

# Package ‘bayefdr’

September 29, 2021

**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](https://doi.org/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](https://doi.org/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** 7.1.2

**Encoding** UTF-8

**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](mailto:alan.ocallaghan@outlook.com)>

**Repository** CRAN

**Date/Publication** 2021-09-29 16:20:02 UTC

## R topics documented:

bayefdr-package . . . . .	2
cumplot . . . . .	2

efdr . . . . .	3
efdr_search . . . . .	3
optimal . . . . .	4
plot.bayefdr . . . . .	5
print.bayefdr . . . . .	5
traceplot . . . . .	6

<b>Index</b>	<b>7</b>
--------------	----------

---

bayefdr-package	<i>The 'nibbles' package.</i>
-----------------	-------------------------------

---

## 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	<i>Plot the cumulative median, mean, and 95% high posterior density region.</i>
---------	---

---

## 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	<i>Plot the EFDR, EFNR grids of a bayefdr object.</i>
--------------	---

---

**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	<i>Print methods for bayefdr objects.</i>
---------------	---

---

**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	<i>Trace, marginal density histogram, and autocorrelation plot of MCMC draws.</i>
-----------	---

---

**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

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](#)