**Fri Feb 9th Lab 3**

Outline

-directories

-anatomy of a command

-getting around

-changing file structure

Directories

-where all files are stored (ex. Users – name – desktop)

Linux file paths

/Users/sara/Desktop/gen711-811

-Starts with / known as the root directory

-Includes all directions between the root and your current directory

- command “pwd” – will output the absolute path to your current directory

-pwd – outputs the full path name of your current directory from the root directory

Relative paths

-a relative path specifies location of a file or directory relative to the current working directory (CWD)

-often shorter and more convenient

-starts with one of three things:

- “.” current directory

- “..” previous directory

- “~” home directory

Anatomy of a command

-specification of how a program should execute

-macse -I ./species.fasta -o species\_aligned.fasta

-some programs have optional arguments, some are required

-ones that start with “-“ are flags

Help

-**man** “”

-“” **-h**

-“” **–help**

Getting Around  
-to move to new directories

-“ls” command short for list will list contents of CWD if no arguments are given

- “ls -F” shows “/” on ends of directions and “\*” on ends of scripts to help diff contents – shows file names

-“ls -l” additional info (size/owner/mod date)

-“ls -a” shows hidden files/directories that are normally hidden with just “ls”

- “ls-lh” – list of human readable sizes

-“clear”

-“ls -S”

- “ls” tab twice to see ever place you could go, then type in first initial or two then tab complete

-“cd” short for change directory, will change your CWD to whichever directory is put as argument. – ex. cd /home/users/smc1079. -ex. cd nameofdesiredfolder/

- cd / -goes to root, then use “..” to go to home

-echo nameoffolder

-echo $HOME

How to make, delete, and change file/directory locations

-mkdir, - make new directory

-mkdir -p – makes new sub directories ex. fasta/fasta1/fasta2

-rmdir, - remove directory

Rmdir ~/empty\_directory first before deleting it

-mv, - short for move, rename, or move + rename

Ex. mv ../notes.txt ~notebook (renames and moves txt file to notebook)

Ex. mv /tmp/important\_data.fasta . (moves to CWD)

Ex. mv “name of what you want to change” “name of what youre renaming it too”

-cp, -short for copy

Ex. cp “name of file” “name of file in CWD”

Ex. cp -R filename .. (copies filename from CWD into parent directory

Ex. cp -r filename . (copies into CWD)

-touch, creates empty file if argument doesn’t exist

-rm, short for remove

-rm -R

-ln

-cat combines and displays files

> : redirect output command to file specified, overwrites it

>> : redirects output of command to file specified, appending to it

Head: first 10 lines

Head -n#: print out requested #

Tail: last 10 lines of file

control C -stops what youre running

**Friday Feb 16th**

3a "3 ways to change directories to HOME from untrimmed\_fastq"

1. echo $HOME
2. cd ~
3. cd $HOME

3b. How many programs in /bin

Wc = 1922 - cd /bin -> ls | wc

Do each of the following tasks from your current directory using a single ls command for each:

List all of the files in /Applications that start with the letter ‘c’. ls c\* | wc

List all of the files in /Applications that contain the letter ‘a’. ls a\* | wc

List all of the files in /Applications that end with the letter ‘o’. ls o\* | wc

Bonus: List all of the files in /Applications that contain the letter ‘a’ or the letter ‘c’.

Start with the letter c \_105\_\_\_ Start with the letter a \_\_55\_\_ Start with the letter o \_\_21\_\_ Contain the letter ‘a’ or the letter ‘c’ \_160\_\_\_

Find the line number in your history for the command that listed all the .fastq files using the absolute path. Paste the command that you used to do this below.

**Friday February 23rd**

Less – up/down arrow to scroll, q to exit

Ex. less “name of file”

Nano – easy to use text editor

Ex. nano “file name”

Ex. nano new\_notes.text - > new text file

Wildcard character = \* , will match any character or amount of charaters

Ex. head -n5 \*.fasta >> fasta\_heads.fasta

Ex. rm samples/\*.fastq

Ex. Cd ../labs/\*.md ./lab\_notes

Ex. Cat \*.fasta > fastas.fasta

To get files back: cp /tmp/shell\_data/untrimmed\_fastq/\*.fastq .

GREP – when given a search term will find all instances of that term within the given search area

Ex. grep “@SRR” \*.fastq

Find all quality headers and sequence and output them all to a new file named “qualities”

Answer: grep -A1 “+SRR” \*.fastq > qualities

grep -A1 -B1 “+SRR” \*.fastq > qualities -> actual sequence, quality header, quality sequence

Flags:

-A# lines after

-B# lines before

-o prints out specific search term in file – gets rid of rest of line

-v leaves out what you input

- | pipe symbol

- ex. input | head -> will output you first 10 lines from initial input

- ex. input | head | grep “root”

- wc: word count

-l only show lines

-w only show words

-c only show bytes

Ex. wc -lwc SRR097977.fastq SRR098026.fastq

Ex. cat \*.fastq | grep “>” (headers) | wc-1  
-sort -> sort lines of stdin

-h human readable #s (not 10 before 2)

-uniq -> removes duplicate lines, input has to be sorted previously,

-c shows how many times each line occurs

-d only prints duplicates

-u only prints lines without duplicates