

Lab00

How to get your computer ready

It would be best if you had a computer connected to the Internet. You need to be an admin to install essential bioinformatics software.

Text editor

Copying biological sequences and/or commands from Word or other sophisticated word processors to the terminal leads to all sorts of problems. You'll want to use a simple text editor.

Additional text editors.

windows

Windows has [Notepad](#).

mac

Mac has [text edit](#).

Linux/Ubuntu

You can use the GNOME [text editor](#). It is a small and lightweight text editor for the GNOME Desktop.

Feel free to explore your preferred text editor.

Documenting your projects/assignments

It is important to store your inputs, steps, software, parameters, code, and outputs, so that

1. You (or anyone else) can repeat your analysis.
2. We can help you to troubleshoot any problem that you might encounter.

This is part of your course grade. I will guide you through each analysis step, but I was hoping you could document all your steps to arrive at your conclusions.

I strongly encourage you not to use Word (.docx) or other sophisticated word processing programs to save your code. These programs embed many additional lines of code that will be misinterpreted by the terminal and the programs you will be using. Even "saving as" a text file may not remove all these symbols.

I recommend using a text editor, [Visual Studio Code](#) or free websites like [HackMD](#), GitLab ([RIT GitLab](#)) or [Github](#).

RIT Research Computing uses GitLab (git.rc.rit.edu) for documentation. RIT students and staff can create and share projects using their RIT usernames.

I have created the repo <https://git.rc.rit.edu/biol-530-630> , where I plan to upload some examples done through the class. You should be able to access it with your RIT credentials.

The **Final Project** will consist of many parts. One of them will be the documentation of all steps taken to get your results (e.g., a PDF of your documentation).

Software

We need specific software installed on our computers to work in the dry labs. Although there are good online alternatives, running them locally on your computer (or *oedipus* server) is preferred.

The PHYLIP package

<https://phylipweb.github.io/phylip/>

MEGA software

Graphical (GUI) and command line (CC)

<https://www.megasoftware.net/>

Tree visualization

<https://github.com/rambaut/figtree/releases>

...and more that will be mentioned for each Lab.

Online phylogenetic programs:

Phylogeny.fr

http://phylogeny.lirmm.fr/phylo_cgi/index.cgi

AliView: alignment viewer and editor

<https://ormbunkar.se/aliview/>

Clustal Omega: multiple sequence alignment program

<https://www.ebi.ac.uk/jdispatcher/msa/clustalo>

Interactive Tree of Life

<https://itol.embl.de/upload.cgi>

Galaxy Tools: Web-based platform for data-intensive biomedical research

<https://usegalaxy.org>

Sequence conversion tools

<https://mafft.cbrc.jp/alignment/server/cgi-bin/readseq.txt>

https://www.ebi.ac.uk/jdispatcher/sfc/emboss_seqret

Using the Terminal: basic Unix commands

We will use the terminal to run different programs. Please **make sure your computer has a working terminal**.

Since Windows Command Prompt is different from the Unix-like terminal from Mac and Linux distros, I highly recommend having installed an equivalent, like WSL or Cygwin and you will be able to use the same commands as on Mac or Linux.

WSL: <https://learn.microsoft.com/en-us/windows/wsl/install>

mv, cp, ls, cd, rm... not familiar?

There are many, many tutorials and cheat sheets.

This is a good cheat sheet

<https://files.fooswire.com/2007/08/fwunixref.pdf>

Tutorials

<http://www.ee.surrey.ac.uk/Teaching/Unix/>

<https://people.ischool.berkeley.edu/~kevin/unix-tutorial/toc.html>

You should be familiar with:

mkdir directory (creates a new directory)

cd navigates to a directory

ls list the the folders or files in a directory

ls -l list the the folders or files with specs

rm file removes a file

rm -r directory remove directories and their contents recursively

mv moves a file

pwd actual directory path

cd ~ home dir

cd .. go back one step in the dir path

cd ../../ go back two steps

in the dir path

for all these commands, typing the flag -h or --help usually list the options of usage.

In summary ... READ THE DOCUMENTATION!

Connect to oedipus

Open the terminal and type

```
`ssh -X user@oedipus.bioinformatics.rit.edu`
```

```
`password: type here`
```

Workspace in oedipus.bioinformatics.rit.edu

Class directory

/mnt/classes/biol_530_630

Lab datasets

/mnt/classes/biol_530_630/data/

Class Software

/mnt/classes/biol_530_630/bioware/

YOUR directory

/mnt/classes/biol_530_630/home/xyz1234/

General Software

/mnt/sde_dir/software/

To transfer files from and to your computer

File transfer software: check <https://en.wikipedia.org/wiki/FileZilla>

Download the appropriate FileZilla version: Client <https://filezilla-project.org/>

You are welcome to use other options.

screen

While working in a **server (ssh protocol)**, to avoid stopping your run because you lose your connection (wifi...), log into the server, and before running anything, invoke **screen**. A blank new terminal will show up, which has your previous environment. Run your script, and (if no error occurs) you can close your terminal, turn off your computer, etc. When you log back in, just type **screen -dr**. Your previous terminal will show up.

<https://linuxize.com/post/how-to-use-linux-screen/>