

# Skeleton Key for RNAseq analysis

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## About

This is the script used to perform differential gene expression analysis using **edgeR**. The tissue came from p4 leaves of *Solanum lycopersicum* using Laser Capture Microdissection.

## Key to Samples

genotype: either wildtype of *tf2*

region: A. tip B. early emerging leaflet C. base

type: MBR = Marginal Blastozone Region, other = the rachis or midvein region

Samples:

```
print(sample1)
```

```
## [1] "tf2cmbr"
```

```
print(sample2)
```

```
## [1] "wtcmbr"
```

*See README.md for more detailed instructions of how to use script*

Run the **render()** function below and everything will be run with report at end.

```
library(rmarkdown)
render("skeletonDE.Rmd", "pdf_document", output_file = paste(sample1,"_",sample2,"_", "DE.pdf",sep=""))
```

## Analysis (Acutal start)

### libraries

```
library(edgeR)
library(yaml)
```

### Read in YAML guide

This reads in the information in the **de.yaml** file which has the two names of the samples you are interested in comparing.

```
yamls <- yaml.load_file("de.yml")
```

This part assigns your YMAL to a object in R. This will be used throughout the script to specify which sample types you are comparing.

```
sample1 <- yamls$sample1
sample2 <- yamls$sample2

sample1
```

```
## [1] "tf2bother"
```

```
sample2
```

```
## [1] "wtbother"
```

## Read in Data

Read in raw count data per gene.

```
counts <- read.delim("../requisiteData/sam2countsResults.tsv",row.names=1)

#check the file
head(counts)
colnames(counts)
#need to convert NA to 0 counts
counts[is.na(counts)] <- 0
```

## Subset DE expirement

Start by subsetting the particular treatments which are being compared. This might need to be modified depending on the naming of your samples. In my case each sample is named by sample and rep number, so the script is identifying any sample with the sample name given in the de.yml file.

```
colnames(counts)
```

```
## [1] "tf2ambr1"      "tf2ambr3"      "tf2ambr4"      "tf2ambr6"
## [5] "tf2aother1"    "tf2aother2"    "tf2aother4"    "tf2aother7"
## [9] "tf2bmr2"       "tf2bmr5"       "tf2bmr6"       "tf2bother1"
## [13] "tf2bother3"    "tf2bother4"    "tf2bother6"    "tf2cmbr1.4"
## [17] "tf2cmbr3"      "tf2cmbr6"      "tf2cmbr7"      "tf2cother2"
## [21] "tf2cother5"    "tf2cother6"    "tf2cother7"    "wtambr2"
## [25] "wtambr4"       "wtambr5"       "wtaother1"     "wtaother5"
## [29] "wtaother6"     "wtaother7"     "wtaother8"     "wtbmr2"
## [33] "wtbmr3"        "wtbmr6"        "wtbmr8"        "wtbother1.4"
## [37] "wtbother3"     "wtbother5"     "wtbother8"     "wtcmbr10"
## [41] "wtcmbr1.4.6"   "wtcmbr2"       "wtcmbr3"       "wtcmbr7"
## [45] "wtcmbr9"       "wtcother1.3.4" "wtcother2"     "wtcother6"
```

```
counts1 <- counts[,grep(sample1, colnames(counts), value = TRUE)]
count1Len <- length(colnames(counts1)) #used in to specify library group in next step.

counts2 <- counts[,grep(sample2, colnames(counts), value = TRUE)]
count2Len <- length(colnames(counts2)) #used to specify library group in next step.

counts <- cbind(counts1, counts2)

head(counts)
```

```
##                tf2bother1 tf2bother3 tf2bother4 tf2bother6 wtbother1.4
## Solyc00g005040.2.1         6         3         5         2         0
## Solyc00g005050.2.1        46         9        23        22         0
## Solyc00g005060.1.1         0         1         1         1         0
## Solyc00g005070.1.1        25         4        11        11         0
## Solyc00g005080.1.1        52        12        15        12         0
## Solyc00g005150.1.1        11         0         0         1         0
##                wtbother3 wtbother5 wtbother8
## Solyc00g005040.2.1         8         0         3
## Solyc00g005050.2.1        25         0        14
## Solyc00g005060.1.1         0         0         0
## Solyc00g005070.1.1         6         2         4
## Solyc00g005080.1.1        29         0        11
## Solyc00g005150.1.1         2         0         2
```

### Add column specifying library Group

Make a vector called group that will be used to make a new column named group to identify library region type.

```
group <- c(rep(sample1, count1Len), rep(sample2, count2Len))
d <- DGEList(counts=counts,group=group)
```

Check to see if the group column matches your sample name and they are appropriate.

```
d$samples
```

```
##                group lib.size norm.factors
## tf2bother1  tf2bother  2415227           1
## tf2bother3  tf2bother   626786           1
## tf2bother4  tf2bother  1003586           1
## tf2bother6  tf2bother   854903           1
## wtbother1.4 wtbother    1421           1
## wtbother3   wtbother  1076939           1
## wtbother5   wtbother   200587           1
## wtbother8   wtbother   499487           1
```

### Differential expression using edgeR

Make sure there is full understanding of each edgeR command being used. The manual is amazing so read it *before* running the DE analysis below [edgeR manual](#). There are many options and they must be set to be appropriate for your analysis.

```
cpm.d <- cpm(d) #counts per mutant
d <- d[rowSums(cpm.d>5)>=3,] #This might be a line to adjust. It is removing genes with low counts.
d <- estimateCommonDisp(d,verbose=T)
```

```
## Disp = 0.327 , BCV = 0.5718
```

```
d <- calcNormFactors(d)
d <- estimateCommonDisp(d)

DEtest <- exactTest(d,pair=c(sample1,sample2))
head(DEtest$table)
```

```
##               logFC logCPM   PValue
## Solyc00g005050.2.1 -0.12332  5.171 5.771e-01
## Solyc00g005070.1.1 -0.38788  4.028 7.088e-01
## Solyc00g005080.1.1  0.06034  4.796 7.598e-01
## Solyc00g005440.1.1 -0.64142  5.222 2.673e-01
## Solyc00g005840.2.1  3.21142  7.672 7.769e-06
## Solyc00g005880.1.1  0.45501  3.491 6.026e-01
```

```
results <- topTags(DEtest, n=Inf)
head(results)
```

```
## Comparison of groups: wtbother-tf2bother
##               logFC logCPM   PValue   FDR
## Solyc04g074380.2.1  7.792 12.140 1.382e-20 2.089e-16
## Solyc10g078540.1.1  7.573 13.679 3.602e-20 2.722e-16
## Solyc04g074390.2.1  6.989 10.519 1.278e-17 6.440e-14
## Solyc02g076780.2.1  6.702 10.766 7.274e-17 2.749e-13
## Solyc09g059140.1.1  6.585  8.743 1.108e-15 3.350e-12
## Solyc12g097060.1.1  6.792  8.043 7.946e-15 2.002e-11
```

```
dim(results$table)
```

```
## [1] 15118      4
```

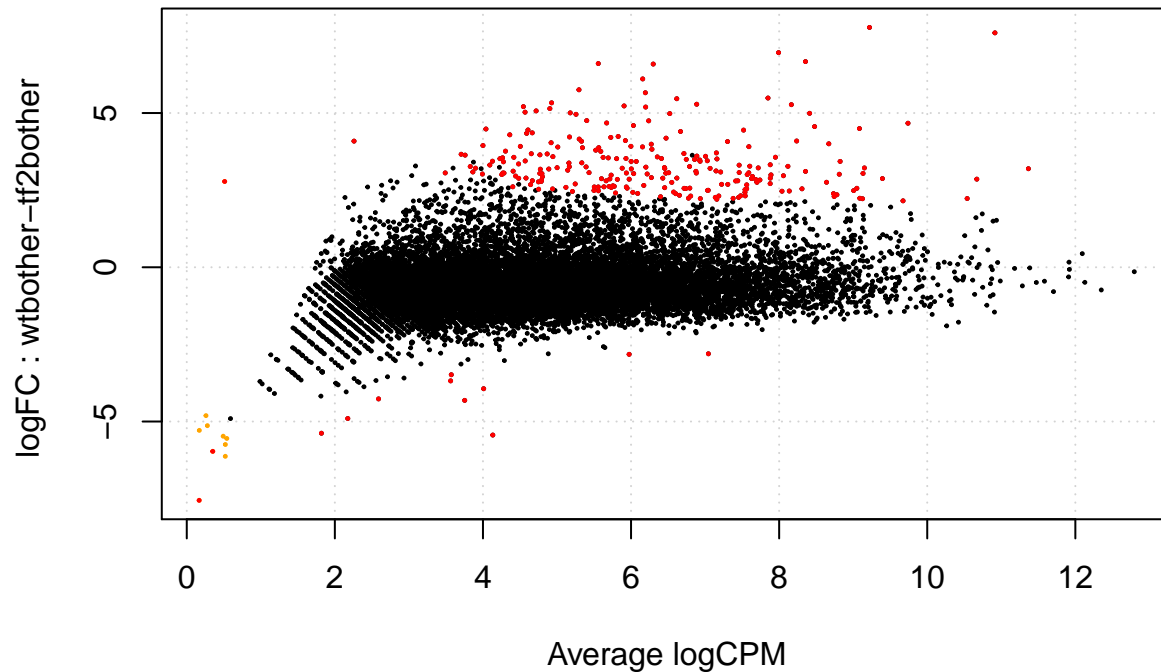
```
sum(results$table$FDR<.05) # How many are DE genes?
```

```
## [1] 252
```

```
summary(decideTestsDGE(DEtest,p.value=.05))
```

```
##      [,1]
## -1      12
##  0    14866
##  1      240
```

```
sig.genes <- rownames(results$table[results$table$FDR<0.05,]) # outputs just significant gene names
plotSmear(d,de.tags=sig.genes)
```



Subset all the genes with a significant FDR score less than .05.

```
results.sig <- subset(results$table, results$table$FDR < 0.05)
```

```
dim(results.sig)
```

What are the genes that are misexpressed? For this we need to add some annotation.

Essentially we are merging two annotations files to 1.) only sig genes 2.) all genes

```
annotation1<- read.delim("../requisiteData/ITAG2.3_all_Arabidopsis_ITAG_annotations.tsv", header=FALSE)
colnames(annotation1) <- c("ITAG", "SGN_annotation")
annotation2<- read.delim("../requisiteData/ITAG2.3_all_Arabidopsis_annotated.tsv")
annotation <- merge(annotation1,annotation2, by = "ITAG")
head(annotation)
```

```
##          ITAG
## 1 Solyc00g005000.2.1
## 2 Solyc00g005040.2.1
## 3 Solyc00g005050.2.1
## 4 Solyc00g005080.1.1
## 5 Solyc00g005900.1.1
## 6 Solyc00g006490.2.1
##
## 1
## 2
## 3
## 4
```

```
Aspartic proteinase nepenthesin I (AHRD V1 ***-
Potassium channel (AHRD V1 ***- DOEM91_9ROSI
```

```

## 5 Oxygen-evolving enhancer protein 1, chloroplastic (AHRD V1 ***- PSBO_SOLTU); contains Interpro dom
## 6 Serine/threonine-protein phosphatase 6 regulatory subunit 3 (AHRD V1 ***- SAPS3_HUMAN); contain
## AGI symbol
## 1 AT3G20015 <NA>
## 2 AT5G46240 KAT1
## 3 AT5G11680 <NA>
## 4 ATCG01280 YCF2.2
## 5 AT5G66570 MSP-1
## 6 AT1G07990 <NA>
##
## 1
## 2
## 3
## 4
## 5
## 6 SIT4 phosphatase-associated family protein; similar to SIT4 phosphatase-associated family protein
## X..identity alignment.length e.value bit.score percent.query.align
## 1 63.76 447 7e-148 520 89.94
## 2 66.02 103 2e-37 150 85.71
## 3 76.96 204 1e-88 322 98.98
## 4 91.25 80 2e-38 153 79.80
## 5 69.62 79 4e-26 112 78.79
## 6 61.92 856 0e+00 979 99.77

```

```

#Making the only significant gene table
results.sig$ITAG <- rownames(results.sig) #change row.names to ITAG for merging
results.sig.annotated <- merge(results.sig,annotation,by = "ITAG", all.x=TRUE) #This is merging only si

#Making all table

results$table$ITAG <- rownames(results$table)
results.all.annotated <- merge(results$table, annotation,by = "ITAG")

```

Write table with results.

```

write.table(results.all.annotated, file=paste(sample1,"_",sample2,"_", "DE_all.txt",sep=""),sep="\t",row
write.table(results.sig.annotated, file=paste(sample1,"_",sample2,"_", "DE_sig.txt",sep=""),sep="\t",row

```

Now run the script below for a full knitr report of what was run and leave this report in the folder that the analysis was done with output files.