

DEGreport

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```
library(DEGreport)
data(humanSexDEedgeR)
library(edgeR)
```

We are going to do a differential expression analysis with edgeR. We have an object that is coming from the edgeR package. It contains a gene count matrix for 85 TSI HapMap individuals, and the gender information. With that, we are going to apply the 'glmFit' function to get genes differentially expressed between males and females.

```
des<-humanSexDEedgeR$design
fit <- glmFit(humanSexDEedgeR,des)
lrt <- glmLRT(fit)
tab<-cbind(lrt$table,p.adjust(lrt$table$PValue,method="BH"))
detags <- rownames(tab[tab[,5]<=0.1,])
plotSmear(humanSexDEedgeR, de.tags=detags)
```

We need to extract the experiment design data.frame where the condition is Male or Female.

```
counts<-cpm(humanSexDEedgeR,log=FALSE)
g1<-colnames(counts)[1:41]
g2<-colnames(counts)[42:85]
design<-data.frame(condition=sub("1","Male",sub("0","Female",des[,2])))
```

We are getting the chromosome information for each gene. This way we can colour genes according autosomic,X or Y chromosomes.

```
data(geneInfo)
```

Create the report. The main parameters are the column names in group1, and group2. Then, the count matrix, gene names that are DE, p-values, fold changes and path to create the report. As optional, you can give colours for each gene, and the number of permutation.

```
detag10<-detags[1:10]
pval<-tab[,4]
fc<-tab[detag10,1]
```

Run the following lines to create the file

```
pathreport<-"~/report" #change this to a proper path  
createReport(g1,g2,counts,detag10,pval,fc,pathreport,colors,pop=400)
```

Run the following lines if you want to visualize your expression values by condition:

```
degObj(counts,design,"/tmp/degObj.rda")  
library(shiny)  
runGist(9930881)
```

You can use individual functions, like degRank or degMean. This will create specific figures and tables that are included in the report.

```
degMean(pval,counts)  
degVar(pval,counts)  
degMV(g1,g2,pval,counts)  
degMB(detags,g1,g2,counts)  
degVB(detags,g1,g2,counts)
```

```
library(coda)  
library(rjags)  
rank<-degRank(g1,g2,counts[detag10,],fc,400,500)  
degPR(rank)
```