

Setting up for the MIG workshop

Rob Lanfear

2025-09-17

This document outlines the software you need to install in preparation for the MIG phylogenetics workshop. You'll install a few pieces of software, and it shouldn't take more than 30 minutes (perhaps a little longer if you have a Windows machine, and haven't installed Linux on it yet). Please make sure to complete this before the start of the workshop.

By the end of this document, you'll be able to run IQ-TREE and MAFFT from the command line, and view/edit results in FigTree, Geneious, and Sublime Text.

Note: if you get stuck during any of these instructions, ChatGPT can be incredibly helpful if you describe the problem in detail - feel free to upload this HTML to ChatGPT so it knows what you are trying to do when you describe your problem!

Software to install

If you have a Mac or Linux, everything should work “straight out of the box”. These operating systems are command-line based, so you can run everything from the command line.

Windows users only: Linux

Most bioinformatics software works seamlessly in Linux, but can be frustrating or impossible to use on Windows. Luckily, Windows allows you to install Linux.

If you use Windows, you will need to install Linux by following these instructions:

<https://learn.microsoft.com/en-us/windows/wsl/setup/environment>

You will need to follow up to and including the section “Update and upgrade packages”.

Once you are done, you can see if it worked by going to the Start Menu, typing “Ubuntu” and opening that application. You should see a terminal window.

Note: In the Ubuntu shell on Windows, file paths are Linux file paths, and your C drive is at `/mnt/c/`. So for example, the path to your Downloads folder should be `/mnt/c/Users/<YourUsername>/Downloads`, e.g. for me it would be `/mnt/c/Users/Rob/Downloads`. To change directories in Linux, you use the `cd` command, and the `ls` command lists what's in a directory. So you should be able to see what's in your downloads folder by using these lines in your Ubuntu shell (adding your username where it's required!):

```
cd /mnt/c/Users/<YourUsername>/Downloads
ls
```

If you can do this, you're up and running!

Once Ubuntu is installed, everything we do at the command line in this workshop will be done inside the Ubuntu shell, which is accessed from the Start Menu.

1. Geneious

Geneious is software that is useful for looking at alignments. The free version is fine (you do not need to sign up for a free trial). You do not need to pay for a license. We will only use features available in the free version in this workshop.

Download Geneious here: <https://www.geneious.com/updates>

Please check that you can run it after you have installed it.

2. FigTree

FigTree is a lightweight tree viewer. If you already have a favourite phylogenetic tree viewer, you can skip this step.

Otherwise, please download FigTree from the GitHub repo:

- For *Windows*, download the zip file here
- For *Mac*, download the dmg file here

Unzip the zip file (Windows) or open the disk image (Mac), then put the FigTree executable where you keep your programs, and then make sure you can use it to open the two example tree files that come with the download, `carnivore.tree` and `influenza.tree`.

3. Sublime Text

Sublime Text is a plain text editor. If you already have a favourite plain text editor (note, not MS Word!), then you can skip this step.

Otherwise, please download Sublime Text from here, then check that it works by running it and making sure you can edit and save a text document.

A good plain text editor is really important for bioinformatics.

4. Miniconda

Miniconda is a package manager. The workshop will use Miniconda as a way of installing and managing software. Miniconda (and its relative Anaconda, which is the same thing but comes with more prepackaged software) are widely used package managers in bioinformatics. They allow you to create ‘environments’, which are isolated areas on your computer in which you can install and run software. They allow you to very easily install and run pretty much every piece of widely-used bioinformatics software. When you get used to them they are incredibly helpful, and remove most of the headaches associated with dealing with bioinformatics software.

Installation

If you already have Miniconda or Anaconda installed (using Linux if you’re on Windows) and are comfortable using them, you can skip the installation and move to ‘Adding channels to conda’, below.

To install Miniconda:

- For *Windows*, open your Ubuntu shell and use it to follow the instructions for installing Miniconda using the Linux Terminal Installer
- For *Mac*, follow either the macOS graphical installer or macOS terminal installer instructions

Those instructions are all under the ‘Basic install instructions’ header here: <https://www.anaconda.com/docs/getting-started/miniconda/install>

Once you have Miniconda installed, make sure to test your install as described in the final step of the instructions.

Adding channels

Conda is accessed from the Linux command line. How you get to the command line depends on your operating system:

- On **Windows**: open “Ubuntu” from the Windows Start Menu
- On **Mac/Linux**: open the “Terminal” application

Before we install anything with conda, we need to tell it where to look for the software we’ll need. You only need to do this once when you are setting up conda.

Copy and paste the following lines into your command line:

```
conda config --add channels conda-forge
conda config --add channels bioconda
```

These two channels are where about 99% of bioinformatics software is made available.

Setting up an environment

Next we’ll set up a conda environment for the workshop, and install the two pieces of software we need. An environment is a place that you can install software. You can use different environments for different pieces of software when the software has different requirements. Environments are also reproducible. Once you have an environment set up, you can set up exactly the same environment on other machines, making your analysis easy to reproduce elsewhere. If you’re interested, you can read a lot more about conda environments [here](#).

To set up your conda environment type this at the command line (you can copy/paste it) and hit Return. When prompted, answer the question it asks you by typing ‘y’ and hitting Return.

```
conda create -n phylo
```

At this point, you have created your new environment called ‘phylo’. Let’s check it worked. Type this at your command line:

```
conda env list
```

You should see your new ‘phylo’ environment listed.

5. IQ-TREE and MAFFT

Now your environment exists, we’ll use it to install the software we need for the workshop.

First we need to activate our conda environment. At your command line, type this and hit Return:

```
conda activate phylo
```

When you do this, you should see that the bit at the start of your command line has changed from (base) to (phylo), something like this:

```
(base) aquila:tutorial roblanfear$ conda activate phylo
(phylo) aquila:tutorial roblanfear$
```

The first part of your command line tells you which environment you’re in.

You are now working inside the ‘phylo’ environment. You can get out of that environment at any time using the command `conda deactivate` but don’t do that now.

Finally we’ll install the software we need: IQ-TREE (for building trees) and MAFFT (for aligning sequences). Copy/paste the commands below, and type ‘y’ and hit Return when prompted:

```
conda install iqtree
conda install mafft
```

You can now check that those installations work by typing `iqtree -h` and `mafft -h` at the command line (hitting Return after each). In each case, you should see some basic instructions.

The convention for command line software is that if you type the name and `-h` you get a simple help file.

Most software has far more useful information in online documentation. E.g.:

- IQ-TREE has its documentation here: <https://iqtree.github.io/doc/>
- MAFFT has its documentation here: <https://mafft.cbrc.jp/alignment/software/>

If at any point you want to know what software you have installed in your environment, you can type:

```
conda list
```

When you do that, you should see something like this:

```
(phylo) aquila:tutorial roblanfear$ conda list
# packages in environment at /Users/roblanfear/opt/anaconda3/envs/phylo:
#
# Name                                Version                                Build      Channel
gawk                                  5.3.1                                h0631170_0  conda-forge
gmp                                   6.3.0                                hf036a51_2  conda-forge
iqtree                               3.0.1                                h6ed3961_0  bioconda
libasprintf                           0.25.1                               h3184127_1  conda-forge
libcxx                                21.1.1                               h3d58e20_0  conda-forge
libgettextpo                          0.25.1                               h3184127_1  conda-forge
libiconv                              1.18                                 h57a12c2_2  conda-forge
libintl                               0.25.1                               h3184127_1  conda-forge
llvm-openmp                           21.1.0                               hf4e0ed4_0  conda-forge
mafft                                 7.526                                hfdf4475_0  conda-forge
mpfr                                   4.2.1                                haed47dc_3  conda-forge
ncurses                               6.5                                  h0622a9a_3  conda-forge
readline                              8.2                                  h7cca4af_2  conda-forge
```

There's a lot more than just `iqtree` and `mafft`, because conda installed all the *other* stuff that these pieces of software require to work.

As a general rule, if you want to install bioinformatics software, just google the name of the software and 'bioconda'. You'll usually find clear installation instructions. For example, the `iqtree` instructions are here: <https://anaconda.org/bioconda/iqtree>. ChatGPT is also incredibly useful if you get stuck!

That's it!

Once you have `iqtree`, `mafft`, FigTree, Geneious, and Sublime Text installed, and you can run them all successfully, you're ready for the workshop.