Skeleton Key for RNAseq analysis

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

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.

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

Analysis

libraries

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

Read in YAML guide

```
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] "tf2ambr"
```

```
sample2
```

```
## [1] "wtambr"
```

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.

```
colnames(counts)
```

```
##  [1] "tf2ambr1"      "tf2ambr3"      "tf2ambr4"      "tf2ambr6"
##  [5] "tf2aother1"    "tf2aother2"    "tf2aother4"    "tf2aother7"
##  [9] "tf2bmbr2"      "tf2bmbr5"      "tf2bmbr6"      "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"     "wtbmbr2"
## [33] "wtbmbr3"       "wtbmbr6"       "wtbmbr8"       "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)
```

```
##                   tf2ambr1 tf2ambr3 tf2ambr4 tf2ambr6 wtambr2 wtambr4
## Solyc00g005040.2.1       12        0        3       12       0       2
## Solyc00g005050.2.1       33        1       14       17       0       6
## Solyc00g005060.1.1        1        5        1        1       0       0
## Solyc00g005070.1.1       14       22       23        5      24       3
## Solyc00g005080.1.1       19        2       25       32       9      15
## Solyc00g005150.1.1        3        0        0        4       0       1
##                   wtambr5
## Solyc00g005040.2.1       8
## Solyc00g005050.2.1       6
## Solyc00g005060.1.1       1
## Solyc00g005070.1.1       9
## Solyc00g005080.1.1      19
## Solyc00g005150.1.1       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
## tf2ambr1 tf2ambr  1313540            1
## tf2ambr3 tf2ambr    91726            1
## tf2ambr4 tf2ambr  1438416            1
## tf2ambr6 tf2ambr  1088653            1
## wtambr2   wtambr   395165            1
## wtambr4   wtambr   792542            1
## wtambr5   wtambr   632686            1
```

Differential expression using edgeR

Make sure there is full understanding on each edgeR command being used. The manual is amazing so read it *before* running the DE analysis below edgeR manual.

```
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 = 0.432 , BCV = 0.6573
```

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

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

```
##                       logFC logCPM PValue
## Solyc00g005040.2.1 -0.1208  3.194 1.0000
## Solyc00g005050.2.1 -1.1173  3.896 0.1451
## Solyc00g005070.1.1 -0.1168  5.566 0.8295
## Solyc00g005080.1.1  0.7194  4.803 0.3426
## Solyc00g005160.1.1 -0.1018  2.784 0.6612
## Solyc00g005440.1.1 -0.9405  4.828 0.2010
```

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

```
## Comparison of groups:  wtambr-tf2ambr
##                      logFC logCPM    PValue       FDR
## Solyc08g079850.1.1 6.596  9.407 7.328e-16 1.036e-11
## Solyc12g010020.1.1 6.344  6.947 1.890e-13 1.336e-09
## Solyc00g187050.2.1 6.572  6.619 4.085e-13 1.925e-09
## Solyc06g024350.1.1 5.578  8.390 1.721e-12 5.314e-09
## Solyc03g062850.1.1 6.467  7.246 1.879e-12 5.314e-09
## Solyc03g098790.1.1 6.287  6.238 3.996e-12 9.416e-09
```

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

```
## [1] 14139     4
```

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

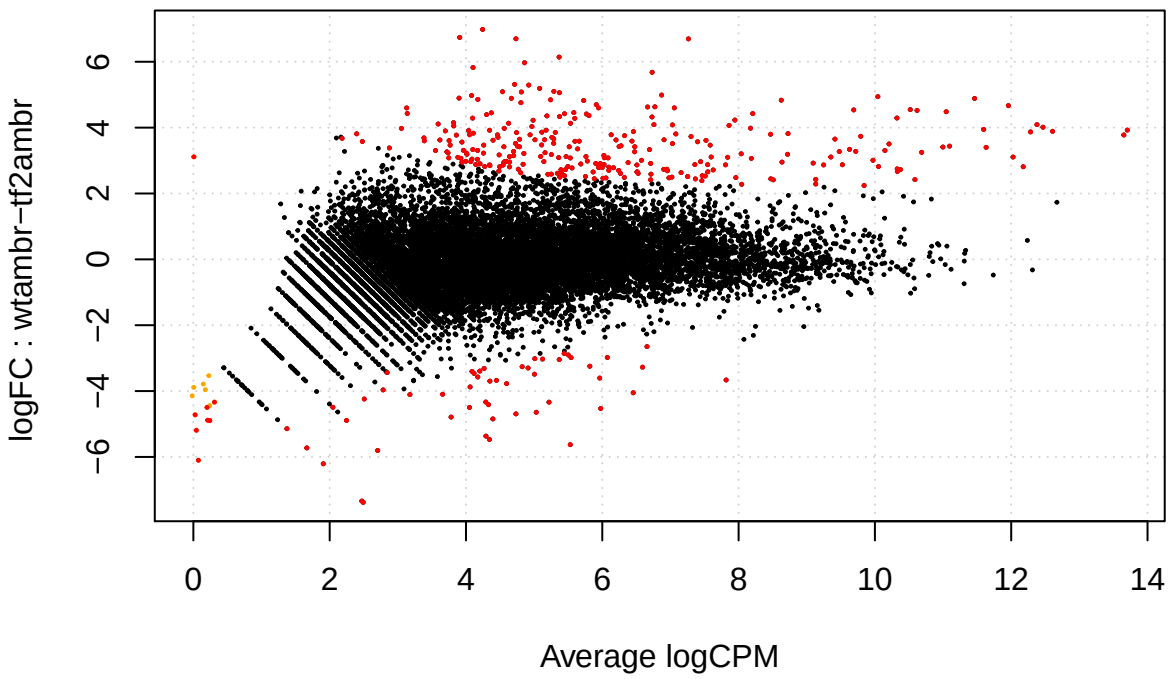
```
## [1] 330
```

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

```
##    [,1]
## -1    57
## 0  13809
## 1    273
```

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

plotSmear(d,de.tags=sig.genes)
```



Subset by all the genes with a significant FDR score.

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

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")

#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") #This is merging to only sig genes

#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
```