qvalue

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hedenfalk Gene expression dataset from Hedenfalk et al. (2001)

Description

The data come from the breast cancer cDNA microarray experiment of Hedenfalk et al. (2001). In the original experiment, comparison was made between 3,226 genes of two mutation types, BRCA1 (7 arrays) and BRCA2 (8 arrays). The data included here are p-values obtained from a two-sample t-test analysis on a subset of 3,170 genes, as described in Storey and Tibshirani (2003).

Usage

data(hedenfalk)

Value

hedenfalk Vector of 3,170 p-values of tests comparing BRCA1 to BRCA2.

References


Description

Graphical display of qvalue objects

Usage

```r
qplot(qobj, rng = c(0, 0.1), smooth.df = 3, smooth.log.pi0 = FALSE, ...)
```

## S3 method for class 'qvalue':

```r
plot(x, ...)
```

Arguments

- `qobj`, `x` : Qvalue object.
- `rng` : Range of q-values to consider. Optional.
- `smooth.df` : Number of degrees-of-freedom to use when estimating $\pi_0$ with a smoother. Optional.
- `smooth.log.pi0` : If TRUE and `pi0.method = "smoother"`, $\pi_0$ will be estimated by applying a smoother to a scatterplot of $\log \pi_0$ estimates against the tuning parameter $\lambda$. Optional.
- `...` : Any other arguments.

Details

The function `qplot` allows one to view several plots:

1. The estimated $\pi_0$ versus the tuning parameter $\lambda$.
2. The q-values versus the p-values.
3. The number of significant tests versus each q-value cutoff.
4. The number of expected false positives versus the number of significant tests.

This function makes four plots. The first is a plot of the estimate of $\pi_0$ versus its tuning parameter $\lambda$. In most cases, as $\lambda$ gets larger, the bias of the estimate decreases, yet the variance increases. Various methods exist for balancing this bias-variance trade-off (Storey 2002, Storey & Tibshirani 2003, Storey, Taylor & Siegmund 2004). Comparing your estimate of $\pi_0$ to this plot allows one to gauge its quality. The remaining three plots show how many tests are significant, as well as how many false positives to expect for each q-value cut-off. A thorough discussion of these plots can be found in Storey & Tibshirani (2003).

Value

Nothing of interest.

Author(s)

John D. Storey (jstorey@u.washington.edu)
References


See Also
qvalue, qwrite, qsummary, qvalue.gui

Examples

```r
## Not run:
p <- scan(pvalues.txt)
qobj <- qvalue(p)
qplot(qobj)
qwrite(qobj, filename=myresults.txt)

# view plots for q-values between 0 and 0.3:
plot(qobj, rng=c(0.0, 0.3))
## End(Not run)
```

qsummary

Display qvalue object

Description
Display summary information for a qvalue object.

Usage

```r
qsummary(qobj, cuts = c(1e-04, 0.001, 0.01, 0.025, 0.05, 0.1, 1),
  digits = getOption("digits"), ...)
```

## S3 method for class 'qvalue':
summary(object, ...)

Arguments

- `qobj`, `object` Qvalue object
- `cuts` Vector of significance value to use for table (optional)
- `digits` Significant digits to display (optional)
- `...` Any other arguments
Details

qsummary shows the original call, estimated proportion of true null hypotheses, and a table comparing the number of significant calls for the raw p-values and for the calculated q-values using a set of cutoffs given by cuts.

Value

Invisibly returns the original object.

Author(s)

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See Also

qvalue, qplot, qwrite, qvalue.gui

Examples

## Not run:
qobj <- qvalue(p)
print(qobj)
summary(qobj, cuts=c(0.01, 0.05))
## End(Not run)
**qvalue**

See Also

qvalue, qplot, qwrite, qsummary

Examples

```r
## Not run:
qvalue.gui()
## End(Not run)
```

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**qvalue**

Estimate the q-values for a given set of p-values

Description

Estimate the q-values for a given set of p-values. The q-value of a test measures the proportion of false positives incurred (called the false discovery rate) when that particular test is called significant.

Usage

```r
qvalue(p=NULL, lambda=seq(0,0.90,0.05), pi0.method="smoother", fdr.level=NULL, robust=FALSE, gui=FALSE, smooth.df=3, smooth.log.pi0=FALSE)
```

Arguments

- `p` A vector of p-values (only necessary input)
- `lambda` The value of the tuning parameter to estimate \( \pi_0 \). Must be in \([0,1)\). Optional, see Storey (2002).
- `pi0.method` Either "smoother" or "bootstrap"; the method for automatically choosing tuning parameter in the estimation of \( \pi_0 \), the proportion of true null hypotheses.
- `fdr.level` A level at which to control the FDR. Must be in \((0,1]\). Optional; if this is selected, a vector of TRUE and FALSE is returned that specifies whether each q-value is less than fdr.level or not.
- `robust` An indicator of whether it is desired to make the estimate more robust for small p-values and a direct finite sample estimate of pFDR. Optional.
- `gui` A flag to indicate to 'qvalue' that it should communicate with the gui. Should not be specified on command line. Optional.
- `smooth.df` Number of degrees-of-freedom to use when estimating \( \pi_0 \) with a smoother. Optional.
- `smooth.log.pi0` If TRUE and pi0.method = "smoother", \( \pi_0 \) will be estimated by applying a smoother to a scatterplot of log \( \pi_0 \) estimates against the tuning parameter \( \lambda \). Optional.

Details

If no options are selected, then the method used to estimate \( \pi_0 \) is the smoother method described in Storey and Tibshirani (2003). The bootstrap method is described in Storey, Taylor & Siegmund (2004).
Value

A list containing:

- `call` function call
- `pi0` an estimate of the proportion of null p-values
- `qvalues` a vector of the estimated q-values (the main quantity of interest)
- `pvalues` a vector of the original p-values
- `significant` if `fdr.level` is specified, and indicator of whether the q-value fell below `fdr.level` (taking all such q-values to be significant controls FDR at level `fdr.level`)

Author(s)

John D. Storey ⟨jstorey@u.washington.edu⟩

References


See Also

qplot, qwrite, qsummary, qvalue.gui

Examples

```r
## Not run:
p <- scan("pvalues.txt")
qobj <- qvalue(p)
qplot(qobj)
qwrite(qobj, filename="myresults.txt")
qobj <- qvalue(p, lambda=0.5, robust=TRUE)
qobj <- qvalue(p, fdr.level=0.05, pi0.method="bootstrap")
## End(Not run)
```
Write the results of the q-value object qobj to a file

Description
Write the results of the q-value object qobj to a file.

Usage
qwrite(qobj, filename = "my-qvalue-results.txt")

Arguments
qobj  Qvalue object
filename  Output filename (optional)

Details
The output file lists the estimate of \( \pi_0 \), which is the proportion of true null hypotheses. It also lists each p-value and corresponding q-value, one per line. If an FDR significance level was specified in the call to \texttt{qvalue}, the significance level is printed below the estimate of \( \pi_0 \), and an indicator of significance is included as a third column for each p-value and q-value.

Value
Nothing of interest.

Author(s)
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See Also
\texttt{qvalue}, \texttt{qplot}, \texttt{qsummary}, \texttt{qvalue.gui}

Examples
## Not run:
p <- scan("pvalues.txt")
qobj <- qvalue(p)
qplot(qobj)
qwrite(qobj, filename="myresults.txt")
## End(Not run)
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