

# Linux

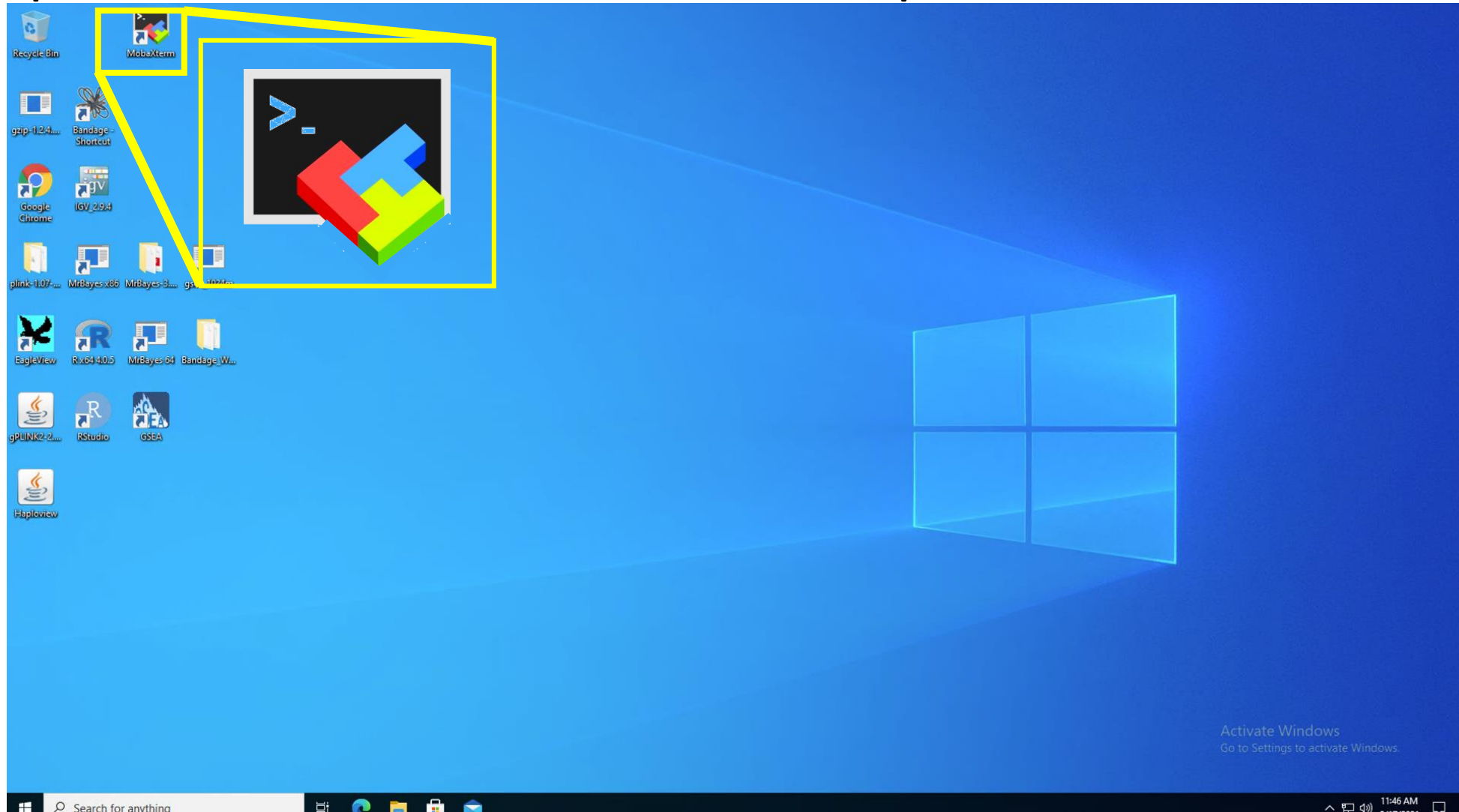
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# Linux commands

Using ClustalW to align two sequences

# Step 0: Connect to VPN & Open MobaXterm

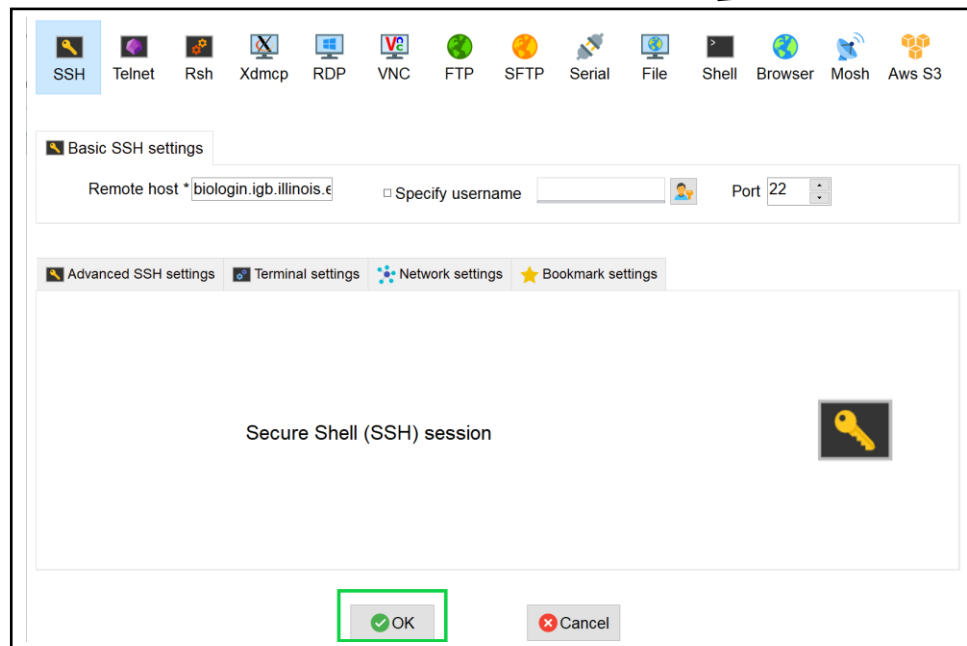
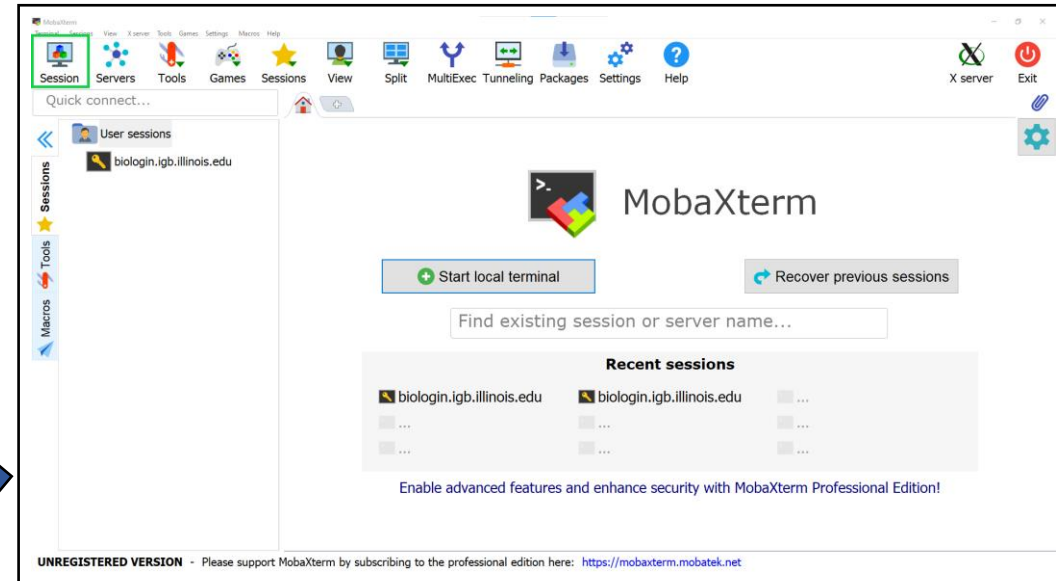


# Step 1A: Accessing the IGB Biocluster

- Open **MobaXterm** on your desktop
- In a new session, select **SSH** and type the following host name:

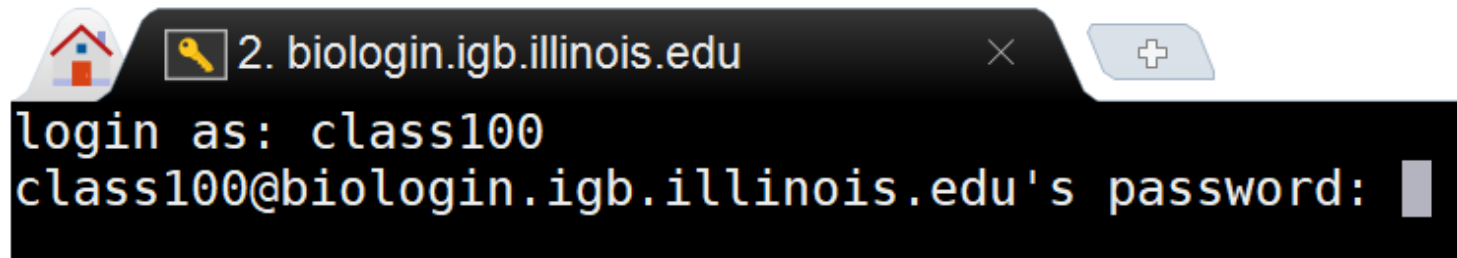
`biologin.igb.illinois.edu`

- Click **OK**



# Step 1A: Accessing the IGB Biocluster

- Enter login credentials assigned to you.
- Example username: **class100**.
- You will not see any characters on screen when typing in password. Just type it.



A screenshot of a terminal window. The window title bar shows a home icon, a key icon, and the text "2. biologin.igb.illinois.edu". The terminal content displays the prompt "login as: class100" followed by "class100@biologin.igb.illinois.edu's password:" and a cursor. The password field is obscured by a grey rectangle.

```
login as: class100
class100@biologin.igb.illinois.edu's password: █
```

• MobaXterm 10.5 •  
(SSH client, X-server and networking tools)

- > SSH session to `class101@biologin.igb.illinois.edu`
  - SSH compression : ✓
  - SSH-browser : ✓
  - X11-forwarding : ✓ (remote display is forwarded through SSH)
  - DISPLAY : ✓ (automatically set on remote server)
- > For more [info](#), ctrl+click on [help](#) or visit our [website](#)

```
Last login: Fri Jun 18 10:43:45 2021 from phalanx.igb.illinois.edu
#####
#
#           Institute for Genomic Biology           #
#           University of Illinois Urbana-Champaign #
#           http://biocluster.igb.illinois.edu      #
#
#####
*Please follow the guide at http://help.igb.illinois.edu/Biocluster
*All data on this cluster is NOT backed up.  It costs $8.75 per terabyte
per month
*HIPAA data is not allowed on the biocluster
*Please email help@igb.illinois.edu with any questions

[class101@biologin-1 ~]$
```

# Step 1B: Listing files and directories (ls)

```
*Please email help@igb.illinois.edu with any questions
```

```
[class101@biologin-1 ~]$
```

```
$ ls
```

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

\$ = command prompt

# = notes

# 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-completion 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 (cat)

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

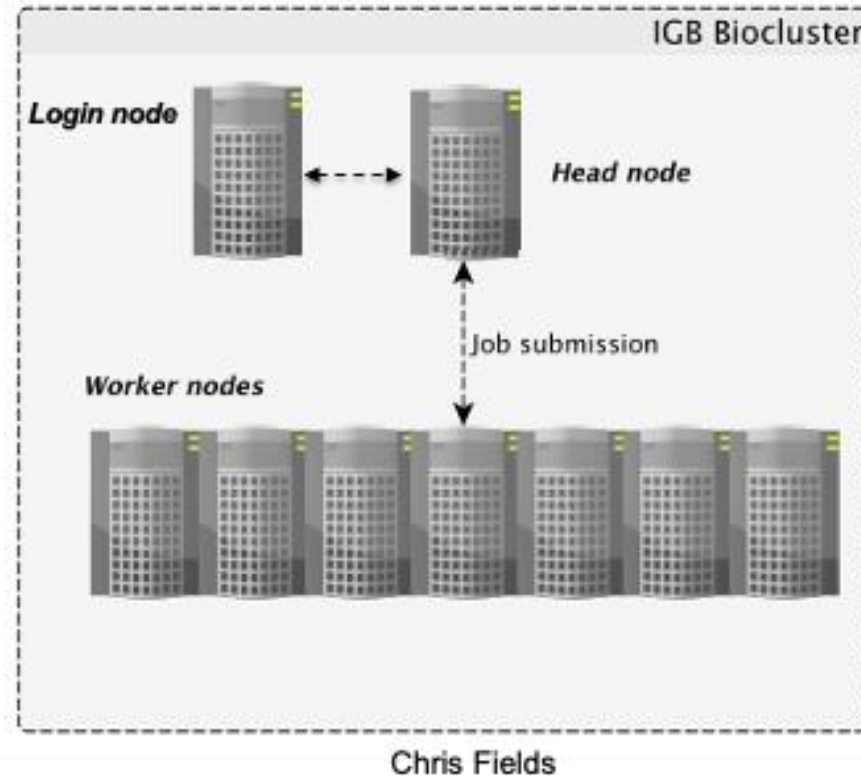
# Commands Summary

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
cat 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
# 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
```

# Step 1H: Run sequence alignment program

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

```
$ cat seqs.aln
# You should see the following on your screen.
CLUSTAL 2.1 multiple sequence alignment

seq1          GATCGAGCGA-TCGTGCAGCGCAGAATGCGCGCTAG
seq2          GGTAGGGTAAATTGCCTACCGTCGATCGAGTA----
              * * * * * * * * * * * * * * * * * *
```



## Exit **MobaXterm** by either of the following:

- Close the window
- Type 'exit' in the command prompt twice and then press <return>.

```
$ exit
```

```
$ exit
```