**Sunday 31 January, 2016**

#moved all \*genes\* to a directory called geneResult (I posted online for students to download,

#put in #Bio343)

#mkdir geneResult

#cp \*genes\* geneResult/

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#Need students to help run Blast2GO. Will discuss in class Tuesday.

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#Named Rstudio file Python\_analysis\_LH\_MC (I posted online for students to download)

#Put into 343 folder, folder called R\_folder

#Open **Rstudio** and keep icon in dock.

#Open Python\_analysis\_LH\_MC via Rstudio

#Run the first three lines (only need to do this once)

#may be prompted where to store, accept suggestions from Rstudio

library (rnaseqWrapper)

setwd (they change username)

#results from RSem:

#Had to change “ to no space

#Had to change ‘ to \_prime

#Had to change \_prime\_prime to ^

#then ran DESeq to generate output files we can download

#then run

countData <- mergeCountFiles("geneResult/")

# View your data

head(countData)

# Pull out counts, make them integers, and view them

myCountData <- round( countData[,grep(".expected\_count",names(countData))],0)

names(myCountData) <- gsub(".expected\_count","",names(myCountData))

head(myCountData)

# Run DESeq - this saves files to folder given by outNamePrefix

deOut <- DESeqWrapper(myCountData, # Our count data to use

 conditions=c("intestine","Liver"), # conditions to compare

 outNamePrefix="DEseq/") # Where to save the outputs

#renamed RSem output file names so that we can compare by organ and treatment

#continue through the next few lines of code to generate first graphical output to compare liver

#and intestine. We will discuss and then students will run their first experiments solo.