**Molecular, Cellular and Tissue Bioengineering Symposium 2019:**

**Single Cell Technologies from Method Development to Application**

Friday April 5th, 2019

**Hands-on session setup guide**

This document will guide you through installation of R and RStudio and performing some basic tests to ensure you have the right environment setup.

**1. Download R**

RStudio requires R version 3.1.1. Here are links to the R installers:

• **Windows install –** <https://cran.r-project.org/bin/windows/base/R-3.5.3-win.exe>

• **Macintosh install** – <https://cran.r-project.org/bin/macosx/R-3.5.3.pkg>

• **Linux install** – https://cran.r-project.org/bin/linux/

Please download the file corresponding to your operating system.

**2. Install R**

**Windows:**The distribution is distributed as an installer R-3.5.3-win.exe. Just run this for a Windows-style installer.

**MacOSX:**Once downloaded and executed, the installer will install the current release of R and a R.app Mac OS X GUI.

**Linux:**Grab the appropriate installer for your distribution and install.

**3. Download RStudio**

Please download the latest version of RStudio (0.99.902) from the Rstudio website corresponding to your operating system: <https://www.rstudio.com/products/rstudio/download/>

**4. Install RStudio**

Double-click on the installation package and follow onscreen instructions to install RStudio into directory of your choice.

**5. Run and test your installation**

After you open the RStudio you will have several windows depending on your system. The most commonly used windows are **“Source”, “Console”, “History” and “Plots”.**  
You can type your command directly into the console and execute them by pressing Enter or you can write your commands in the console and execute by **“Run”**button on the top right corner of Source window.

Let’s run few commands and get familiar with code execution. Type the following commands in the Console and execute:

version  # This will show you R version information  
data(CO2) # This will load sample CO2 dataset into your environment.  
summary(CO2)  # Get summary information for this dataset.  
head(CO2) # Show the first 6 records  
plot(CO2$Plant, CO2$uptake) # Plot some columns

**6. Installing Seurat**

The hands-on session will exclusively utilize the single cell analysis R package Seurat (<https://satijalab.org/seurat/>). Please install this package by copying the command below into the RStudio console:

install.packages(‘Seurat’)  # This will install the Seurat R package, and any dependencies

If it asks you to update any packages please choose “yes”. Then test the Seurat install by running:

library(Seurat)  # This will load the Seurat package

You should see a list of additional packages that Seurat loads. If you see any warnings or errors please come to the hands-on session early so we can ensure your computer is prepared to run the code for the session.

**7. Resources for learning R or for quick reference**

* [RStudio Support](https://support.rstudio.com/hc/en-us)
* [Basic R Cheat Sheet](https://sites.ualberta.ca/~ahamann/teaching/renr690/R_Cheat_Data.pdf)
* [RStudio Cheat Sheets](https://www.rstudio.com/resources/cheatsheets/)
* [Basic R Tutorial](http://www.cyclismo.org/tutorial/R/)
* [R codeschool](http://tryr.codeschool.com/)