Pasilla Analysis in EdgeR

Duncan Brian

Put your code to load edgeR and locate the count file setwd("/home/participant/Course_Materials"

```
library(edgeR)
```

```
datafile = system.file( "extdata/pasilla_gene_counts.tsv", package="pasilla" )
datafile
```

```
pasillaCountTable = read.table(datafile, header=TRUE, row.names=1)

head(pasillaCountTable)
```

```
##             untreated1 untreated2 untreated3 untreated4 treated1 treated2
## FBgn0000003          0          0          0          0        0        0
## FBgn0000008         92        161         76         70      140       88
## FBgn0000014          5          1          0          0        4        0
## FBgn0000015          0          2          1          2        1        0
## FBgn0000017       4664       8714       3564       3150     6205     3072
## FBgn0000018        583        761        245        310      722      299
##             treated3
## FBgn0000003        1
## FBgn0000008       70
## FBgn0000014        0
## FBgn0000015        0
## FBgn0000017     3334
## FBgn0000018      308
```

Read the count table and print out

Construct the design and setup the conditions. Report how many samples were in the treated and untreated groups

Normalise

Do the differential expression test and print the table of top hits

Use the results of the previous code-chunk to comment on how many up and down regulated genes were found at a p-value cut-off of 0.05. [Embed your answers in this section of text quoting the p-value cut-off and number of genes]

Produce the smear plot, but hide the code