Connecting to the High Performance Computer cluster (HPC)

We hope that you all applied for an account. You will have your username, which is your Staff Number/Matric Number (normally 5 characters long, mine is to16r) – and a password.

For simplicity, **where you see username, replace it with your ID**. So everywhere you see that during the logging, replace it with yours.

First: Connect to HPC
There are many ways to connect to the HPC.

1. **Linux**

If you are running on a Linux, and you are in the university network, just do
ssh -X username@headnode03.cent.gla.ac.uk

2. **Mac**

Some as Linux. Open a terminal (Application/Utilities -> terminal). Once open
ssh -X username@headnode03.cent.gla.ac.uk

3. **Windows machine at the University of Glasgow**

If you are working on a windows university computer, like in the computer room, we will use the tool mobaxterminal.
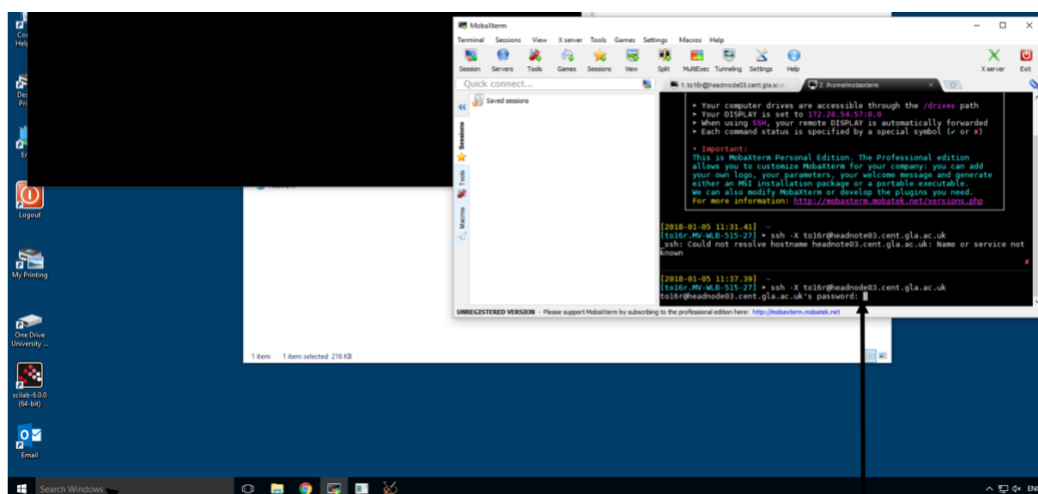
1. Write here "mobaxterminal" and open the software

2. Once it is running, type "ssh -X username@headnode03.cent.gla.ac.uk "
(**replace username with your user id**).
3. Answer
- yes if they ask to connect,
- type your password for the clutser once asked
- no save the password,

4. Running from private windows machine

Download and install mobaxterminal (https://mobaxterm.mobatek.net/download.html).
When working over the wireless you need to run the university VPN.
Proceed as in 3.

Second: Connect to server

Once you are logging, please type (use the tab key to automatically complete the command)

~to16r/bioinfo/start.sh

This will launch a session on the bioinformatics server, from where we are going to work most of the time.

Third: Set the environment

Once this is done you need to set the correct environment:

source ~to16r/bioinfo/setpath.sh

This script will initialize some settings we need. You should get a little message, like hello…

IMPORTANT

Once you are finished with the exercises, type exit, until the connection to the HPC is closed!

Thank you.