Package ‘bacon’

May 8, 2026

Type Package

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

Version 1.41.0

Author Maarten van Iterson [aut, cre], Erik van Zwet [ctb]

Maintainer Maarten van Iterson `<mviterson@gmail.com>`

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

Collate 'BaconClass.R' 'BaconMethods.R' 'bacon.R' 'normmixture.R'

VignetteBuilder knitr

NeedsCompilation yes

git_url https://git.bioconductor.org/packages/bacon

git_branch devel

git_last_commit 9777412

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-08

Contents

`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))
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`	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

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))
```

`estimates` *Method to extract the estimated parameters from the ’bacon’-object*

Description

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

Usage

```
estimates(object)

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

Arguments

`object`	’bacon’-object

Value

vector or matrix of estimates

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)
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, col = "grey75", border = "grey75", ...)
```

Arguments

`object`	'bacon'-object
`index`	if multiple sets of test-statsistics where 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

```
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, ...)
```

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

`plotnormmix` *plot normal mixtures*

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)
```

`posteriors` *Method to plot posterior distribution*

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-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

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)
posteriors(bc)
```

`pval` *Method to extract inflation- and bias-corrected P-values*

Description

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

Usage

```
pval(object, corrected = TRUE)

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

Arguments

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

Value

vector or matrix of P-values

See Also

`bacon`

Examples

```
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, 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)

## 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

```
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` *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)
```

`traces` *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-statsistics 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))
```

Index