

Dimensionality reduction, differential expression analysis using single-cell RNA-seq data

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Install required packages

```
if (!require("pacman")) install.packages("pacman")

pacman::p_load(tidyverse, Seurat, stringr,
               Rtsne, cluster, limma, edgeR, statmod)
```

- Make sure you have the latest version of RStudio (<https://www.rstudio.com/products/rstudio/download/>).

Navigate to working directory

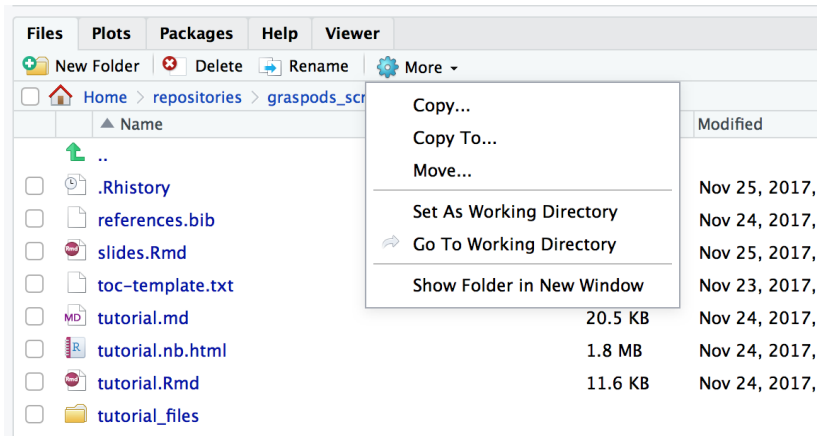


Figure 1: