

For our next lab, we will be back at the computer performing an analysis of RNA sequencing data.

The data set is RNA-sequencing gene expression of maternal heart, liver and lungs on day 14 post conception compared to non-pregnant female mice.

This is the link to access the online version of R studio. It was in the presentation link but here it is again.

<https://jupyter.utoronto.ca>

Make sure to select RStudio.

This link will automatically open Rstudio and bring in the data files needed for next week. You may need to log into your utor account.

<https://jupyter.utoronto.ca/hub/user-redirect/git-pull?repo=https%3A%2F%2Fgithub.com%2Flungboyz%2FRNAseqAnalysis&urlpath=rstudio%2F&branch=main>

BEFORE TUESDAY:

1. click the data file hyperlink above and ensure the data loads in!
2. create a new project in the fold that was created when the data loaded in. the folder should be called "RNAseqAnalysis"
2. test if all needed libraries are installed.

Run the library() code at the top of the rmd document.

If the library is not found, you will need to install it.

My tests showed that only these three libraries need to be installed.

```
BiocManager::install("biomaRt")  
BiocManager::install("genefilter")  
BiocManager::install("qusage")
```

The code is in the rmd file, but it has a # in front. The # needs to be deleted so the code will run. After installation, add the # back to prevent accidental installation.

The installation will take about 15-30 minutes!!!! Depending on your internet connection. SO install this BEFORE Tuesday's class, so we have time to fix any issues.

See you next week

Brian