Bulk RNAseq exercise

Bulk RNAseq workshop from Danish National Sandbox project

The aim of this exercise is to get familiar with the DESeq2 R package and downstream analysis of a RNAseq experiment. You can select one of the three data sets under the folder Data/exercise\_data. Check the README.md file to read a small description of each of the datasets presented there. One dataset is a bit more complex than the other two, and it is perfect if you want to practice with a multiple factor design matrix.

Create a Rmarkdown file and proceed with the analysis of the data. You can play around as much as you want! Try to understand each step of the analysis and create beautiful plot of your exploratory analysis, DEA and functional annotation. Describe and discuss the results of each step and try to find meaning on the data. You are welcome to check on the original manuscripts and follow their results!

Finally, create an html report with the “Knit” functionality of Rstudio. This would create a report that can be easily presented to your colleages! It is also a great way to reproduce your results and save it for the future.

Down below there are several questions dedicated to each dataset:

DATASET XXXX

DATASET XXXX

DATASET XXXX