Package ‘bayefdr’

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Type Package

Title Bayesian Estimation and Optimisation of Expected False Discovery Rate

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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

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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

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)
```

---

**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**

```r
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.

---

**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

<table>
<thead>
<tr>
<th>probs</th>
<th>Vector of probabilities.</th>
</tr>
</thead>
<tbody>
<tr>
<td>target_efdr</td>
<td>Numeric scalar specifying the expected false discovery rate to match.</td>
</tr>
<tr>
<td>min_threshold</td>
<td>Minimum probability threshold. If the optimal probability threshold is below this number, it is rejected and\nmin_threshold is used instead.</td>
</tr>
<tr>
<td>prob_thresholds</td>
<td>Vector for probability thresholds to scan, with the aim of finding the threshold that matches the target EFDR.</td>
</tr>
</tbody>
</table>

Value

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

Examples

```r
probs <- runif(100)
efdr <- efdr_search(probs, target_efdr = 0.1)
plot(efdr)
```

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

Description

Retrieve the index of the optimal probability threshold.

Usage

```r
optimal(x)
```

Arguments

| x             | An object of class "bayefdr". |

Value

The integer index of the optimal probability threshold.

Examples

```r
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

```r
## 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

```r
## 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**

```r
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)
```
Index

bayefdr (bayefdr-package), 2
bayefdr-package, 2

cumplot, 2

efdr, 3
efdr_search, 3
efnr (efdr), 3

head.bayefdr (print.bayefdr), 5

optimal, 4

plot.bayefdr, 5
plot_grid, 6
print.bayefdr, 5

traceplot, 6