

# qvalue

April 19, 2009

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hedenfalk

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

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## 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*

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## 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**

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

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qsummary

*Display qvalue object*

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**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)**

Alan Dabney (adabney@u.washington.edu) and Gregory R. Warnes (gregory\_r\_warnes@groton.pfizer.com)

**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*

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**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](mailto:adabney@u.washington.edu)>

**See Also**

`qvalue`, `qplot`, `qwrite`, `qsummary`

**Examples**

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

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qvalue	<i>Estimate the q-values for a given set of p-values</i>
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### 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,
       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**

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)
```

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qwrite

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

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**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 `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**

[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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