

# quasispectral

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**2019-05-11**

## Using quasispectral

To download the library, first install the “devtools” package, which will allow you to install packages from github; this only needs to be done once:

```
install.packages("devtools")
```

Then install the quasispectral package from github:

```
devtools::install_github("mooredf22/quasispectral")
```

This will make the functions and data in the package available to you in R.

Next, load the libraries; the libraries `QuasiSeq` and `fdrtool` must have been previously installed from CRAN.

```
library(QuasiSeq)
library(fdrtool)
library(quasispectral)
```

The first few lines of the data may be examined:

```
head(spectralData_CLN1_late)
#>   geneName CLN1.1 CLN1.2 CLN1.3 CLN1.4 CLN1.5 CLN1.6 wt.1 wt.2 wt.3 wt.4
#> 1    Aga    149    142     67    135    150    142    135    155    159    202
#> 2   Arsa    577    542    314    601    569    590    602    639    617    599
#> 3   Arsb    466    482    258    409    465    465    624    599    645    688
#> 4   Arsg     68     65     41     55     69     63     87     84     46     98
#> 5   Arsk     59     60     22     39     45     54     75     75     80    107
#> 6  Asah1    806    905    533    729    748    827    865    812    887    861
#>   wt.5 wt.6
#> 1  195  181
#> 2  613  631
#> 3  662  667
#> 4  107   99
#> 5   77   79
#> 6  918  904
```

The first column is the gene name, the next 6 columns are spectral counts for mutant animals, and the final 6 columns are counts for wildtype animals.

Finally, call the package as follows, and look at the first few lines of output:

```
result.QLfit <- quasiSpectral(spectralDataAll=spectralData_CLN1_late, n.mut=6, n.wt=6)
#> Currently, bias reduction has not yet been implemented for Poisson model.
#> Spline scaling factor: 0.983018553199358
#> Warning in fdrtool(p.values, statistic = "pvalue"): There may be too few
```

```
#> input test statistics for reliable FDR calculations!
#> Step 1... determine cutoff point
#> Step 2... estimate parameters of null distribution and eta0
#> Warning: Censored sample for null model estimation has only size 8 !
#> Step 3... compute p-values and estimate empirical PDF/CDF
#> Step 4... compute q-values and local fdr
#> Step 5... prepare for plotting
```

```
QLfit.out <- result.QLfit$QLfit
```

```
head(QLfit.out)
```

```
#>  geneName CLN1.1 CLN1.2 CLN1.3 CLN1.4 CLN1.5 CLN1.6 wt.1 wt.2 wt.3 wt.4
#> 1      Aga    149    142     67    135    150    142    135    155    159    202
#> 2     Arsa    577    542    314    601    569    590    602    639    617    599
#> 3     Arsb    466    482    258    409    465    465    624    599    645    688
#> 4     Arsg     68     65     41     55     69     63     87     84     46     98
#> 5     Arsk     59     60     22     39     45     54     75     75     80    107
#> 6    Asah1    806    905    533    729    748    827    865    812    887    861
#>  wt.5 wt.6 coef.main      p.values p.values.bonf p.values.holm
#> 1   195   181 0.3129084 1.254920e-03 1.016486e-01 4.141237e-02
#> 2   613   631 0.1382393 5.303151e-03 4.295553e-01 1.198925e-01
#> 3   662   667 0.5354857 4.922626e-11 3.987327e-09 3.790422e-09
#> 4   107    99 0.4545213 3.430625e-03 2.778806e-01 8.919292e-02
#> 5    77    79 0.7465593 6.204245e-06 5.025439e-04 2.978038e-04
#> 6   918   904 0.1314973 1.497866e-02 1.000000e+00 2.845946e-01
#>  q.values.BH q.values.strimmer
#> 1 2.074460e-03    2.914893e-04
#> 2 7.159254e-03    1.029129e-03
#> 3 7.974655e-10    1.120724e-10
#> 4 4.875099e-03    7.007858e-04
#> 5 1.478070e-05    2.104575e-06
#> 6 1.925828e-02    2.698284e-03
```

To see the estimated proportion of null samples in the population, from `fdrtool`, look at `eta0`:

```
result.QLfit$eta0      # estimated proportion of null samples in population
#> [1] 0.143748
```