

## Final Exam (100 pts + 6 extra credit, 30% of grade)

Name: \_\_\_\_\_

**NOTE: this is only the section of the final exam related to weeks 2-3.**

1. Which of the following is the most accurate description for what the commands more and less display?
  - a. The first 10 lines of a file
  - b. The last 10 lines of a file
  - c. The entire file
  - d. One terminal window worth of a file at a time
  - e. More and less are not used to display the contents of a file
2. Which of the following commands is commonly used to transfer files between computers?
  - a. scp
  - b. cd
  - c. ls
  - d. grep
  - e. tr
3. Which of the following commands is commonly used to connect to a remote server?
  - a. pwd
  - b. cut
  - c. echo
  - d. sort
  - e. ssh
4. Which of the following commands is commonly used to retrieve files from a remote server?
  - a. more
  - b. less
  - c. cat
  - d. grep
  - e. ftp
5. Which of the following commands is commonly used to compress a file?
  - a. ssh
  - b. gzip
  - c. grep
  - d. ftp
  - e. mv
6. Which of the following options is used to decompress a file using the command from question 4?
  - a. -d
  - b. -a

- c. -x
- d. -c
- e. -l

7. Which of the following commands is commonly used to combine files into a single archive?

- a. tar
- b. gzip
- c. grep
- d. ftp
- e. mv

8. Which of the following commands can be used to return lines containing a specified pattern?

- a. tar
- b. gzip
- c. grep
- d. awk
- e. both c and d

9. The regular expression for a new line is \_\_\_\_\_

10. The regular expression for a tab is \_\_\_\_\_

11. Fill in the blank:

\_\_\_\_\_ is a graphical user interface (gui) program for transferring files using between computers (there is more than one correct answer).

12. At the prompt below, write code to substitute the Ts, found in DNA, for Us, found in RNA, in a file called DNA.txt and specify for the output to be inserted into a new file called RNA.txt:

\$

13. At the prompt below, write code to determine the reverse complement of the sequence ACTG (the reverse complement is CAGT):

\$

14. Circle the number next to each line of the following text file (miRNAs.txt) that would be returned using the command below:

\$ grep ".\*U" <miRNAs.txt

1. hsa-miR-15a-5p	UAGCAGCACAUAAUGGUUUGUG
2. hsa-miR-15a-3p	CAGGCCAUUUUGUGCUGCCUCA
3. hsa-miR-16-5p	UAGCAGCACGUAAAUAUUGGCG
4. hsa-miR-16-1-3p	CCAGUAUUAACUGUGCUGCUGA
5. hsa-miR-17-5p	CAAAGUGCUUACAGUGCAGGUAG
6. hsa-miR-17-3p	ACUGCAGUGAAGGCACUUGUAG
7. hsa-miR-18a-5p	UAAGGUGCAUCUAGUGCAGAUAG
8. hsa-miR-18a-3p	ACUGCCCUAAGUGCUCUUCUGG

15. At the prompt below, write code to extract the seventh line of a text file (e.g. lines.txt):

\$

16. At the prompt below, write code to extract the first 1,000 lines of fastq file (e.g. fastq.txt):

\$

17. Fill in the blanks:

In the script below, next to the # signs indicate what each line of code does:

```
#!/bin/bash
```

```
# Infinite loop
```

```
while
```

```
# _____
read -p "Enter text:" text
```

```
# _____
length=`echo -n $text | wc -c`
```

```
# _____
```

```
do
```

```
echo "The text you entered contains $length characters"
```

```
done
```

18. At the prompt below, write the command to execute a program named final.sh (i.e. how are bash scripts executed from the command line?):

\$

19. **Extra credit:** how do you perform a search in more or less?

- a. ctrl + f search term
- b. ctrl + h search term
- c. \ search term
- d. /search term
- e. find search term

20. **Extra credit:** Identify the error in this example of variable assignment from the command line:

```
$ sequence==ACTGATCAGTGTGTTTAGGAC
```