R analysis

System requirement:

* macOS Mojave 10.14.6
* R version 3.6.0 (2019-04-26)
* Platform: x86\_64-apple-darwin15.6.0 (64-bit)

Installation:

* R

https://cran.r-project.org/

* R studio

https://rstudio.com/products/rstudio/download/

Installation of R packages:

* Launch R studio:
  + install.packages("readr")
  + install.packages("tidyverse")
  + install.packages("dplyr")
  + install.packages("ggplot2")
  + install.packages("gplots")
  + install.packages("calibrate")
  + install.packages("fdrtool")
  + install.packages("BiocManager")
  + install.packages("RColorBrewer")
  + install.packages("vsn")
  + install.packages("tidyr")
  + install.packages("plotly")
  + install.packages("shiny")
  + install.packages("rmarkdown")
  + install.packages("ClassDiscovery")
  + BiocManager::install('tximport')
  + BiocManager::install('rhdf5')
  + BiocManager::install('DESeq2')
  + BiocManager::install('ensembldb')
  + BiocManager::install('GenomicFeatures')
  + BiocManager::install('biomaRt')
  + BiocManager::install("genefilter")
  + BiocManager::install("topGO")
  + BiocManager::install("org.Mm.eg.db")
  + BiocManager::install("Rgraphviz")

Instructions:

* Scripts with .R ending:
  + Launch R studio
  + source(“scriptname.R”)
* scripts with .Rmd ending:
  + Launch R studio
  + open the script in R studio, and click “Knit”, default output document is html, default output directory is the Document directory.