

RNA-seq workshop

Differential expression analysis in R (subset of slides)

Mik Black
Genomics Aotearoa & University of Otago

What are we doing in this session?

- Differential expression analysis in R
- So far we have:
 - QC'd
 - Trimmed
 - Aligned
 - Generated counts per gene
- What is next?
 - use count data to detect differentially expressed genes
 - that involves some statistics....

But first...

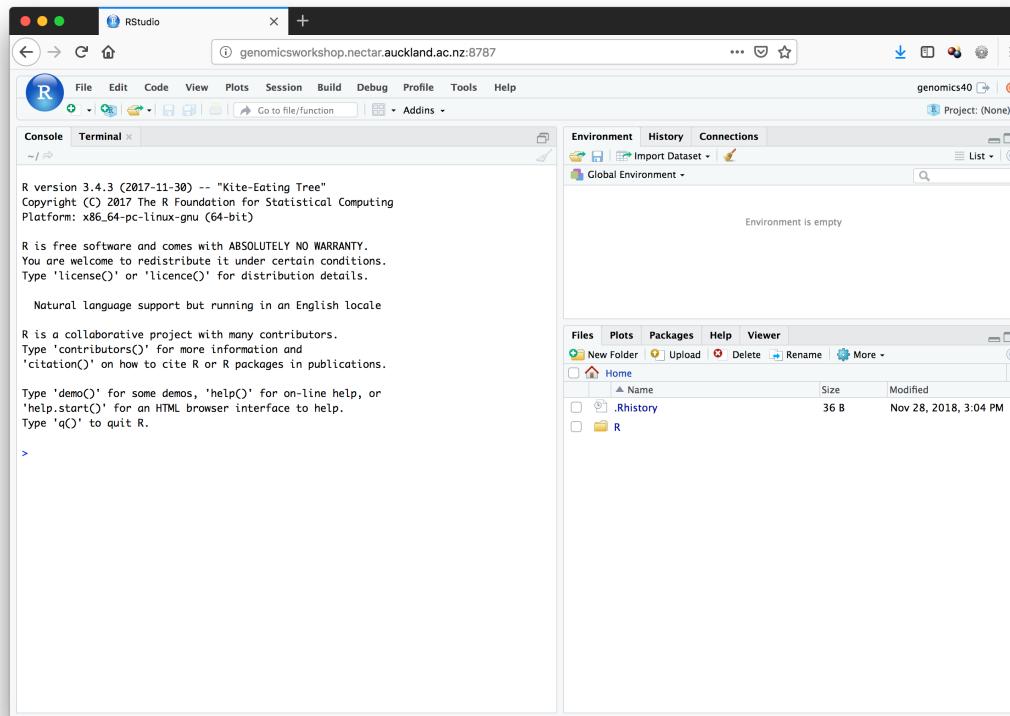
HUGE THANKS TO:

**Centre for eResearch
University of Auckland**

nectarinfo@auckland.ac.nz

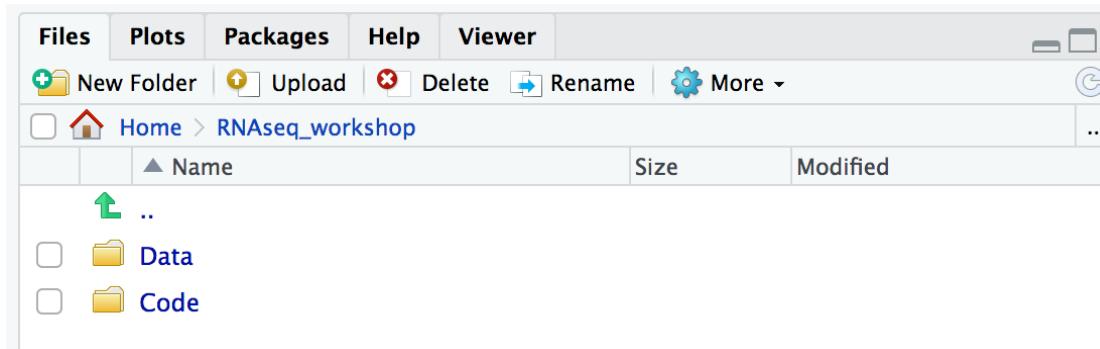
Working in R/RStudio

- Our virtual machine has an instance of RStudio Server running
- Log in at: <http://genomicsworkshop.nectar.auckland.ac.nz:8787>



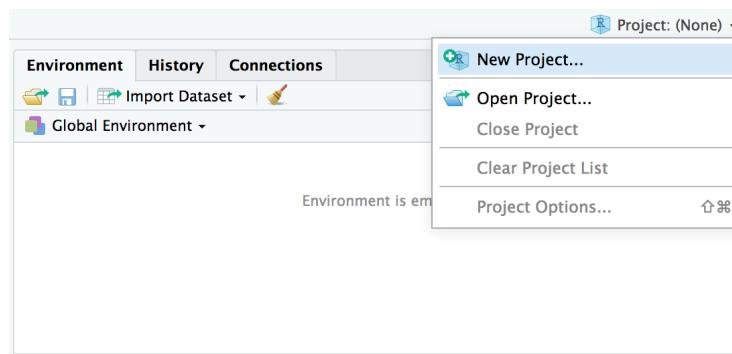
Gettings things set up

- Before we get started, we're going to set up a directory structure to work in, and create an "R project"
- It is good to keep things organised within an analysis project: here we'll set up a project folder called "RNAseq_workshop" using the "New Folder" button in RStudio, and then inside that folder we'll add two additional folders: "Data" and "Code".



Creating a "project"

- RStudio provides functionality to help us keep things organised across analysis projects.
- Use the "Project" menu in the upper right to create a "New Project":



- Choose to use an "Existing Directory" and then select the "RNAseq_workshop"" folder.
- Once you select "Create Project", R will restart, and we will be (almost) ready to do some analysis.

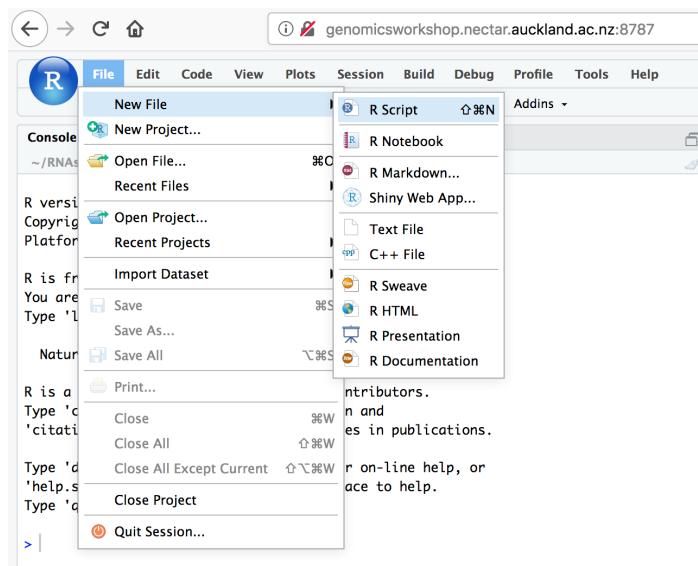
Getting our data

- The only data we need to identify differentially expressed genes is the file of count data that is generated with the `featureCounts` command.
 - We need to place this file in the "Data" folder.
 - To do this we will use the "terminal" feature of the RStudio interface (access this by clicking the "Terminal" tab next to the "Console" tab) to download the data.
 - In the terminal, navigate to the "Data"" directory, and then use the `wget` command to directly download the data from GitHub: the `wget` command and the link to the data can be copied from GitHub:

https://github.com/gregomics/RNAseqWorkshop2018/tree/master/differential_expression

One last thing..

- We are going to save our R commands in a file, in the "Code" folder.
- Create a new file using the "File" menu (choose "New File", "R Script"):



- You can then use "Save As..." (in the "File" menu) to save this file in the "Code" folder.

FeatureCounts

- Let's have a look at the count data:

```
readcounts <- read.table("Data/CountMat_NCBIM37.67.dat", header = TRUE)
```

```
dim(readcounts)
```

```
## [1] 37991     12
```

```
names(readcounts)
```

```
##  [1] "Geneid"    "Chr"       "Start"      "End"       "Strand"     "Length"     "WT1.bam"  
##  [8] "WT2.bam"   "WT3.bam"   "KO1.bam"   "KO2.bam"   "KO3.bam"
```

- What did we just do?

Viewing the data

```
head(readcounts)[,-c(2:6)]
```

```
##           Geneid WT1.bam WT2.bam WT3.bam KO1.bam KO2.bam KO3.bam
## 1 ENSMUSG00000000702      0      0      0      0      0      0
## 2 ENSMUSG00000078423      0      0      0      0      0      0
## 3 ENSMUSG00000078424      0      0      0      0      0      0
## 4 ENSMUSG00000071964      0      0      0      0      0      0
## 5 ENSMUSG00000093774      0      0      0      0      0      0
## 6 ENSMUSG00000093444      0      0      0      0      0      0
```

- You can also use the `View` command to open the internal viewer
- Best to combine with `head` unless you want to look at the whole file...

```
View( head(readcounts) )
```

Convert to nicer format

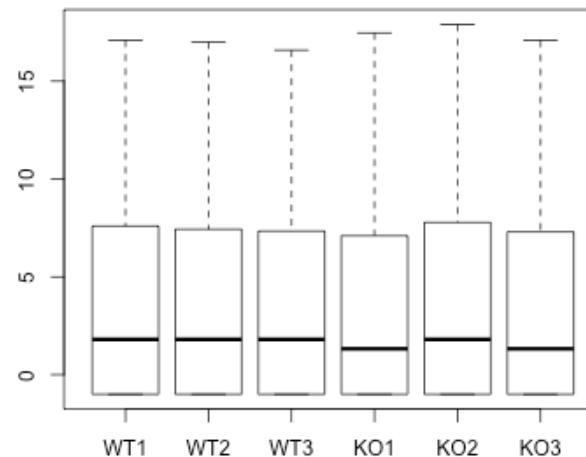
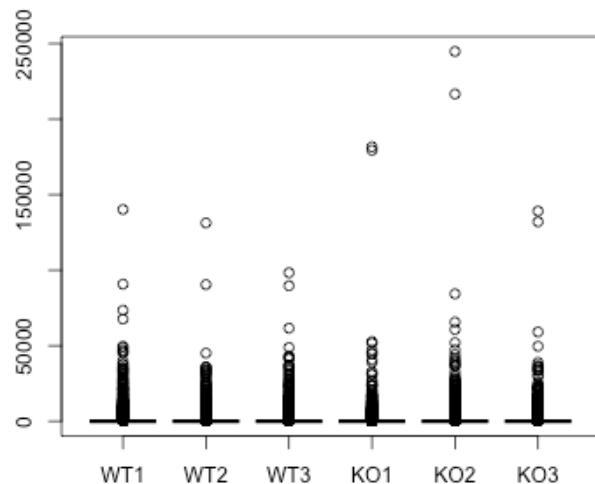
```
## Use the transcript IDs as the row names
row.names(readcounts) <- readcounts$Geneid
## Remove the non-count columns (and convert to a matrix)
counts <- as.matrix(readcounts[ , -c(1:6)])
## Remove the ".bam" suffix from the name of each column
colnames(counts) <- gsub(".bam", "", colnames(counts))
## Show the first 6 rows of the counts object
head(counts)
```

```
##                               WT1 WT2 WT3 KO1 KO2 KO3
## ENSMUSG00000000702      0   0   0   0   0   0
## ENSMUSG00000078423      0   0   0   0   0   0
## ENSMUSG00000078424      0   0   0   0   0   0
## ENSMUSG00000071964      0   0   0   0   0   0
## ENSMUSG00000093774      0   0   0   0   0   0
## ENSMUSG00000093444     0   0   0   0   0   0
```

Visualize the data: boxplots

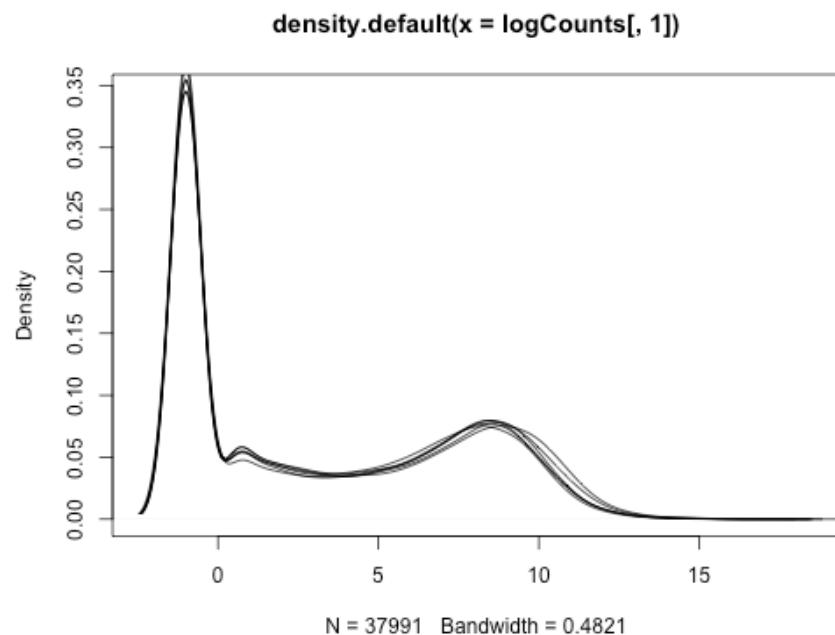
```
## Take logs of data (add 0.5 to avoid log(0) issues)
logCounts <- log2(counts + 0.5)
```

```
## Boxplots of original and logged data
boxplot(counts ~ col(counts), names=colnames(counts))
boxplot(logCounts ~ col(logCounts), names=colnames(counts))
```



Visualize the data: density plots

```
## Plot the density (distribution) for the first sample  
plot( density(logCounts[,1]) )  
## Use a loop to add the densities for the other samples  
for(i in 2:6) lines( density(logCounts[,i]) )
```



Data pre-processing

- Before we can do any statistical analysis, we need to do some "pre-processing" of the data to:
 - make sure the data are comparable across samples
 - make sure the data are suitable for statistical methods
- We will use the `edgeR` package to help with this (we'll hear more about `edgeR` and `limma` later).

```
library(edgeR)  
library(limma)
```

Create a DGEList object to work with

```
## Create DGEList object - use counts and gene length information  
dge <- DGEList(counts=counts, genes=data.frame( length=readcounts$Length) )  
names(dge)
```

```
## [1] "counts"  "samples" "genes"
```

```
dge$counts[1:2, ]
```

```
##                               WT1  WT2  WT3  KO1  KO2  KO3  
## ENSMUSG00000000702      0    0    0    0    0    0  
## ENSMUSG00000078423      0    0    0    0    0    0
```

```
dge$genes[1:2, ]
```

```
## [1] 1037 1051
```

Create a **DGEList** object to work with

```
dge$samples
```

```
##      group lib.size norm.factors
## WT1      1 12108291          1
## WT2      1  9772751          1
## WT3      1  9855150          1
## KO1      1  8868643          1
## KO2      1 13422084          1
## KO3      1  9638012          1
```

- Note that the **lib.size** info is the total number of reads for each sample.
- This gets used in the preprocessing stage so that the amount of data for each sample is taken into account.

Define our groups and the "design matrix"

```
groups <- rep(c("WT", "KO"), c(3,3))
groups
```

```
## [1] "WT" "WT" "WT" "KO" "KO" "KO"
```

```
design <- model.matrix(~groups)
design
```

```
## (Intercept) groupsWT
## 1           1           1
## 2           1           1
## 3           1           1
## 4           1           0
## 5           1           0
## 6           1           0
## attr(,"assign")
## [1] 0 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
```

Use filtering to remove very low count genes

```
## Figure out what to keep: output is TRUE/FALSE for each gene
keep <- filterByExpr(dge, design)
## Make table of TRUE and FALSE
table(keep)
```

```
## keep
## FALSE  TRUE
## 21651 16340
```

```
## Apply filtering and recalculate library sizes
dge <- dge[keep, keep.lib.sizes=FALSE]
## Calculate normalisation factor (i.e., account for total reads per sample)
dge <- calcNormFactors(dge)
```

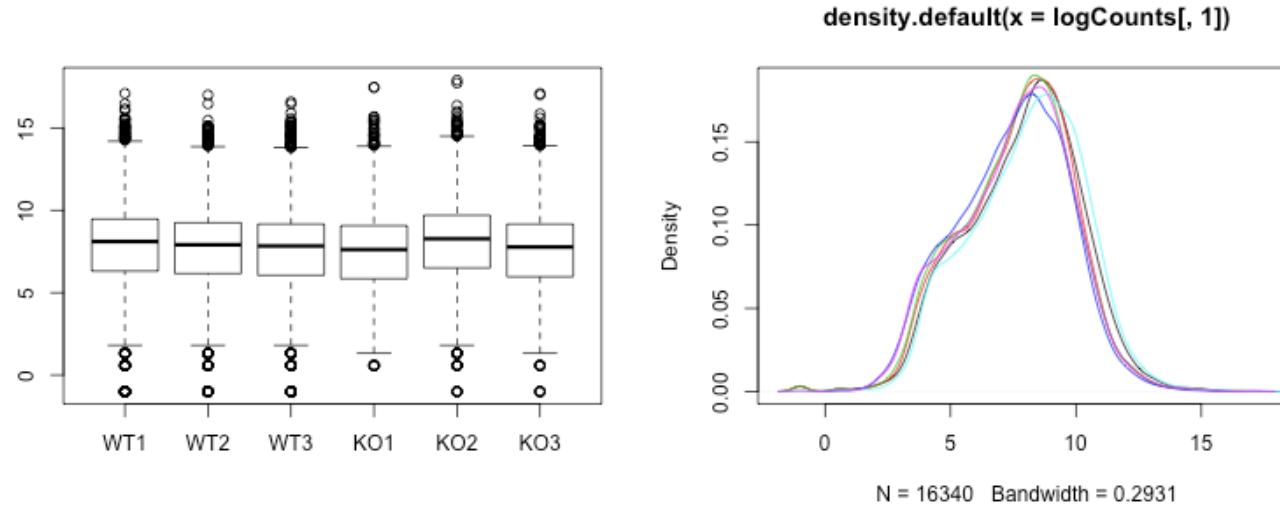
New DGEList object

```
dge
```

```
## An object of class "DGEList"
## $counts
##                               WT1  WT2  WT3  KO1  KO2  KO3
## ENSMUSG00000063889    79   69   43   63  104   66
## ENSMUSG00000024231   324  356  299  453  725  369
## ENSMUSG00000024232   389  344  317  174  302  222
## ENSMUSG00000073647    63   95   69  127  182   67
## ENSMUSG00000024235   281  222  177  326  390  148
## 16335 more rows ...
##
## $samples
##      group lib.size norm.factors
## WT1     1 12083144      1.0015
## WT2     1  9752121      1.0494
## WT3     1  9831590      0.9952
## KO1     1  8849450      0.9627
## KO2     1 13398664      0.9938
## KO3     1  9622437      0.9992
```

Visualise the new data

```
## Make log count data  
logCounts <- log2(dge$counts + 0.5)  
## Boxplots  
boxplot(logCounts ~ col(logCounts), names=colnames(logCounts))  
## Density plots  
plot(density(logCounts[,1]))  
for(i in 2:ncol(logCounts)) lines(density(logCounts[,i]), col=i)
```



Counts per million

```
## Generate "counts per million", based on gene lengths
logCPM <- cpm(dge, log=TRUE, prior.count=0.5)
head(logCPM)
```

```
##                               WT1     WT2     WT3      KO1      KO2      KO3
## ENSMUSG00000063889 2.7171 2.763 2.151 2.8956 2.974 2.789
## ENSMUSG00000024231 4.7453 5.122 4.936 5.7338 5.768 5.264
## ENSMUSG00000024232 5.0087 5.073 5.020 4.3555 4.506 4.532
## ENSMUSG00000073647 2.3932 3.222 2.828 3.9024 3.778 2.811
## ENSMUSG00000024235 4.5403 4.442 4.181 5.2597 4.875 3.949
## ENSMUSG00000090484 0.3637 1.001 1.064 0.6536 1.745 1.089
```

Aside: RPKM values

- RPKM stands for "reads per kilobase of exon model per million mapped reads"
- Used to adjust for:
 - total number of reads generated per sample
 - gene length
- Similar measure (FPKM, F='Fragments') used for paired-end data.

$$\begin{aligned} RPKM &= \frac{\text{Reads per transcript}}{\frac{\text{total reads}}{1,000,000} \times \frac{\text{transcript length}}{1000}} \\ &= \frac{\text{Reads per transcript}}{\text{million reads} \times \text{transcript length (kb)}} \end{aligned}$$

RPKM in R

- Here is how to calculate RPKM values in R, but we are not going to use them.

```
## Use genelength data from dge to calculate rpkm values (not on log scale)
rpkmData <- rpkm(dge)
head(rpkmData)
```

```
##          WT1      WT2      WT3      KO1      KO2      KO3
## ENSMUSG00000063889 1.0996  1.1356  0.7402  1.2455  1.315  1.1562
## ENSMUSG00000024231 6.0020  7.7978  6.8500  11.9189 12.205  8.6030
## ENSMUSG00000024232 6.3782  6.6693  6.4280  4.0522  4.500  4.5812
## ENSMUSG00000073647 6.9416  12.3770 9.4024  19.8753 18.224  9.2911
## ENSMUSG00000024235 5.1557  4.8162  4.0163  8.4955  6.503  3.4176
## ENSMUSG00000090484 0.3775  0.5951  0.6224  0.4646  1.006  0.6334
```

Analysis with `limma`

- Once the data have been normalized, the `limma` package can be used to detect genes undergoing differential expression.
 - On the log scale this is simply a difference between two means, for each gene/transcript represented in the pre-processed count data.
- There are many tools available to do this (both in `R`, and elsewhere), but my favourite is the `limma` package.

The limma package

- The `limma` package is available as part of Bioconductor (<http://www.bioconductor.org>)
- Developed by Gordon Smyth and colleagues at the Walter and Eliza Hall Institute in Melbourne: <http://bioinf.wehi.edu.au/limma/>
- Provides tools for the normalization and analysis of gene expression data: microarrays and RNA-seq data.

Fold changes

- Differential expression (i.e., a change in gene activation level) is often reported as a *fold change* in activity.
- Often the \log_2 scale is used (i.e., log fold change).
- Initially, genes with fold changes greater than 2 ($\log_2(2) = 1$) or less than $1/2$ ($\log_2(\frac{1}{2}) = -1$) were considered to have undergone differential expression.

Determining differential expression

- Assume that we want to investigate differences in gene expression between our two cell lines, WT and KO.
- We have three replicates of the WT samples and three replicates of the KO samples.
- For each gene we have 6 data points for each gene (3 in each group, WT and KO).
- For gene k this gives:
 - Group 1 (WT): x_{11}, x_{12}, x_{13}
 - Group 2 (KO): x_{21}, x_{22}, x_{23}

Hypothesis testing

- In statistics, we think of our sample means as providing estimates of the underlying (true) population means for each gene, μ_1 and μ_2 .
- For each gene, we want to test the following null hypothesis: $H_0 : \mu_1 = \mu_2$ against the alternative hypothesis: $H_A : \mu_1 \neq \mu_2$
- If we reject the null hypothesis for a particular gene, we think that gene is likely to be differentially expressed.

Hypothesis testing

- In order to conduct the hypothesis test, we need a test statistic. A simple approach (but not the best!) is to utilize the test statistic of the standard t-test:

$$T = \frac{\hat{\mu}_1 - \hat{\mu}_2}{SE(\hat{\mu}_1 - \hat{\mu}_2)}$$

where $\hat{\mu}_1$ and $\hat{\mu}_2$ are the sample means of the data, and $SE(\hat{\mu}_1 - \hat{\mu}_2)$ is some appropriate measure of variability (in this case the *standard error*).

- Various choices are possible for the denominator depending on the structure of the data.

Two sample t-test in R

```
## The function "t.test"" performs a two sample t-test in R.  
## Perform t-test on first gene in data set (first row of matrix:  
## first three values are WT, second three are KO):  
t.test(logCPM[1,] ~ groups)
```

```
##  
## Welch Two Sample t-test  
##  
## data: logCPM[1, ] by groups  
## t = 1.7, df = 2.3, p-value = 0.2  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## -0.4355 1.1202  
## sample estimates:  
## mean in group KO mean in group WT  
## 2.886 2.544
```

Two sample t-test in R

```
## very first gene does not appear to be  
## differentially expressed between the two groups:  
t.test(logCPM[1,]~groups)$p.value
```

```
## [1] 0.219
```

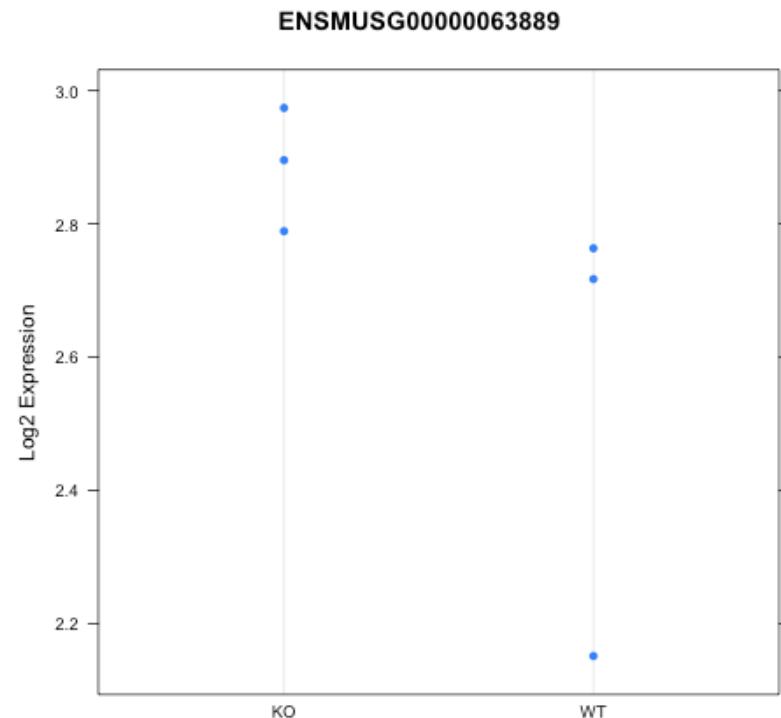
```
## How big is the change?  
2^(2.886-2.544)
```

```
## [1] 1.268
```

- Expression is 27% higher in the KO samples relative to the WT samples.
- Our statistical test tells us that this is not a significant result.

Visualize the data

```
## Examine expression graphically using a dotplot:  
lattice::dotplot(logCPM[1, ] ~ groups, main = rownames(logCPM)[1], ylab = "Log2 Expression")
```



P-values

- Once we have calculated a gene-specific test statistic, we can either use a t distribution, or resampling methods (e.g., randomization test) to calculate a p -value for each gene, p_k .
- The p -value represents the probability of observing this (or a more extreme) result, if no differential expression occurred. (i.e., what is the chance we are just observing noise?)
- We reject H_{0k} (i.e., say gene k is differentially expressed) if p_k is small.
- Question: what does small mean?

Type I errors

- Using a Type I error rate of $\alpha= 0.05$ means that we are willing to make a Type I error in 5% of our hypothesis tests (i.e., 5% of the time that the null hypothesis is true, we will say that it's false).
- So for every 20 hypothesis tests we perform, on average we expect 1 Type I error.
- What if we are performing 20,000 hypothesis tests?

1000 TYPE I ERRORS!

Adjusting the α level

- Obviously using an α level of 0.05 (or even 0.01) is not suitable when testing large numbers of hypotheses.
- To get around this problem we use Multiple Comparison Procedures (MCPs).
- MCPs provide error rate control, allowing us to keep a lid on how many Type I errors we make.

Family-wise error rate control

- Control of the family-wise error rate (FWER) is very common in multiple testing problems.
- MCPs which control the FWER guarantee that the $\text{FWER} < \alpha$, where a "family-wise error" is defined to be the occurrence of a single Type I error in the entire family (set) of hypotheses being tested.
- In a transcriptomic experiment we test each gene for differential expression, so there are as many hypothesis tests as there are genes.
- The Bonferroni and Holm procedures both provide control of the FWER.

False Discovery Rate control

- The False Discovery Rate was introduced by Benjamini and Hochberg (1995 - JRSS(B)).
- Provides a less conservative approach to error rate control than FWER controlling procedures.
- Greater power comes at the cost of an increased likelihood of Type I errors.
- Has become very popular in genomic data analysis, plus astronomy, brain imaging, and genetics (all test large numbers of hypotheses).

FDR control versus FWER control

- FWER control is concerned with making sure that the probability of a single testing error is small.
- FDR control is concerned with keeping the proportion of Type I errors out of the total number of rejected hypotheses small.
 - This value can be anything from 0 to 1.
- FDR controlling procedures provide more error rate protection than not adjusting at all, but are a lot more likely to make Type I errors than FWER controlling procedures.
- The flip side is that FDR controlling methods are more likely to reject false null hypotheses (i.e., they achieve greater power).

Comparing approaches

- Instead of adjusting the significance threshold, we can adjust the p-values themselves.
- The table below contains unadjusted p-values ("P-value"), and p-values adjusted using the Bonferroni, Holm, and FDR methods.
- For $\alpha=0.05$, the four approaches find 7, 2, 4, or 6 tests significant.

TEST NUMBER	P-VALUE	BONFERRONI	HOLM	FDR
1	0.002	0.016	0.016	0.0160
2	0.004	0.032	0.028	0.0160
3	0.007	0.056	0.042	0.0187
4	0.010	0.080	0.050	0.0200
5	0.020	0.160	0.080	0.0320
6	0.030	0.240	0.090	0.0400
7	0.050	0.400	0.100	0.0571
8	0.080	0.640	0.100	0.0800

Multiple t-tests for transcriptome data

- P-values for multiple genes (first 10).

```
pvalues = c()  
for(i in 1:10) pvalues[i] = t.test( logCPM[i,] ~ groups )$p.value  
sort( round(pvalues,4) )
```

```
## [1] 0.0047 0.0353 0.1862 0.1880 0.2190 0.4202 0.4482 0.4999 0.5177 0.5758
```

Multiple t-tests for transcriptomic data

- Use `p.adjust` to apply correction (default is Holm):

```
round(p.adjust(sort(pvalues)), 4)
```

```
## [1] 0.0469 0.3177 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000 1.0000
```

```
round(p.adjust(sort(pvalues), "BH"), 4) # BH is the FDR method
```

```
## [1] 0.0469 0.1765 0.4380 0.4380 0.4380 0.5752 0.5752 0.5752 0.5752 0.5752 0.5758
```

- So here the test with the smallest p-value remains (just) significant, but the remainder do not.

Modification to t-test procedure

- One problem with the t-statistic approach to determining significance is that some genes with small, but consistent fold changes can end up with very large t-statistics.
- This is especially common in experiments involving only a few samples.
- Generally feel that genes with small fold changes shouldn't be considered as having undergone significant differential expression.
- Need a way to prevent these genes showing up as significant.

Significance Analysis for Microarrays (SAM)

- Tusher et al. (2001) proposed a modification to the denominator of the t-statistic to reduce the influence of tiny standard deviations.

$$T = \frac{\hat{\mu}_1 - \hat{\mu}_2}{SE(\hat{\mu}_1 - \hat{\mu}_2) + s_0}$$

- Although this modification looks somewhat arbitrary, it can be derived by taking a Bayesian approach to analysis (and various other ways).
- The Bayesian derivation relies on the assumption that the standard errors for each gene have an underlying common distribution. The s_0 parameter then contains information from this underlying distribution.

Significance Analysis for Microarrays (SAM)

- Has the effect of restricting significant genes to those exhibiting large fold changes.
- Although the distribution of T is unknown, resampling methods (e.g., bootstrapping) can be used to approximate the null distribution, allowing calculation of p -values.
- Multiple comparison procedures can then be used to provide control of the Type I error rate (FWER or FDR).

Empirical Bayes analysis

- Limma uses Empirical Bayes methods to produce a modified test statistic.
- The idea is similar to that employed by the SAM procedure, but is more sophisticated, and has more solid mathematical foundations.
- The goal is to modify the denominator of a standard t test statistic, by making large standard errors smaller, and small standard errors larger.
- This is known as *shrinkage estimation*.

Background: linear models

- Simple linear regression: $y = mx + b$
- Linear model equivalent: $y_i = \beta_0 + \beta_1 x_i + \epsilon_i$
- In linear regression, x and y are continuous variables. Here we have y (gene expression) as continuous, but x (group) is discrete, so our linear model is actually equivalent to ANOVA (analysis of variance).
- For a single gene:
 - y_i are our gene expression values
 - x_i is the group (WT or KO) for the i^{th} sample
 - β_0 and β_1 are the intercept and slope coefficients
 - ϵ_i is the residual (or error) associated with observation y_i (the difference between our predicted, \hat{y}_i and observed, y_i , values that cannot be explained by the model).

Background: linear algebra

- In practice, we represent our linear model in matrix form:

$$Y = X\beta + \epsilon$$

and use basic linear algebra to solve the equation and determine the value of the coefficients.

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_1 \\ 1 & x_2 \\ \vdots & \vdots \\ 1 & x_n \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \vdots \\ \epsilon_n \end{bmatrix}$$

$\downarrow \quad \downarrow \quad \downarrow$

$$Y = X\beta + \epsilon$$

Image from: <https://onlinecourses.science.psu.edu/stat501/node/382>

The design matrix

- Remember our design matrix:

```
design
```

```
##   (Intercept) groupsWT
## 1           1      1
## 2           1      1
## 3           1      1
## 4           1      0
## 5           1      0
## 6           1      0
## attr(,"assign")
## [1] 0 1
## attr(,"contrasts")
## attr(,"contrasts")$groups
## [1] "contr.treatment"
```

The design matrix

- For our simple two-group differential expression analysis, the design matrix has two columns:
 - the first is all ones, and relates to the intercept coefficient: it is the average level of log-expression for the gene (remember the linear model is fit to each gene, so we have an intercept and a "slope" term *per gene*),
 - the second has zeroes for one group, and ones for the other, and relates to the coefficient for group ("slope"): it is the average difference in log-expression between the groups for that gene).
This is what we are interested in.
- The residuals (the ϵ_i 's) for each gene are used to determine whether the observed expression difference is statistically significant.

Determining differential expression

- Limma also reports the *log odds* of differential expression.
- This quantity has a more Bayesian "feel" to it, providing a measure of how likely it is for a gene to have undergone differential expression, relative to the null hypothesis of no differential expression.
- Genes with high (positive) log odds are considered likely to have undergone differential expression.

Limma: detecting differential expression

```
## Load the limma package
library(limma)
## Fit linear model
fit = lmFit(logCPM, design)
fit = eBayes(fit)
tt = topTable(fit, coef=2, adjust="BH", n=nrow(logCPM))
options(digits=4)
tt[1:5,]
```

```
##          logFC AveExpr      t  P.Value adj.P.Val      B
## ENSMUSG00000079112 -7.019 -0.8959 -53.32 2.245e-10 2.130e-06 12.16
## ENSMUSG00000086445 -7.494 -0.6582 -52.19 2.607e-10 2.130e-06 12.10
## ENSMUSG00000087318 -6.514 -1.1483 -39.51 1.807e-09 7.543e-06 11.25
## ENSMUSG00000020673 -7.560 -0.6252 -39.39 1.846e-09 7.543e-06 11.24
## ENSMUSG00000085973 -6.205 -1.3030 -30.77 1.026e-08 3.353e-05 10.23
```

Check output against t-test (top gene)

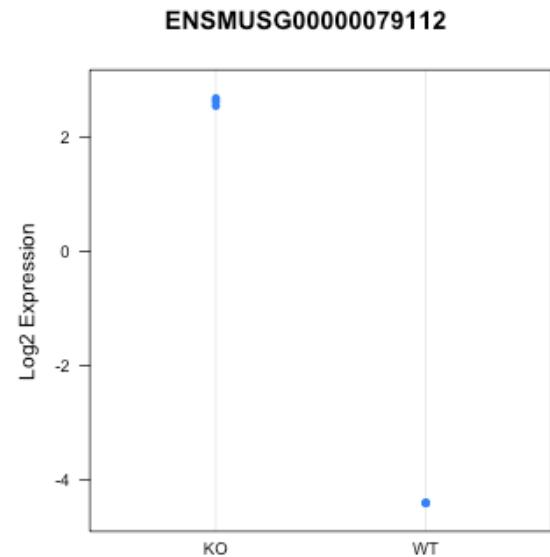
```
topGene = match(rownames(tt)[1], rownames(logCPM))  
t.test(logCPM[topGene, ] ~ groups)
```

```
##  
## Welch Two Sample t-test  
##  
## data: logCPM[topGene, ] by groups  
## t = 180, df = 2, p-value = 3e-05  
## alternative hypothesis: true difference in means is not equal to 0  
## 95 percent confidence interval:  
## 6.853 7.184  
## sample estimates:  
## mean in group KO mean in group WT  
## 2.613 -4.405
```

```
# "Raw" data agrees with logFC (WT - KO): -4.405 - 2.613 = -7.018
```

Dotplot of expression (top gene)

```
lattice::dotplot(logCPM[topGene,] ~ groups, main=rownames(logCPM)[topGene],  
                 ylab='Log2 Expression')
```



Clearly there is a major difference in expression between the WT and KO samples for this gene.

Limma: detecting differential expression

```
sum( tt$adj.P.Val < 0.05 )
```

```
## [1] 598
```

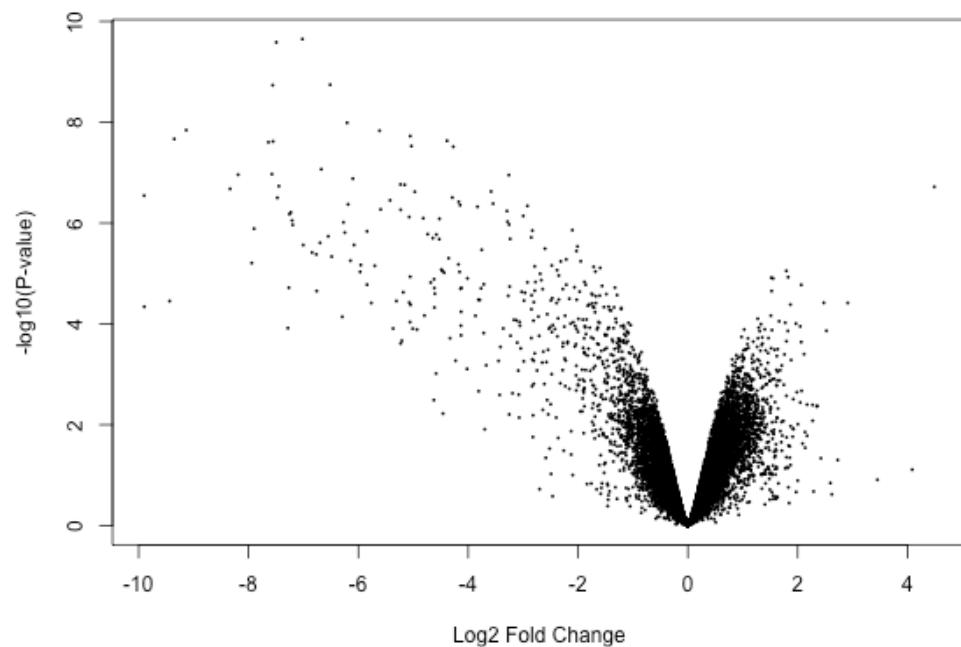
598 transcripts found to be differentially expressed using the False Discovery Rate (FDR) criterion.

Get the rows for the significant genes (we'll use these later):

```
limmaPadj <- tt[tt$adj.P.Val <= 0.05, ]
```

Volcano Plot

```
## Plot log fold-change _versus_ -log(P-value)
## (i.e., higher number = lower p-value):
volcanoplot(fit, coef=2)
```



- Volcanoplots are a useful tool for visualising the results of a differential expression analysis.
- Easy to identify significant changes that are also large in magnitude.

Annotation: additional information

- From wikipedia.org: "Annotation is extra information associated with a particular point in a document or other piece of information."
- Here our "document" is the genome.
- The goal of annotating the genome is to link *all* information relating to sequences, genes, protein, function...

Which genes are significant?

```
## Load Entrez-centric annotation for Mouse (Mus musculus: Mm)
library(org.Mm.eg.db)
## Get the IDs for the significant transcripts
sigGenes <- rownames(limmaPadj)
## Get the gene symbols and names associated with these transcripts (first 6, via head)
options(width=100)
select(org.Mm.eg.db, keys = head(sigGenes), column = c("SYMBOL", "GENENAME"),
      keytype="ENSEMBL")
```

	ENSEMBL	SYMBOL	GENENAME
## 1	ENSMUSG00000079112	Fam90a1a	family with sequence similarity 90, member A1A
## 2	ENSMUSG00000086445	<NA>	<NA>
## 3	ENSMUSG00000087318	<NA>	<NA>
## 4	ENSMUSG00000020673	Tpo	thyroid peroxidase
## 5	ENSMUSG00000085973	<NA>	<NA>
## 6	ENSMUSG00000043110	Lrrn4	leucine rich repeat neuronal 4

List of significant genes

```
allSigGenes <- select(org.Mm.eg.db, keys = sigGenes, column = "SYMBOL",  
keytype="ENSEMBL")[,2]
```

```
## 'select()' returned 1:many mapping between keys and columns
```

```
na.omit(allSigGenes)
```

```
## [1] "Fam90a1a"      "Tpo"          "Lrrn4"        "Iqcf5"  
## [5] "Hnf4aos"       "Chrm3"        "Sp110"        "Fbxo16"  
## [9] "Dhtkd1"         "Olfr815"      "Slc14a2"      "Prr18"  
## [13] "AI427809"      "Krt2"         "Abcb5"        "Tie1"  
## [17] "Echdc3"         "Mecom"        "Cryz12"       "Ccdc60"  
## [21] "Loxhd1"         "Aqp9"         "4930432K21Rik" "Oas1a"  
## [25] "Artn"           "H2-M10.4"     "Ccser1"       "A530032D15Rik"  
## [29] "LOC100041708"   "Apol7b"       "Stox1"        "Slfn2"  
## [33] "BB557941"       "Rasd2"        "Dlgap2"       "Oas1g"  
## [37] "0610040J01Rik"  "Defb13"       "Supt3"        "Colgalt2"  
## [41] "B3gnt11"        "Lmx1a"        "Dcc"          "Acslf2"  
## [45] "Iars"           "Sp140"        "Chit1"        "Kcnk15"
```

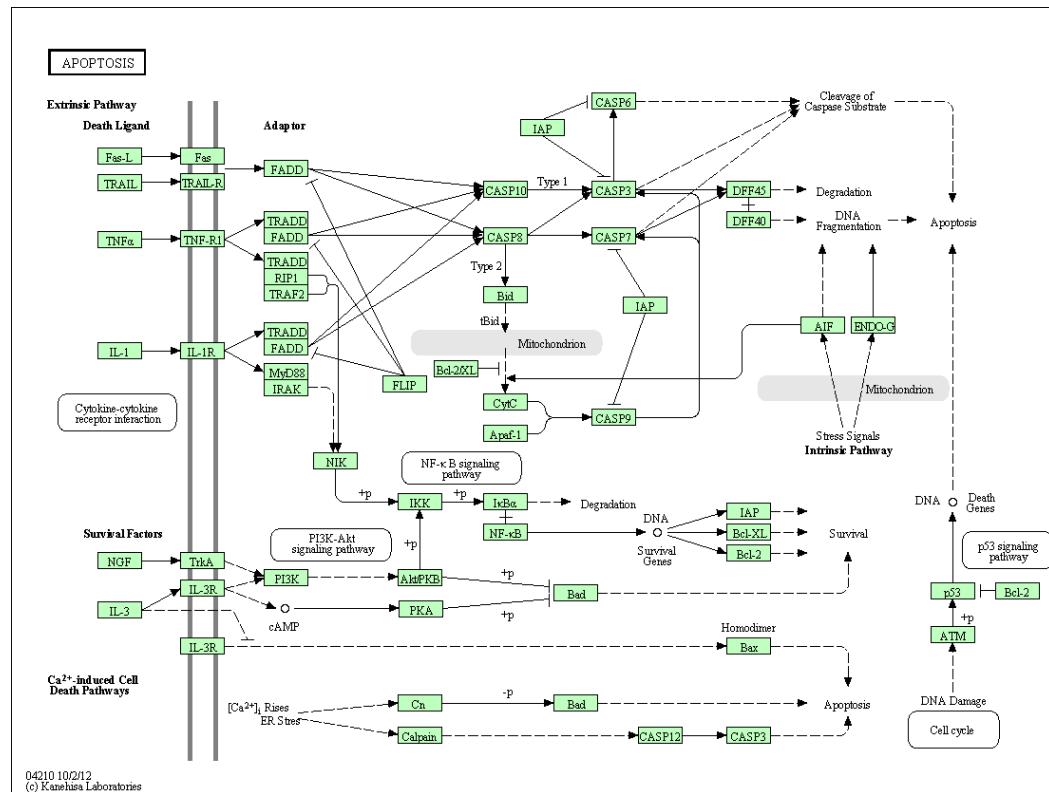
Biological pathways

- In reality genes are members of *pathways*, which perform major biological functions.
- As more biological experimentation is done, researchers are able to build a better picture of how genes interact, and how pathways function.
- Information about pathway membership and gene function are stored in publicly available databases.
- This information can be used to define *gene sets* (groups of genes which are functionally related), to which statistical analysis can be applied.

Biological pathways: KEGG

- Kyoto Encyclopedia of Gene and Genomes:
<http://www.genome.jp/kegg/kegg4.html>
- Provides nice (user-created) pathway diagrams.
- XML output includes information about genes involved in pathways, and inter-gene (and gene product) relationships.
 - Can produce graphic representation of pathway based on XML alone.
- Access to database now requires a subscription (can still view pathway maps for free though).

KEGG pathway diagram (apoptosis)



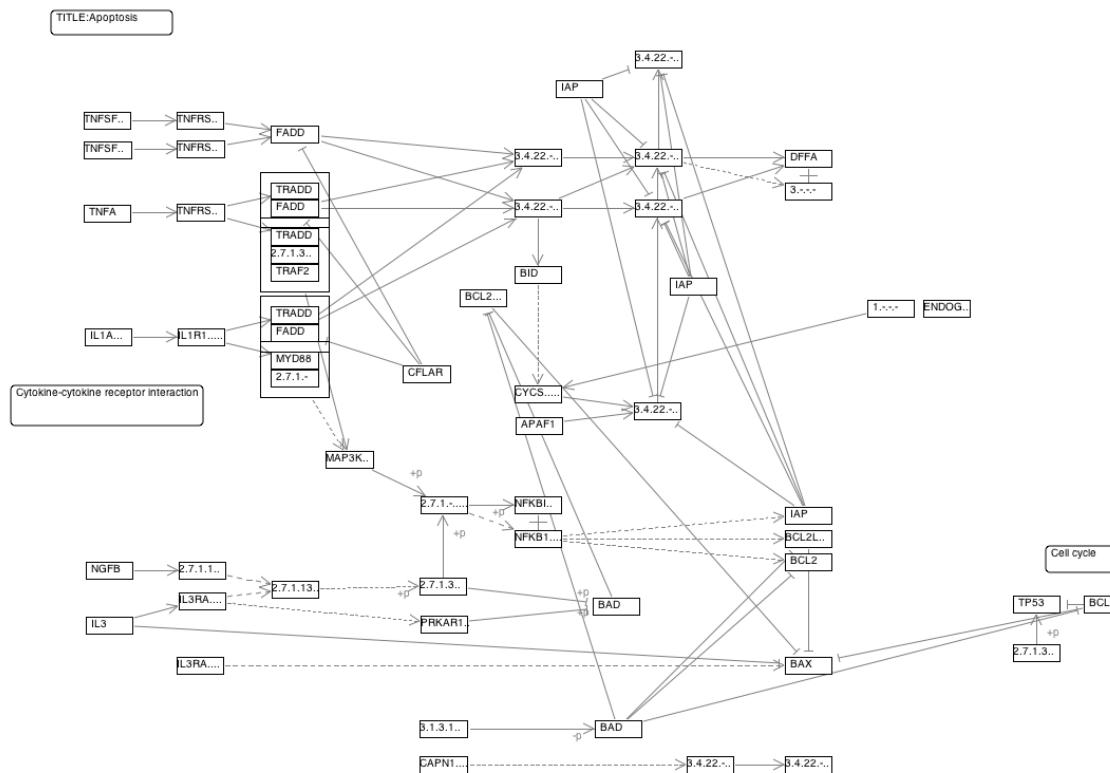
http://www.genome.jp/kegg-bin/show_pathway?org_name=hsa&mapno=04210&mapscale=&show_description=show

XML output file for apoptosis pathway

```
:<?xml version="1.0"?>
<!DOCTYPE pathway SYSTEM "http://www.kegg.jp/kegg/xml/KGML_v0.7.1_.dtd">
<!-- Creation date: Oct 2, 2012 11:48:00 +0900 (GMT+09:00) -->
<pathway name="path:hsa04210" org="hsa" number="04210"
    title="Apoptosis"
    image="http://www.kegg.jp/kegg/pathway/hsa/hsa04210.png"
    link="http://www.kegg.jp/kegg-bin/show_pathway?hsa04210">
    <entry id="1" name="path:hsa04115" type="map"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa04115"
        <graphics name="p53 signaling pathway" fgcolor="#000000" bgcolor="#FFFFFF"
            type="roundrectangle" x="1049" y="572" width="95" height="39"/>
    </entry>
    <entry id="2" name="path:hsa04060" type="map"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa04060"
        <graphics name="Cytokine-cytokine receptor interaction" fgcolor="#000000" bgcolor="#FFFFFF"
            type="roundrectangle" x="111" y="427" width="124" height="39"/>
    </entry>
    <entry id="3" name="hsa:5530 hsa:5532 hsa:5533 hsa:5534 hsa:5535" type="gene"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa:5530+hsa:5532+hsa:5533+hsa:5534+hsa:5535"
        <graphics name="PPP3CA, CALN, CALNA1, CCN1, CNA1, PPP2B..." fgcolor="#000000" bgcolor="#BFFFBF"
            type="rectangle" x="430" y="733" width="46" height="17"/>
    </entry>
    <entry id="4" name="hsa:581" type="gene"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa:581"
        <graphics name="BAK, BCL2L4" fgcolor="#000000" bgcolor="#BFFFBF"
            type="rectangle" x="776" y="673" width="46" height="17"/>
    </entry>
    <entry id="5" name="hsa:598" type="gene"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa:598"
        <graphics name="BCL2L1, BCL-XL/S, BCL2L, BCLX, BCLXL, BCLX5, Bcl-X, PPP1R52, bcl-xL, bcl-xS" fgcolor="#000000" bgcolor="#BFFFBF"
            type="rectangle" x="776" y="553" width="46" height="17"/>
    </entry>
    <entry id="6" name="hsa:1676" type="gene"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa:1676"
        <graphics name="DFFA, DFF-45, DFF1, ICAD" fgcolor="#000000" bgcolor="#BFFFBF"
            type="rectangle" x="776" y="192" width="46" height="17"/>
    </entry>
    <entry id="7" name="hsa:596" type="gene"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa:596"
        <graphics name="BCL2, Bcl-2, PPP1R50" fgcolor="#000000" bgcolor="#BFFFBF"
            type="rectangle" x="1059" y="615" width="46" height="17"/>
    </entry>
    <entry id="8" name="hsa:472" type="gene"
        link="http://www.kegg.jp/dbget-bin/www_bget?hsa:472">
```

<http://www.kegg.jp/kegg-bin/download?entry=hsa04210&format=kgml>

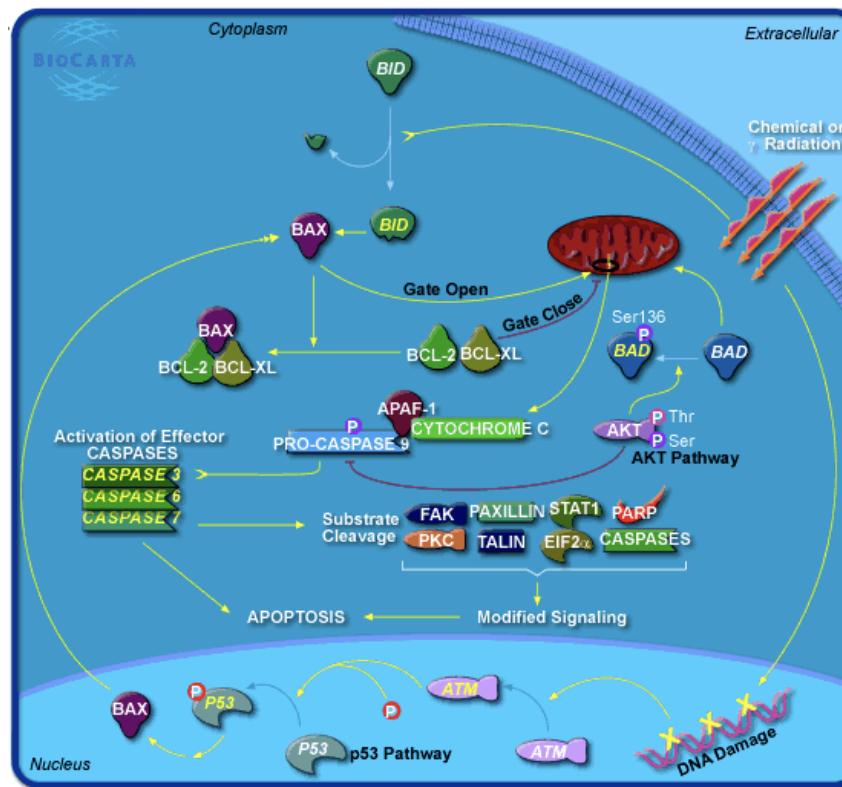
XML-based KEGG diagram (apoptosis)



Biological pathways: Biocarta

- Maintain "open source" pathway database, and provide lab supplies for related experiments: <http://www.biocarta.com>
- Pathway database is edited by "gurus".
- Very nice pathway diagrams (user created).
- No non-html output.

Biocarta pathway diagram (apoptosis)



User-curated database: Reactome

The screenshot shows the Reactome website homepage. At the top is a dark blue header with the Reactome logo (three white ovals) and a banner image of a cell membrane with various proteins and molecules. Below the header is a navigation menu with links: Home, About, Content, Documentation, Tools, Download, Contact Us, and Outreach. The main content area has a light blue sidebar on the left containing a search bar, a 'Search examples...' button, and four buttons: 'Browse Pathways', 'Map IDs to Pathways', 'Compare Species', and 'Analyze Expression Data'. A red link at the bottom of this sidebar says 'If you would prefer to use our old website, click here.' To the right of the sidebar is a dark blue box titled 'About Reactome' which contains text about the database being open-source, peer-reviewed, and manually curated. It also mentions cross-referencing to other databases like NCBI, Ensembl, and UniProt. A blue link '[more]' is at the bottom of this box. To the right of the 'About Reactome' box is another dark blue box titled 'Featured pathway: Integrin cell surface interactions'. This box contains a detailed diagram of the pathway. The diagram shows an integrin receptor on the cell surface. Upon activation by clustering, it triggers a series of intracellular signaling events involving proteins like FAK1, p190NCab, Grb2, and SOS, leading to Arkin Polymerization, Cytoskeletal Reorganization and Lamellipodia Formation, and MAPK Pathway. The diagram uses various colors (blue, green, purple) to represent different protein families or domains.

<http://www.reactome.org>

Gene ontology

- Gene Ontology (GO) defines a collection of words (an ontology) which are used to classify the function of a gene.
- Three broad classifications:
 - Molecular function.
 - Biological process.
 - Cellular component.
- Each of these broad terms contains a hierarchy of categories, going from general to specific.
- Each category is indexed by an identifier.

Example of GO hierarchy (apoptosis)

```
* all : all  ( 218850 )
  o GO:0008150 : biological_process ( 145098 )
    + GO:0009987 : cellular process ( 91236 )
      # GO:0050875 : cellular physiological process ( 81383 )
        * GO:0008219 : cell death ( 2714 )
          o GO:0012501 : programmed cell death ( 2395 )
            + GO:0006915 : apoptosis ( 2061 )
    + GO:0007582 : physiological process ( 96419 )
      # GO:0050875 : cellular physiological process ( 81383 )
        * GO:0008219 : cell death ( 2714 )
          o GO:0012501 : programmed cell death ( 2395 )
            + GO:0006915 : apoptosis ( 2061 )
  # GO:0016265 : death ( 3054 )
    * GO:0008219 : cell death ( 2714 )
      o GO:0012501 : programmed cell death ( 2395 )
        + GO:0006915 : apoptosis ( 2061 )
```

Annotation available in `org.Mm.eg.db`

```
options(width=100)
ls("package:org.Mm.eg.db")
```

```
## [ 1] "org.Mm.eg"                                "org.Mm.eg_dbconn"          "org.Mm.eg_dbfile"
## [ 4] "org.Mm.eg_dbInfo"                           "org.Mm.eg_dbschema"        "org.Mm.eg.db"
## [ 7] "org.Mm.egACCTNUM"                           "org.Mm.egACCTNUM2EG"       "org.Mm.egALIAS2EG"
## [10] "org.Mm.egCHR"                               "org.Mm.egCHRLLENGTHS"     "org.Mm.egCHRLOC"
## [13] "org.Mm.egCHRLOCEND"                          "org.Mm.egENSEMBL"          "org.Mm.egENSEML2EG"
## [16] "org.Mm.egENSEMLPROT"                          "org.Mm.egENSEMLPROT2EG"    "org.Mm.egENSEMLTRANS"
## [19] "org.Mm.egENSEMLTRANS2EG"                      "org.Mm.egENZYME"           "org.Mm.egENZYME2EG"
## [22] "org.Mm.egGENENAME"                           "org.Mm.egGO"                "org.Mm.egGO2ALLEGS"
## [25] "org.Mm.egGO2EG"                             "org.Mm.egMAPCOUNTS"        "org.Mm.egMGI"
## [28] "org.Mm.egMGI2EG"                            "org.Mm.egORGANISM"         "org.Mm.egPATH"
## [31] "org.Mm.egPATH2EG"                            "org.Mm.egPFAM"              "org.Mm.egPMID"
## [34] "org.Mm.egPMID2EG"                            "org.Mm.egPROSITE"           "org.Mm.egREFSEQ"
## [37] "org.Mm.egREFSEQ2EG"                           "org.Mm.egSYMBOL"            "org.Mm.egSYMBOL2EG"
## [40] "org.Mm.egUNIGENE"                            "org.Mm.egUNIGENE2EG"        "org.Mm.egUNIPROT"
```

GO annotation

```
na.omit( select(org.Mm.eg.db, keys = head(sigGenes),  
                column = c("SYMBOL", "ENSEMBL", "GO"), keytype="ENSEMBL" ) )
```

```
## 'select()' returned 1:many mapping between keys and columns
```

##	ENSEMBL	SYMBOL	GO	EVIDENCE	ONTOLOGY
## 1	ENSMUSG00000079112	Fam90a1a	GO:0003674	ND	MF
## 2	ENSMUSG00000079112	Fam90a1a	GO:0005575	ND	CC
## 3	ENSMUSG00000079112	Fam90a1a	GO:0008150	ND	BP
## 6	ENSMUSG00000020673	Tpo	GO:0004447	IEA	MF
## 7	ENSMUSG00000020673	Tpo	GO:0004601	IBA	MF
## 8	ENSMUSG00000020673	Tpo	GO:0005509	IEA	MF
## 9	ENSMUSG00000020673	Tpo	GO:0005615	IBA	CC
## 10	ENSMUSG00000020673	Tpo	GO:0005615	ISO	CC
## 11	ENSMUSG00000020673	Tpo	GO:0005739	IDA	CC
## 12	ENSMUSG00000020673	Tpo	GO:0005886	ISO	CC
## 13	ENSMUSG00000020673	Tpo	GO:0006590	IEA	BP
## 14	ENSMUSG00000020673	Tpo	GO:0006979	IEA	BP
## 15	ENSMUSG00000020673	Tpo	GO:0009986	ISO	CC
## 16	FNSMUSG00000020673	Tpo	GO:0016020	TFA	CC

Detecting pathway-level changes

- Transcriptomic experiments are able to measure changes in gene expression across treatment conditions.
- Can obtain information about gene sets (e.g., GO, KEGG, Reactome).
- Allows transcriptomic data to be used to assess whether changes in expression occur at the *group* level.
- Such changes often provide greater information than single gene changes.

Over-representation analysis

- Simple approach for investigating coordinated gene expression - involves hypergeometric distribution.
- Look for functional groupings within a set of significantly differentially expressed genes:
 - e.g., what is the probability of getting 10 apoptosis genes in my 100 differentially expressed genes?
- Similar to classic hypergeometric problem:
 - e.g., what is the probability of selecting k white balls in a sample of size n from a bag containing m white and $N - m$ black balls?

Fisher's Exact Test

- In practice we can use *Fisher's Exact Test* to determine whether a functional grouping is *over-represented* (or *enriched*) in our list of differentially expressed genes.
 - This is a test for independence in a 2×2 table.
- Suppose that we observe 10 apoptosis genes in our 100 differentially expressed genes, and there are 10,000 genes in our experiment, of which 500 are apoptosis genes.
- Fisher's Exact Test uses the hypergeometric distribution to test whether being involved in apoptosis is independent of being significantly differentially expressed in our hypothetical experiment.

Tools for over-representation analysis

- There are MANY R-based and online tools for assessing functional enrichment of gene lists.
- We'll look at two: GeneSetDB, Enrichr
- Each provides access to multiple types of gene set annotation

Start with a list of genes

MMP7	matrix metalloproteinase 7
PTGS2	prostaglandin-endoperoxide synthase 2
IL8	interleukin 8
BIRC5	baculoviral IAP repeat-containing 5
CEACAM1	carcinoembryonic antigen-related cell adhesion molecule 1
GZMB	granzyme B
GNLY	granulysin
IFNG	interferon, gamma
IRF1	interferon regulatory factor 1
CD3Z	CD3Z antigen, zeta polypeptide
CD8A	CD8 antigen, alpha polypeptide
TBX21	T-box 21
TNFRSF10A	tumor necrosis factor receptor superfamily, member 10a
B7H3	B7 homolog 3
CD4	CD4 antigen (p55)
IL10	interleukin 10
TGFB1	transforming growth factor, beta 1
VEGF	vascular endothelial growth factor

GeneSetDB: input

Enrichment Analysis

Enrichment Analysis

1. Gene List
paste gene list

MMP7
PTGS2
IL8
BIRC5
CEACAM1
GZMB
GNLY
IFNG
IRF1
CD3Z
CD8A
TBX21
TNFRSF10A
B7H3
CD4

Or

upload gene list file

2. Input ID type

3. Choose DB

All
SubClass Pathway
SubClass Disease/Phenotype
SubClass Drug/Chemical
SubClass Gene Regulation

4. FDR

5. Submit
After submit is pressed it can take a little while until the page refreshes.

Sample data
[Enrichment Analysis tutorial](#)

Enrichment analysis used: 2295

<http://genesetdb.auckland.ac.nz>

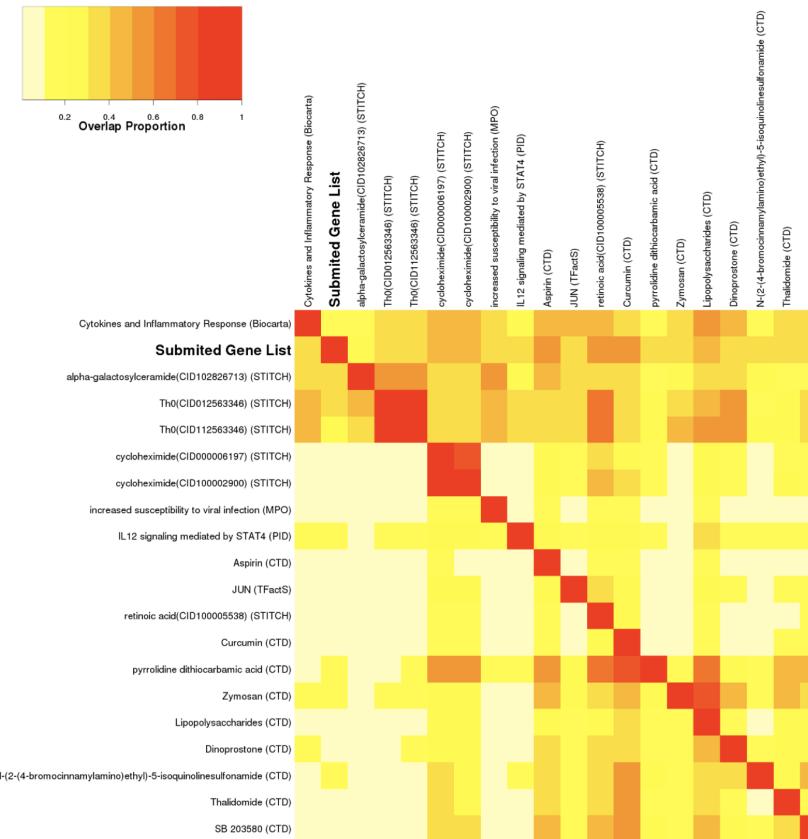
GeneSetDB: output

18 symbol input ids were converted into 15 unique gene ids.
19 entries for fdr cutoff 0.0000001 estimated.

Sub Class	Gene Set Name	Source DB	Gene #	Gene # with Anno	Gene # without Anno	p-value	FDR
Drug/Chemical	Th0(CID012563346)	STITCH	16	5	11	6.9E-13	2.2E-9
Drug/Chemical	Th0(CID112563346)	STITCH	18	5	13	1.4E-12	2.2E-9
Pathway	Cytokines and Inflammatory Response	Biocarta	26	5	21	1.0E-11	1.1E-8
Drug/Chemical	Aspirin	CTD	461	9	452	1.4E-11	1.1E-8
Drug/Chemical	Dinoprostone	CTD	90	6	84	5.1E-11	2.3E-8
Drug/Chemical	cycloheximide(CID100002900)	STITCH	179	7	172	4.0E-11	2.3E-8
Pathway	IL12 signaling mediated by STAT4	PID	35	5	30	5.1E-11	2.3E-8
Disease/Phenotype	increased susceptibility to viral infection	MPO	93	6	87	6.3E-11	2.5E-8
Drug/Chemical	Zymosan	CTD	39	5	34	9.0E-11	3.2E-8
Drug/Chemical	Lipopolysaccharides	CTD	204	7	197	1.0E-10	3.2E-8
Drug/Chemical	N-(2-(4-bromocinnamylamino)ethyl)-5-isoquinolinesulfonamide	CTD	42	5	37	1.3E-10	3.9E-8
Drug/Chemical	SB 203580	CTD	108	6	102	1.6E-10	4.2E-8
Drug/Chemical	alpha-galactosylceramide(CID102826713)	STITCH	13	4	9	1.9E-10	4.7E-8
Drug/Chemical	pyrrolidine dithiocarbamic acid	CTD	46	5	41	2.1E-10	4.9E-8
Drug/Chemical	cycloheximide(CID000006197)	STITCH	233	7	226	2.6E-10	5.4E-8
Drug/Chemical	Thalidomide	CTD	125	6	119	3.8E-10	6.8E-8
Drug/Chemical	retinoic acid(CID100005538)	STITCH	421	8	413	3.5E-10	6.8E-8
GeneRegulation	JUN	TFactS	125	6	119	3.8E-10	6.8E-8
Drug/Chemical	Curcumin	CTD	438	8	430	4.8E-10	8.1E-8

<http://genesetdb.auckland.ac.nz>

GeneSetDB: gene set overlap



<http://genesetdb.auckland.ac.nz>

Enrichr

 **Enrichr**

[Login](#) | [Register](#)
9,169,953 lists analyzed
234,849 terms
128 libraries

Analyze What's New? Libraries Find a Gene About Help

Input data

Choose an input file to upload. Either in BED format or a list of genes. For a quantitative set, add a comma and the level of membership of that gene. The membership level is a number between 0.0 and 1.0 to represent a weight for each gene, where the weight of 0.0 will completely discard the gene from the enrichment analysis and the weight of 1.0 is the maximum.

Try an example [BED file](#).

No file selected.

Or paste in a list of gene symbols optionally followed by a comma and levels of membership. Try two examples:
[crisp set example](#), [fuzzy set example](#)

IRF1
CD3Z
CD8A
TBX21
TNFRSF10A
B7H3
CD4
IL10
TGFB1
VEGF

18 gene(s) entered

Enter a brief description for the list in case you want to share it. (Optional)

Contribute

Please acknowledge Enrichr in your publications by citing the following references:
Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics*. 2013;128(14).

Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.

<http://amp.pharm.mssm.edu/Enrichr/>

Enrichr

 Enrichr

Login | Register

Transcription Pathways Ontologies Disease/Drugs Cell Types Misc Legacy Crowd

Description No description available (18 genes)  

KEGG 2016 Inflammatory bowel disease (IBD)_Homo sapiens Leishmaniasis_Homo sapiens_hsa05140 T cell receptor signaling pathway_Homo sapiens Allograft rejection_Homo sapiens_hsa05330 Malaria_Homo sapiens_hsa05144	WikiPathways 2016 Cytokines and Inflammatory Response_Homo sapiens Cytokines and Inflammatory Response (BioCyc) Allograft Rejection_Homo sapiens_WP2328 Apoptosis_Mus musculus_WP1254 Apoptosis_Homo sapiens_WP254	ARCHS4 Kinases Coexp PLK3_human_kinase_ARCHS4_coexpression PIM3_human_kinase_ARCHS4_coexpression LCK_human_kinase_ARCHS4_coexpression MAP3K8_human_kinase_ARCHS4_coexpression PRKCH_human_kinase_ARCHS4_coexpression
Reactome 2016 TP53 Regulates Transcription of Cell Death C Extracellular matrix organization_Homo sapiens Interferon gamma signaling_Homo sapiens Apoptosis_Homo sapiens_R-HSA-109581 Programmed Cell Death_Homo sapiens_R-HSA-109581	BioCarta 2016 IFN gamma signaling pathway_Homo sapiens Granzyme A mediated Apoptosis Pathway_Homo sapiens Apoptotic DNA fragmentation and tissue homeostasis_Homo sapiens NO2-dependent IL 12 Pathway in NK cells_Homo sapiens IL-10 Anti-inflammatory Signaling Pathway_Homo sapiens	Humancyc 2016 C20 prostanoid biosynthesis_Homo sapiens
NCI-Nature 2016 IL12 signaling mediated by STAT4_Homo sapiens IL12-mediated signaling events_Homo sapiens Calcineurin-regulated NFAT-dependent transcriptional network_Homo sapiens AP-1 transcription factor network_Homo sapiens IL27-mediated signaling events_Homo sapiens	Panther 2016 Apoptosis signaling pathway_Homo sapiens CCKR signaling map ST_Homo sapiens_P069 Inflammation mediated by chemokine and cytokine_Homo sapiens Interferon-gamma signaling pathway_Homo sapiens Toll receptor signaling pathway_Homo sapiens	BioPlex 2017 CD320 ALDH3B1 MED4 MED14 CNOT2

<http://amp.pharm.mssm.edu/Enrichr/>

Enrichr

 Enrichr

Login | Register

Transcription Pathways Ontologies Disease/Drugs Cell Types Misc Legacy Crowd

Description No description available (18 genes)  

KEGG 2016

WikiPathways 2016 Bar Graph Table Grid Network Clustergram  

Hover each row to see the overlapping genes.

10 entries per page Search:

Index	Name	P-value	Adjusted p-value	Z-score	Combined score
1	Cytokines and Inflammatory Response_Homo sapiens_WP530	6.780e-9	1.831e-7	-2.11	39.61
2	Cytokines and Inflammatory Response (BioCarta)_Mus musculus_WP222	5.740e-9	1.831e-7	-2.06	39.12
3	Allograft Rejection_Homo sapiens_WP2328	6.523e-9	1.831e-7	-2.00	37.66
4	Apoptosis_Mus musculus_WP1254	0.00004638	0.0009244	-1.93	19.22
5	Apoptosis_Homo sapiens_WP254	0.00005978	0.0009244	-1.90	18.52
6	TCR Signaling Pathway_Homo sapiens_WP69	0.00006847	0.0009244	-1.91	18.28
7	Senescence and Autophagy in Cancer_Homo sapiens_WP615	0.0001083	0.001254	-1.77	16.12
8	Spinal Cord Injury_Homo sapiens_WP2431	0.0001570	0.001590	-1.80	15.74
9	Interleukin-11 Signaling Pathway_Homo sapiens_WP2332	0.0007077	0.005211	-1.78	12.91
10	Aryl Hydrocarbon Receptor Pathway_Homo sapiens_WP2873	0.0007735	0.005221	-1.68	12.01

Showing 1 to 10 of 81 entries | [Export entries to table](#)

Terms marked with an * have an overlap of less than 5

Previous Next

<http://amp.pharm.mssm.edu/Enrichr/>

Limitations of enrichment testing

- The hypergeometric-based enrichment tests only take the size of gene sets into account.
- All genes for the same group that are not significant are treated the same.
 - What if they are "almost" significant?
 - We are now thinking about the *ranks* of the genes.
 - Can we incorporate this rank information into our calculations?
- More sophisticated methods (e.g., Gene Set Enrichment Analysis) take a rank-based approach.

We can stop here...

Detecting differential expression: DESeq2

- The DESeq2 package uses the *Negative Binomial* distribution to model the count data from each sample.
- Statistical test based on the Negative Binomial distribution (via a generalized linear model, GLM) can be used to assess differential expression for each gene.
- Negative Binomial distribution attempts to accurately capture the variation that is observed for count data.

M. I. Love, W. Huber, S. Anders: Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology* 2014, 15:550.

Detecting differential expression: DESeq2

```
library(DESeq2)
# Specify "conditions" (groups: WT and KO)
# Create object of class CountDataSet derived from eSet class
dds <- DESeqDataSetFromMatrix(countData = counts,
                               colData = data.frame(groups),
                               design = ~groups)
counts(dds)[1:4, ]
```

		WT1	WT2	WT3	KO1	KO2	KO3
FALSE	ENSMUSG00000000702	0	0	0	0	0	0
FALSE	ENSMUSG00000078423	0	0	0	0	0	0
FALSE	ENSMUSG00000078424	0	0	0	0	0	0
FALSE	ENSMUSG00000071964	0	0	0	0	0	0

Detecting differential expression: DESeq2

```
## Fit DESeq model to identify DE transcripts
dds <- DESeq(dds)
res <- DESeq2::results(dds)
## Remove rows with NAs
res = na.omit(res)
options(digits=2, width=100)
head(res, 4)
```

```
## log2 fold change (MLE): groups WT vs KO
## Wald test p-value: groups WT vs KO
## DataFrame with 4 rows and 6 columns
##           baseMean log2FoldChange      lfcSE      stat     pvalue     padj
##           <numeric>      <numeric> <numeric> <numeric> <numeric> <numeric>
## ENSMUSG00000063889       69        -0.35     0.28    -1.2    0.2131    0.454
## ENSMUSG00000024231      414        -0.70     0.21    -3.3    0.0011    0.015
## ENSMUSG00000024232      284         0.53     0.17     3.1    0.0018    0.023
## ENSMUSG00000073647       99        -0.76     0.35    -2.2    0.0312    0.145
```

DESeq2: adjusted p-values

```
sum(res$padj <= 0.05)
```

```
## [1] 2043
```

```
## Get the rows of "res" with significant adjusted p-values
resPadj<-res[res$padj <= 0.05 , ]
```

Detecting differential expression: edgeR

- The edgeR package also uses the negative binomial distribution to model the RNA-seq count data.
- Takes an empirical Bayes approach to the statistical analysis, in a similar way to how the `limma` package handles transcriptomic data.

Detecting differential expression: edgeR

```
library(edgeR)
# Construct DGEList object
y <- DGEList(counts=counts, group=groups)

# Calculate library size (counts per sample)
y <- calcNormFactors(y)

# Estimate common dispersion (overall variability)
y <- estimateCommonDisp(y)

# Estimate tagwise dispersion (per gene variability)
y <- estimateTagwiseDisp(y)

# Compute exact test for the negative binomial distribution.
et <- exactTest(y)
```

Detecting differential expression: edgeR

```
topTags(et, n=4)$table
```

```
##          logFC  logCPM    PValue      FDR
## ENSMUSG00000070034 -7.6     8.7 1.8e-103 6.9e-99
## ENSMUSG00000079455 -9.6     7.5 2.1e-98 3.9e-94
## ENSMUSG00000033634 -8.8     6.5 1.2e-97 1.5e-93
## ENSMUSG00000024552 -8.4     4.8 1.2e-92 1.1e-88
```

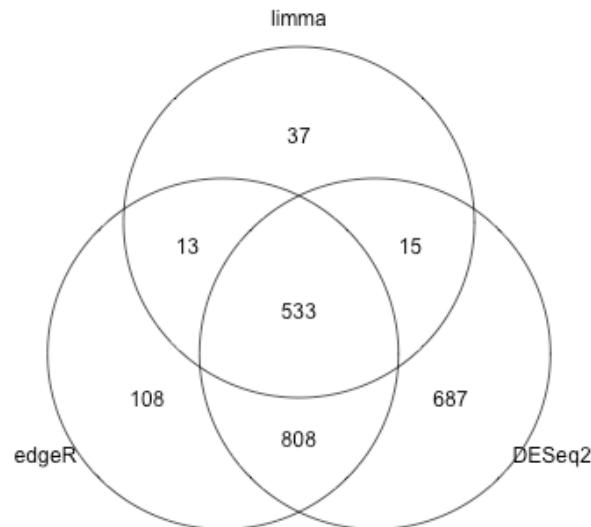
```
edge <- as.data.frame(topTags(et, n=nrow(counts)))
sum(p.adjust(edge$FDR <= 0.05))
```

```
## [1] 1462
```

```
## Get the rows of "edge" with significant adjusted p-values
edgePadj <- edge[edge$FDR <= 0.05, ]
```

limma vs edgeR vs DESeq2

```
library(gplots)
venn(list(edgeR=rownames(edgePadj), DESeq2=rownames(resPadj), limma=rownames(limmaPadj)))
```



Other normalisation methods (limma-voom)

Re-make our original DGEList object:

```
## Create DGEList object from count data
dge <- DGEList(counts=counts)

## Figure out which genes to keep
keep <- filterByExpr(dge, design)

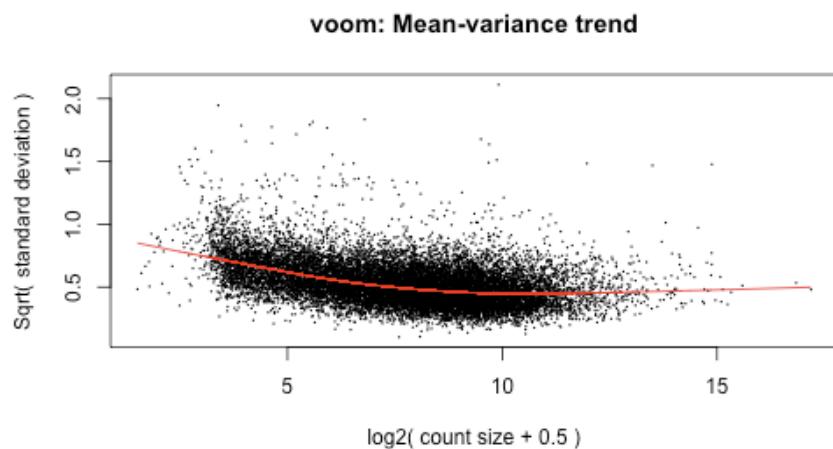
## Apply filtering and recalculate library sizes
dge <- dge[keep, keep.lib.sizes=FALSE]

## Calculate normalisation factor (i.e., account for total reads per sample)
dge <- calcNormFactors(dge)
```

limma-voom

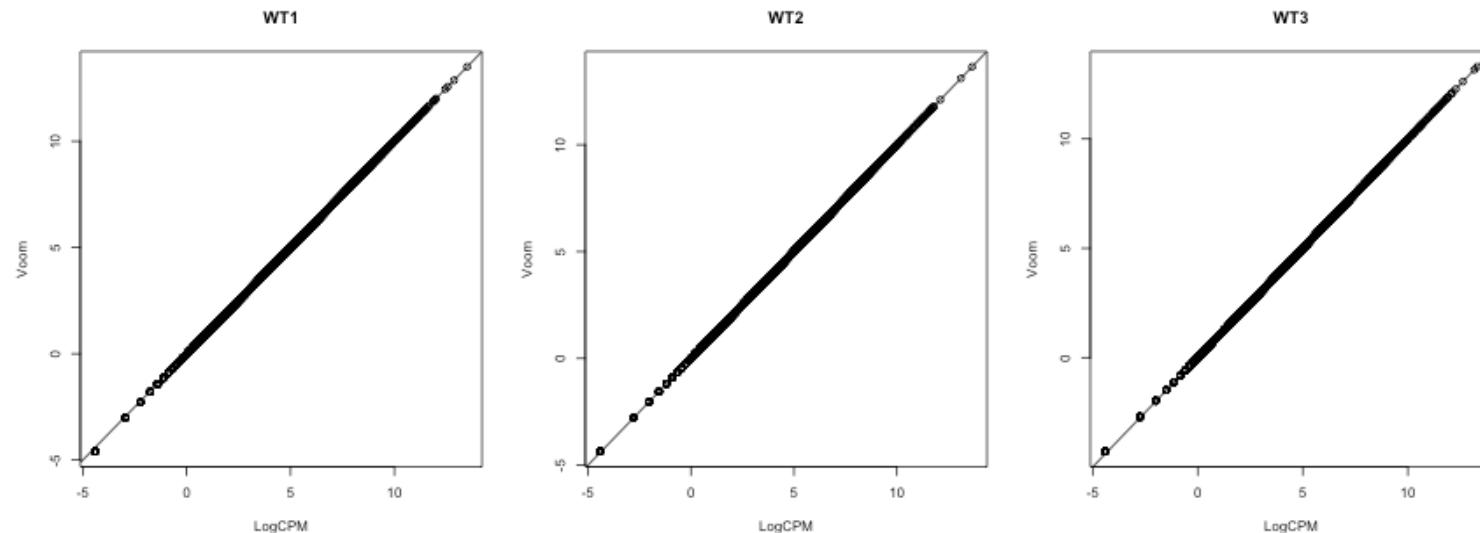
- The "voom" function estimates relationship between the mean and the variance of the logCPM data, normalises the data, and creates "precision weights" for each observation that are incorporated into the limma analysis.

```
v <- voom(dge, design, plot=TRUE)
```



Limma-voom (impact on first three samples)

```
par(mfrow=c(1,3))
for(i in 1:3){
  plot(logCPM[,i], v$E[,i], xlab="LogCPM", ylab="Voom", main=colnames(logCPM)[i])
  abline(0,1)
}
```



limma-voom

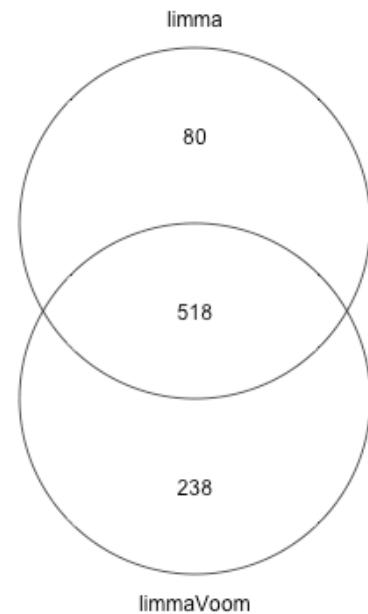
```
options(digits=4)
fit <- lmFit(v, design)
fit <- eBayes(fit)
tt <- topTable(fit, coef=ncol(design), n=nrow(v))
head(tt)
```

```
##          logFC AveExpr      t  P.Value adj.P.Val      B
## ENSMUSG00000025815 -4.265  4.8430 -24.37 5.556e-09 4.539e-05 11.251
## ENSMUSG00000070034 -7.565  5.8920 -24.00 6.287e-09 4.539e-05 11.013
## ENSMUSG00000064201  4.491  8.9488  21.30 1.662e-08 4.539e-05 10.413
## ENSMUSG00000033191 -3.586  6.9315 -21.29 1.667e-08 4.539e-05 10.411
## ENSMUSG00000032204 -2.921  6.0643 -18.20 5.939e-08 8.432e-05  9.170
## ENSMUSG00000086445 -7.511 -0.6625 -22.31 1.139e-08 4.539e-05  8.831
```

```
## Get the rows of top table with significant adjusted p-values
limmaVoomPadj <- tt[tt$adj.P.Val <= 0.05, ]
```

limma vs limma-voom

```
venn( list(limmaVoom = rownames(limmaVoomPadj), limma = rownames(limmaPadj)) )
```



limma-voom vs edgeR vs DESeq2

```
venn(list(edgeR = rownames(edgePadj), DESeq2 = rownames(resPadj),
          limmaVoom = rownames(limmaVoomPadj)))
```

