

## Micro B3 EU-US Bioinformatics Course: Day 1

### Nasko Introduction to Linux I: Linux File System

Commands to type at the command prompt will be followed by a \$:   \$ whoami

#### 1. Login (ssh) to biohen

```
$ ssh -X user@biohen.dbi.udel.edu
```

#### 2. Who am I?

```
$ whoami           – prints your user name (who you are)
```

#### 3. Where am I?

```
$ pwd              – prints your current directory
```

#### 4. List Directory Contents

```
$ ls               – prints the contents of the current directory (may be blank)
```

```
$ ls /home/microb3
```

#### 5. Command History and Command Arguments

Try pressing:   [arrow up]   then edit your previous command

```
$ ls -l /home/microb3
```

```
$ ls -lh /home/microb3
```

These are called options, arguments, or parameters, they change the behavior of the command. Most Linux commands have various options.

#### 6. Manual (Help)

```
$ man ls
```

This will display the help for the list command.  
(scroll with [ up/down arrows ], press q to exit)

## 7. Change the directory

```
$ cd /home/microb3
```

Now list the contents.

Change back to your home directory:

```
$ cd ~           -same as: $ cd /home/username
```

(~ is the Linux shortcut to your home directory)

## 8. Create a symbolic link (shortcut)

```
$ ln -s /home/microb3 ~/microb3-shared
```

```
$ ls -l
```

```
$ ls -l /home/microb3
```

```
$ ls -l ~/microb3-shared
```

## 9. Make a new directory

```
$ mkdir test
```

Now change into that directory. And type:

```
$ pwd
```

To get back to your original directory (one level up):

```
$ cd ../
```

## 10. Copy a file: `cp [from] [to]`

```
$ cp ~/ microb3-shared/file1.txt ./
```

( `./` is how Linux refers to the current directory)

Now list the directory contents

```
$ cp ~/ microb3-shared/file2.txt ./
```

## 11. Move a file: `mv [from] [to]`

```
$ mv fi          (then hit [tab])
```

now hit: [tab][tab]

```
$ mv file* test/
```

## 12. Rename a file

Change into the 'test' directory and list the contents

type:

```
$ mv file1.txt file-one.txt
```

## 13. File Permissions

```
$ ls -l
```

Now see what 'groups' you are in

```
$ groups
```

Now change permissions so only you can read and write

```
$ chmod 600 file-one.txt
```

```
$ ls -l
```

Now change permissions so you can read and write, AND group AND world can read

```
$ chmod 644 file-one.txt
```

```
$ ls -l
```

#### **14. Redirection and Piping (with grep and wc)**

```
$ ls -l
```

Redirect the output (new file)

```
$ ls -l > list.out
```

```
$ cat list.out
```

Redirect the output (add to file)

```
$ ls -l >> list.out
```

```
$ cat list.out
```

Pipe output to grep command (search)

```
$ ls -l | grep "file"
```

Pipe output to wc command (word count)

```
$ ls -l | wc
```

#### **15. Delete file (NO UNDO: use with caution)**

```
$ rm -i file2.txt
```

List the directory contents

## 16. Remove Directory

```
$ cd ..  
$ rmdir test
```

rmdir only removes empty directories

```
$ rm -i test/file-one.txt  
$ rm -i test/list.out  
$ rmdir test
```

List the directory contents

### ACTIVITY

Use what you've learned to do the following:

- Under your home directory make a folder called microb3-work
- Copy all the files in: ~/microb3-shared/raw\_sequences to the new directory you created (~/microb3-work)

## Micro B3 EU-US Bioinformatics Course: Day 1

### Nasko Introduction to Linux II: Viewing and Editing Files

#### 1. Learn about the PATH

```
$ metagene
```

```
$ echo $PATH  Displays the directories where programs are  
              located
```

Go to: <http://bioinformatics.udel.edu/Core/BioHen-Software>

#### 2 . View a file (read only)

```
$ less /home/microb3/class_env
```

#### 3 . Edit a file

```
$ nano ~/.bashrc
```

Add this line to the end of your `.bashrc`:

```
source /home/microb3/class_env
```

```
[ctrl-o]  to save; [enter] confirm file name
```

```
[ctrl-x]  to exit
```

Any command in your `.bashrc` will run automatically when you login. To make the change take effect:

```
$ exit  to logoff from biohen
```

Now ssh back in to biohen again and try the `tophat` command again:

```
$ metagene
```

#### 4. Unzip a file (Gzip format)

Change to the directory you just copied the sequence files to in the previous exercise

```
$ cd ~/microb3-work
```

```
$ gunzip *.gz
```

#### 5 . View the file

```
$ less FL1-1.fastq
```

[Learn about FASTQ format](#)

## Micro B3 EU-US Bioinformatics Course: Day 1

### Nasko Introduction to Linux III: Using Torque PBS

#### 1 . List Torque nodes

```
$ pbsnodes
```

#### 2 . List jobs currently running on Torque

```
$ qstat -aln
```

#### 3 . Start Interactive Torque session

```
$ qsub -N intrctv-users1 -I -V -l nodes=1:ppn=1:class
```

```
$ qstat -aln
```

#### 4 . Ends interactive Torque session

```
$ exit
```

#### 5. Alias to make interactive session easier

```
$ less /home/microb3/class_env
```

#### 6. Run a Torque job in batch mode

```
$ less ~/microb3-shared/bin/test.qs
```

```
$ qsub ~/microb3-shared/bin/test.qs
```

```
$ qstat -aln
```

#### 7. Open result files with less

```
$ less Test.o#####
```



## 8. Delete an active or queued job

```
$ qsub ~/microb3-shared/bin/test.qs
```

```
$ qstat -aln
```

```
$ qdel #####
```