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

qplot
Graphical display of qvalue objects

Description
Graphical display of qvalue objects

Usage
qplot(qobj, rng = c(0, 0.1), smooth.df = 3, smooth.log.pi0 = FALSE, ...)## S3 method for class 'qvalue':
plot(x, ...)

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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"), ...)
```

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)

Alan Dabney (adabney@u.washington.edu) and Gregory R. Warnes (gregory_r_warnes@groton.pfizer.com)
qvalue.gui

See Also

cvalue, qplot, qwrite, qvalue.gui

Examples

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

qvalue.gui

A graphical user interface for QValue

Description

A graphical user interface for QValue

Usage

qvalue.gui(dummy = NULL)

Arguments

dummy

Dummy argument to facilitate documentation (no arguments required)

Details

This is a point-and-click version of cvalue. See the manual at http://faculty.washington.edu/~jstorey/qvalue/manual.pdf for documentation.

Value

Nothing of interest.

Author(s)

Alan R. Dabney (adabney@u.washington.edu)

See Also

cvalue, qplot, qwrite, qsummary

Examples

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

---

**qwrite**

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**

```r
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)

Alan Dabney (adabney@u.washington.edu) and John D. Storey (jstorey@u.washington.edu)

See Also

\texttt{qvalue, qplot, qsummary, qvalue.gui}

Examples

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