Linux

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Linux commands

Using ClustalW to align two sequences

Step 1A: Accessing the IGB Biocluster

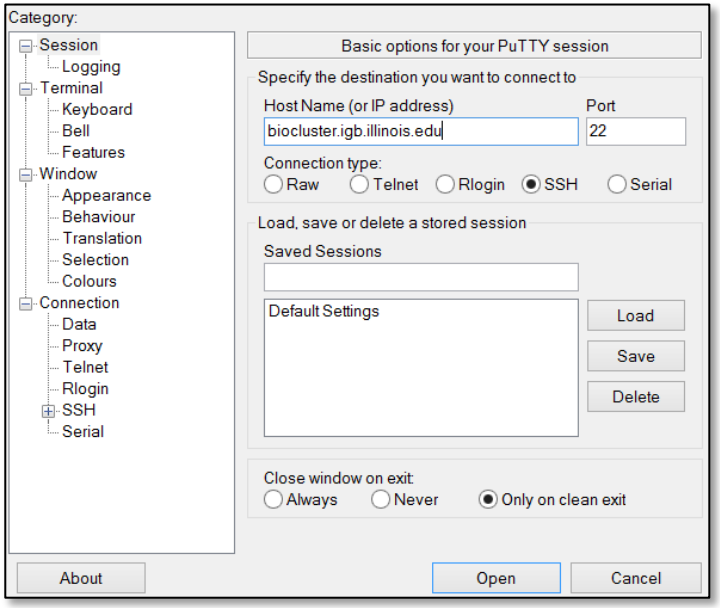
Open Putty.exe

In the **hostname** textbox type:

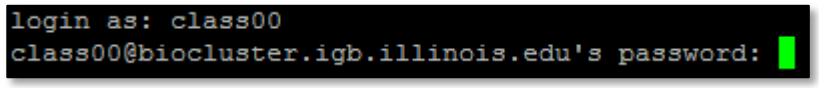
```
biologin.igb.illinois.edu
```

Click **Open**

If popup appears, Click **Yes**



Enter login credentials assigned to you; example, user **class00**. You will not see any characters on screen when typing in password. Just type it.



Now you are all set!

Step 1B: Listing files and directories (ls)

```
$ ls

# listing files in your current directory. When you first login, your
directory is your home directory.
```

Step 1C: Making Directories (mkdir)

```
$ mkdir ~/01_Linux

# create a subdirectory in your home directory. The tilde ~ character refers to your home directory.

$ ls

# to see the directory you just created.
```

Step 1D: Changing directory (cd)

The lab is located in the following directory:

/home/classroom/mayo/2020/01_Linux

```
$ cd /home/classroom/mayo/2020/01_Linux
# tip: use “tab” for auto-completetion for path
$ ls
# to see the contents. You should see seqs.fa
```

Step 1E: Print working directory (pwd)

```
$ pwd
# to see the full pathname. You should see
“/home/classroom/mayo/2020/01_Linux”
```

Step 1F: Copying files (cp)

Copy `seqs.fa` from the data directory to your working directory.

```
$ cp /home/classroom/mayo/2020/01_Linux/seqs.fa ~/01_Linux/
# tip: use “tab” for autocompletetion for path
$ cd ~/01_Linux/
```

Step 1G: Displaying the contents of a file on the screen (more)

```
$ more seqs.fa
# you should see two sequences on your screen
>seq1
GATCGAGCGATCGTGCAGC
GCAGAATGCGCGCTAG
>seq2
```

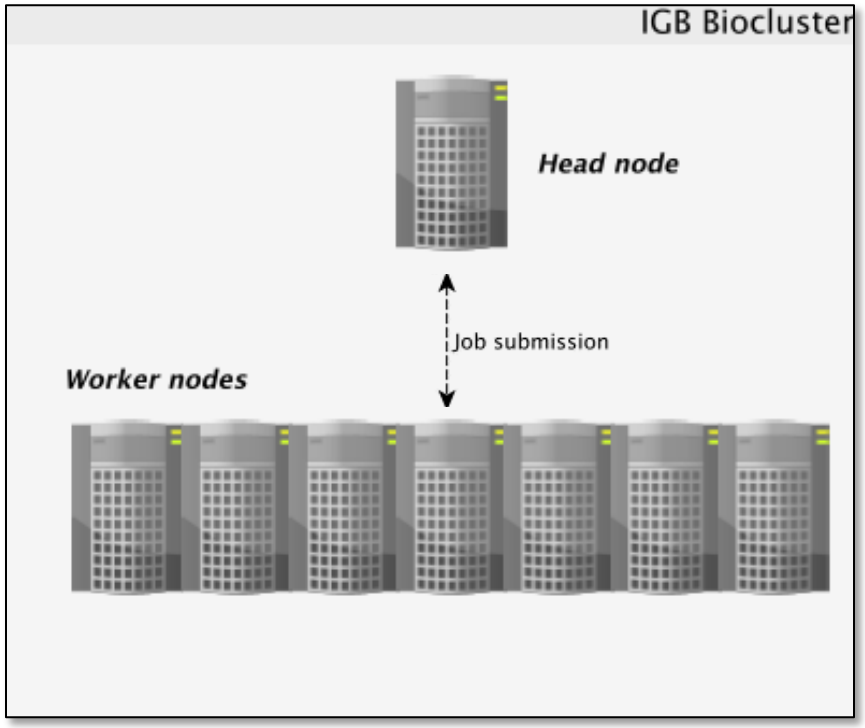
Commands Summary

Command	Meaning
ls	list files and directories
mkdir directory	make a directory
cd directory	change to named directory
cd ~	change to home directory
cd ..	change to parent directory
pwd	display the path of the current directory
cp file1 file2	cp file1 and call it file2
more file	display the contents of a file

Useful tips

Command	Meaning
tab	auto-complete path
↑	retrieve previous commands

Step 1H: Run sequence alignment program



Accessing the IGB Biocluster

Step 1H: Run sequence alignment program

```
$ srun -p classroom  -c 2 --mem 8000 --pty bash  # SKIP IF DONE

# Open interactive session on biocluster with 2 cpus and 8G memory.


$ module load ClustalW2     # Load sequence aligner into the shell environment.


$ module list #See loaded tools


$ clustalw2 -INFILE=seqs.fa  # Run the clustalW sequence aligner.
```

Step 1H: Run sequence alignment program

You will see this on your screen, when the program is done.

```
CLUSTAL 2.1 Multiple Sequence Alignments

Sequence format is Pearson
Sequence 1: seq1          35 bp
Sequence 2: seq2          32 bp
Start of Pairwise alignments
Aligning...

Sequences (1:2) Aligned. Score:  21
Guide tree file created:   [seqs.dnd]

There are 1 groups
Start of Multiple Alignment

Aligning...
Group 1:                    Delayed
Alignment Score 47

CLUSTAL-Alignment file created  [seqs.aln]
```

Step 1H: Run sequence alignment program

The alignment result is in **`seqs.aln`**. Use **more** command to see the result.

```
$ more seqs.aln

# You should see the following on your screen.

CLUSTAL 2.1 multiple sequence alignment

seq1            GATCGAGCGA-TCGTGCAGCGCAGAATGCGCGCTAG

seq2            GGTAGGGTAAATTGCCTACCGTCGATCGAGTA----

                * * * *  * * *   * **  **  * *
```

Exit putty by either closing the window or typing ‘exit’ in the command prompt.