**Pre-Workshop To-Dos**

To make sure the workshop progresses as smoothly as possible (given that we have a few steps to cover), please complete the following to-dos before the course.

1. **Download R and R studio**

Download R from <https://mirror.rcg.sfu.ca/mirror/CRAN/>

Download RStudio from <https://www.rstudio.com/products/rstudio/download/#download>

1. **Install necessary packages**

Here's the list of all the packages you will need for this workshop. You can simply copy and paste the following command into your RStudio console and run.

install.packages(c("rmarkdown", "formatR", "knitr", "tidyverse", "here", "scales",

"kableExtra", "reshape2", "pheatmap", "ggpubr"))

if (!require("BiocManager", quietly = TRUE))

install.packages("BiocManager")

BiocManager::install("edgeR", force = TRUE)

1. **Download the course materials (RNAseq\_Workshop1.zip)**
2. **Read the sections 0.0 – 3.0 of the compiled html file (RNA-seq Workshop\_part1.html)**