Package ‘bacon’
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Type Package
Title Controlling bias and inflation in association studies using the empirical null distribution
Version 1.2.0
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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)
Depends R (>= 3.3), methods, stats, ggplot2, graphics, BiocParallel, ellipse
Suggests BiocStyle, knitr, rmarkdown, testthat, roxygen2
biocViews StatisticalMethod, Bayesian, Regression,
GenomeWideAssociation, Transcriptomics, RNASeq,
MethylationArray, BatchEffect, MultipleComparison
RoxygenNote 5.0.1
VignetteBuilder knitr
NeedsCompilation yes
URL https://github.com/mvaniterson/bacon
BugReports https://github.com/mvaniterson/bacon/issues

R topics documented:

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**bacon**

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

**Usage**

```r
bacon(teststatistics = NULL, effectsizes = NULL, standarderrors = NULL, 
niter = 5000L, nburnin = 2000L, nbins = 1000, trim = 0.999, 
level = 0.05, verbose = FALSE, 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))))
```

**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 leve used to determine prop. null for starting values
- `verbose`: default FALSE
- `priors`: list of parameters of for the prior distributions

**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))
## inspect the Gibbs Sampling output
traces(bc)
posteriors(bc)
fit(bc)
## simulate multiple sets of test-statistic from a normal mixture
## and run bacon
y <- matrix(rnormmix(10*2000, c(0.9, 0, 1, 0, 4, 1)), ncol=10)
bc <- bacon(y)
## extract all estimated mixture parameters
estimates(bc)
## extract only the inflation
inflation(bc)
## extract only the bias
bias(bc)
## extract bias and inflation corrected P-values
head(pval(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**: similar to 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**

```r
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)

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>'bacon'-object</td>
</tr>
<tr>
<td>corrected</td>
<td>optional return uncorrected</td>
</tr>
</tbody>
</table>

Value

vector or matrix of effect-sizes

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))
```

## 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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>'bacon'-object</td>
</tr>
</tbody>
</table>

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)
```
fit

Method to plot mixture fit

Description
Method to plot mixture fit

Usage

fit(object, index = 1, ...)

## S4 method for signature 'Bacon'
fit(object, index = 1, ...)

Arguments

object 'bacon'-object
index if multiple sets of test-statistics where provided
... additional plotting parameters

Value
plot of the Gibbs Sampler mixture fit

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)
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)

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, ...)

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

```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)
mbc <- meta(bc)
```

Description

simple ggplot2 plotting function for 'bacon'-object

Usage

```r
## 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

```r
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

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'
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-statistics where provided
alphas significance level confidence ellipses
xlab optional xlab
ylab optional ylab
... additional plotting parameters

Value

plot of the Gibbs Sampler posterior probabilities

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)
```

---

pval

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))
bc <- bacon(y, nbins=100) #nbins = 100 to speed up the calculations
head(pval(bc))
```
rnormmix  sample from a normal mixture

Description
sample from a normal mixture

Usage
rnormmix(n, theta)

Arguments
- n: size
- theta: parameters

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)

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

Arguments

object 'bacon'-object
corrected optional return uncorrected

Value

vector or matrix of 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)
head(se(bc))

topTable

description

Extract top features after meta analysis

Usage

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

## 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)

---

Method to plot Gibbs sampling traces

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

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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