**How to Setup for Section 2 (Lab Section)**

We will be using R in RStudio for Section 2, which is the coding lab section. You will need to download R, RStudio, and R packages if you haven’t already. PLEASE READ THE INSTRUCTIONS CAREFULLY!

**Setup R:**

1. Go to R’s website
   1. <https://www.r-project.org/>
2. Click on “CRAN”, which is under the header “Download” in the left sidebar

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1. Scroll down and find ‘MBNI, University of Michigan, Ann Arbor, MI” and click on link

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1. Click on the Windows or macOS link (depending on what operating system you have)

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* 1. If have Windows operating system:
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* + 1. Graphical user interface, text, application, email

       Description automatically generatedClick on “Download R 4.1.3 for Windows” and download .exe file

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* + 1. Click .exe file and install with **default settings**
  1. If have Mac operating system (macOS):
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        Description automatically generated with medium confidenceClick on “R-4.1.3.pkg” and “XQuartz” (if have OS X) in that section and download both files

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* + 1. Click .pkg file and install with default settings

**Setup RStudio:**

1. Go to RStudio’s website
   1. <https://www.rstudio.com/>

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1. Click on “Download” in the top bar

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1. Scroll down to the “All Installers” section
2. Click on the Windows or macOS download link

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1. Install RStudio (either by clicking .exe or .dmg file)

Install packages used in the workshop:

1. **If using macOS**, then open terminal:
   1. Log in or sign up here:
   2. Find “Command Line Tools for Xcode 13.3” and download .dmg file
   3. Click .dmg file to install Xcode
   4. Reboot computer
2. Open RStudio
3. In the console, copy and paste and enter the code (in gray) below:

list.of.packages <-c('tidyverse','Seurat','SeuratObject','pheatmap','RColorBrewer','scales','cowplot','patchwork','grid','gridExtra','harmony','knitr','rmarkdown',’ BiocManager’)

new.packages <- list.of.packages[!(list.of.packages %in% installed.packages()[,"Package"])]

if(length(new.packages)) install.packages(new.packages)

BiocManager::install(c('clusterProfiler','org.Hs.eg.db','ReactomePA','msigdbr'))

If prompted if want to restart R, choose “No”.

If prompted in console if want to update packages, pick “No”.

If prompted in console if want to install packages from sources, pick “Yes”.

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Description automatically generated The console is right here (in yellow box):

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1. Check if packages were install correctly with the code (in gray) below (copy and paste and enter in the console):

library(tidyverse)

library(Seurat)

library(pheatmap)

library(RColorBrewer)

library(scales)

library(cowplot)

library(patchwork)

library(grid)

library(gridExtra)

library(harmony)

library(clusterProfiler)

library(org.Hs.eg.db)

library(ReactomePA)

library(msigdbr)