

Computer Setup

To fully participate in the hands-on sections of this course you will need access to the software described below on your **own laptop**. Note that you may need Administrator privileges/permissions to install some of these.

Students in this course will learn that Bioinformatics frequently requires analyzing large complex datasets. The recommended approach to such analysis is to work with a computer that offers **UNIX** integration. Together we will lean the fundamentals of the UNIX command line and the R environment for data analysis and graphics.

Student Computers & Software Setup Instructions

To fully participate in this course students will need access to a modern computer to which they have administrator privileges (that is a computer where they can install software without restriction).

I much prefer **Mac** and Linux based computers as they already have a UNIX base. If you can, please use one of these. However, don't worry if you are running Windows as we will be able to login to a campus based UNIX machine from your laptop or windows desktop for classwork. Chromebooks and iPads will not work for this class.

Regardless of your computer type you will need to install the software described below.

An up-to-date web browser

Current versions of [Chrome](#), [Firefox](#) and [Safari](#) are preferred.

The Zoom virtual meeting software

We will use [Zoom](#) on a weekly basis for office hours and other meetings. Please make sure you have Zoom installed and running to allow you to join these meetings.

The data analysis environment R and RStudio

R Binaries for Windows, MacOSX and Linux can be downloaded and installed from [CRAN](#) (Comprehensive R Archive Network). If possible download the latest binary version of R for your operating system. As of course launch (Sept 18) the latest release (2023-06-16, “Beagle Scouts”) is R-4.3.1.

After installing R itself we recommend installing [RStudio Desktop](#) (version 2023.06.2+561 or above), a slick visual interface for R. **N.B.** You will want the Open Source **FREE** version. If you have an older version of RStudio (without Quarto, i.e. pre-2023) you will benifit from updating.

RTools for windows

PC users will benefit from installing [RTool](#). This is needed for building R packages with C/C++/Fortran code from source - something we will describe later in the course. Look for the **Rtools42 installer** link. **N.B. Rtools is only needed for Windows users.**

Xcode Command Line Tools (Mac only)

Mac users will benefit from installing *Xcode Command Line Tools*. If you try to run any recognized command line tool in the Terminal application, macOS will prompt you to install these tools. For example. if you try to run `git --version` at the Terminal and don't have this software then you will be prompted to install. You can also install directly from the command line. Open your **Terminal** (found in `/Applications/Utilities`) and type the command `xcode-select --install` this will open a dialog for installation of the command line tools. Note that the time estimate for installation is usually ridiculously off so don't panic. Also please don't worry if you don't know what this means yet as I will explain when we get to this point in the course.

The Bash Shell

Bash is a commonly-used UNIX shell that gives you the power to do simple tasks more quickly.

Mac OS X: You do not need to install anything. You can access bash from the **Terminal** (found in `/Applications/Utilities`). You may want to keep Terminal in your dock for this class.

Linux: There is no need to install anything.

Windows: Install *Git for Windows* from <https://gitforwindows.org> by downloading their latest .exe installer file, double click on the installer file, click “Next” and follow their default setup (latest version).

To check if your install worked you can click on the “*Windows Menu button*” > “*All Apps*” and scroll down to **Git** and click to expand and select **Git Bash**. This should open a mostly black command line window. Success!! We can go ahead and close this for now.

XQuartz (Mac only)

Please install [XQuartz](#) a windowing environment required by some R packages. **N.B. This is only required on macs.** Download the linked DMG file (e.g. `XQuartz-2.8.1.dmg`). Once fully downloaded, double click to launch the installer and follow the regular steps.