**November 15, 2019**

**DESeq2 – log2foldchange**

<https://support.bioconductor.org/p/77021/>

The default log fold change calculated by DESeq2 use statistical techniques to "moderate" or shrink imprecise estimates toward zero. So these are not simple ratios of normalized counts (for more details see vignette or for full details see DESeq2 paper).

You can obtain standard log fold changes (no shrinkage) by using:

DESeq(dds, betaPrior=FALSE)

Here is another link: <https://support.bioconductor.org/p/79950/>

They are all very helpful!

Get log2foldchange issue resolve, get normalized read for human for downstream analysis

PCA

Clustering

Etc.

**IPA analysis**

For some reason, IPA does not take the input data file

**Making salmon index for hg38 and mm10**

And, test run generateDecoyTransciptome (SalmonTools) for both human and mouse

Need to install “mashmap”: <https://github.com/marbl/MashMap/releases>

**EMMA for Heather Vellers**

(zoom conference with Heather and remember to say hi from Heather L)

Found out that I have worked on nuVar for mm10 in March, modifying the mm9 version of SNP, lifted over to mm10, had a few python scripts for modifying the annotation, and preparing for mongoDB!!

Met with Heather and Michael, will accept files and run EMMA for them.

ID, chr-pos : lift to mm10

Phenotype data: 4-6 replicates/line, 95% no missing values! Will do individual data points instead of mean

**November 19, 2019**

**DESeq2 – extreme small p-value**

I noticed that the p-values are extremely low and want to figure out what is going on. Here is the note as usual from the Bioconductor support: <https://support.bioconductor.org/p/70928/>. However, it turns out that Michael seems to misunderstand the question. Here is the much more comprehensive documentation on how to understand the p-value produced from DEseq2: <https://www.huber.embl.de/users/klaus/Teaching/DESeq2Predoc2014.html#inspection-and-correction-of-pvalues>

Will learn from Klaus (<https://github.com/b-klaus>) and Huber from here,

To resolve some of the dependencies, I need to get dev\_tools (<https://www.r-project.org/nosvn/pandoc/devtools.html>) work, and it requires Rtools (<https://cran.r-project.org/bin/windows/Rtools/>), which I already have. It turns out that I have “devtools” but I do not have those dependencies, and after I have them installed, I can load “devtools” with a snap of a fingers.

**JAVA JDK & JRE**

In order to run EPIG-Seq on my linux machine, I need to recompile the Java code under version 1.7. So, I need to get the 1.7 JDK. I got it and was able to compile the java code. But, running still gives me errors.

noticed that the p-values are extremely low and want to figure out what is going on. Here is the note as

**November 20, 2019**

**Python web application, credit goes to Brian Yu (**<https://cs50.harvard.edu/web/>**)**

I need to install Flask: <https://gist.github.com/dineshviswanath/af72af0ae2031cd9949f>

On my linux desktop,

I used “virtual environment” to get python 3.7, then

I am able to use sudo -H pip install Flask to get system wide installation

But, I need to specifically issue export FLASK\_APP=application.py

**November 21, 2019**

**Working on the Rshiny app – add a radio button**

I reviewed shiny note and tested those 11 examples: <https://shiny.rstudio.com/tutorial/written-tutorial/lesson1/#Go%20Further> .

I am able to update our SignatureAnalysis Rshiny application.

**November 22, 2019**

**Working with R markdown – how to arrange figure order**

When I try to add two figures into R markdown, I found out it puts my figures in different orders. Very annoying! It turns out to have something to do with LaTex, and someone has the same struggle like me. <https://stackoverflow.com/questions/29216662/images-and-text-coming-out-in-a-different-order-to-how-i-expected>

Even I tried to change the LaTex, it does not solve the problem.

For some reason, I need to get help for R with argument: <https://www.r-bloggers.com/passing-arguments-to-an-r-script-from-command-lines/>

I have always been struggle with “apply” series of functions, I have gone back to my only post on R tricks : <https://sites.duke.edu/workblog/2016/04/01/r-tricks-version-ii/>

m <- matrix( as.character(sample(1:12)), nrow=4 )

#Here, problem solved.

m2 <- data.frame(sapply(m, function(x) as.numeric(as.character(x))))

m2

Found a very interesting post:

word <- c('apple-orange-strawberry','chocolate')

sapply(strsplit(word,"-"), `[`, 1)

#[1] "apple" "chocolate"

vapply(strsplit(word,"-"), `[`, 1, FUN.VALUE=character(1))

#[1] "apple" "chocolate"

vapply(strsplit(word,"-"), `[`, 2, FUN.VALUE=character(1))

#[1] "orange" NA

**November 25, 2019**

**Reviewing my R trick code to save file with column name or row names arrangement**

write.table (dmObject, fileTowrite, sep = “\t”, row.names = TRUE, col.names = NA)

**November 26, 2019**

**I encounter an error when I try to copy file when the file names contain special character, i.e. space, comma etc.**

Putting the double quote does not seem to work for me: <https://askubuntu.com/questions/648577/copying-files-from-directories-having-spaces-in-its-name>

This is not what I wanted: <https://www.hecticgeek.com/2014/02/spaces-file-names-command-line/>