Package ‘FDRestimation’

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**Title**  Estimate, Plot, and Summarize False Discovery Rates
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**Depends**  R (>= 3.4.0)
**Imports**  stats, utils, graphics, Rdpack
**Description**  The user can directly compute and display false discovery rates from inputted p-values or z-scores under a variety of assumptions. p.fdr() computes FDRs, adjusted p-values and decision reject vectors from inputted p-values or z-values. get.pi0() estimates the proportion of data that are truly null. plot.p.fdr() plots the FDRs, adjusted p-values, and the raw p-values points against their rejection threshold lines.
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Description

This function estimates the null proportion of data or pi0 value.

Usage

```r
get.pi0(
  pvalues,
  set.pi0 = 1,
  zvalues = "two.sided",
  estim.method = "last.hist",
  threshold = 0.05,
  default.odds = 1,
  hist.breaks = "scott",
  na.rm = TRUE
)
```

Arguments

- **pvalues**: A numeric vector of raw p-values.
- **set.pi0**: A numeric value to specify a known or assumed pi0 value in the interval \([0, 1]\). Defaults to 1. Which means the assumption is that all inputted raw p-values come from the null distribution.
- **zvalues**: A numeric vector of z-values to be used in pi0 estimation or a string with options "two.sided", "greater" or "less". Defaults to "two.sided".
- **estim.method**: A string used to determine which method is used to estimate the pi0 value. Defaults to "last.hist".
- **threshold**: A numeric value in the interval \([0, 1]\) used in a multiple comparison hypothesis tests to determine significance from the null. Defaults to 0.05.
- **default.odds**: A numeric value determining the ratio of pi1/pi0 used in the computation of lower bound FDR. Defaults to 1.
- **hist.breaks**: A numeric or string variable representing how many breaks in the pi0 estimation histogram methods. Defaults to "scott".
- **na.rm**: A Boolean TRUE or FALSE value indicating whether NA's should be removed from the inputted raw p-value vector before further computation. Defaults to TRUE.

Details

We run into errors or warnings when pvalues, zvalues, threshold or default.odds are not inputted correctly.
get.pi0

Value

An estimated null proportion:

\( \pi_0 \)

A numeric value representing the proportion of the given data that come from the null distribution. A value in the interval \([0, 1]\).

References

Romain Francois (2014). bibtex: bibtex parser. R package version 0.4.0.


See Also

plot.p.fdr,p.fdr,summary.p.fdr

Examples

# Example 1
pi0 = 0.8
pi1 = 1-pi0
n = 10000
n.0 = ceiling(n*pi0)
n.1 = n-n.0
sim.data = c(rnorm(n.1,3,1),rnorm(n.0,0,1))
sim.data.p = 2*pnorm(-abs(sim.data))
get.pi0(sim.data.p, estim.method = "last.hist")
get.pi0(sim.data.p, estim.method = "storey")
get.pi0(sim.data.p, estim.method = "set.pi0")
Description

This function computes FDRs and Method Adjusted p-values.

Usage

```r
p.fdr(
  pvalues = NA,
  zvalues = "two.sided",
  threshold = 0.05,
  adjust.method = "BH",
  BY.corr = "positive",
  just.fdr = FALSE,
  default.odds = 1,
  estim.method = "set.pi0",
  set.pi0 = 1,
  hist.breaks = "scott",
  ties.method = "random",
  sort.results = FALSE,
  na.rm = TRUE
)
```

Arguments

- `pvalues` A numeric vector of raw p-values.
- `zvalues` A numeric vector of z-values to be used in pi0 estimation or a string with options "two.sided", "greater" or "less". Defaults to "two.sided".
- `threshold` A numeric value in the interval \([0, 1]\) used in a multiple comparison hypothesis tests to determine significance from the null. Defaults to 0.05.
- `adjust.method` A string used to identify the p-value and false discovery rate adjustment method. Defaults to BH. Options are BH, BY, codeBon, Holm, Hoch, and Sidak.
- `BY.corr` A string of either "positive" or "negative" to determine which correlation is used in the BY method. Defaults to positive.
- `just.fdr` A Boolean TRUE or FALSE value which output only the FDR vector instead of the list output. Defaults to FALSE.
- `default.odds` A numeric value determining the ratio of pi1/pi0 used in the computation of one FDR. Defaults to 1.
- `estim.method` A string used to determine which method is used to estimate the null proportion or pi0 value. Defaults to set.pi0.
- `set.pi0` A numeric value to specify a known or assumed pi0 value in the interval \([0, 1]\). Defaults to 1. Which means the assumption is that all inputed raw p-values come from the null distribution.
**hist.breaks**
A numeric or string variable representing how many breaks are used in the pi0 estimation histogram methods. Defaults to "scott".

**ties.method**
A string a character string specifying how ties are treated. Options are "first", "last", "average", "min", "max", or "random". Defaults to "random".

**sort.results**
A Boolean TRUE or FALSE value which sorts the output in either increasing or non-increasing order dependent on the FDR vector. Defaults to FALSE.

**na.rm**
A Boolean TRUE or FALSE value indicating whether NA's should be removed from the inputted raw p-value vector before further computation. Defaults to TRUE.

**Details**
We run into errors or warnings when pvalues, zvalues, threshold, set.pi0, BY.cor, or default.odds are not inputted correctly.

**Value**
A list containing the following components:

- **fdrs**
  A numeric vector of method adjusted FDRs.

- **Results Matrix**
  A numeric matrix of method adjusted FDRs, method adjusted p-values, and raw p-values.

- **Reject Vector**
  A vector containing Reject.H0 and/or FTR.H0 based off of the threshold value and hypothesis test on the adjusted p-values.

- **pi0**
  A numeric value for the pi0 value used in the computations.

- **threshold**
  A numeric value for the threshold value used in the hypothesis tests.

- **Adjustment Method**
  The string with the method name used in computation(needed for the plot.fdr function).

**References**
Romain Francois (2014). *bibtex: bibtex parser*. R package version 0.4.0.


See Also

plot.p.fdr, summary.p.fdr, get.pi0

Examples

# Example 1
pi0 = 0.8
pi1 = 1-pi0
n = 10000
n.0 = ceiling(n*pi0)
n.1 = n-n.0
sim.data = c(rnorm(n.1,3,1),rnorm(n.0,0,1))
sim.data.p = 2*pnorm(-abs(sim.data))

fdr.output = p.fdr(pvalues=sim.data.p, adjust.method="BH")

fdr.output$fdrs
fdr.output$pi0

# Example 2

sim.data.p = output = c(runif(800),runif(200, min=0, max=0.01))
fdr.output = p.fdr(pvalues=sim.data.p, adjust.method="Holm", sort.results = TRUE)
Description

This function creates a plot using a p.fdr object.

Usage

```r
## S3 method for class 'p.fdr'
plot(
x, 
raw.pvalues = TRUE, 
adj.pvalues = TRUE, 
sig.line = TRUE, 
adj.sig.line = TRUE, 
threshold = NA, 
x.axis = "Rank", 
xlim = NA, 
ylim = c(0, 1), 
zvalues = "two.sided", 
legend.where = NA, 
legend.on = TRUE, 
main = NA, 
pch.adj.p = 17, 
pch.raw.p = 20, 
pch.adj.fdr = 20, 
col = c("dodgerblue", "firebrick2", "black"), 
...
)
```

Arguments

- **x**: A p.fdr object that contains the list of output.
- **raw.pvalues**: A Boolean TRUE or FALSE value to indicate whether or not to plot the raw p-value points. Defaults to TRUE.
- **adj.pvalues**: A Boolean TRUE or FALSE value to indicate whether or not to plot the adjusted p-value points. Defaults to TRUE.
- **sig.line**: A Boolean TRUE or FALSE value to indicate whether or not to plot the raw p-value significance line. Defaults to TRUE.
- **adj.sig.line**: A Boolean TRUE or FALSE value to indicate whether or not to plot the adjusted significance threshold. Defaults to TRUE.
threshold  A numeric value to determine the threshold at which we plot significance. Defaults to value used in the p.fdr.object.

x.axis  A string variable to indicate what to plot on the x-axis. Can either be "Rank" or "Zvalues". Defaults to "Rank".

xlim  A numeric interval for x-axis limits.

ylim  A numeric interval for y-axis limits. Defaults to c(0,1).

zvalues  A numeric vector of z-values to be used in pi0 estimation or a string with options "two.sided", "greater" or "less". Defaults to "two.sided".

legend.where  A string "bottomright", "bottomleft", "topleft", "topright". Defaults to "topleft" if x.axis="Rank" and "topright" if x.axis="Zvalues".

legend.on  A Boolean TRUE or FALSE value to indicate whether or not to print the legend.

main  A string variable for the title of the plot.

pch.adj.p  A plotting "character", or symbol to use for the adjusted p-value points. This can either be a single character or an integer code for one of a set of graphics symbols. Defaults to 17.

pch.raw.p  A plotting "character", or symbol to use for the raw p-value points. This can either be a single character or an integer code for one of a set of graphics symbols. Defaults to 20.

pch.adj.fdr  A plotting "character", or symbol to use for the adjusted FDR points. This can either be a single character or an integer code for one of a set of graphics symbols. Defaults to 20.

col  A vector of colors for the points and lines in the plot. If the input has 1 value all points and lines will be that same color. If the input has length of 3 then col.adj.fdr will be the first value, col.adj.p will be the second, and col.raw.p is the third. Defaults to c("dodgerblue","firebrick2","black").

...  Graphical parameters. Any argument that can be passed to image.plot and to base plot, such as axes=FALSE, main='title', ylab='latitude'

Details

We run into errors or warnings when zvalues or col are inputted incorrectly.

References

Romain Francois (2014). *bibtex: bibtex parser*. R package version 0.4.0.


print.summary.p.fdr


See Also

`summary.p.fdr, p.fdr, get.pi0`

Examples

```r
# Example 1

sim.data.p = c(runif(80), runif(20, min=0, max=0.01))
fdr.output = p.fdr(pvalues=sim.data.p)

plot(fdr.output)
plot(fdr.output, x.axis="Zvalues")
```

print.summary.p.fdr  
Print the summary of p.fdr.object

Description

This function prints the summary a p.fdr.object.

Usage

```r
## S3 method for class 'summary.p.fdr'
print(x, digits = 3, ...)
```

Arguments

- `x` A list of output from the summary.p.fdr function.
- `digits` A numeric value for the number of desired digits in the summary output. Defaults to 3.
- `...` Further arguments passed to or from other methods.

Details

We run into errors or warnings when
References

Romain Francois (2014). \textit{bibtex: bibtex parser}. R package version 0.4.0.


See Also

\texttt{plot.p.fdr, p.fdr, get.pi0}

Examples

\begin{verbatim}
# Example 1
pi0 = 0.8
pi1 = 1-pi0
n = 10
n.0 = ceiling(n*pi0)
n.1 = n-n.0

sim.data = c(rnorm(n.1,5,1),rnorm(n.0,0,1))
sim.data.p = 2*pnorm(-abs(sim.data))

fdr.output = p.fdr(pvalues=sim.data.p, adjust.method="BH")

summary(fdr.output)
\end{verbatim}

**summary.p.fdr**

Summary of \texttt{p.fdr} object

Description

This function summarizes a \texttt{p.fdr} object.

Usage

\begin{verbatim}
## S3 method for class 'p.fdr'
summary(object, digits = 5, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{object} A list of output from the \texttt{p.fdr} function.
  \item \texttt{digits} A numeric value for the number of desired digits in the summary output. Defaults to 3.
  \item \ldots Additional arguments affecting the summary produced.
\end{itemize}
Details

We run into errors or warnings when

Value

A list containing the following components:

Range
The range on the false discovery rates.

Significant Findings
The number of significant findings. Found using the adjusted p-values and the
given threshold. This is also the number of times we decide to reject the null
hypothesis that the data is generated from a standard normal distribution.

Inconclusive Findings
The number of inconclusive findings. Found using the adjusted p-values and
the given threshold. This is also the number of times we fail to reject the null
hypothesis that the data is generated from a standard normal distribution.

Assumed/Estimated pi0
the assumed or estimated pi0 value depending on how the p.fdr function was
run.

Number of Tests
The total number of multiple comparison tests completed.

Adjustment Method
The adjustment method used in the p.fdr function.

References

Romain Francois (2014). bibtex: bibtex parser. R package version 0.4.0.

R Core Team (2016). R: A Language and Environment for Statistical Computing. R Foundation for

Murray MH, Blume JD (2020). “False Discovery Rate Computation: Illustrations and Modifica-
tions.” 2010.04680.

See Also

plot.p.fdr,p.fdr,get.pi0

Examples

# Example 1
pi0 = 0.8
pi1 = 1-pi0
n = 10
n.0 = ceiling(n*pi0)
n.1 = n-n.0

sim.data = c(rnorm(n.1,5,1),rnorm(n.0,0,1))

sim.data.p = 2*pnorm(-abs(sim.data))
fdr.output = p.fdr(pvalues=sim.data.p, adjust.method="BH")

summary(fdr.output)
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