Accessing the Command Line

Before using the Linux command line to perform bioinformatic analysis, you will need to figure out how to access the command line. Follow the appropriate instructions for your computer type below.

Regardless of the operating systems running on your computer (Windows, Mac, or Linux), you will use a program called *Terminal* to access the command line. A terminal is a program which opens a text-based interface through which you can use the command line.

Linux

We recommend using the Ubuntu 20.04 LTS distribution of Linux. On any Linux system, the terminal application is called *Terminal* and is pre-installed. No additional setup is needed.

Mac

On any Mac system, the terminal application is called *Terminal* and is pre-installed. You can run Linux commands on the Mac terminal with minimal modification. No additional setup is needed.

Windows

Windows computers do have a terminal installed, but it cannot accept Linux commands. Therefore, you will need to add a new terminal application (specifically, a *bash* shell) to run Linux commands on a Windows computer.

If your computer is running Windows 10 (64-bit edition), you can activate a *bash* shell by following these instructions: https://www.howtogeek.com/249966/how-to-install-and-use-the-linux-bash-shell-on-windows-10/.

If you are running an older version of Windows, you will need to install external software. There are several options for Windows-compatible software that will allow you to run a Linux terminal:

- Option 1: Install PuTTY, freely available at this website: https://www.putty.org/.
- Option 2: Install cygwin, freely available at this website: https://www.cygwin.com/. Additional instructions for how to install this software are available here: https://www.youtube.com/watch?v=QonIPpKodCw.

Once you have set up the Linux command line, you will use the newly installed *bash* terminal to enter commands. You only have to perform these setup steps once. Once your computer is properly configured, you can run any Linux command (though you may still need to install software packages required to perform your specific bioinformatic analyses).