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

Name:_____

1. Adobe Illustrator is an example of what type of program:
    a. a GUI
    b. a command line interface application
    c. a shell
    d. a kernel

2. Which of the following key strokes is used to terminate a process from the command line:
    a. Ctrl + C
    b. Ctrl + A
    c. Ctrl + E
    d. Ctrl + B

3. At the prompt below, write the single command line that would navigate from directory A to directory B using a relative path:

    i. Directory A = /Users/erin/Documents/proj/160912_assignment1
    ii. Directory B = /Users/erin/Documents/proj/160915_test_prep

    $

4. At the prompt below, write the single command line that would navigate from directory A to directory B using an absolute path:

    i. Directory A = /Users/erin/Documents/proj/160915_test_prep
    ii. Directory B = /Users/erin/Documents/website/content/

    $

5. At the prompt below, write the single command line that would navigate from directory A to directory B, in which *home* stands for the current user's home directory:

    i. Directory A = /Users/erin/Documents/proj/160915_test_prep
    ii. Directory B = *home*

    $

6. Read the following man page and assume all the options work as specified:

Table 3- 1: Common ls Options

Option	Long Option	Description
-a	--all	List all files, even those with names that begin with a period, which are normally not listed (i.e., hidden).
-A	--almost-all	Like the -a option above except it does not list . (current directory) and .. (parent directory).
-d	--directory	Ordinarily, if a directory is specified, ls will list the contents of the directory, not the directory itself. Use this option in conjunction with the -l option to see details about the directory rather than its contents.
-F	--classify	This option will append an indicator character to the end of each listed name. For example, a "/" if the name is a directory.
-h	--human-readable	In long format listings, display file sizes in human readable format rather than in bytes.
-l		Display results in long format.
-r	--reverse	Display the results in reverse order. Normally, ls displays its results in ascending alphabetical order.
-S		Sort results by file size.
-t		Sort by modification time.

Circle the commands that will yield the same results as ls –alh:
   a. ls --almost-all -lh
   b. ls -all -lh
   c. ls --all -lh
   d. ls --all --human-readable -l
   e. ls --allhuman-readable -l
   f. ls -a -h -l .
   g. ls -a -h -l ..
   h. ls --allhl ..

7. Assume you are in an empty directory. List the contents of your directory after you execute the following sequence of commands:

```
$ touch file1.txt file2.txt
$ mkdir dir1 dir2 dir3
$ mv dir1 dir4
$ cp file1.txt file3.txt
$ mv dir2 ..
$ mv file2.txt dir3
$ rm –Ri dir3
```

8. What will the following two commands do:

```
$ rm *.txt
```

```
$ rm * .txt
```

9. Explain where **stdout** and **stderr** will be sent when the following commands are executed:

```
$ wc –l file1.txt *.docx fdklsj > output.txt
```

```
$ wc –w file1.txt *.docx fdklsj 2> output.txt
```

```
$ wc –lw file1.txt *.docx fdklsj | tee output.txt
```

10. You perform the following series of commands. How would you **pipe** these commands together into a single command?

```
$ sort file1.txt > 01_file_sorted.tmp
$ uniq 01_file_sorted.tmp > 02_file_uniq.tmp
$ wc –l 02_file_uniq.tmp > output.txt
```

11. How would you **chain** the commands together from question 10 onto a single line using ';' ?

12. Explain what **each of the four steps** of the piped command below do:

```
$ more C_briggsae.gff
# Caenorhabditis elegans annotation
# Wormbase Annotation file
# 1/25/2012
# Wormbase Consortium
chrISGD tRNA    139152  139254  .   +   ID=A67A13.2
chrISGD CDS     166267  166339  .   +   ID=elt-2
chrISGD gene    166267  166339  .   +   ID=elt-2
chrISGD snoRNA  181141  181254  .   -   ID=sno_18742
chrISGD CDS     182522  182603  .   +   ID=A23B23.2
$ grep -v '^#' C_briggsae.gff | cut -f 3 | grep -i 'CDS' | wc -l
```

Step 1 (grep):

Step 2 (cut):

Step 3 (grep):

Step 4 (wc):

13. Given the file contents displayed using more, what will be the output of the commands in question 12?

14. At the prompt below, indicate how you would change the permissions of a file genome.fa to allow the owner all privileges, the group read-only privileges, and the world no privileges: Use the following permissions chart as a guide.

OWNER			GROUP			WORLD		
r	w	x	r	w	x	r	w	x
4	2	1	4	2	1	4	2	1
= 7			= 7			= 7		

$

15. At the prompt below, indicate how you would change permissions on the directory 03_annotations and all its contents such that the owner will have all privileges, the group will have read-only privileges:

$

16. 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

17. Which of the following commands is commonly used to transfer files between computers?
    a. scp
    b. cd
    c. ls
    d. grep
    e. tr

18. Which of the following commands is commonly used to connect to a remote server?
    a. pwd
    b. cut
    c. echo
    d. sort
    e. ssh

19. 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

20. Which of the following commands is commonly used to compress a file?
    a. ssh
    b. gzip
    c. grep
    d. ftp
    e. mv

21. 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

22. 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

23. 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

24. The regular expression for a new line is _____

25. The regular expression for a tab is _____

26. Fill in the blank:

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

27. 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:

    $

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

    $

29. 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   CAGGCCAUAUUGUGCUGCCUCA
    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   ACUGCCCUAAGUGCUCCUUCUGG

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

    $

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

    $

32. 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
    ```

33. 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?):

    $

34. **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

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

    $ sequence==ACTGATCAGTGTGTTTAGGAC