R version 3.5.1 (2018-07-02) -- "Feather Spray"

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Platform: x86\_64-w64-mingw32/x64 (64-bit)

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[Workspace loaded from C:/Users/jet06/Desktop/MBallgown/samples/.RData]

Loading required package: ballgown

Attaching package: ‘ballgown’

The following object is masked from ‘package:base’:

structure

> View(bg\_chrX\_filt)

Warning message:

In sample.int(.Machine$integer.max - 1L, 1L) :

'.Random.seed[1]' is not a valid integer, so ignored

> results\_transcripts = stattest(bg\_chrX\_filt, feature="transcript", covariate="status", getFC=TRUE, meas="FPKM")

Error in stattest(bg\_chrX\_filt, feature = "transcript", covariate = "status", :

to do statistical tests, either gown must contain pData or you must specify models.

> library(ballgown)

> library(devtools)

> library(genefilter)

> library(RSkittleBrewer)

> library(dplyr)

Attaching package: ‘dplyr’

The following objects are masked from ‘package:ballgown’:

contains, expr, last

The following objects are masked from ‘package:stats’:

filter, lag

The following objects are masked from ‘package:base’:

intersect, setdiff, setequal, union

Warning message:

package ‘dplyr’ was built under R version 3.5.3

> pheno\_data = read.csv ("pheno\_data.csv")

> View(pheno\_data)

> bg\_chrX = ballgown(dataDir = ".", samplePattern = "M", pData=pheno\_data)

Sat Jul 20 13:06:03 2019

Sat Jul 20 13:06:03 2019: Reading linking tables

Sat Jul 20 13:06:04 2019: Reading intron data files

Sat Jul 20 13:06:14 2019: Merging intron data

Sat Jul 20 13:06:17 2019: Reading exon data files

Sat Jul 20 13:06:40 2019: Merging exon data

Sat Jul 20 13:06:45 2019: Reading transcript data files

Sat Jul 20 13:06:56 2019: Merging transcript data

Wrapping up the results

Sat Jul 20 13:06:58 2019

> bg\_chrX\_filt = subset(bg\_chrX, "rowVars(texpr(bg\_chrX)) > 1", genomesubset=TRUE)

> results\_transcripts = stattest(bg\_chrX\_filt, feature="transcript", covariate="organ", adjustvars = c("infection"), getFC=TRUE, meas="FPKM")

> results\_genes = stattest(bg\_chrX\_filt, feature="gene", covariate="organ", adjustvars = c("infection"), getFC=TRUE, meas="FPKM")

> results\_transcripts= data.frame(geneNames=ballgown::geneNames(bg\_chrX\_filt), geneIDs=ballgown::geneIDs(bg\_chrX\_filt), results\_transcripts)

>

> results\_transcripts = arrange(results\_transcripts, pval)

>

> results\_genes = arrange(results\_genes, pval)

> write.csv(results\_transcripts, "Mresults.csv", row.names=FALSE)

> write.csv(results\_genes, "Mgresults.csv", row.names=FALSE)

> subset (results\_transcripts,results\_transcripts$qval<0.05)

> subset(results\_genes,results\_genes$qval<0.05)

> tropical=c('darkorange', 'dodgerblue', 'hotpink', 'limegreen', 'yellow')

> palette(tropical)

> fpkm = texpr(bg\_chrX, meas="FPKM")

> fpkm= log2(fpkm+1)

> boxplot(fpkm, col=as.numeric(pheno\_data$status), las=2, ylab='log2(FPKM+1)')

> View(fpkm)

> View(fpkm)

> View(results\_transcripts)

> View(results\_genes)