

Single-cell RNA Seq Training Course: 10x Genomics Data Analysis software requirements

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Software Requirements

Introduction

To help you get the most out of the course and to make sure you hit the ground running during the hands-on session, we ask that you complete as many steps as you can from this document.

Most importantly - if you cannot complete any steps or have any issues then feel free to message us and we will try and help where we can. If you cannot get these steps completed before the hands-on session, do not worry as we will find time before this session to help you and check everything is set up correctly. Some of the steps are optional and are there only if you are curious or have additional time to play around with Rstudio.

NOTE: *You may require administrator rights to complete this. If you are using a company/university laptop you will need to get permission from your IT support.*

R Language

Background (optional)

R is a scripting/programming language for statistical computing and graphics. It is used heavily for bioinformatics mainly due to its ability to create high-resolution graphics/plots to represent biological data. It is not just limited to bioinformatics, with industries such as finance, government services, chemistry, astronomy and many more statistical fields using it. Much like other programming languages such as Python or Java, R has its own syntax (or grammar).

It should be noted that for this course you will not be expected to have any previous experience in R. The majority of the code will be provided to you in a workbook during the hands-on session. However, if you would like to get some experience beforehand, we have provided a link to a free resource below:

To get familiar with R's syntax we recommend the following free tutorials. These will introduce you to basics of R: <https://www.codecademy.com/learn/learn-r>

To install R

If you already have R installed on your computer please skip this step. If you have any issues installing R please reach out to us on the slack channel or by email.

1. Go to <https://cran.r-project.org/>
2. Click download for your operating system
3. Depending on your Operating System (OS) do the following:
 - a. Windows: select "Latest release: base" → click "Download R"
 - b. Mac: select "Latest release: 4.X.X.pkg"
4. Once they have downloaded the correct follow through the menus to install the software

The Comprehensive R Archive Network

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#) ([Debian](#), [Fedora/Redhat](#), [Ubuntu](#))
- [Download R for macOS](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Rstudio

Background

RStudio is an Integrated Development Environment for R. You can think of this as the “MS Word” for R. Here you are able to write, run, compile and document your scripts/code. One of the most powerful features of R is its interactive nature. Meaning you can run the code in real-time. R studio gives you the ability to access all the powerful features R has to offer in a graphical and interactive manner.

Install Rstudio

To download RStudio use the following link:

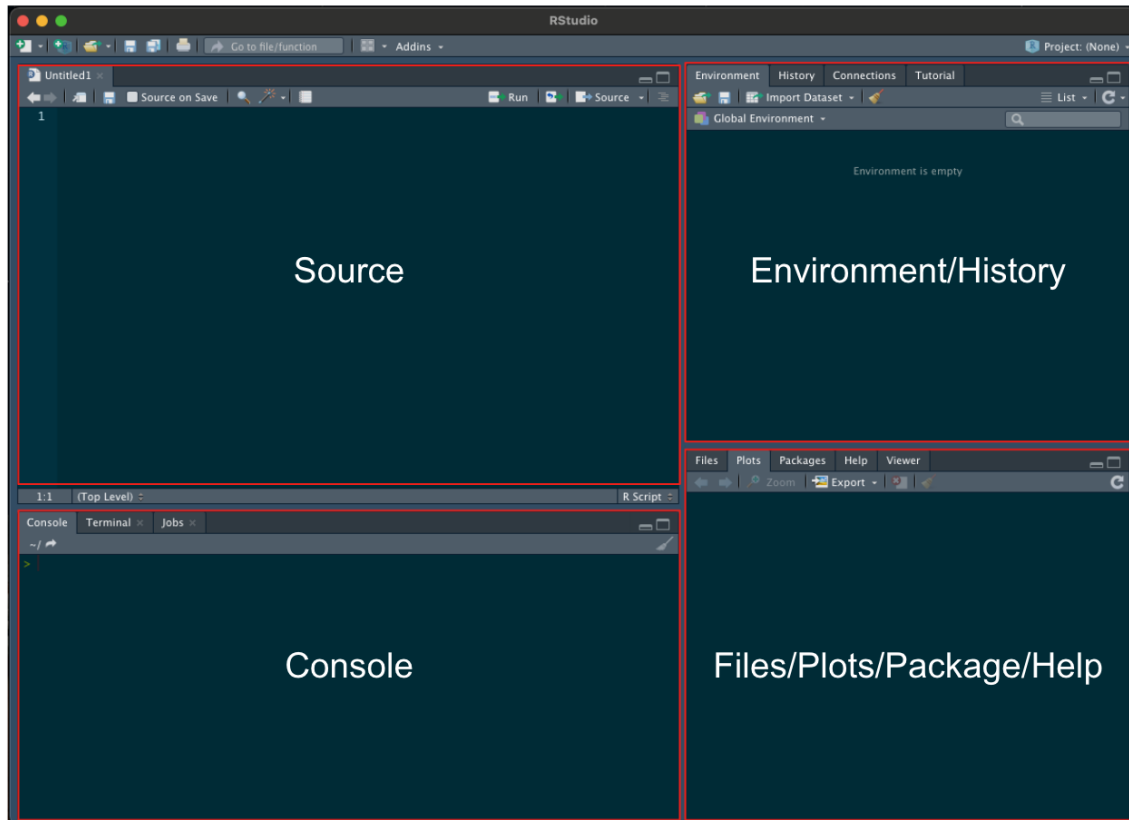
<https://www.rstudio.com/products/rstudio/download/>

1. Click the link above and then click the “**Download**” button on Rstudio (Free).
2. It will recognise what OS you have so then you can just download the latest version
3. Once downloaded, left click to open the setup wizard. Follow the instructions and select all the defaults.



Introduction to RStudio (optional)

When you open Rstudio you will see the interface seen below. This will be divided into 4 main panels (if the source panel does not open do not panic this is because you have not yet created your first script).



- **Source:** This panel is where you will write/view R scripts
- **Console:** This is actually where you see the execution of commands.
 - This is also where you can install the required packages (see [Seurat/Tidyverse](#) sections for more information).
- **Environment/History:** RStudio will show here you what datasets and objects (variables) you have created and which are defined in memory.
- **Files/Plots/Packages/Help:** This multipurpose panel will show you the contents of directories on your computer
 - **Files:** You can also use this tab to navigate and set the working directory
 - **Plots:** This tab will show the output of any plots generated
 - **Package:** In this tab you will see what packages are actively loaded, or you can attach installed packages
 - **Help:** It will display help files for R functions and packages.

Creating your first Script (optional)

Now that we are ready to start exploring R, we will want to keep a record of the commands we are using. To do this we can create an R script.

1. Click the File menu
2. Select New File
3. Click on R Script
4. A new panel appears on the top left.

5. Click the save icon (Save current document) in the bar above the first line in the source script editor. Alternatively, you can use the shortcut: **CTRL+S** (**CMD+S** on OSX)
6. Finally you can give your script a new file name. By convention we try to avoid putting spaces in file names. Instead we replace the white space with an underscore. I.e. `hello_word.R`

Seurat - A software package for Single-cell Data

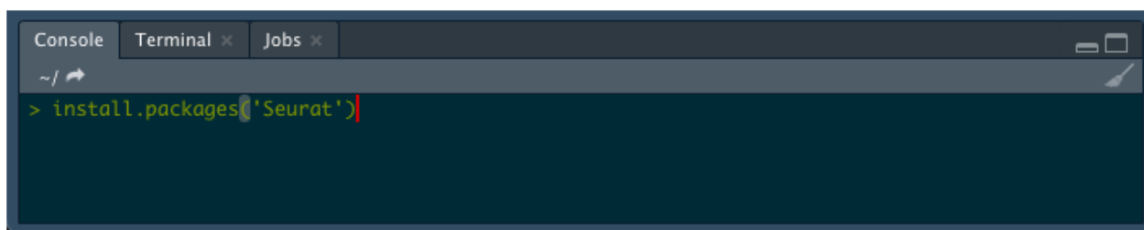
Background

Seurat is an R package designed for quality control (QC), analysis, and exploration of single-cell RNA-seq data. Seurat aims to enable users to identify and interpret sources of heterogeneity from single-cell transcriptomic measurements and to integrate diverse types of single-cell data.

To install Seurat you will need to use an R tool called: The Comprehensive R Archive Network (CRAN), you may remember this from when you installed base R. CRAN is built into R, and allows you to download any software packages or tools that you may need. This saves you time as you won't have to write all your code from scratch!

To install Seurat

1. Open Rstudio
2. Go to the console tab
3. Enter the following: `install.packages('Seurat')`
4. If you are asked for a location, select the location nearest to you. E.g. 74. London you would need to enter: 74 then press enter.

A screenshot of the RStudio interface. The 'Console' tab is active, showing a prompt character followed by the command `install.packages('Seurat')` entered. The 'Terminal' and 'Jobs' tabs are also visible but inactive. The background of the console is dark blue.

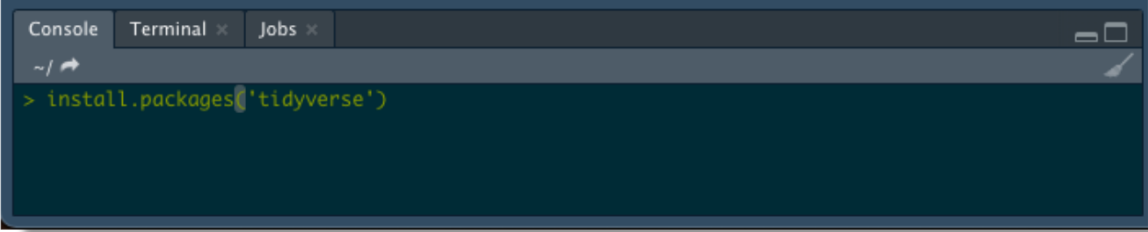
Tidyverse - A software package for data science

Background

Another very useful R package is Tidyverse. The tidyverse is a collection of R packages designed for data science. All packages share an underlying design philosophy, grammar, and data structures. This means that once you learn the syntax of one, you will know the syntax for all the others. You can install it in the same way as you did above for Seurat:

To install Tidyverse

1. Open Rstudio
2. Go to the console tab
3. Enter the following: `install.packages('tidyverse')`
4. If you are asked for a location, select the location nearest to you. E.g. 74. London
you would need to enter: 74 then press enter.

A screenshot of the RStudio interface. The 'Console' tab is active, showing a terminal window with a dark background. The prompt is '>' followed by the command 'install.packages('tidyverse')'. The cursor is positioned at the end of the command. The window title bar shows 'Console', 'Terminal x', and 'Jobs x'. There are also icons for window management in the top right corner.

```
> install.packages('tidyverse')
```