

DEGreport

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Package

DEGreport 1.14.1

Contents

1	General QC figures from DE analysis	2
1.1	Size factor QC	2
1.2	Mean-Variance QC plots	3
1.3	Covariates effect on count data	4
1.4	Covariates correlation with metrics	5
1.5	QC report	5
2	Report from DESeq2 analysis	5
2.1	Contrasts.	6
2.2	Volcano plots.	8
2.3	Gene plots	9
2.4	Full report	10
2.5	Interactive shiny-app	13
3	Detect patterns of expression.	13
4	Useful functions.	14

```
library(DEGreport)
data(humanGender)
```

1 General QC figures from DE analysis

We are going to do a differential expression analysis with edgeR/DESeq2. We have an object that is coming from the edgeR package. It contains a gene count matrix for 85 TSI HapMap individuals, and the gender information. With that, we are going to apply the 'glmFit' function or 'DESeq2' to get genes differentially expressed between males and females.

```
library(DESeq2)
idx <- c(1:10, 75:85)
dds <- DESeqDataSetFromMatrix(assays(humanGender)[[1]][1:1000, idx],
                             colData(humanGender)[idx,], design=~group)

dds <- DESeq(dds)
res <- results(dds)
```

We need to extract the experiment design data.frame where the condition is Male or Female.

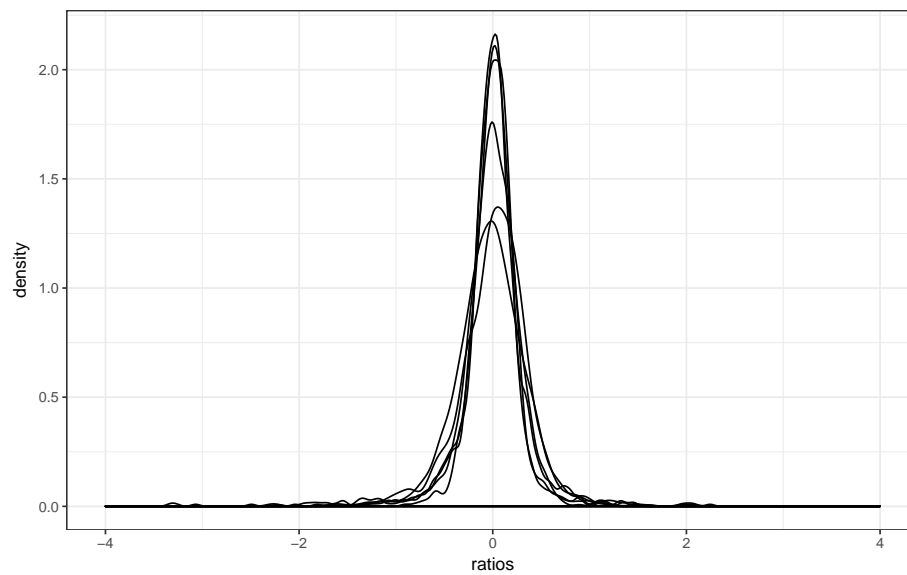
```
counts <- counts(dds, normalized = TRUE)
design <- as.data.frame(colData(dds))
```

1.1 Size factor QC

A main assumption in library size factor calculation of edgeR and DESeq2 (and others) is that the majority of genes remain unchanged. Plotting the distribution of gene ratios between each gene and the average gene can show how true this is. Not super useful for many samples because the plot becomes crowded.

```
degCheckFactors(counts[, 1:6])

## Warning in bind_rows_(x, .id): Unequal factor levels: coercing to character
## Warning in bind_rows_(x, .id): binding character and factor vector, coercing
## into character vector
## Warning in bind_rows_(x, .id): binding character and factor vector, coercing
## into character vector
## Warning in bind_rows_(x, .id): binding character and factor vector, coercing
## into character vector
## Warning in bind_rows_(x, .id): binding character and factor vector, coercing
## into character vector
## Warning in bind_rows_(x, .id): binding character and factor vector, coercing
## into character vector
## Warning in bind_rows_(x, .id): binding character and factor vector, coercing
## into character vector
```



1.2 Mean-Variance QC plots

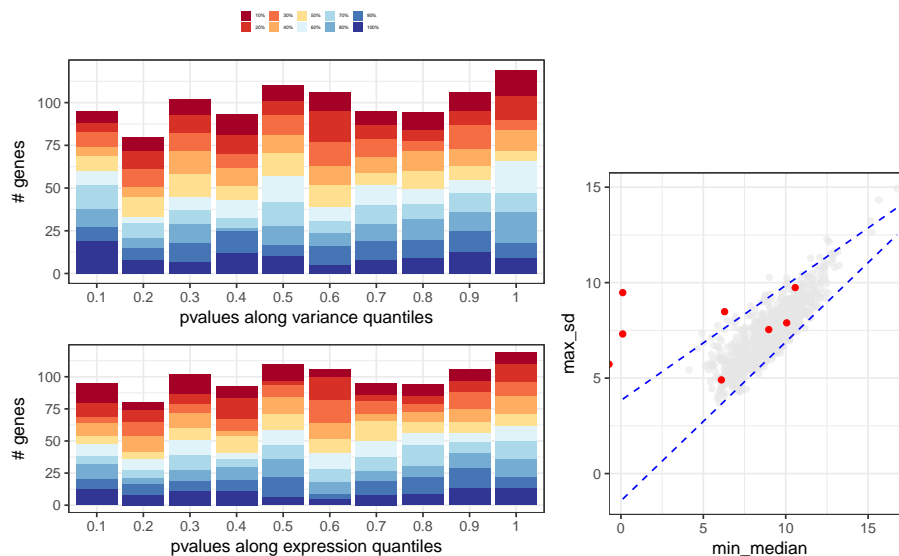
p-value distribution gives an idea on how well your model is capturing the input data and as well whether it could be some problem for some set of genes. In general, you expect to have a flat distribution with peaks at 0 and 1. In this case, we add the mean count information to check if any set of genes are enriched in any specific p-value range.

Variation (dispersion) and average expression relationship shouldn't be a factor among the differentially expressed genes. When plotting average mean and standard deviation, significant genes should be randomly distributed.

In this case, it would be good to look at the ones that are totally outside the expected correlation.

You can put these plots together using `degQC`.

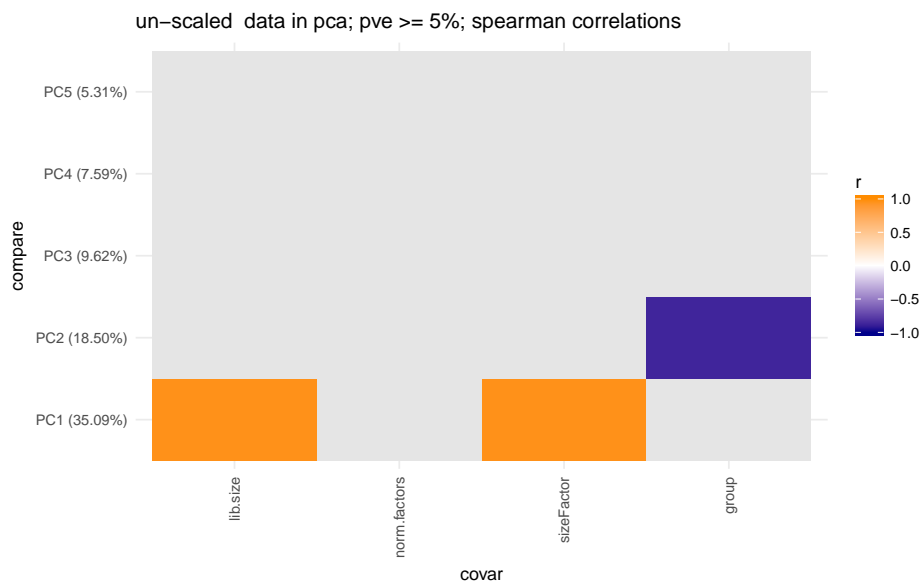
```
degQC(counts, design[["group"]], pvalue = res[["pvalue"]])
```



1.3 Covariates effect on count data

Another important analysis to do if you have covariates is to calculate the correlation between PCs from PCA analysis to different variables you may think are affecting the gene expression. This is a toy example of how the function works with raw data, where clearly library size correlates with some of the PCs.

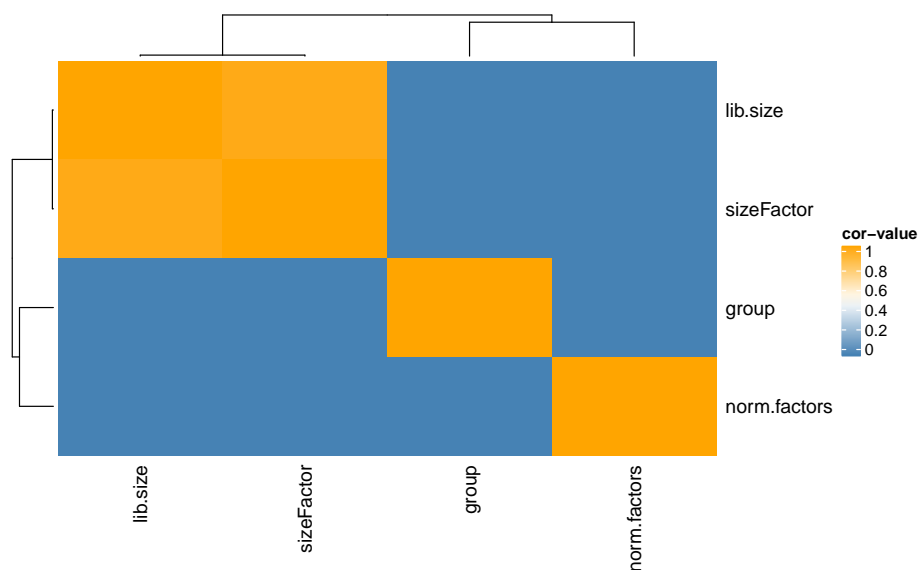
```
resCov <- degCovariates(log2(counts(dds)+0.5),
                        colData(dds))
```



1.4 Covariates correlation with metrics

Also, the correlation among covariates and metrics from the analysis can be tested. This is useful when the study has multiple variables, like in clinical trials. The following code will return a correlation table, and plot the correlation heatmap for all the covariates and metrics in a table.

```
cor <- degCorCov(colData(dds))
```



```
names(cor)
## [1] "cor"      "corMat"   "fdrMat"   "plot"
```

1.5 QC report

A quick HTML report can be created with `createReport` to show whether a DE analysis is biased to a particular set of genes. It contains the output of `degQC`, `degVB` and `degMB`.

```
createReport(colData(dds)[["group"]], counts(dds, normalized = TRUE),
             row.names(res)[1:20], res[["pvalue"]], path = "~/Downloads")
```

2 Report from DESeq2 analysis

Here, we show some useful plots for differentially expressed genes.

2.1 Contrasts

DEGSet is a class to store the DE results like the one from `results` function. *DESeq2* offers multiple way to ask for contrasts/coefficients. With `degComps` is easy to get multiple results in a single object:

```
degs <- degComps(dds, combs = "group",
                 contrast = list("group_Male_vs_Female",
                                c("group", "Female", "Male")))

names(degs)

## [1] "group_Male_vs_Female" "group_Female_vs_Male"
```

`degs` contains 3 elements, one for each contrast/coefficient asked for. It contains the results output in the element `raw` and the output of `lfcShrink` in the element `shrunk`. To obtain the results from one of them, use the method `dge`:

```
deg(degs[[1]])

## log2 fold change (MAP): group Male vs Female
## Wald test p-value: group Male vs Female
## DataFrame with 1000 rows and 6 columns
##
```

	baseMean	log2FoldChange	lfcSE	stat
	<numeric>	<numeric>	<numeric>	<numeric>
ENSG000000067048	1025.03783	1.9394875	0.10069402	23.994380
ENSG00000012817	411.54387	3.7005640	0.09898885	21.804517
ENSG000000067646	169.81477	3.3228457	0.09951933	15.483847
ENSG000000005889	670.86191	-0.4894347	0.09293631	-5.263708
ENSG000000006757	92.66111	-0.4729262	0.09927492	-4.757006
...
ENSG000000068120	1214.0967	-0.0001143219	0.07972266	-0.001433998
ENSG000000072062	935.3172	0.0005592191	0.09153522	0.006108720
ENSG000000076770	1019.7964	0.0008500818	0.10166633	0.008361930
ENSG000000078967	166.4221	0.0004157454	0.09597580	0.004329710
ENSG000000079246	5226.3390	0.0001495843	0.09262051	0.001614995

```
##
```

	pvalue	padj
	<numeric>	<numeric>
ENSG000000067048	3.183020e-127	3.183020e-124
ENSG00000012817	2.102139e-105	1.051070e-102
ENSG000000067646	4.459844e-54	1.486615e-51
ENSG000000005889	1.411785e-07	3.529463e-05
ENSG000000006757	1.964856e-06	3.929713e-04
...
ENSG000000068120	0.9988558	0.9988558
ENSG000000072062	0.9951260	0.9988558
ENSG000000076770	0.9933282	0.9988558
ENSG000000078967	0.9965454	0.9988558
ENSG000000079246	0.9987114	0.9988558

By default it would output the `shrunk` table always, as defined by `degDefault`, that contains the default table to get.

To get the original results table, use the parameter as this:

DEGreport

```
deg(degs[[1]], "raw", "tibble")

## # A tibble: 1,000 x 7
##       gene      baseMean log2FoldChange      lfcSE      stat
## *    <chr>      <dbl>          <dbl>      <dbl>      <dbl>
## 1 ENSG00000067048 1025.03783      10.1571705 0.42331456 23.994380
## 2 ENSG00000012817  411.54387       9.2394007 0.42373792 21.804517
## 3 ENSG00000067646  169.81477     10.1874916 0.65794317 15.483847
## 4 ENSG00000005889   670.86191     -0.6919265 0.13145228 -5.263708
## 5 ENSG00000006757    92.66111     -0.7666012 0.16115204 -4.757006
## 6 ENSG00000073282   220.15603     -1.8685615 0.42061202 -4.442482
## 7 ENSG00000005302  2026.54990     -0.7418952 0.17634123 -4.207157
## 8 ENSG00000005020  1233.86316      0.3888370 0.09523118  4.083085
## 9 ENSG00000003400   393.62677      0.6803243 0.17664751  3.851310
## 10 ENSG00000069702  106.67010     -1.6323189 0.45856109 -3.559654
## # ... with 990 more rows, and 2 more variables: pvalue <dbl>, padj <dbl>
```

Note that the format of the output can be changed to tibble, or data.frame with a third parameter `tidy`.

The table will be always sorted by `padj`.

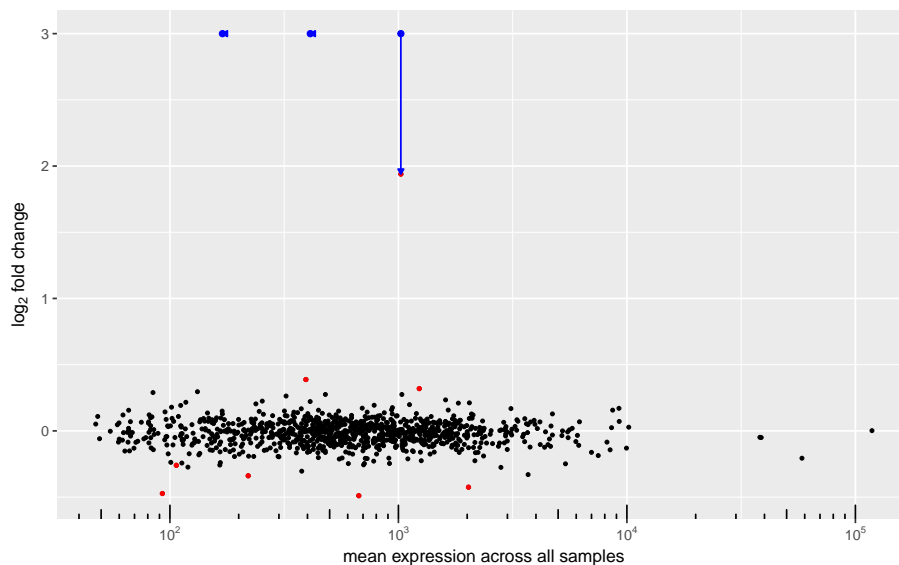
And easy way to get significant genes is:

```
significants(degs[[1]], fc = 0, fdr = 0.05)

## [1] "ENSG00000012817" "ENSG00000067646" "ENSG00000067048" "ENSG00000005889"
## [5] "ENSG00000006757" "ENSG00000005302" "ENSG00000003400" "ENSG00000073282"
## [9] "ENSG00000005020" "ENSG00000069702"
```

Since `log2FoldChange` are shrunken, the method for `DEGSet` class now can plot these changes as follow:

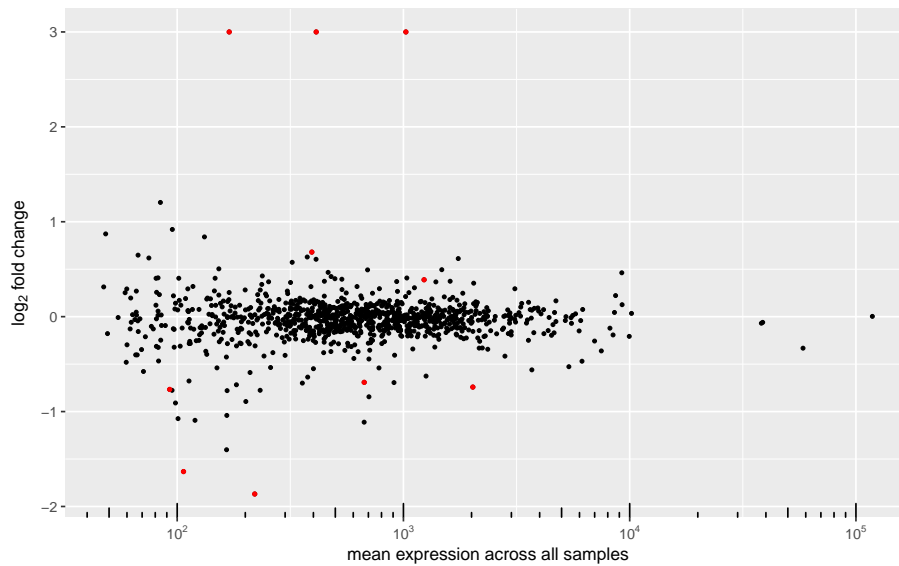
```
plotMA(degs[[1]], diff = 2, limit = 3)
```



The blue arrows indicate how foldchange is affected by this new feature.

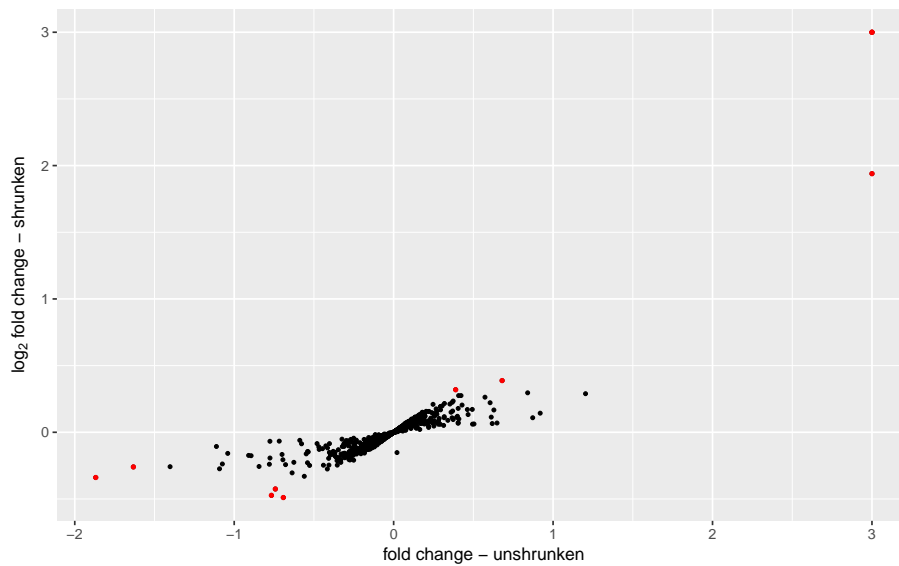
As well, it can plot the original MA plot:

```
plotMA(degs[[1]], diff = 2, limit = 3, raw = TRUE)
```



or the correlation between the original log2FoldChange and the new ones:

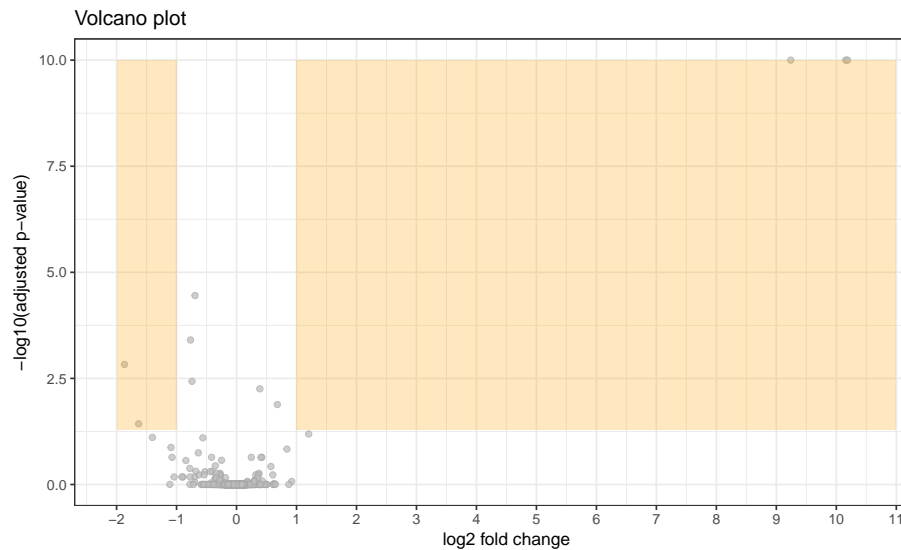
```
plotMA(degs[[1]], limit = 3, correlation = TRUE)
```



2.2 Volcano plots

Volcano plot using the output of *DESeq2*. It mainly needs data.frame with two columns (logFC and pVal). Specific genes can be plot using the option `plot_text` (subset of the previous data.frame with a 3rd column to be used to plot the gene name).


```
res[["id"]] <- row.names(res)
# show <- as.data.frame(res[1:10, c("log2FoldChange", "padj", "id")])
degVolcano(res[,c("log2FoldChange", "padj")])
```

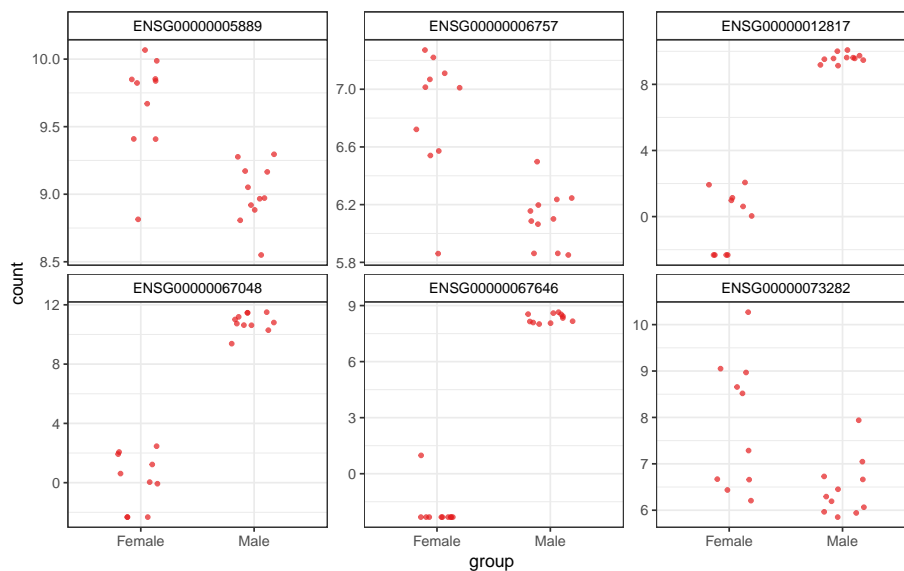


Note that the function is compatible with DEGset. Using `degVolcano(degs[[1]])` is valid.

2.3 Gene plots

Plot top genes coloring by group. Very useful for experiments with nested groups. 'xs' can be 'time' or 'WT'/'KO', and 'group' can be 'treated'/'untreated'. Another classification can be added, like 'batch' that will plot points with different shapes.

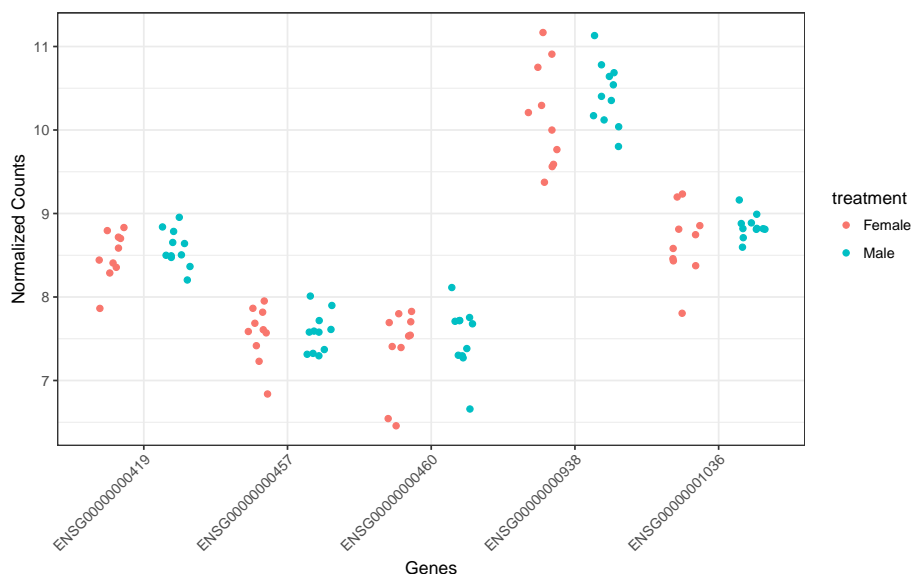
```
degPlot(dds = dds, res = res, n = 6, xs = "group")
```



DEGreport

Another option for plotting genes in a wide format:

```
degPlotWide(dds, rownames(dds)[1:5], group="group")
```



2.4 Full report

If you have a DESeq2 object, you can use `degResults` to create a full report with markdown code inserted, including figures and table with top de-regulated genes, GO enrichment analysis and heatmaps and PCA plots. If you set `path_results`, different files will be saved there.

```
resreport <- degResults(dds = dds, name = "test", org = NULL,  
                        do_go = FALSE, group = "group", xs = "group",  
                        path_results = NULL)
```

```
## ## Comparison: test {.tabset}
```

```
##
```

```
##
```

```
## <br>out of 1000 with nonzero total read count<br>adjusted p-value < 0.1<br>LFC > 0 (up) : 6, 0.6% <br>
```

```
##
```

```
##
```

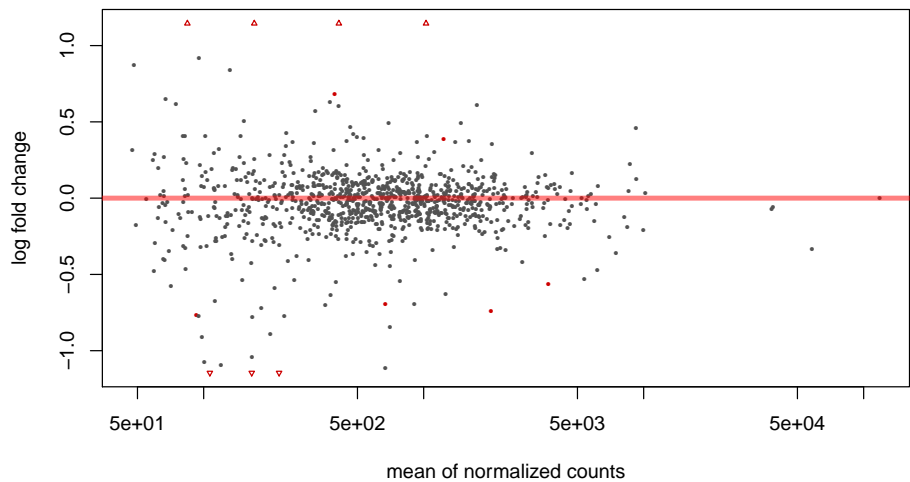
```
## Differential expression file at: test_de.csv
```

```
##
```

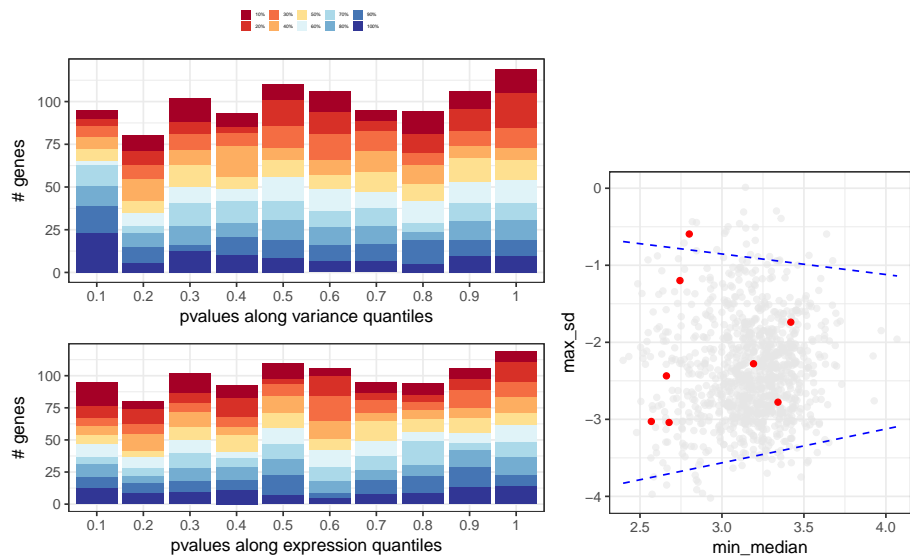
```
## Normalized counts matrix file at: test_log2_counts.csv
```

```
##
```

```
## ### MA plot plot
```

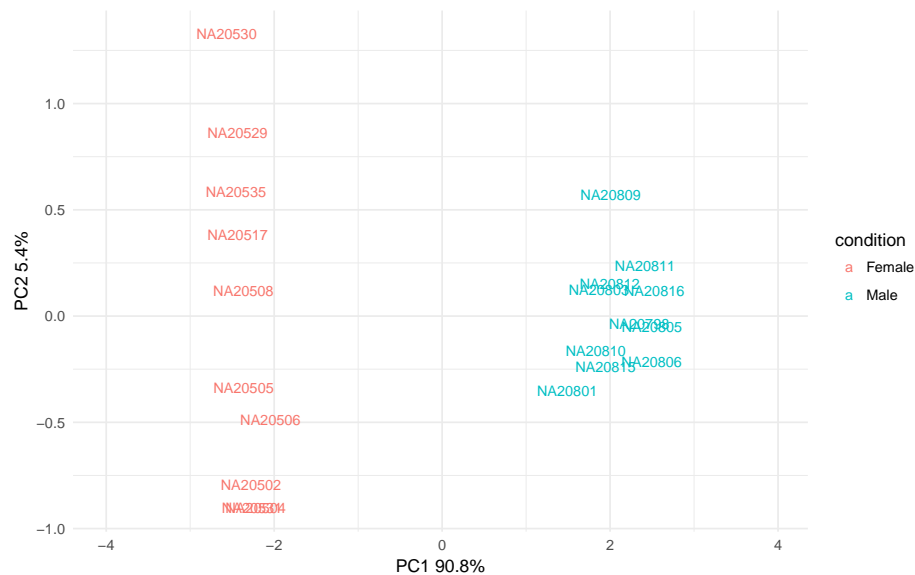


```
##
##
## ### Volcano plot
##
##
##
## ### QC for DE genes
```



```
##
##
## ### Most significants, FDR< 0.05 and log2FC > 0.1 : 10
```

DEGreport



```
##
##
##
## ### Plots top 9 most significant
##
##
##
## ### Top DE table
##
##
## \begin{tabular}{l|r|r|r|r|r|r|r}
## \hline
##   & baseMean & log2FoldChange & lfcSE & stat & pvalue & padj & absMaxLog2FC\\
## \hline
## ENSG00000067048 & 1025.03783 & 10.1571705 & 0.4233146 & 23.994380 & 0.0000000 & 0.0000000 & 10.1571705\\
## \hline
## ENSG00000012817 & 411.54387 & 9.2394007 & 0.4237379 & 21.804517 & 0.0000000 & 0.0000000 & 9.2394007\\
## \hline
## ENSG00000067646 & 169.81477 & 10.1874916 & 0.6579432 & 15.483847 & 0.0000000 & 0.0000000 & 10.1874916\\
## \hline
## ENSG00000005889 & 670.86191 & -0.6919265 & 0.1314523 & -5.263708 & 0.0000001 & 0.0000353 & 0.6919265\\
## \hline
## ENSG00000006757 & 92.66111 & -0.7666012 & 0.1611520 & -4.757006 & 0.0000020 & 0.0003930 & 0.7666012\\
## \hline
## ENSG00000073282 & 220.15603 & -1.8685615 & 0.4206120 & -4.442482 & 0.0000089 & 0.0014821 & 1.8685615\\
## \hline
## ENSG00000005302 & 2026.54990 & -0.7418952 & 0.1763412 & -4.207157 & 0.0000259 & 0.0036943 & 0.7418952\\
## \hline
## ENSG00000005020 & 1233.86316 & 0.3888370 & 0.0952312 & 4.083085 & 0.0000444 & 0.0055552 & 0.3888370\\
## \hline
## ENSG00000003400 & 393.62677 & 0.6803243 & 0.1766475 & 3.851310 & 0.0001175 & 0.0130542 & 0.6803243\\
## \hline
## ENSG000000069702 & 106.67010 & -1.6323189 & 0.4585611 & -3.559654 & 0.0003713 & 0.0371343 & 1.6323189\\
```

```
## \hline
## ENSG00000010278 & 84.30823 & 1.2035871 & 0.3554857 & 3.385754 & 0.0007098 & 0.0645300 & 1.2035871\\
## \hline
## ENSG00000023171 & 165.31692 & -1.4022259 & 0.4236024 & -3.310240 & 0.0009322 & 0.0776799 & 1.4022259\\
## \hline
## ENSG00000072501 & 3694.76013 & -0.5604815 & 0.1707989 & -3.281529 & 0.0010325 & 0.0794200 & 0.5604815\\
## \hline
## ENSG00000070018 & 119.89049 & -1.0921227 & 0.3512409 & -3.109327 & 0.0018751 & 0.1339388 & 1.0921227\\
## \hline
## ENSG00000059377 & 131.98111 & 0.8405094 & 0.2744635 & 3.062372 & 0.0021959 & 0.1463935 & 0.8405094\\
## \hline
## ENSG00000008277 & 377.43955 & -0.6368732 & 0.2136506 & -2.980910 & 0.0028739 & 0.1796208 & 0.6368732\\
## \hline
## ENSG00000005059 & 479.12528 & 0.4225402 & 0.1492246 & 2.831571 & 0.0046320 & 0.2289281 & 0.4225402\\
## \hline
## ENSG00000012963 & 1829.21224 & 0.2471040 & 0.0861859 & 2.867104 & 0.0041425 & 0.2289281 & 0.2471040\\
## \hline
## ENSG00000038427 & 100.87217 & -1.0743654 & 0.3810269 & -2.819658 & 0.0048075 & 0.2289281 & 1.0743654\\
## \hline
## ENSG00000068079 & 1035.17996 & 0.4075632 & 0.1415563 & 2.879160 & 0.0039874 & 0.2289281 & 0.4075632\\
## \hline
## \end{tabular}
```

2.5 Interactive shiny-app

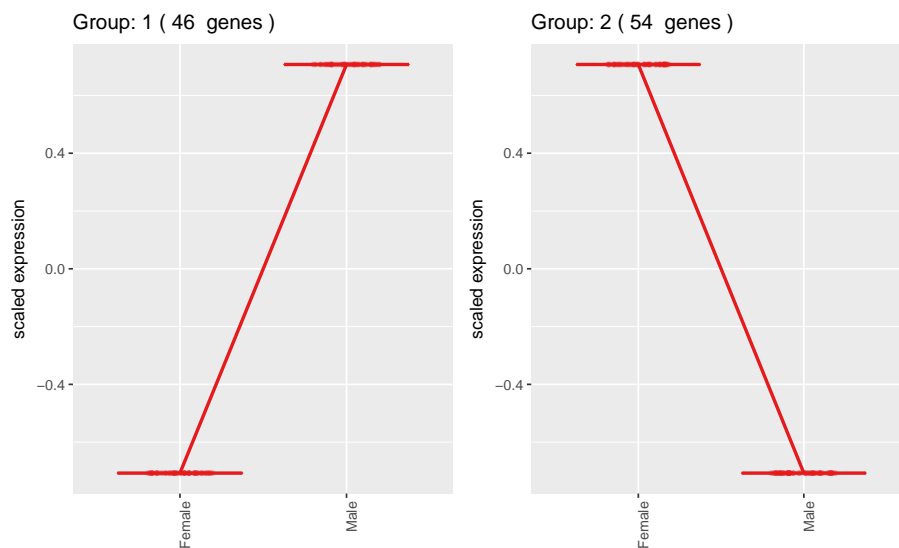
Browsing gene expression can help to validate results or select some gene for downstream analysis. Run the following lines if you want to visualize your expression values by condition:

```
degObj(counts, design, "degObj.rda")
library(shiny)
shiny::runGitHub("lpantano/shiny", subdir="expression")
```

3 Detect patterns of expression

In this section, we show how to detect pattern of expression. Mainly useful when data is a time course experiment. `degPatterns` needs a expression matrix, the design experiment and the column used to group samples.

```
ma = assay(rlog(dds))[row.names(res)[1:100],]
res <- degPatterns(ma, design, time = "group", col=NULL)
```



4 Useful functions

This section shows some useful functions during DEG analysis.

`degFilter` helps to filter genes with a minimum read count by group.

```
cat("gene in original count matrix: 1000")
## gene in original count matrix: 1000
filter_count <- degFilter(counts(dds),
                          design, "group",
                          min=1, minreads = 50)
cat("gene in final count matrix", nrow(filter_count))
## gene in final count matrix 940
```