

# class12

Jacob Gil

```
library(BiocManager)
library(DESeq2)
```

Loading required package: S4Vectors

Loading required package: stats4

Loading required package: BiocGenerics

Attaching package: 'BiocGenerics'

The following objects are masked from 'package:stats':

IQR, mad, sd, var, xtabs

The following objects are masked from 'package:base':

anyDuplicated, aperm, append, as.data.frame, basename, cbind,  
colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,  
get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,  
match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,  
Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort,  
table, tapply, union, unique, unsplit, which.max, which.min

Attaching package: 'S4Vectors'

```
The following object is masked from 'package:utils':
```

```
  findMatches
```

```
The following objects are masked from 'package:base':
```

```
  expand.grid, I, unname
```

```
Loading required package: IRanges
```

```
Loading required package: GenomicRanges
```

```
Loading required package: GenomeInfoDb
```

```
Warning: package 'GenomeInfoDb' was built under R version 4.3.2
```

```
Loading required package: SummarizedExperiment
```

```
Warning: package 'SummarizedExperiment' was built under R version 4.3.2
```

```
Loading required package: MatrixGenerics
```

```
Loading required package: matrixStats
```

```
Attaching package: 'MatrixGenerics'
```

```
The following objects are masked from 'package:matrixStats':
```

```
  colAlls, colAnyNAs, colAnyNs, colAvgsPerRowSet, colCollapse,
  colCounts, colCummaxs, colCummins, colCumprods, colCumsums,
  colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,
  colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,
  colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,
  colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,
  colWeightedMeans, colWeightedMedians, colWeightedSds,
  colWeightedVars, rowAlls, rowAnyNAs, rowAnyNs, rowAvgsPerColSet,
  rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,
  rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,
```

```
rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,
rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,
rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,
rowWeightedMads, rowWeightedMeans, rowWeightedMedians,
rowWeightedSds, rowWeightedVars
```

Loading required package: Biobase

Welcome to Bioconductor

```
Vignettes contain introductory material; view with
'browseVignettes()'. To cite Bioconductor, see
'citation("Biobase")', and for packages 'citation("pkgname")'.
```

Attaching package: 'Biobase'

The following object is masked from 'package:MatrixGenerics':

```
rowMedians
```

The following objects are masked from 'package:matrixStats':

```
anyMissing, rowMedians
```

```
counts <- read.csv("airway_scaledcounts.csv", row.names=1)
metadata <- read.csv("airway_metadata.csv")
head(counts)
```

	SRR1039508	SRR1039509	SRR1039512	SRR1039513	SRR1039516
ENSG000000000003	723	486	904	445	1170
ENSG000000000005	0	0	0	0	0
ENSG00000000419	467	523	616	371	582
ENSG00000000457	347	258	364	237	318
ENSG00000000460	96	81	73	66	118
ENSG00000000938	0	0	1	0	2
	SRR1039517	SRR1039520	SRR1039521		
ENSG000000000003	1097	806	604		
ENSG000000000005	0	0	0		
ENSG00000000419	781	417	509		

```

ENSG000000000457      447      330      324
ENSG000000000460      94       102      74
ENSG000000000938      0        0        0

```

```
head(metadata)
```

```

  id      dex celltype      geo_id
1 SRR1039508 control    N61311 GSM1275862
2 SRR1039509 treated    N61311 GSM1275863
3 SRR1039512 control    N052611 GSM1275866
4 SRR1039513 treated    N052611 GSM1275867
5 SRR1039516 control    N080611 GSM1275870
6 SRR1039517 treated    N080611 GSM1275871

```

Q1. How many genes are in this dataset?

```
ncol(counts)
```

```
[1] 8
```

Q2. How many ‘control’ cell lines do we have?

```
sum(metadata$dex == "control")
```

```
[1] 4
```

```

control <- metadata[metadata[, "dex"] == "control",]
control.counts <- counts[ , control$id]
control.mean <- rowSums( control.counts )/4
head(control.mean)

```

```

ENSG000000000003 ENSG000000000005 ENSG000000000419 ENSG000000000457 ENSG00000000460
      900.75          0.00        520.50        339.75        97.25
ENSG000000000938
      0.75

```

Q3. How would you make the above code in either approach more robust? Is there a function that could help here?

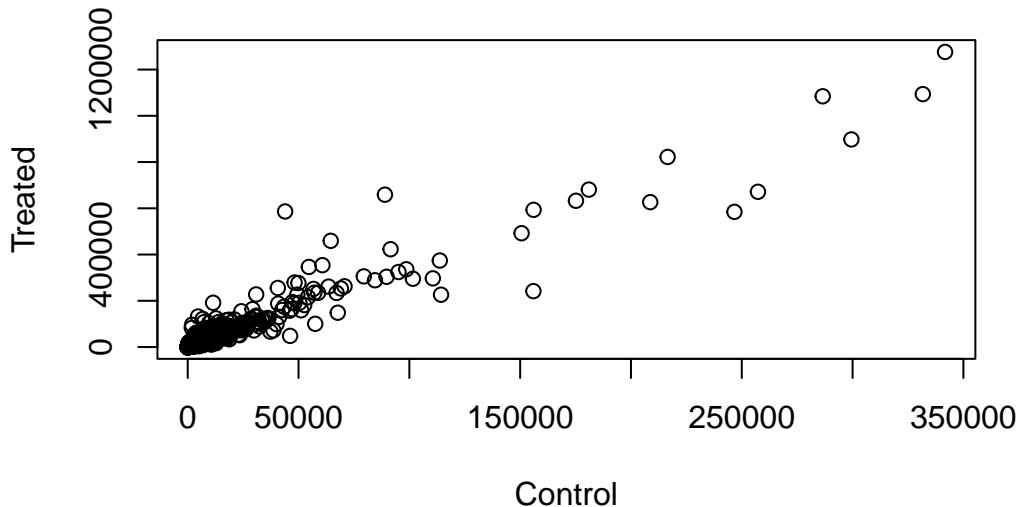
The average would be incorrect because the number of samples would not be 4. A function that took the number of samples as a parameter would be able to resolve this issue.

Q4. Follow the same procedure for the treated samples (i.e. calculate the mean per gene across drug treated samples and assign to a labeled vector called treated.mean)

```
treated <- metadata[metadata[, "dex"]=="treated",]  
treated.mean <- rowSums( counts[ ,treated$id] )  
  
meancounts <- data.frame(control.mean, treated.mean)
```

Q5 (a). Create a scatter plot showing the mean of the treated samples against the mean of the control samples. Your plot should look something like the following.

```
plot(meancounts[,1],meancounts[,2], xlab="Control", ylab="Treated")
```



Q5 (b). You could also use the ggplot2 package to make this figure producing the plot below. What geom\_?() function would you use for this plot?

```
geom_point()
```

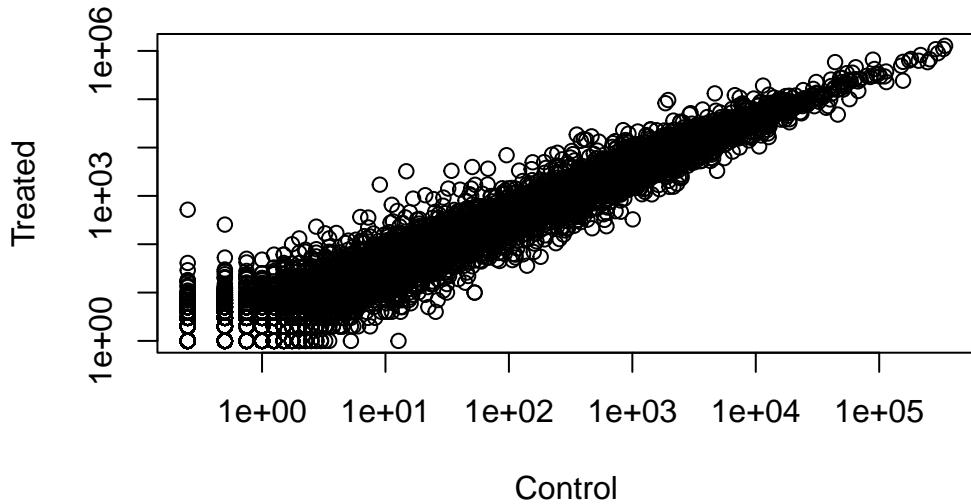
Q6. Try plotting both axes on a log scale. What is the argument to plot() that allows you to do this?

```
log = "xy"
```

```
plot(meancounts[,1],meancounts[,2], xlab="Control", ylab="Treated", log = "xy")
```

Warning in xy.coords(x, y, xlabel, ylabel, log): 15032 x values <= 0 omitted from logarithmic plot

Warning in xy.coords(x, y, xlabel, ylabel, log): 15281 y values <= 0 omitted from logarithmic plot



```
meancounts$log2fc <- log2(meancounts[, "treated.mean"] / meancounts[, "control.mean"])
head(meancounts)
```

	control.mean	treated.mean	log2fc
ENSG000000000003	900.75	2632	1.546961
ENSG000000000005	0.00	0	NaN
ENSG000000000419	520.50	2184	2.069003
ENSG000000000457	339.75	1266	1.897732
ENSG000000000460	97.25	315	1.695582
ENSG000000000938	0.75	0	-Inf

```

zero.vals <- which(meancounts[,1:2]==0, arr.ind=TRUE)

to.rm <- unique(zero.vals[,1])
mycounts <- meancounts[-to.rm,]
head(mycounts)

```

	control.mean	treated.mean	log2fc
ENSG00000000003	900.75	2632	1.546961
ENSG00000000419	520.50	2184	2.069003
ENSG00000000457	339.75	1266	1.897732
ENSG00000000460	97.25	315	1.695582
ENSG00000000971	5219.00	26750	2.357694
ENSG00000001036	2327.00	7143	1.618059

Q7. What is the purpose of the arr.ind argument in the which() function call above? Why would we then take the first column of the output and need to call the unique() function?

The arr.ind argument allows us to find the instances in which there are zero counts. unique() prevents us from counting these instances twice.

```

up.ind <- mycounts$log2fc > 2
down.ind <- mycounts$log2fc < (-2)

```

Q8. Using the up.ind vector above can you determine how many up regulated genes we have at the greater than 2 fc level?

```
sum(up.ind)
```

[1] 7151

Q9. Using the down.ind vector above can you determine how many down regulated genes we have at the greater than 2 fc level?

```
sum(down.ind)
```

[1] 6

Q10. Do you trust these results? Why or why not?

No, because this does not determine if the change is statistically significant or not.

```
library(DESeq2)
citation("DESeq2")
```

To cite package 'DESeq2' in publications use:

Love, M.I., Huber, W., Anders, S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2 Genome Biology 15(12):550 (2014)

A BibTeX entry for LaTeX users is

```
@Article{,
  title = {Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2},
  author = {Michael I. Love and Wolfgang Huber and Simon Anders},
  year = {2014},
  journal = {Genome Biology},
  doi = {10.1186/s13059-014-0550-8},
  volume = {15},
  issue = {12},
  pages = {550},
}
```

```
dds <- DESeqDataSetFromMatrix(countData=counts,
                               colData=metadata,
                               design=~dex)
```

converting counts to integer mode

Warning in DESeqDataSet(se, design = design, ignoreRank): some variables in design formula are characters, converting to factors

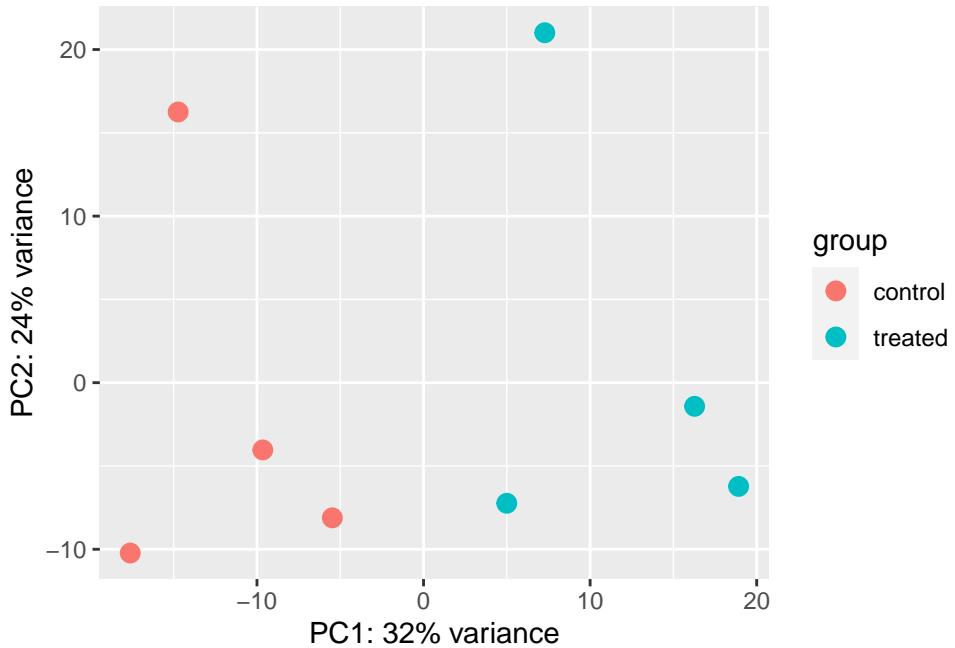
```
dds
```

```
class: DESeqDataSet
dim: 38694 8
metadata(1): version
assays(1): counts
rownames(38694): ENSG00000000003 ENSG00000000005 ... ENSG00000283120
```

```
ENSG00000283123
rowData names(0):
colnames(8): SRR1039508 SRR1039509 ... SRR1039520 SRR1039521
colData names(4): id dex celltype geo_id
```

```
vsd <- vst(dds, blind = FALSE)
plotPCA(vsd, intgroup = c("dex"))
```

using ntop=500 top features by variance



```
pcaData <- plotPCA(vsd, intgroup=c("dex"), returnData=TRUE)
```

using ntop=500 top features by variance

```
head(pcaData)
```

	PC1	PC2	group	dex	name
SRR1039508	-17.607922	-10.225252	control	control	SRR1039508

```

SRR1039509  4.996738 -7.238117 treated treated SRR1039509
SRR1039512 -5.474456 -8.113993 control control SRR1039512
SRR1039513  18.912974 -6.226041 treated treated SRR1039513
SRR1039516 -14.729173 16.252000 control control SRR1039516
SRR1039517  7.279863  21.008034 treated treated SRR1039517

```

```

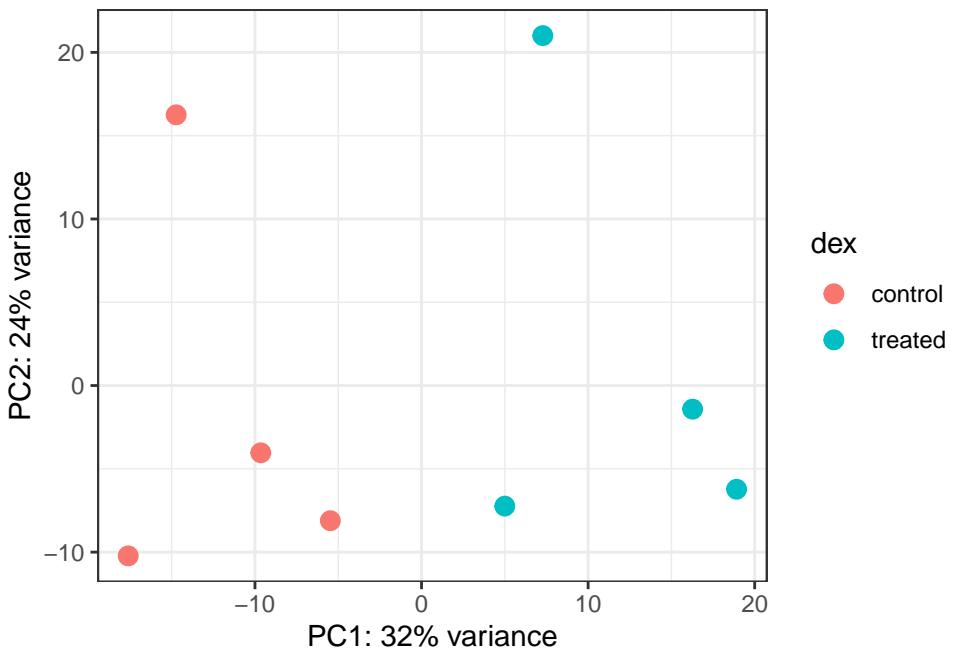
# Calculate percent variance per PC for the plot axis labels
percentVar <- round(100 * attr(pcaData, "percentVar"))

```

```

library(ggplot2)
ggplot(pcaData) +
  aes(x = PC1, y = PC2, color = dex) +
  geom_point(size = 3) +
  xlab(paste0("PC1: ", percentVar[1], "% variance")) +
  ylab(paste0("PC2: ", percentVar[2], "% variance")) +
  coord_fixed() +
  theme_bw()

```



```
#results(dds)
```

```
  dds <- DESeq(dds)
```

estimating size factors

estimating dispersions

gene-wise dispersion estimates

mean-dispersion relationship

final dispersion estimates

fitting model and testing

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

log2 fold change (MLE): dex treated vs control

Wald test p-value: dex treated vs control

DataFrame with 38694 rows and 6 columns

	baseMean	log2FoldChange	lfcSE	stat	pvalue
	<numeric>	<numeric>	<numeric>	<numeric>	<numeric>
ENSG000000000003	747.1942	-0.3507030	0.168246	-2.084470	0.0371175
ENSG000000000005	0.0000	NA	NA	NA	NA
ENSG000000000419	520.1342	0.2061078	0.101059	2.039475	0.0414026
ENSG000000000457	322.6648	0.0245269	0.145145	0.168982	0.8658106
ENSG000000000460	87.6826	-0.1471420	0.257007	-0.572521	0.5669691
...	...	...	...	...	...
ENSG00000283115	0.000000	NA	NA	NA	NA
ENSG00000283116	0.000000	NA	NA	NA	NA
ENSG00000283119	0.000000	NA	NA	NA	NA
ENSG00000283120	0.974916	-0.668258	1.69456	-0.394354	0.693319
ENSG00000283123	0.000000	NA	NA	NA	NA
	padj				
	<numeric>				
ENSG000000000003	0.163035				
ENSG000000000005	NA				
ENSG000000000419	0.176032				

```
ENSG00000000457 0.961694
ENSG00000000460 0.815849
...
ENSG00000283115 NA
ENSG00000283116 NA
ENSG00000283119 NA
ENSG00000283120 NA
ENSG00000283123 NA
```

```
summary(res)
```

```
out of 25258 with nonzero total read count
adjusted p-value < 0.1
LFC > 0 (up)      : 1563, 6.2%
LFC < 0 (down)    : 1188, 4.7%
outliers [1]       : 142, 0.56%
low counts [2]     : 9971, 39%
(mean count < 10)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results
```

```
res05 <- results(dds, alpha=0.05)
summary(res05)
```

```
out of 25258 with nonzero total read count
adjusted p-value < 0.05
LFC > 0 (up)      : 1236, 4.9%
LFC < 0 (down)    : 933, 3.7%
outliers [1]       : 142, 0.56%
low counts [2]     : 9033, 36%
(mean count < 6)
[1] see 'cooksCutoff' argument of ?results
[2] see 'independentFiltering' argument of ?results
```

```
library("AnnotationDbi")
library("org.Hs.eg.db")
```

```

columns(org.Hs.eg.db)

[1] "ACCNUM"      "ALIAS"       "ENSEMBL"      "ENSEMBLPROT"  "ENSEMLTRANS"
[6] "ENTREZID"    "ENZYME"     "EVIDENCE"    "EVIDENCEALL" "GENENAME"
[11] "GENETYPE"    "GO"         "GOALL"       "IPI"         "MAP"
[16] "OMIM"        "ONTOLOGY"   "ONTOLOGYALL" "PATH"        "PFAM"
[21] "PMID"        "PROSITE"    "REFSEQ"      "SYMBOL"     "UCSCKG"
[26] "UNIPROT"

res$symbol <- mapIds(org.Hs.eg.db,
                      keys=row.names(res), # Our genenames
                      keytype="ENSEMBL",      # The format of our genenames
                      column="SYMBOL",        # The new format we want to add
                      multiVals="first")

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

head(res)

log2 fold change (MLE): dex treated vs control
Wald test p-value: dex treated vs control
DataFrame with 6 rows and 7 columns
  baseMean log2FoldChange      lfcSE      stat      pvalue
  <numeric>      <numeric> <numeric> <numeric> <numeric>
ENSG000000000003 747.194195     -0.3507030  0.168246 -2.084470 0.0371175
ENSG000000000005  0.000000        NA        NA        NA        NA
ENSG000000000419 520.134160      0.2061078  0.101059  2.039475 0.0414026
ENSG000000000457 322.664844      0.0245269  0.145145  0.168982 0.8658106
ENSG000000000460  87.682625     -0.1471420  0.257007 -0.572521 0.5669691
ENSG000000000938  0.319167     -1.7322890  3.493601 -0.495846 0.6200029
  padj      symbol
  <numeric> <character>
ENSG000000000003  0.163035      TSPAN6
ENSG000000000005    NA          TNMD
ENSG000000000419  0.176032      DPM1
ENSG000000000457  0.961694      SCYL3
ENSG000000000460  0.815849      FIRRM
ENSG000000000938    NA          FGR

```

Q11. Run the mapIds() function two more times to add the Entrez ID and UniProt accession and GENENAME as new columns called res\$entrez, res\$uniprot and res\$genename.

```
res$entrez <- mapIds(org.Hs.eg.db,
                      keys=row.names(res),
                      column="ENTREZID",
                      keytype="ENSEMBL",
                      multiVals="first")

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

res$uniprot <- mapIds(org.Hs.eg.db,
                      keys=row.names(res),
                      column="UNIPROT",
                      keytype="ENSEMBL",
                      multiVals="first")

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

res$genename <- mapIds(org.Hs.eg.db,
                      keys=row.names(res),
                      column="GENENAME",
                      keytype="ENSEMBL",
                      multiVals="first")

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

head(res)

log2 fold change (MLE): dex treated vs control
Wald test p-value: dex treated vs control
DataFrame with 6 rows and 10 columns
  baseMean log2FoldChange      lfcSE      stat     pvalue
  <numeric>      <numeric> <numeric> <numeric> <numeric>
ENSG000000000003 747.194195     -0.3507030  0.168246 -2.084470 0.0371175
ENSG000000000005  0.0000000      NA         NA         NA         NA
ENSG000000000419 520.134160     0.2061078  0.101059  2.039475 0.0414026
```

ENSG000000000457	322.664844	0.0245269	0.145145	0.168982	0.8658106
ENSG000000000460	87.682625	-0.1471420	0.257007	-0.572521	0.5669691
ENSG000000000938	0.319167	-1.7322890	3.493601	-0.495846	0.6200029
	padj	symbol	entrez	uniprot	
	<numeric>	<character>	<character>	<character>	
ENSG000000000003	0.163035	TSPAN6	7105	AOA024RCIO	
ENSG000000000005	NA	TNMD	64102	Q9H2S6	
ENSG000000000419	0.176032	DPM1	8813	060762	
ENSG000000000457	0.961694	SCYL3	57147	Q8IZE3	
ENSG000000000460	0.815849	FIRRM	55732	AOA024R922	
ENSG000000000938	NA	FGR	2268	P09769	
	genename				
	<character>				
ENSG000000000003		tetraspanin 6			
ENSG000000000005		tenomodulin			
ENSG000000000419		dolichyl-phosphate m..			
ENSG000000000457		SCY1 like pseudokina..			
ENSG000000000460		FIGNL1 interacting r..			
ENSG000000000938		FGR proto-oncogene, ..			

```
ord <- order( res$padj )
#View(res[ord,])
head(res[ord,])
```

log2 fold change (MLE): dex treated vs control  
 Wald test p-value: dex treated vs control  
 DataFrame with 6 rows and 10 columns

	baseMean	log2FoldChange	lfcSE	stat	pvalue
	<numeric>	<numeric>	<numeric>	<numeric>	<numeric>
ENSG00000152583	954.771	4.36836	0.2371268	18.4220	8.74490e-76
ENSG00000179094	743.253	2.86389	0.1755693	16.3120	8.10784e-60
ENSG00000116584	2277.913	-1.03470	0.0650984	-15.8944	6.92855e-57
ENSG00000189221	2383.754	3.34154	0.2124058	15.7319	9.14433e-56
ENSG00000120129	3440.704	2.96521	0.2036951	14.5571	5.26424e-48
ENSG00000148175	13493.920	1.42717	0.1003890	14.2164	7.25128e-46
	padj	symbol	entrez	uniprot	
	<numeric>	<character>	<character>	<character>	
ENSG00000152583	1.32441e-71	SPARCL1	8404	AOA024RDE1	
ENSG00000179094	6.13966e-56	PER1	5187	015534	
ENSG00000116584	3.49776e-53	ARHGEF2	9181	Q92974	
ENSG00000189221	3.46227e-52	MAOA	4128	P21397	

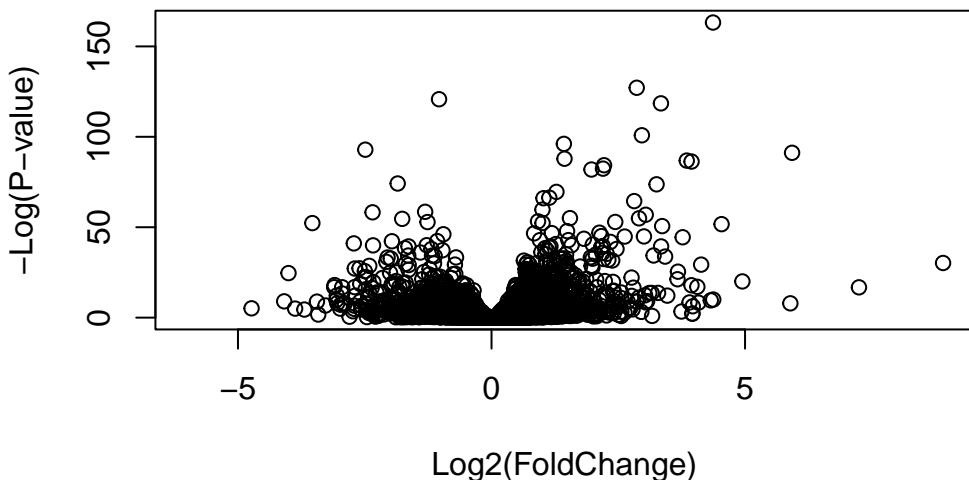
```

ENSG00000120129 1.59454e-44      DUSP1      1843      B4DU40
ENSG00000148175 1.83034e-42      STOM      2040      F8VSL7
genename
<character>
ENSG00000152583      SPARC like 1
ENSG00000179094 period circadian reg..
ENSG00000116584 Rho/Rac guanine nucl..
ENSG00000189221 monoamine oxidase A
ENSG00000120129 dual specificity pho..
ENSG00000148175      stomatin

```

```
write.csv(res[ord,], "deseq_results.csv")
```

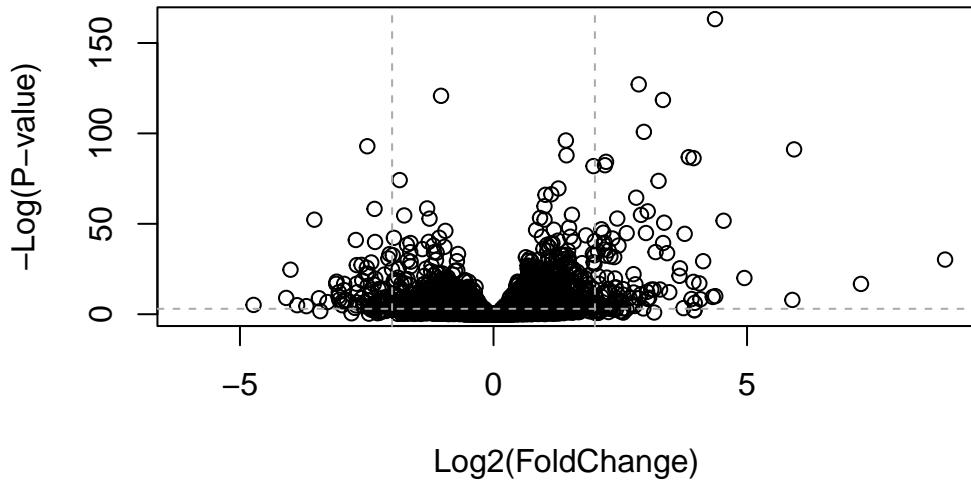
```
plot( res$log2FoldChange, -log(res$padj),
      xlab="Log2(FoldChange)",
      ylab="-Log(P-value)")
```



```
plot( res$log2FoldChange, -log(res$padj),
      ylab="-Log(P-value)", xlab="Log2(FoldChange)")
```

```
# Add some cut-off lines
```

```
abline(v=c(-2,2), col="darkgray", lty=2)
abline(h=-log(0.05), col="darkgray", lty=2)
```

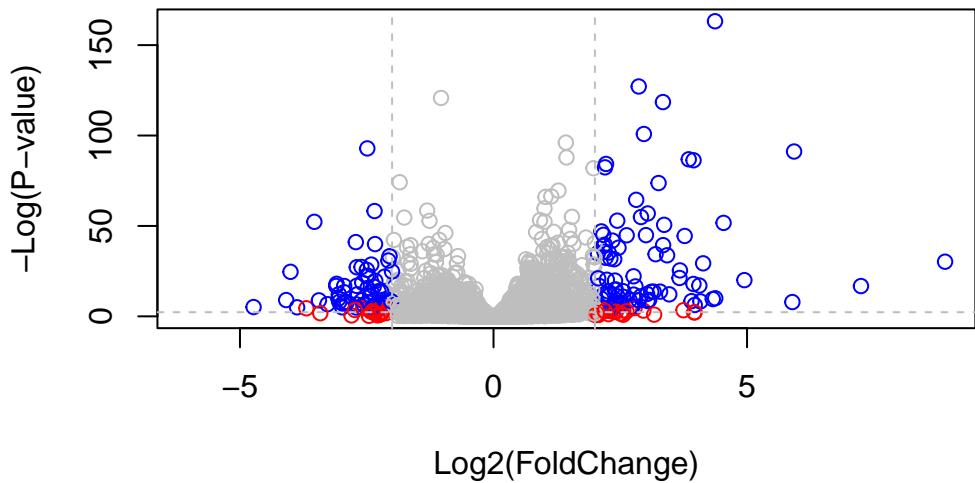


```
# Setup our custom point color vector
mycols <- rep("gray", nrow(res))
mycols[ abs(res$log2FoldChange) > 2 ] <- "red"

inds <- (res$padj < 0.01) & (abs(res$log2FoldChange) > 2 )
mycols[ inds ] <- "blue"

# Volcano plot with custom colors
plot( res$log2FoldChange, -log(res$padj),
col=mycols, ylab="-Log(P-value)", xlab="Log2(FoldChange)" )

# Cut-off lines
abline(v=c(-2,2), col="gray", lty=2)
abline(h=-log(0.1), col="gray", lty=2)
```



```
library(EnhancedVolcano)
```

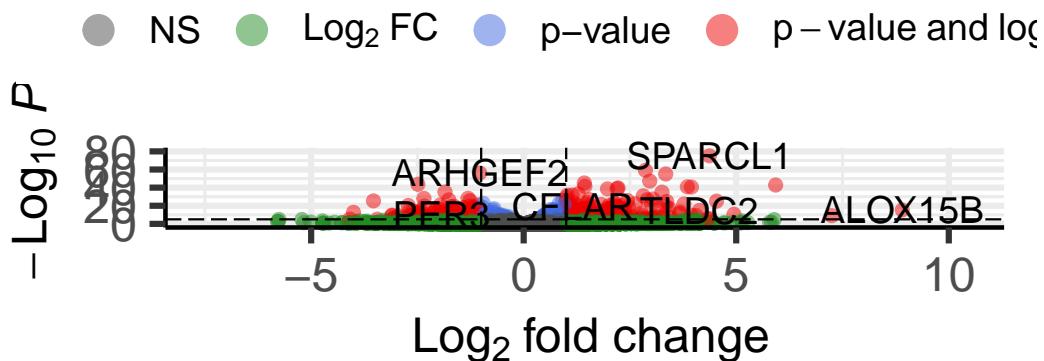
```
Loading required package: ggrepel
```

```
x <- as.data.frame(res)

EnhancedVolcano(x,
  lab = x$symbol,
  x = 'log2FoldChange',
  y = 'pvalue')
```

# Volcano plot

## Enhanced Volcano



```
library(pathview)
```

```
#####
# Pathview is an open source software package distributed under GNU General
# Public License version 3 (GPLv3). Details of GPLv3 is available at
# http://www.gnu.org/licenses/gpl-3.0.html. Particullary, users are required to
# formally cite the original Pathview paper (not just mention it) in publications
# or products. For details, do citation("pathview") within R.
```

```
The pathview downloads and uses KEGG data. Non-academic uses may require a KEGG
license agreement (details at http://www.kegg.jp/kegg/legal.html).
```

```
library(gage)
```

```
library(gageData)
```

```

data(kegg.sets.hs)

# Examine the first 2 pathways in this kegg set for humans
head(kegg.sets.hs, 2)

$`hsa00232 Caffeine metabolism`
[1] "10"    "1544"  "1548"  "1549"  "1553"  "7498"  "9"

$`hsa00983 Drug metabolism - other enzymes`
[1] "10"    "1066"  "10720" "10941" "151531" "1548"  "1549"  "1551"
[9] "1553"  "1576"  "1577"  "1806"  "1807"  "1890"  "221223" "2990"
[17] "3251"  "3614"  "3615"  "3704"  "51733"  "54490" "54575"  "54576"
[25] "54577" "54578" "54579" "54600" "54657"  "54658" "54659"  "54963"
[33] "574537" "64816" "7083"  "7084"  "7172"  "7363"  "7364"  "7365"
[41] "7366"  "7367"  "7371"  "7372"  "7378"  "7498"  "79799" "83549"
[49] "8824"  "8833"  "9"     "978"

foldchanges = res$log2FoldChange
names(foldchanges) = res$entrez
head(foldchanges)

 7105       64102       8813       57147       55732       2268
-0.35070302      NA  0.20610777  0.02452695 -0.14714205 -1.73228897

# Get the results
keggres = gage(foldchanges, gsets=kegg.sets.hs)

attributes(keggres)

$names
[1] "greater" "less"    "stats"

# Look at the first three down (less) pathways
head(keggres$less, 3)

          p.geomean stat.mean      p.val
hsa05332 Graft-versus-host disease 0.0004250461 -3.473346 0.0004250461

```

```

hsa04940 Type I diabetes mellitus 0.0017820293 -3.002352 0.0017820293
hsa05310 Asthma 0.0020045888 -3.009050 0.0020045888
q.val set.size exp1
hsa05332 Graft-versus-host disease 0.09053483 40 0.0004250461
hsa04940 Type I diabetes mellitus 0.14232581 42 0.0017820293
hsa05310 Asthma 0.14232581 29 0.0020045888

pathview(gene.data=foldchanges, pathway.id="hsa05310")

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

Info: Working in directory /Users/jacobgil/Downloads/BIMM 143/class13

Info: Writing image file hsa05310.pathview.png

# A different PDF based output of the same data
pathview(gene.data=foldchanges, pathway.id="hsa05310", kegg.native=FALSE)

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

Info: Working in directory /Users/jacobgil/Downloads/BIMM 143/class13

Info: Writing image file hsa05310.pathview.pdf

i <- grep("CRISPLD2", res$symbol)
res[i,]

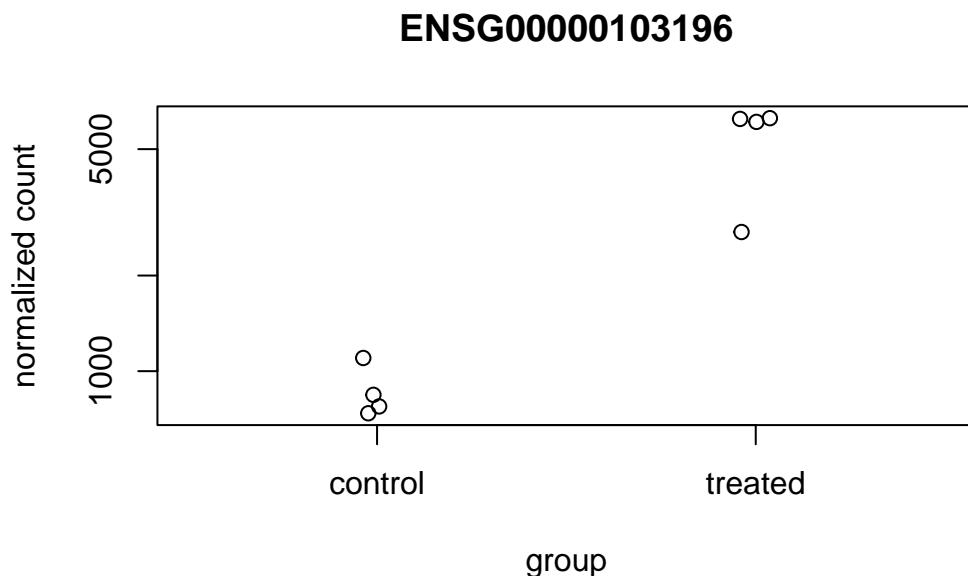
log2 fold change (MLE): dex treated vs control
Wald test p-value: dex treated vs control
DataFrame with 1 row and 10 columns
  baseMean log2FoldChange      lfcSE      stat      pvalue
  <numeric>      <numeric> <numeric> <numeric>  <numeric>
ENSG00000103196  3096.16      2.62603  0.267444  9.81899 9.32747e-23
  padj      symbol      entrez      uniprot
  <numeric> <character> <character> <character>
ENSG00000103196 3.36344e-20    CRISPLD2      83716  AOA140VK80
  genename
  <character>
ENSG00000103196 cysteine rich secret..

```

```
rownames(res[i,
```

```
[1] "ENSG00000103196"
```

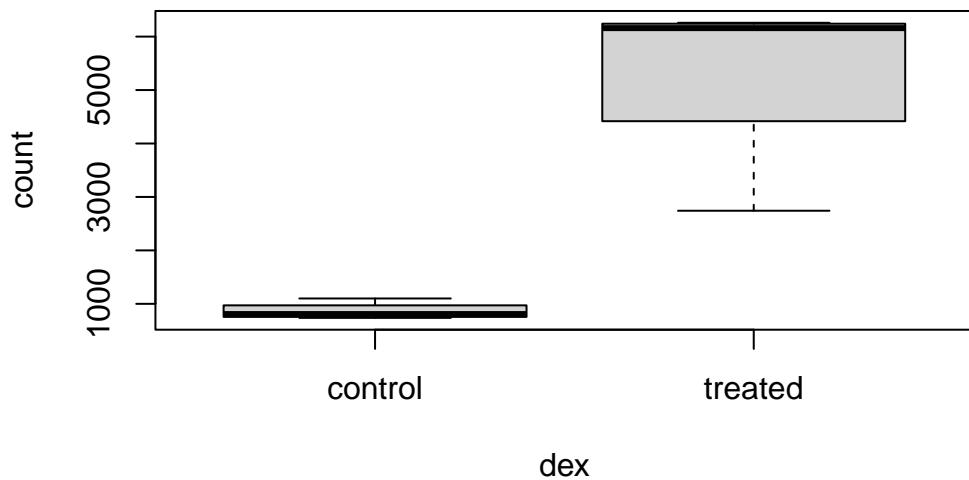
```
plotCounts(dds, gene="ENSG00000103196", intgroup="dex")
```



```
# Return the data
d <- plotCounts(dds, gene="ENSG00000103196", intgroup="dex", returnData=TRUE)
head(d)
```

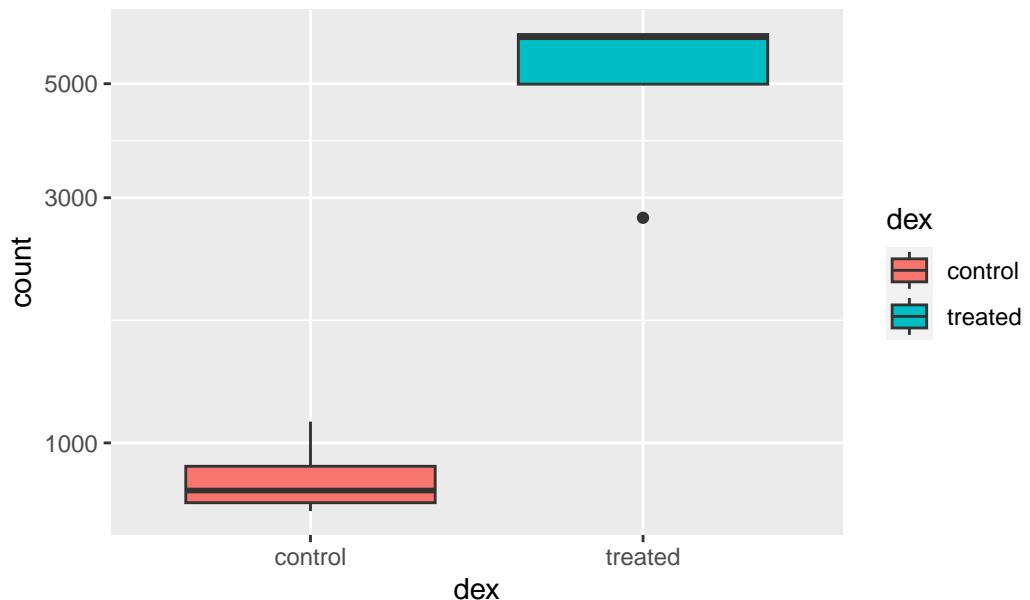
	count	dex
SRR1039508	774.5002	control
SRR1039509	6258.7915	treated
SRR1039512	1100.2741	control
SRR1039513	6093.0324	treated
SRR1039516	736.9483	control
SRR1039517	2742.1908	treated

```
boxplot(count ~ dex , data=d)
```



```
library(ggplot2)
ggplot(d, aes(dex, count, fill=dex)) +
  geom_boxplot() +
  scale_y_log10() +
  ggtitle("CRISPLD2")
```

## CRISPLD2



**ASTHMA**