Package ‘bacon’

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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.

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Encoding UTF-8

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Suggests BiocStyle, knitr, markdown, testthat, roxygen2

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bacon  Gibbs sampler

Description

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

Usage

bacon(
  teststatistics = NULL,
  effectsizes = NULL,
  standarderrors = NULL,
  niter = 5000L,
  nburnin = 2000L,
  nbins = 1000,
  trim = 0.999,
  level = 0.05,
  na.exclude = FALSE,
  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)),
  globalSeed = 42,
  parallelSeed = 42
)
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

Examples

##simulate some test-statistic from a normal mixture
##and run bacon
y <- rnormmix(2000, c(0.9, 0, 1, 0, 4, 1))
b <- 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)
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
   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 plot mixture fit

Description

Method to plot mixture fit

Usage

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

## 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

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**  

```r  
inflation(object)  
```

### S4 method for signature 'Bacon'

```r  
inflation(object)  
```

**Arguments**

- `object`  'bacon'-object

**Value**

vector or matrix of inflation

**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)  
inflation(bc)  
```

---

**meta**  
*fixed meta-analysis*

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

**Usage**

```r  
meta(object, corrected = TRUE, ...)  
```

### S4 method for signature 'Bacon'

```r  
meta(object, corrected = TRUE, ...)  
```

**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)  
inflation(bc)  
```
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)

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
plotnormmix

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)
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 were 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)
posteriors(bc)
```

```r
pval <- function(object, corrected = TRUE) {
  if (corrected) {
    pvals <- object$pvals_corrected
  } else {
    pvals <- object$pvals
  }
  return(pvals)
}
```

Description

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

Usage

```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))
```
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)

Description

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

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

## S4 method for signature 'Bacon'
```r
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))
```

Description

Extract top features after meta analysis

Usage

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

## S4 method for signature 'Bacon'
```r
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

```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)
topTable(mbc)
```

---

**traces**

Method to plot Gibbs sampling traces

Description

Method to plot Gibbs sampling traces

Usage

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

## S4 method for signature 'Bacon'

```r
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

```r
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

<table>
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<tr>
<th>Method to extract inflation- and bias-corrected test-statistics</th>
</tr>
</thead>
</table>

Description

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

Usage

```r
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

```r
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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