Bioconductor's **qvalue** package Version 2.30.0

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1 Introduction

The qvalue package performs false discovery rate (FDR) estimation from a collection of p-values or from a collection of test-statistics with corresponding empirical null statistics. This package produces estimates of three key quantities: q-values, the proportion of true null hypotheses (denoted by π_0), and local false discovery rates.

When carrying out multiple hypothesis tests, one typically starts either with a set of p-values or test-statistics.

Either quantity yields a natural ordering of tests from most significant to least significant. For example, using p-values one would order the tests from smallest p-value (most significant) to largest p-value (least significant). As another example, using F-statistics one would order the tests from largest F-statistic (most significant) to smallest F-statistic (least significant).

One may then ask: "If I draw a significance threshold somewhere along this list, how much can I trust the top of the list, i.e., those I choose to call statistically significant?" Another possible question is: "Where should I draw a line of significance along this list so that we can expect that at most 10% of the list I call significant is composed of false positives?" We may also wish to know the reliability of a set of tests called significant for all possible thresholds simultaneously or we may want to estimate the probability that any given test is a true null hypothesis.

The qualue package forms various estimates that allow one to answer these and other questions. The quantity of interest is the false discovery rate – sometimes abbreviated as FDR – which is roughly defined to be the expected proportion of false discoveries (also known as false positives) among all tests that are called significant.

An overview of the FDR and its well-established methods and theory may be found in Storey (2011) [1] (preprint freely available at http://genomine.org/papers/Storey_FDR_2011.pdf). We recommend this paper for users of qvalue who want a quick start and are unfamiliar with FDR, q-value, and local FDR estimation.

2 Citing this package

The statistical techniques implemented in the package come from the following publications. We ask that you cite the most appropriate paper(s) from this list when reporting results from the qvalue package.

J. D. Storey. A direct approach to false discovery rates. *Journal of the Royal Statistical Society, Series B*, 64:479–498, 2002.

Proposed the key strategy and derived the main estimators used in this package.

J. D. Storey. The positive false discovery rate: A Bayesian interpretation and the q-value. *Annals of Statistics*, 31:2013–2035, 2003.

Developed and proved theorems showing a direct relationship between FDR and Bayesian classification, giving a direct Bayesian version and interpretation of the quantities estimated in this package.

J. D. Storey and R. Tibshirani. Statistical significance for genome-wide experiments. *Proceedings of the National Academy of Sciences*, 100:9440–9445, 2003.

Proposed that the FDR and q-value estimators from Storey (2002) [2] be used in a wide range of genomics studies as a way to determine statistical significance.

J. D. Storey, J. E. Taylor, and D. Siegmund. 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, 2004.

Unified the point estimation approach of Storey (2002) [2] with the more traditional sequential p-values method approaches from the multiple hypothesis testing literature (e.g., Benjamini and Hochberg 1995 [6]), and proved a number of theorems establishing that the methods in this package provide conservative FDR estimation and control for fixed FDR levels, fixed significance thresholds, and over all levels or thresholds simultaneously.

J. D. Storey. False discovery rates. In Miodrag Lovric, editor, *International Encyclopedia of Statistical Science*. Springer, 2011. http://genomine.org/papers/Storey_FDR_2011.pdf.

Provides a concise summary of the main methods and theory on FDR.

The format of a citation to the qvalue package itself is obtained from:

```
citation("qvalue")
```

3 Getting help

Many questions about qvalue will hopefully be answered by this documentation and references therein. As with any R package, detailed information on functions, their arguments and values, can be obtained in the help files. To view the help for qvalue within R, type

```
help(package = "qvalue")
```

If you identify bugs related to basic usage please contact the authors directly, preferably via GitHub at https://github.com/jdstorey/qvalue. Otherwise, any questions or problems regarding qvalue will most efficiently be addressed on the Bioconductor support site, https://support.bioconductor.org/.

4 Quick start guide

Given a set of p-values, the qvalue object can be calculated by using the qvalue function:

```
library(qvalue)
data(hedenfalk)
pvalues <- hedenfalk$p
qobj <- qvalue(p = pvalues)</pre>
```

Additionally, the qualue object can be calculated given a set of empirical null statistics:

```
library(qvalue)
data(hedenfalk)
obs_stats <- hedenfalk$stat
null_stats <- hedenfalk$stat0
pvalues <- empPvals(stat = obs_stats, stat0 = null_stats)
qobj <- qvalue(p = pvalues)</pre>
```

Once the qvalue object is created, estimates of the q-values, the proportion of true null hypotheses π_0 , and the local false discovery rates can be accessed from qobj:

```
qvalues <- qobj$qvalues
pi0 <- qobj$pi0
lfdr <- qobj$lfdr</pre>
```

The object can be summarized and visualized by:

```
summary(qobj)
hist(qobj)
plot(qobj)
```

The following sections of the manual go through a case study to show additional features of the qvalue package.

5 Case study: differential gene expression

We demonstrate the functionality of this package using gene expression data from the breast cancer study of Hedenfalk et al. (2001) [7]. The test-statistics and p-values from our analysis are included with the qvalue package:

```
data(hedenfalk)
names(hedenfalk)
## [1] "p" "stat" "stat0"
```

A test of differential gene expression was performed between two types of genetic mutations that are associated with an increased risk of breast cancer, BRCA1 and BRCA2. There were 7 and 8 cDNA arrays for BRCA1 and BRCA2, respectively. The example considered here is restricted to 3170 genes as described in Storey and Tibshirani (2003) [4].

The list hedenfalk has three variables: p, stat, stat0. The p variable is a vector of p-values from the tests of differential expression (one per gene for a total of 3170); stat is a vector also of length 3170 that contains the observed test-statistics calculated on the original data (the statistic is the absolute values of a two-sample t-test); and stat0 is a 3170×100 matrix that contains the empirical "null statistics", which were generated by permuting the BRCA1 and BRCA2 group labels 100 times and recalculating the absolute t-statistics for each permutation.

5.1 Calculating p-values

One will typically already have a vector of p-values calculated using an appropriate method before utilizing the qvalue package. Sometimes users will instead have a vector of "observed statistics" that have been calculated on the original data, and then simulated or data-resampled (e.g., bootstrap, permutation) "null statistics". As long as the statistics are constructed such that the larger a statistic is, the more evidence there is against the null hypothesis in favor of the alternative hypothesis (e.g., the larger it is the "more extreme" it is), then there is a function in qvalue called empPvals that allows one to efficiently calculate p-values to be input into qvalue:

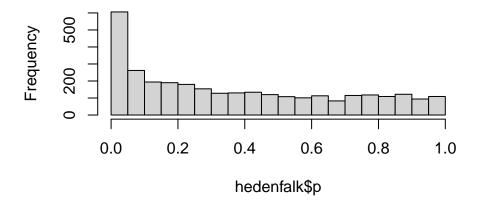
The documentation on empPvals, which can be accessed via ?empPvals, explains how to use this function to calculate test-specific or test-nonspecific pooled p-values using this function.

5.2 Checking the p-value histogram

Before running qvalue, we strongly recommend that you view a histogram of the p-values:

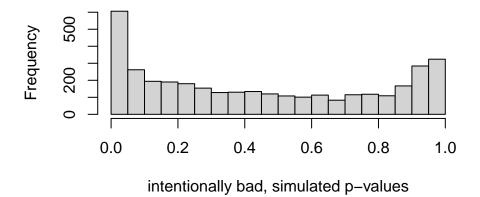
¹The original data and code for pre-processing can be found at http://genomine.org/qvalue.

Histogram of hedenfalk\$p



The p-values are relatively flat at the right tail of the histogram. This is an important step in determining whether the true null p-values are distributed according to a Uniform(0,1) distribution. Suppose the p-value histogram instead looked like this simulated set of p-values:

Problematic p-values



The "U-shaped" p-value histogram is a red flag. An important assumption behind the estimation performed in this package is that null p-values follow a Uniform(0,1) distribution, which would result in a p-value histogram where the right tail is fairly flat as in the Hedenfalk et al. p-values. U-shaped p-value histograms can indicate that a one-sided test was performed on data where there is signal in both directions, or it can indicate that there is dependence among the variables in the data. In the latter case, we suggest considering the sva Bioconductor package. In either case, it is usually possible to compute the p-values using a different model or method that will yield p-values that better match the underlying assumptions of the methods

implemented in this package.

5.3 The qualue function

Once you've examined the distribution of the p-values and confirmed they are well-behaved, the function qualue can be used to calculate the q-values:

```
qobj <- qvalue(p = hedenfalk$p)</pre>
```

Several arguments can be used in the function qvalue:

- p: A vector of p-values. This is the only necessary input.
- fdr.level: The level at which to control the false discovery rate. Optional; if this is selected, a vector of TRUE and FALSE is returned in the fdr.level slot that specifies whether each q-value is less than fdr.level or not.
- pfdr: An indicator of whether it is desired to make the estimate more robust for small p-values. This uses the point estimate of "positive false discovery rate" (pFDR). Optional; see Storey (2002) [2] for more information.
- ...: Arguments passed to the functions pi0est and lfdr, which can include:
 - lambda (passed to pi0est): The values of the tuning parameter to be considered in estimating π_0 . These must be in [0,1] and are set to lambda = seq(0, 0.95, 0.05) by default.
 - pi0.method (passed to pi0est): Either "smoother" or "bootstrap"; the method for automatically handling the tuning parameter in the estimation of π_0 .
 - trunc (passed to 1fdr): If TRUE, local FDR estimates > 1 are set to 1. Default is TRUE.

The user has the most influence on choosing how to estimate π_0 , the overall proportion of true null hypotheses, via lambda and pi0.method. If no options are selected, then by default the smoother method (pi0.method = "smoother") proposed in Storey and Tibshirani (2003) [4] is used. An alternative is the bootstrap method (pi0.method = "bootstrap") proposed in Storey, Taylor & Siegmund (2004) [5].

If one selects lambda = 0 (which estimates π_0 as 1) and fdr.level = 0.05, then this produces a list of significant tests equivalent to the Benjamini and Hochberg (1995) [6] methodology at level $\alpha = 0.05$ (where, of course, 0.05 can be substituted for any number in (0,1]). This can be viewed as a special conservative case of the Storey (2002) [2] methodology.

5.3.1 The qualue object

The object contains several relevant fields:

- call: The function call.
- pi0: An estimate of the proportion of null p-values.

- qvalues: A vector of the estimated q-values.
- pvalues: A vector of the original p-values.
- lfdr: A vector of estimated local FDR values.
- significant: If fdr.level is specified, and indicator of whether the estimated q-value fell below fdr.level (taking all such q-values to be significant controls FDR at level fdr.level).
- pi0.lambda: An estimate of the proportion of null p-values at each lambda value.
- lambda: A vector of lambda values utilized in forming a set of π_0 estimates.

5.3.2 Summarizing results

Running the function qualue in the previous section returns a qualue object. A qualue object can be summarized by using the summary function:

```
summary(qobj)
##
## Call:
## qvalue(p = hedenfalk$p)
## pi0: 0.669926
##
## Cumulative number of significant calls:
##
##
             <1e-04 <0.001 <0.01 <0.025 <0.05 <0.1
                 15
                        76
                              265
                                     424
                                           605 868
## p-value
                          0
                                      73
## q-value
                  0
                                1
                                           162 319
                  0
                          0
                                3
                                      30
## local FDR
                                            85 167
               <1
## p-value
             3170
## q-value
## local FDR 2241
```

The summary function provides a nice way of viewing the π_0 estimate and the number of significant genes at various cutoffs. The cutoffs printed in the summary function can be controlled by changing the cuts argument.

5.3.3 The π_0 estimate

One very important statistic that is obtained with the software is an estimate of the overall proportion of true null hypotheses, π_0 :

```
piO <- qobj$piO
```

An estimate of the proportion of true alternative tests is one minus this number. This is quite a useful number to know, even if all the truly significant tests cannot all be explicitly identified. If the π_0 estimate is the statistic of interest, the function pi0est can be used directly:

The pi0 slot provides the overall π_0 estimate, pi0.lambda are the estimated proportion of null p-values at each lambda values, and pi0.smooth are the estimated proportion of null p-values at each lambda from the spline fit.

5.3.4 The q-values

The q-value is the minimum FDR incurred when calling a test significant. The q-values can be extracted from the qvalue object by:

```
qvalues <- qobj$qvalues
```

We advocate reporting the estimated q-value for each test. However, sometimes one wants to estimate the FDR incurred for a given p-value cut-off, or estimate the p-value cut-off required to control the FDR at a certain level. For example, if one wants to estimate the false discovery rate when calling all p-values ≤ 0.01 significant, then type:

```
max(qvalues[qobj$pvalues <= 0.01])
## [1] 0.07932935</pre>
```

This calculates the maximum estimated q-value among all p-values ≤ 0.01 , which is equivalent to estimating the false discovery rate when calling all p-values ≤ 0.01 significant. When considering all p-values ≤ 1 , the maximum q-value will be the estimate of π_0 . This is because the best estimate of the false discovery rate, when considering all tests, will be the estimate of the rejection region.

If one wants to control the false discovery rate at a pre-determined level α , then calling all tests significant with estimated q-values $\leq \alpha$ accomplishes this under certain mathematical assumptions, including some cases where the p-values are dependent ([5]). If fdr.level is set to α in qvalue, then a vector indicating whether each q-value is $\leq \alpha$ can be obtained by:

```
qobj_fdrlevel <- qvalue(p = hedenfalk$p, fdr.level = 0.1)
qobj$significant</pre>
```

The more likely case is that one will want to investigate the overall behavior of the estimated q-values before making such a decision.

5.3.5 The local false discovery rates

The local FDR is a useful counterpart to the q-values ([1]). The estimated local FDR of a given test is an empirical Bayesian posterior probability that the null hypothesis is true, conditional on the observed p-value. To extract the local FDR estimates, type:

```
localFDR <- qobj$lfdr</pre>
```

The function lfdr can be used to calculate the local FDR estimates directly:

```
localFDR <- lfdr(p = hedenfalk$p)</pre>
```

When calling lfdr directly, the user can provide a pi0 value if desired. If no pi0 value is given, then pi0est

is called, and arguments can be passed to pi0est via the ... argument in lfdr. Type ?lfdr for further details on the various inputs for the lfdr function.

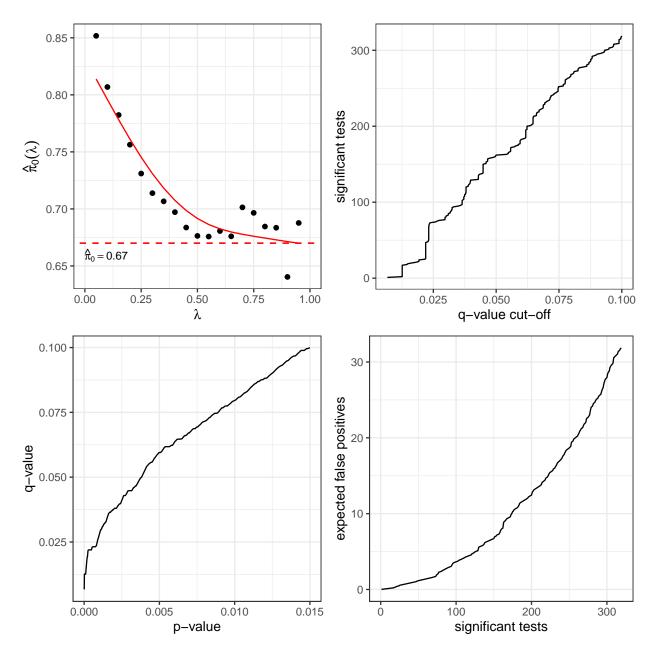
5.4 Visualizing results

The hist and plot functions can be used to visualize the results from qvalue. The function plot allows one to view several useful plots:

- The estimated π_0 versus the tuning parameter λ
- The q-values versus the p-values
- The number of significant tests versus each q-value cut-off
- The number of expected false positives versus the number of significant tests

Applying plot to the hedenfalk qvalue object, we get:

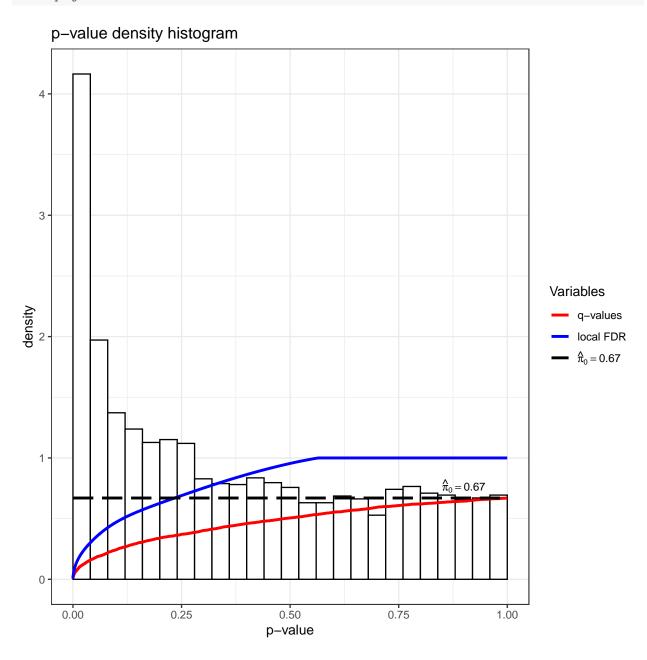
plot(qobj)



The main purpose of the upper-left plot is to gauge the reliability of the π_0 estimate, where the estimated π_0 is plotted versus the tuning parameter λ . The variable λ is called lambda in the package; it can be fixed or automatically handled. As λ gets larger, the bias of the estimate decreases, yet the variance increases. When pi0.method = "smoother" is utilized, the fitted smoother is also shown in this plot. See Storey (2002) [2] for more on λ and its role in estimating π_0 . Comparing your final estimate of π_0 to this plot gives a good sense as to its quality.

The remaining plots show how many tests are significant, as well as how many false positives to expect for each q-value cut-off.

Additionally, running hist on a q-value object can be used to view the histogram of p-values along with line plots of both q-values and local FDR values versus the p-values:



6 Point-and-click implementation

A Shiny implementation of the package written by Andrew Bass can be found at http://qvalue.princeton.edu.

7 Frequently asked questions

1. This package produces "adjusted p-values", so how is it possible that my adjusted p-values are smaller than my original p-values?

The q-value is not an adjusted p-value, but rather a population quantity with an explicit definition (see [1, 2, 3]). The package produces estimates of q-values and the local FDR, both of which are very different from p-values. The package does not perform a Bonferroni correction on p-values, which returns adjusted p-values that are larger than the original p-values. The maximum possible q-value is π_0 , the proportion of true null hypotheses. The maximum possible p-value is 1. When considering a large number of hypothesis tests where there is a nontrivial fraction of true alternative p-values, we will have both an estimate $\pi_0 < 1$ and we will have some large p-values close to 1. Therefore, the maximal estimated q-value will be less than or equal to the estimated π_0 but there will also be a number of p-values larger than the estimated π_0 . It must be the case then that at some point p-values become larger than estimated q-values.

8 Obtaining updates on qualue

The easiest way to obtain the most recent (development) version of qvalue is to visit https://github.com/jdstorey/qvalue/. Bug fixes will appear on GitHub earlier than on Bioconductor, and suggested changes can also be made there.

Acknowledgements

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References

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