Package ‘bayefdr’

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Type Package

Title Bayesian Estimation and Optimisation of Expected False Discovery Rate

Version 0.2.0

Date 2021-09-18

Description Implements the Bayesian FDR control described by
Newton et al. (2004), <doi:10.1093/biostatistics/5.2.155>. Allows optimisation and visualisation of expected error rates based on
tail posterior probability tests.
Based on code written by Catalina Vallejos for BASiCS, see
Beyond comparisons of means: understanding changes in gene expression at the

Imports ggplot2, reshape2, assertthat, utils, cowplot, ggExtra, stats

License GPL-3

BugReports https://github.com/VallejosGroup/bayefdr/issues

RoxygenNote 7.1.2

Encoding UTF-8

Suggests testthat, pkgdown

Language en-gb

NeedsCompilation no

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Repository CRAN

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R topics documented:

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The 'nibbles' package.

Description

A DESCRIPTION OF THE PACKAGE

References

Detecting differential gene expression with a semiparametric hierarchical mixture method Michael A. Newton, Amine Noueiry, Deepayan Sarkar, Paul Ahlquist https://doi.org/10.1093/biostatistics/5.2.155

cumplot

Plot the cumulative median, mean, and 95% high posterior density region.

Description

Plot the cumulative median, mean, and 95% high posterior density region.

Usage

cumplot(x, ylab = NULL, burn = 0, thin = 1, hpd_level = 0.95)

Arguments

x An vector of MCMC draws.
ylab An optional y-axis label.
burn Integer specifying the number of initial iterations to be discarded.
thin Integer specifying the thinning factor to be used on the MCMC steps.
hpd_level Floating point specifying the desired HPD level.

Value

A ggplot showing the cumulative mean, median and HPD.
Examples

```r
x <- rnorm(1000)
cumplot(x)
```

---

efe

**EFDR and EFNR estimation**

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### Description

Calculate the Expected False Discovery Rate (EFDR) or Expected False Negative Rate (EFNR) in a vector of probabilities, given a specified evidence threshold.

### Usage

- `efdr(evidence_threshold, probs)`
- `efnr(evidence_threshold, probs)`

### Arguments

- `evidence_threshold` (Scalar value specifying the evidence threshold at which the EFDR or EFNR should be evaluated.)
- `probs` (Vector of probabilities.)

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efdr_search

**Bayesian EFDR optimisation.**

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### Description

Given a vector of probabilities, this function finds the probability threshold that matches a target expected false discovery rate as closely as possible.

### Usage

```r
efdr_search(
  probs,
  target_efdr,
  min_threshold = 0.7,
  prob_thresholds = seq(0.5, 0.9995, by = 0.00025)
)
```
Arguments

probs Vector of probabilities.
target_efdr Numeric scalar specifying the expected false discovery rate to match.
min_threshold Minimum probability threshold. If the optimal probability threshold is below this number, it is rejected and min_threshold is used instead.
prob_thresholds Vector for probability thresholds to scan, with the aim of finding the threshold that matches the target EFDR.

Value

An object of class "bayefdr" containing the probability thresholds tested, the EFDR and EFNR at each probability threshold, and the optimal threshold.

Examples

probs <- runif(100)
e <- efdr_search(probs, target_efdr = 0.1)
plot(e)

optimal(e)
e[optimal(e), ]

Description

Retrieve the index of the optimal probability threshold.

Usage

optimal(x)

Arguments

x An object of class "bayefdr".

Value

The integer index of the optimal probability threshold.

Examples

probs <- runif(100)
e <- efdr_search(probs, target_efdr = 0.1)
 optimal(e)
e[optimal(e), ]
plot.bayefdr  

Plot the EFDR, EFNR grids of a bayefdr object.

Description

Plot the EFDR, EFNR grids of a bayefdr object.

Usage

## S3 method for class 'bayefdr'
plot(x, ...)

Arguments

x  An object of class bayefdr.
...

Value

A ggplot.

print.bayefdr  

Print methods for bayefdr objects.

Description

Print methods for bayefdr objects.

Usage

## S3 method for class 'bayefdr'
print(x, ...)

## S3 method for class 'bayefdr'
head(x, ...)

Arguments

x  An object of class bayefdr.
...

Unused.
traceplot

Trace, marginal density histogram, and autocorrelation plot of MCMC draws.

Description
Trace, marginal density histogram, and autocorrelation plot of MCMC draws.

Usage
traceplot(x, ylab = NULL, log = FALSE)

Arguments
- x: A vector of MCMC draws.
- ylab: An optional y-axis label.
- log: Logical scalar controlling whether the y-axis should be logged.

Value
A plot created using `plot_grid` showing the trace, marginal density histogram, and autocorrelation function of the MCMC draws in x.

Examples
```r
x <- rnorm(1000)
traceplot(x)
```
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