Unix Cheat Sheet

$ pwd: print working directory. For example, if you just entered your bananas controller, using pwd should give you /home/zz220

$ rm filename: remove a file

$ ls: shows what is in your directory. Folders in blue, files in black

$ ls -l: same as ls command, but gives you more detail (overall format is of the command is specific command- command option). It will Will get you a list of the files, date, and the file size

$ ls -it: similar to ls, will give you list of the files and the file size, but ordered from largest to smallest file size

$ ls -lh: human readable, will give you file size in gigs

$ mkdir new\_directory\_name: makes a new directory called new\_directory\_name—obviously, if you want a different name, put that name instead of new\_directory\_name—(never put spaces in name), then use Is to check that it’s there

$ rmdir directory\_name: remove empty directory called directory\_name—obviously, if you want a different name, put that name instead of directory\_name

$ rm -r directory\_name: remove directory that has files in it

$ cd directory\_name: change directory (i.e move to another directory); for exp, going to HW1, do $ cd /home/zz220/Homework1

$ ..: go up a directory. For example, if you want to copy a file from HW1 to HW2 that are both under the zz220 directory, then you need to go up first to zz220 then HW2: $ cp file\_name ../ifneededsubdirectorynameexp\_homework2

$ cp: copy; when you copy make sure to direct it to the right directory. For an example, see previous command.

$ .: current directory

Wildcard: wildcards (\*): \*.txt means consider every file that ends in .txt

Viewing Files:

$ head file\_name: shows first 10 lines of file. Can use $ head -50 <file\_name> : to show first 50 lines, or other specified number

$ tail file\_name: shows last part of file.

$ more file\_name: displays file content, but obviously more content than less would display. Can use it to scroll down

$ less file\_name: displays file content. Space or return to advance. Can use “/text” to pattern search on text. Can use less to scroll up

$ man command\_you\_want\_to\_search: this pulls up a manual description of the command you are searching for and tells you how what the command does—for example, if you want to know what ls does, use $ man head

$ grep “character” file\_name: this gives you the number of lines with the character of interest. For example, to get number of sequences, see which lines have “>” $ grep “>” file\_name

$ grep -v “character” file\_name: this gives you the number of lines that DO NOT have the character of interest.

|: This is called a pipe you can use it to combine commands: exp: combining grep with wc –l to show how many lines have the character; piping (|) one command into another: grep “character” filename | wc -l

$ wc file\_name: gives you a wordcount of the file. More specifically, will give you: #of lines, words, characters, file\_name—obviously put in an actual file name instead of file\_name

$ wc –l file\_name: will give you: # of lines in the file— obviously put in an actual file name instead of file\_name

$ cat file1name file2name: will give you the contents of both files; in order to combine/place the contents of both files into one: add > (file redirect): $ cat file1name file2name > newfilename Check by viewing new file with: $ less newfilename

Combining grep w/ redirecting to new file: $ grep “character” > newfilename

Put contents of one file to another file: $ cat oldfilename > newfilename

To append text to a file you use >>. To overwrite the data currently in that file, you use >. In general, in bash and other shells, you escape special characters using \.

Nano Text editor:

$ nano filename: invoke test editor for newfilename— obviously use an actual file name instead of filename.

Up arrow on the bottom of nano commands means control

Exit: exit

$wget <url>: will download file specified by URL to current working directory.

Find url by using web browser to locate file you want, right click and “copy url”, then

paste into terminal. exp: $wget <https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/204/515/GCF_002204515.2_AaegL5.0/GCF_002204515.2_AaegL5.0_protein.faa.gz>

https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/204/515/GCF\_002204515.2\_AaegL5.0/

https://ftp.ncbi.nlm.nih.gov/genomes/genbank/fungi/Candida\_albicans/latest\_assembly\_versions/GCA\_000182965.3\_ASM18296v3/[GCA\_000182965.3\_ASM18296v3\_protein.faa.gz](https://ftp.ncbi.nlm.nih.gov/genomes/genbank/fungi/Candida_albicans/latest_assembly_versions/GCA_000182965.3_ASM18296v3/GCA_000182965.3_ASM18296v3_protein.faa.gz)

https://ftp.ncbi.nlm.nih.gov/genomes/genbank/fungi/Candida\_albicans/latest\_assembly\_versions/GCA\_000182965.3\_ASM18296v3/[GCF\_002204515.2\_AaegL5.0\_genomic.gff.gz](https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/204/515/GCF_002204515.2_AaegL5.0/GCF_002204515.2_AaegL5.0_genomic.gff.gz)

$gunzip <file\_name.gz>: will decompress (unzip) a .gz f

$module avail: shows all available modules (programs)

$module load modulename: load a module

$bowtie2: Take a look at online manual for bowtie2

Google bucket: same commands as bash but always put “gsutil” in the front   
Access our class’ bucket with “gsutil”: $ gsutil ls gs://gu-biology-dept-class  
To copy a file from the bucket into your current working directory: $ gsutil cp gs://gu-biology-dept-class/file\_name .

MAKE SURE TO PUT SPACE and then “.” This means cp it to our current working directory

**Tips:**

Press tab to autocomplete

Control C to kill process

q: quit. For example, if you are viewing a file with “more”, and need to stop viewing it you use

Exit: to exit terminal, type exit

Up arrow: fills in with previous command

$ cd ../ .../ to go up two directories

* Quit shell, $ exec –l $SHELL
* ONE IMPORTANT NEW COMMAND! ^X^C = “kill process”
* sbatch slurmname to run

$ squeue -u zz220

To see jobs that are currently running

![Graphical user interface, application

Description automatically generated]()

paa9$ gcloud compute scp file\_name bananas-controller:.

or… paa9$ gcloud compute scp file\_name bananas-controller:/home/paa9/albo\_2020\_genome/

REMEMBER you need to logout of bananas controller i.e. you need to be desktop Cottonelles-MBP:~ cottonellezhou$

Download files to desktop: gcloud compute scp bananas-controller:/home…full path to file ./

Number of reads/sequences: Grep > for fasta, have to do wc -l and /4 for fq

srun --pty bash for compute node