



Molecular, Cellular and Tissue Bioengineering Symposium 2019:  
**Single Cell Technologies from Method Development to Application**

Friday April 5<sup>th</sup>, 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 (1.1.463) from the Rstudio website corresponding to your operating system:

- **Windows install** – <https://download1.rstudio.org/RStudio-1.1.463.exe>
- **Macintosh install** – <https://download1.rstudio.org/RStudio-1.1.463.dmg>
- **Linux install** – <https://www.rstudio.com/products/rstudio/download/#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, dplyr, and ranger

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

```
install.packages(c('Seurat', 'dplyr', 'ranger')) # This will install the Seurat, dplyr and ranger R packages, 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.

Then test the dplyr install by running:

```
library(dplyr) # This will load the dplyr package, and should give no errors
```

Then test the ranger install by running:

```
library(ranger) # This will load the ranger package, and should give no errors
```

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

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