11_04_22_lab

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```
library(BiocManager)
```

```
Bioconductor version '3.15' is out-of-date; the current
release version '3.16'
  is available with R version '4.2'; see
https://bioconductor.org/install
```

```
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, 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 objects are masked from 'package:base':

    expand.grid, I, unname

Loading required package: IRanges

Loading required package: GenomicRanges

Loading required package: GenomeInfoDb

Loading required package: SummarizedExperiment

Loading required package: MatrixGenerics

Loading required package: matrixStats


Attaching package: 'MatrixGenerics'

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

    colAlls, colAnyNAs, colAnys, 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, rowAnys,
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
ENSG00000000003        723        486        904        445
1170
ENSG00000000005          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
ENSG00000000003       1097        806        604
ENSG00000000005          0          0          0
ENSG00000000419        781        417        509
ENSG00000000457        447        330        324
ENSG00000000460         94        102         74
ENSG00000000938          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?

```
cat("We have", ncol(counts), "genes in this dataset")
```

```
We have 8 genes in this dataset
```

Q2. How many 'control' cell lines do we have?

```
cat("We have", ncol(metadata[metadata$dex == "control",]), "cor
```

```
We have 4 control cell lines in this dataset
```

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

```
ENSG00000000003 ENSG00000000005 ENSG00000000419
ENSG00000000457 ENSG00000000460
         900.75             0.00          520.50
339.75           97.25
ENSG00000000938
           0.75
```

```
library(dplyr)
```

```
Attaching package: 'dplyr'

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

    combine

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

    count

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

    intersect, setdiff, union

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

    intersect

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

    collapse, desc, intersect, setdiff, slice, union

The following objects are masked from 'package:S4Vectors':

    first, intersect, rename, setdiff, setequal, union

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

    combine, intersect, setdiff, union

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

    filter, lag

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

    intersect, setdiff, setequal, union
```

```
control <- metadata %>% filter(dex=="control")
control.counts <- counts %>% select(control$id)
control.mean <- rowSums(control.counts)/4
```

```
head(control.mean)
```

```
ENSG00000000003 ENSG00000000005 ENSG00000000419
ENSG00000000457 ENSG00000000460
         900.75             0.00          520.50
339.75           97.25
ENSG00000000938
           0.75
```

Q3. How would you make the above code in either approach more robust? I would change the 4 to nrow(control) This would make the process more robust to different sized datasets. Currently it is hard coded to only be able to deal with specifically 4 controls. Outside of that someone would have to find out how many controls there are and manually change it. That changes the code to this for the 1st process:

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

```
ENSG00000000003 ENSG00000000005 ENSG00000000419
ENSG00000000457 ENSG00000000460
         900.75             0.00          520.50
339.75           97.25
ENSG00000000938
           0.75
```

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.counts <- counts[ ,treated$id]
treated.mean <- rowSums( treated.counts )/nrow(treated)
head(treated.mean)
```

```
ENSG00000000003 ENSG00000000005 ENSG00000000419
ENSG00000000457 ENSG00000000460
         658.00             0.00          546.00
316.50           78.75
ENSG00000000938
```

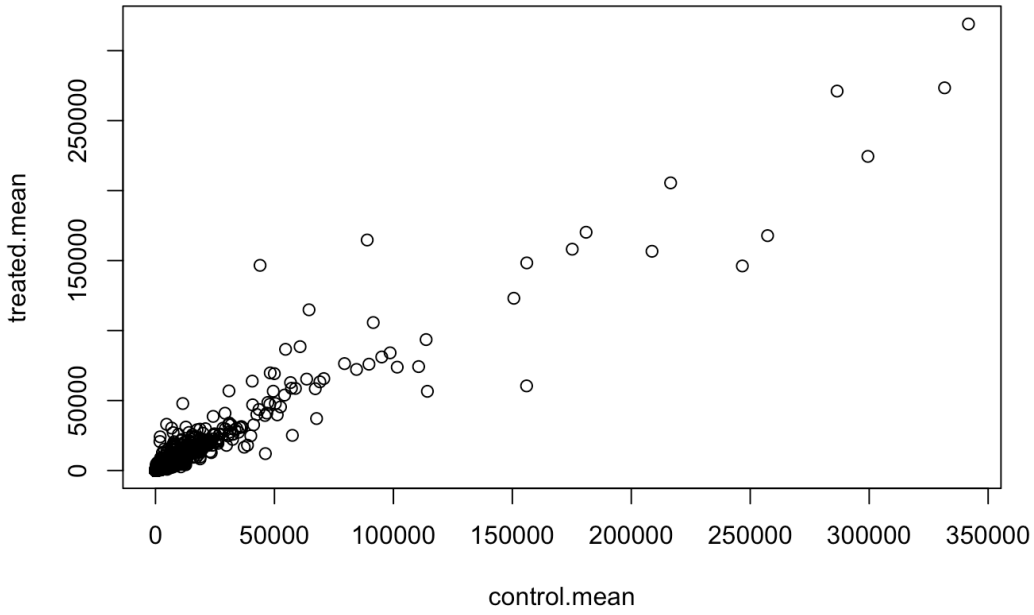
```
0.00
```

```
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.

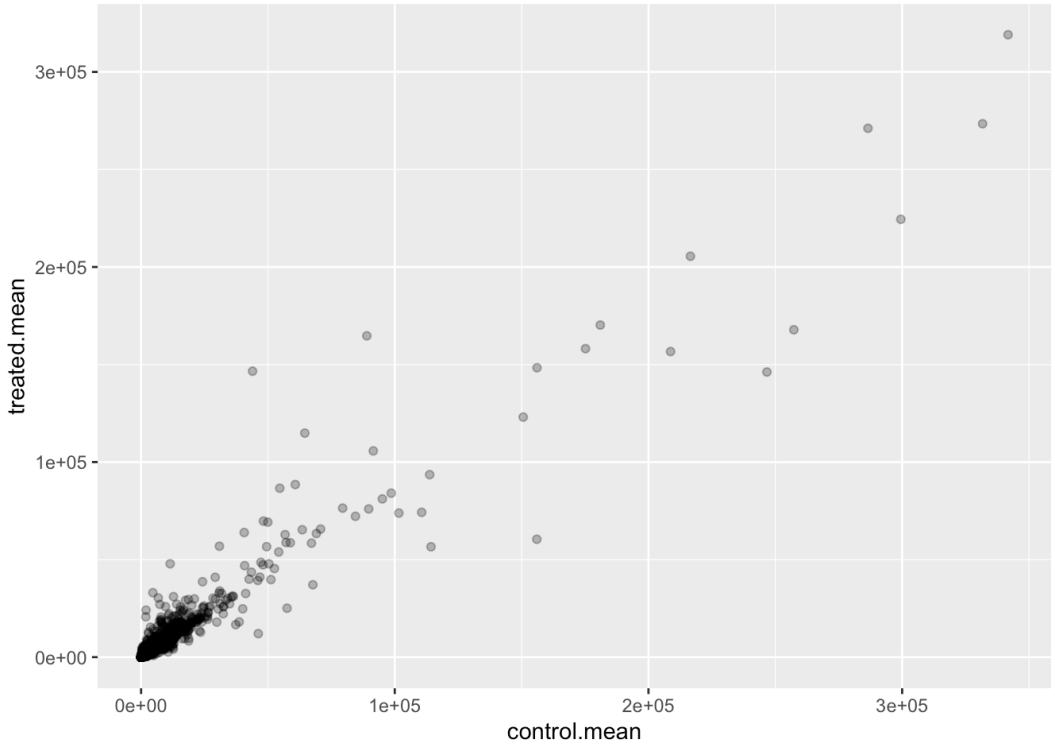
```
library(ggplot2)
```

```
plot(control.mean, treated.mean)
```



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()

```
ggplot(meancounts, aes(control.mean, treated.mean))+
  geom_point(alpha = 0.3)
```

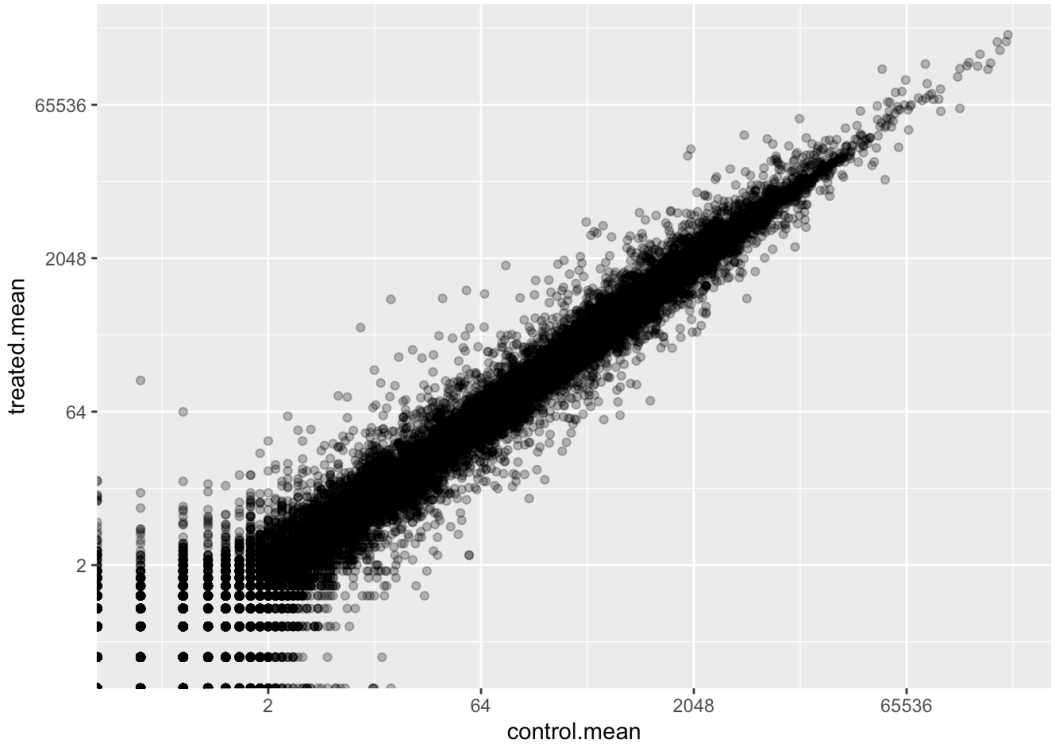


Q6. Try plotting both axes on a log scale. What is the argument to plot() that allows you to do this? scale_x_continuous and scale_y_continuous are the additional functions needed for ggplot

```
ggplot(meancounts, aes(control.mean, treated.mean))+
  geom_point(alpha = 0.3)+
  scale_x_continuous(trans="log2")+
  scale_y_continuous(trans="log2")
```

```
Warning: Transformation introduced infinite values in
continuous x-axis
```

```
Warning: Transformation introduced infinite values in
continuous y-axis
```




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

```
                control.mean treated.mean      log2fc
ENSG00000000003       900.75       658.00 -0.45303916
ENSG00000000005         0.00         0.00         NaN
ENSG00000000419       520.50       546.00  0.06900279
ENSG00000000457       339.75       316.50 -0.10226805
ENSG00000000460        97.25        78.75 -0.30441833
ENSG00000000938         0.75         0.00        -Inf
```

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? First we are looking at which values are 0 and then everytime one is found, arr.ind allows us to know which rowname each row is associated with. Then unique allows us to make sure nothing is double counted if there are 0s in both columns.

```
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       658.00 -0.45303916
ENSG00000000419       520.50       546.00  0.06900279
ENSG00000000457       339.75       316.50 -0.10226805
ENSG00000000460        97.25        78.75 -0.30441833
ENSG00000000971      5219.00      6687.50  0.35769358
ENSG00000001036      2327.00      1785.75 -0.38194109
```

```
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?

```
cat("There are", sum(up.ind), "upregulated genes at a greater t
```

```
There are 250 upregulated genes at a greater than 2x fold
change level
```

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

```
cat("There are", sum(down.ind), "upregulated genes at a greate
```

```
There are 367 upregulated genes at a greater than 2x fold
change level
```

Q10. Do you trust these results? Why or why not? I do trust that all the results are true to the fact that there is a 2x fold change, but in the greater context, I don't have enough information to draw conclusions yet.

```
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
```

```
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>
ENSG00000000003  747.1942     -0.3507030  0.168246 -2.084470
0.0371175
ENSG00000000005    0.0000             NA        NA        NA
NA
ENSG00000000419  520.1342      0.2061078  0.101059  2.039475
0.0414026
ENSG00000000457  322.6648      0.0245269  0.145145  0.168982
0.8658106
ENSG00000000460   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>
```

```
ENSG00000000003  0.163035
ENSG00000000005        NA
ENSG00000000419  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")
```

```
Attaching package: 'AnnotationDbi'
```

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

    select
```

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

```
columns(org.Hs.eg.db)
```

```
 [1] "ACCNUM"       "ALIAS"        "ENSEMBL"
"ENSEMBLPROT"  "ENSEMBLTRANS"
 [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
                     column="SYMBOL",          # The new format
                     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>
ENSG00000000003 747.194195     -0.3507030  0.168246 -2.084470
0.0371175
ENSG00000000005   0.000000             NA        NA        NA
NA
```

```
ENSG00000000419 520.134160      0.2061078  0.101059  2.039475
0.0414026
ENSG00000000457 322.664844      0.0245269  0.145145  0.168982
0.8658106
ENSG00000000460  87.682625     -0.1471420  0.257007 -0.572521
0.5669691
ENSG00000000938   0.319167     -1.7322890  3.493601 -0.495846
0.6200029
                     padj      symbol
                <numeric> <character>
ENSG00000000003  0.163035      TSPAN6
ENSG00000000005        NA        TNMD
ENSG00000000419  0.176032        DPM1
ENSG00000000457  0.961694       SCYL3
ENSG00000000460  0.815849    C1orf112
ENSG00000000938        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), # Our genenames
                     keytype="ENSEMBL",        # The format of
                     column="ENTREZID",          # The new form
                     multiVals="first")
```

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

```
res$uniprot <- mapIds(org.Hs.eg.db,
                     keys=row.names(res), # Our genenames
                     keytype="ENSEMBL",        # The format of
                     column="UNIPROT",          # The new forma
                     multiVals="first")
```

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

```
res$genename <- mapIds(org.Hs.eg.db,
                     keys=row.names(res), # Our genenames
                     keytype="ENSEMBL",        # The format of
                     column="GENENAME",          # The new form
                     multiVals="first")
```

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

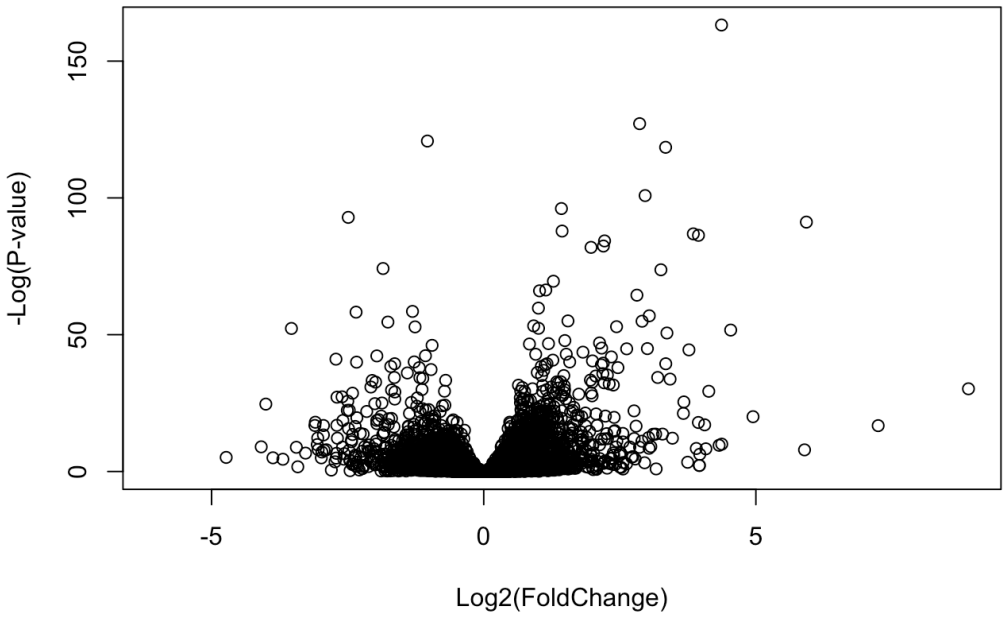
```
ord <- order( res$padj )
#View(res[ord,])
head(res[ord,])
```

```
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
A0A024RDE1
ENSG00000179094 6.13966e-56        PER1        5187
O15534
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
```

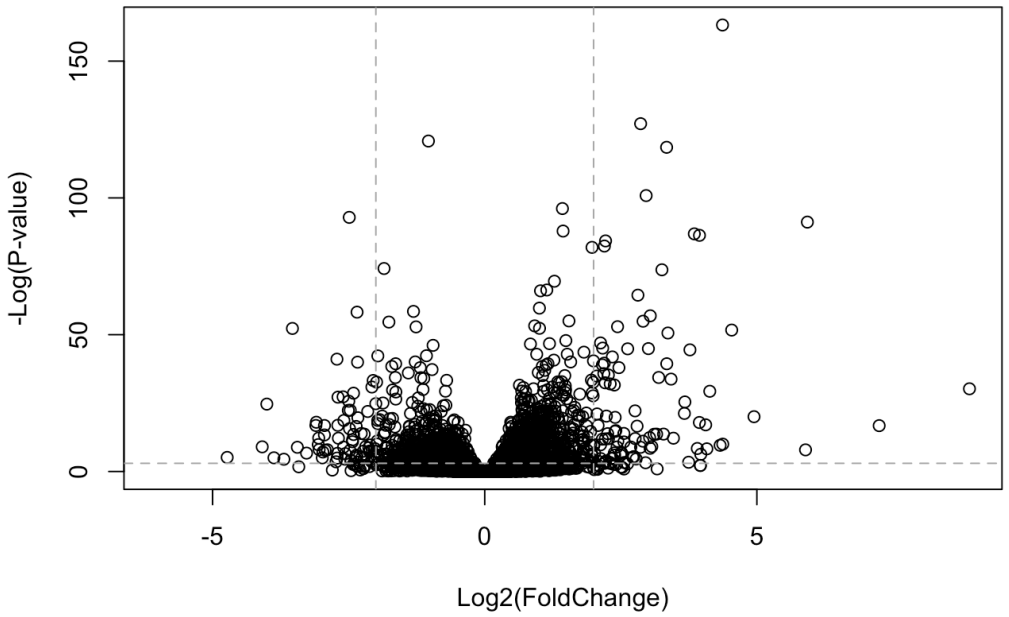
```
write.csv(res[ord,], "deseq_results.csv")
```

```
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)
```

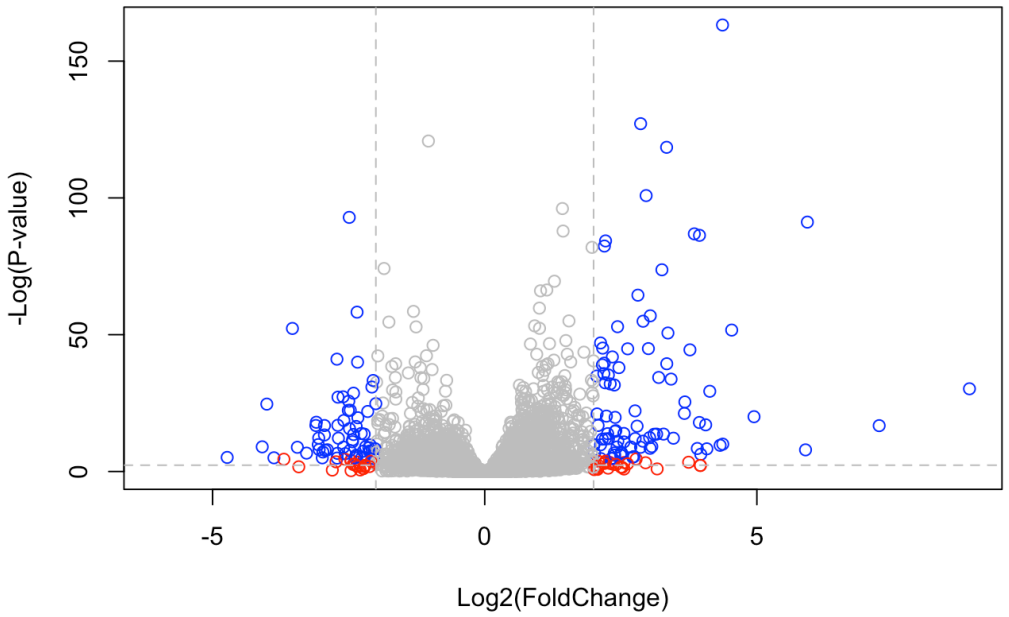



```
# Setup our custom point color vector
mycols <- rep("gray", nrow(res))
mycols[ abs(res$log2FoldChange) > 2 ]  <- "red"

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)
```

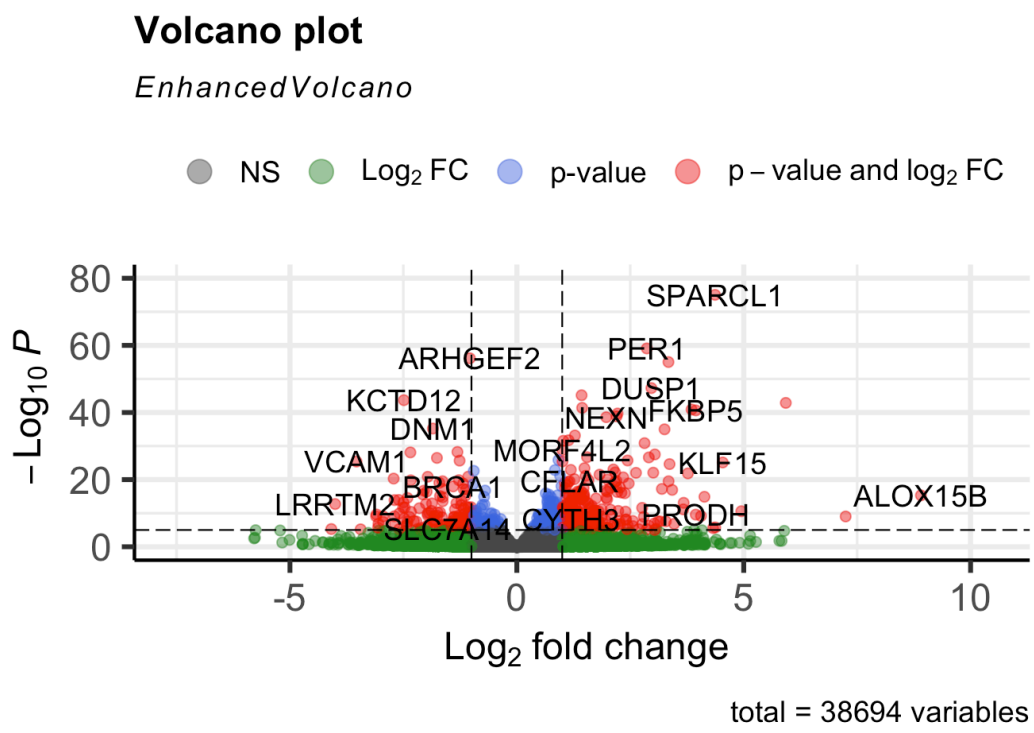



```
library(EnhancedVolcano)
```

```
Loading required package: ggrepel
```

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

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




```
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"
```

```
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/andytong/Downloads/Bioinformatics Work/11_04_22

Info: Writing image file hsa05310.pathview.png
```

Q12. Can you do the same procedure as above to plot the pathview figures for the top 2 down-reguled pathways?

Yes I can do the same for both of these.

```
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
```

Type I diabetes mellitus

```
pathview(gene.data=foldchanges, pathway.id="hsa04940")
```

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

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Info: Writing image file hsa04940.pathview.png
```

Graft-versus-host disease

```
pathview(gene.data=foldchanges, pathway.id="hsa05332")
```

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

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Info: Writing image file hsa05332.pathview.png
```