qvalue

November 11, 2009

R topics documented:

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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

Hedenfalk I et al. (2001). Gene expression profiles in hereditary breast cancer. New Engl. Jour. Medicine, 344: 539-548.

Storey JD and Tibshirani R. (2003). Statistical significance for genome-wide studies. Proceedings of the National Academy of Sciences, 100: 9440-9445.

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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, ...)
```

Arguments

`qobj, x`	Qvalue object.
`rng`	Range of q-values to consider. Optional.
`smooth.df`	Number of degrees-of-freedom to use when estimating π_0 with a smoother. Optional.
`smooth.log.pi0`	
	If TRUE and `pi0.method = "smoother"`, π_0 will be estimated by applying a smoother to a scatterplot of $log\ \pi_0$ estimates against the tuning parameter λ. Optional.
`...`	Any other arguments.

Details

The function qplot allows one to view several plots:

1. The estimated π_0 versus the tuning parameter λ.

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 fours plots. The first is a plot of the estimate of π_0 versus its tuning parameter λ. In most cases, as λ 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 π_0 to this plot allows one to guage 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

Storey JD. (2002) A direct approach to false discovery rates. Journal of the Royal Statistical Society, Series B, 64: 479-498.

Storey JD and Tibshirani R. (2003) Statistical significance for genome-wide experiments. Proceedings of the National Academy of Sciences, 100: 9440-9445.

Storey JD. (2003) The positive false discovery rate: A Bayesian interpretation and the q-value. Annals of Statistics, 31: 2013-2035.

Storey JD, Taylor JE, and Siegmund D. (2004) Strong control, conservative point estimation, and simultaneous conservative consistency of false discovery rates: A unified approach. Journal of the Royal Statistical Society, Series B, 66: 187-205.

QVALUE Manual http://faculty.washington.edu/~jstorey/qvalue/manual.pdf

See Also

qvalue, qwrite, qsummary, qvalue.gui

Examples

```
## 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

```
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)
```

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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 qvalue. 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

qvalue, qplot, qwrite, qsummary

Examples

```
## 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

```
qvalue(p=NULL, lambda=seq(0,0.90,0.05), pi0.method="smoother", fdr.level=NULL, r
    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 π_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 π_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 π_0 with a smoother. Optional.
smooth.log.pi0	
	If TRUE and pi0.method = "smoother", π_0 will be estimated by applying a smoother to a scatterplot of $log\ \pi_0$ estimates against the tuning parameter λ. Optional.

Details

If no options are selected, then the method used to estimate π_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

Storey JD. (2002) A direct approach to false discovery rates. Journal of the Royal Statistical Society, Series B, 64: 479-498.

Storey JD and Tibshirani R. (2003) Statistical significance for genome-wide experiments. Proceedings of the National Academy of Sciences, 100: 9440-9445.

Storey JD. (2003) The positive false discovery rate: A Bayesian interpretation and the q-value. Annals of Statistics, 31: 2013-2035.

Storey JD, Taylor JE, and Siegmund D. (2004) Strong control, conservative point estimation, and simultaneous conservative consistency of false discovery rates: A unified approach. Journal of the Royal Statistical Society, Series B, 66: 187-205.

QVALUE Manual http://faculty.washington.edu/~jstorey/qvalue/manual.pdf

See Also

qplot, qwrite, qsummary, qvalue.gui

Examples

```
## 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

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

Arguments

qobj   Qvalue object

filename   Output filename (optional)

Details

The output file lists the estimate of π_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 qvalue, the significance level is printed below the estimate of π_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

qvalue, qplot, qsummary, 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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