

# Week 1 - Downloading R

September 2024

Welcome to BINF 5003: Data Mining, Modeling, and Biostatistics!

## Tech Requirements

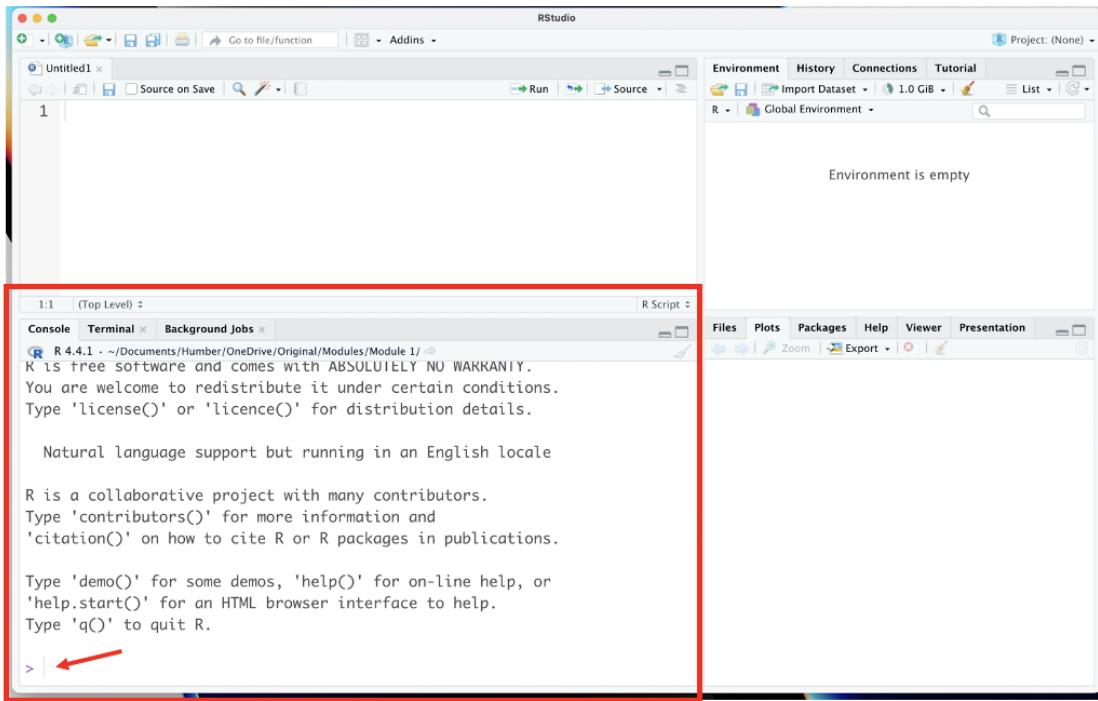
Before we start, you will require your own laptop computer, with the following minimum requirements: 1024×768 screen resolution, 1.5GHz CPU, 2GB RAM, 10GB free disk space, recent versions of Windows, Mac OS X or Linux (most computers purchased in the past 3-4 years likely meet these requirements). Make sure you have a robust internet browser such as Firefox, Safari or Chrome (not Internet Explorer). Make sure you have a PDF viewer (e.g., Adobe Acrobat, Preview or similar), or that you can read PDF files in your Web browser.

## Download R

1. Download R, a free software environment for statistical computing and graphics from [CRAN](#), the Comprehensive R Archive Network. I highly recommend you install a precompiled binary distribution for your operating system – use the links up at the top of the CRAN page!

Note: MacBook users with an Apple Silicon chip (e.g., M1 or M2) should install the “arm64” version of R, while MacBook users with an Intel chip should install the regular (64-bit) version of R. You can check your laptop’s hardware specifications by clicking the Apple icon (top left corner) > About This Mac and verifying whether the chip is Apple or Intel

2. Install [RStudio’s IDE](#) (stands for integrated development environment), a powerful user interface for R. Click the link under “2: Install RStudio”. RStudio comes with a text editor, so there is no immediate need to install a separate stand-alone editor.
3. If R is already installed, ensure that the R version is at least 4.0 or higher. You can do this by opening RStudio, where you should see a multi-section window like below. We’ll take a tour of the interface together. For now, locate the quadrant named “Console” as indicated by the red square in the image below.
4. Put your cursor at the start of the prompt indicated by the > symbol and where the red arrow is pointing. Type or copy sessionInfo() - make sure that only the I at the start of Info is capitalized and you are including the round brackets. Press enter to run this command and R should return an output to you. Then, double check your R version in the first line. Ensure that the R version is at least 4.0 or higher. If you have an older version of R like this image, you can re-install a more current version R (do not need to re-install RStudio).



## TinyTex

There is one package we have to install first before we can create PDF reports, which will be necessary for assignments and the project. Copy and paste into the console (where the > symbol is) the two lines of code below to install a package called tinytex.

```
install.packages('tinytex')
tinytex::install_tinytex()
```

## All packages

Next, let's install all the packages that we will be using in the course (more on what packages are soon!).

Follow the steps below.

1. First, we will be installing packages from the Comprehensive R Archive Network (CRAN). To install these packages, you can copy the code below and paste it into your console.

```
install.packages(c("tidyverse", "gridExtra", "cowplot", "datasauRus", "tidyselect"),
dependencies = TRUE)
```

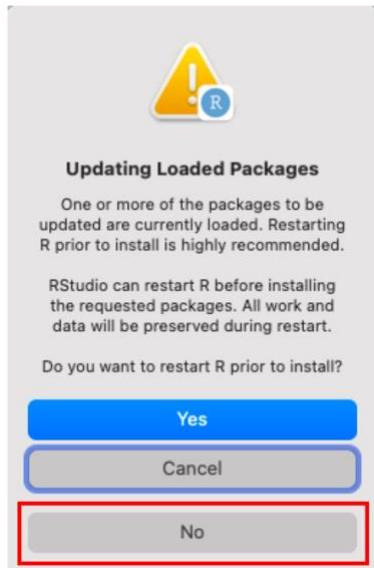
2. Next, we'll be using packages hosted on a different repository. Again, copy and paste the code into your console. These will take a while to download and depend on your internet speed. Budget at least 30-60 mins. The installs will likely also require your input so keep an eye on the console.

```

if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("GEOquery")
BiocManager::install("oligo")
BiocManager::install("limma")
BiocManager::install("hgu133a.db")
BiocManager::install("Biobase")

```

During installation, if you ever get the below message about updating loaded packages, select “No”.



And if you get this message in your console “Do you want to install from sources the packages which need compilation? (Yes/no/cancel)”, type “Yes” in the console.

To check that these packages have been installed correctly, go to the bottom right pane and click the tab for “Packages”. If you can search for and find the below packages, then they have been installed! They do not need to be checked off.

#### Packages

- tidyverse
- gridExtra
- cowplot
- datasauRus
- tidyselect
- ggfortify
- BiocManager