



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](#)
- [Basic R Cheat Sheet](#)
- [RStudio Cheat Sheets](#)
- [Basic R Tutorial](#)
- [R codeschool](#)