Package ‘bayefdr’

May 7, 2026

Type Package

Title Bayesian Estimation and Optimisation of Expected False Discovery Rate

Version 0.2.1

Date 2022-10-26

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 single-cell level Vallejos et al. (2016) <doi:10.1186/s13059-016-0930-3>.

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

License GPL-3

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

RoxygenNote 7.2.1

Encoding UTF-8

URL `https://github.com/VallejosGroup/bayefdr`

Suggests testthat, pkgdown

Language en-gb

NeedsCompilation no

Author Alan O'Callaghan [aut, cre],
Catalina Vallejos [aut]

Maintainer Alan O'Callaghan <`alan.ocallaghan@outlook.com`>

Repository CRAN

Date/Publication 2022-10-26 19:35:06 UTC

Contents

`bayefdr-package` *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

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

`efdr` *EFDR and EFNR estimation*

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.

`efdr_search` *Bayesian EFDR optimisation.*

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

```
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)
efdr <- efdr_search(probs, target_efdr = 0.1)
plot(efdr)
```

`optimal` *Retrieve the index of the optimal probability threshold.*

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.
`...`	Unused.

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

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

Index