
## S4 method for signature 'Bacon'
se(object, corrected = TRUE)
```

**Arguments**

- `object`: 'bacon'-object
- `corrected`: optional return uncorrected

**Value**

vector or matrix of standard-errors

**See Also**

`bacon`

**Examples**

```r
es <- replicate(6, rnormmix(2000, c(0.9, 0, 1, 0, 4, 1)))
se <- replicate(6, 0.8*sqrt(4/rchisq(2000,df=4)))
bc <- bacon(NULL, es, se)
head(se(bc))
```

---

**topTable**

<table>
<thead>
<tr>
<th>topTable</th>
<th>topTable</th>
</tr>
</thead>
</table>

**Description**

Extract top features after meta analysis

**Usage**

```
topTable(
  object,
  number = 10,
  adjust.method = "bonf",
  sort.by = c("pval", "eff.size")
)
```

```R
## S4 method for signature 'Bacon'
topTable(
  object,
  number = 10,
  adjust.method = "bonf",
  sort.by = c("pval", "eff.size")
)
```
Arguments

object 'bacon'-object
number return specified number of top features, n=-1 return all features
adjust.method P-value multiple testing adjustment method default bonferroni
sort.by order results by pval or eff.size

Value

table with top features

See Also

bacon

Examples

es <- replicate(6, rnormmix(2000, c(0.9, 0, 1, 0, 4, 1)))
se <- replicate(6, 0.8*sqrt(4/rchisq(2000,df=4)))
bc <- bacon(NULL, es, se)
mbc <- meta(bc)
topTable(mbc)

description

Method to plot Gibbs sampling traces

Usage

traces(object, burnin = TRUE, index = 1)

## S4 method for signature 'Bacon'
traces(object, burnin = TRUE, index = 1)

Arguments

object 'bacon'-object
burnin include burnin period default true
index if multiple sets of test-statistics where provided

Value

plot of the Gibbs Sampler traces
tstat

See Also

bacon

Examples

y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
#nbins = 100 to speed up the calculations
bc <- bacon(y, nbins=100)
traces(bc)

tstat

Method to extract inflation- and bias-corrected test-statistics

Description

Method to extract inflation- and bias-corrected test-statistics

Usage

tstat(object, corrected = TRUE)

## S4 method for signature 'Bacon'
tstat(object, corrected = TRUE)

Arguments

object 'bacon'-object
corrected optional return uncorrected

Value

vector or matrix of test-statistics

See Also

bacon

Examples

y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
#nbins = 100 to speed up the calculations
bc <- bacon(y, nbins=100)
head(tstat(bc))
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