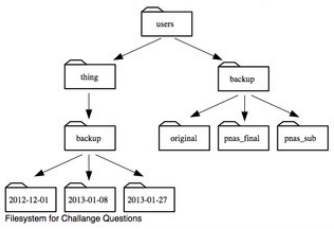
socrative by MasteryConnect

Name: _____ Date: _____

Quiz name: Shell Quiz

1. If pwd displays /users/thing, what will ls ../backup display?



(A) ../backup: No such file or directory

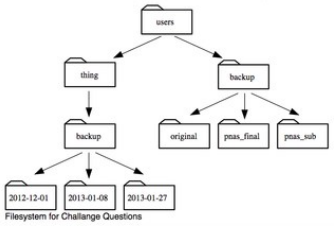
(B) 2012-12-01 2013-01-08 2013-01-27

(C) 2012-12-01/ 2013-01-08/ 2013-01-27/

(D) original pnas_final pnas_sub

2. If pwd displays /users/backup, and -r tells ls to display things in reverse order, what command will display:

pnas-sub/ pnas-final/ original/



(A) ls pwd

(B) ls -r -F

(C) ls -r -F /users/backup

(D) Either #2 or #3 above, but not #1.

3. What does the command cd do if you do not pass it a directory name?

(A) It has no effect

(B) It changes the working directory to /

(C) It changes the working directory to the user's home directory

(D) It produces an error message

4. Suppose that you created a .txt file in your current directory to contain a list of the statistical tests you will need to do to analyze your data, and named it: statstics.txt
After creating and saving this file you realize you misspelled the filename! You want to correct the mistake, which of the following commands could you use to do so?

(A) cp statstics.txt statistics.txt

(B) mv statstics.txt statistics.txt

(C) mv statstics.txt .

(D) cp statstics.txt .

What is the output of the last ls command in the sequence shown below?

```
$ pwd
/home/jamie/data
$ ls
proteins.dat
$ mkdir recombine
$ mv proteins.dat recombine
$ cp recombine/proteins.dat ../proteins-saved.dat
$ ls
```

5.

A proteins-saved.dat recombine

B recombine

C proteins.dat recombine

D proteins-saved.dat

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ls -F in ~/Desktop/Shell/Users/nelle/sugars results in:

analyzed/ glucose.dat mannose.dat sucrose.dat fructose.dat maltose.dat raw/

6.

What code would you use to move all the .dat files into the analyzed sub-directory?

In a directory we want to find the 3 files which have the least number of lines. Which command of those listed below would work?

7.

A wc -l * > sort -n > head -3

B wc -l * | sort -n | head 1-3

C wc -l * | head -3 | sort -n

D wc -l * | sort -n | head -3

What code would allow you to extract the real number values (columns 5-9) for only the rows containing Carbon atoms from cubane.csv in the molecules directory?

hint - use the cut command which allows you to extract columns from a file. For example, to get the first three columns of cubane.csv you could type:

8.

```
cut -f 1-3 -d',' cubane.csv
```

-f flag refers to columns, and -d flag refers to the type of delimiter

```
ATOM,1,C,1,0.789,-0.852,0.504,1,0
ATOM,2,C,1,-0.161,-1.104,-0.624,1,0
ATOM,3,C,1,-1.262,-0.44,0.16,1,0
ATOM,4,C,1,-0.289,-0.202,1.284,1,0
ATOM,5,C,1,1.203,0.513,-0.094,1,0
ATOM,6,C,1,0.099,1.184,0.694,1,0
ATOM,7,C,1,-0.885,0.959,-0.46,1,0
ATOM,8,C,1,0.236,0.283,-1.269,1,0
ATOM,9,H,1,1.41,-1.631,0.942,1,0
ATOM,10,H,1,-0.262,-2.112,-1.024,1,0
ATOM,11,H,1,-2.224,-0.925,0.328,1,0
ATOM,12,H,1,-0.468,-0.501,2.315,1,0
ATOM,13,H,1,2.224,0.892,-0.134,1,0
ATOM,14,H,1,0.24,2.112,1.251,1,0
ATOM,15,H,1,-1.565,1.73,-0.831,1,0
ATOM,16,H,1,0.472,0.494,-2.315,1,0
```

9. In a directory, where ls returns:
fructose.dat glucose.dat sucrose.dat maltose.txt
What would be the output of the following loop?
for datafile in *.dat
do
cat $datafile >> sugar.dat
done

(A) All of the text from fructose.dat, glucose.dat and sucrose.dat would be concatenated and saved to a file called sugar.dat

(B) The text from sucrose.dat will be saved to a file called sugar.dat

(C) All of the text from fructose.dat, glucose.dat, sucrose.dat, and maltose.txt would be concatenated and saved to a file called sugar.dat

(D) All of the text from fructose.dat, glucose.dat and sucrose.dat will be printed to the screen and saved into a file called sugar.dat

10.

1. Write a loop that concatenates all of the .csv files in the ~/nelle/molecules/csvs subdirectory into one file called allmolecules.csv

2. Write a loop that concatenates only the third column of the .csv files in the ~/nelle/molecules/csvs subdirectory into one file called allmolecules_elements.csv

3. Write a loop that concatenates only the unique value of the third column of each .csv file in the ~/nelle/molecules/csvs subdirectory into one file called allmolecules_unique_elements.csv (hint use the uniq command)

4. Why might you want to do this with a loop instead of only using cat?

11. In the molecules directory, you have a shell script called script.sh containing the following commands:
head $2 $1
tail $3 $1
While you are in that current directory, you type the following command:
bash script.sh '*.pdb' -1 -1
Which of the following outputs would you expect to see?

(A) All of the lines between the first and the last lines of each file ending in .pdb in the current directory

(B) The first and the last line of each file ending in .pdb in the current directory

(C) The first and the last line of each file in the current directory

(D) An error because of the quotes around *.pdb

12. 1. Write a shell script that extracts the unique values from the 2nd column (antibiotic names) from antibiotics.csv in nelle's directory and saves these to a file called antibiotics_unique.csv

2. Write a shell script that takes any file and extracts the unique values from the 2nd column of a comma delimited file and saves these to a file specified by the user.

3. Write a shell script that takes any file and extracts the unique values from a specified column of a file and saves these to a file specified by the user. This script should also let the user choose the delimiter.

13. The Tao that is seen
Is not the true Tao, until
You bring fresh toner.
With searching comes loss
and the presence of absence:
"My Thesis" not found.
Yesterday it worked

Today it is not working
Software is like that.
From the above text, contained in the file haiku.txt, which command would result in the following output:
and the presence of absence

- (A) grep of haiku.txt
- (B) grep -E of haiku.txt
- (C) grep -w of haiku.txt

14. The -v flag to grep inverts pattern matching, so that only lines which do not match the pattern are printed. Given that, which of the following commands will find all files in /data whose names end in ose.dat (e.g., sucrose.dat or maltose.dat), but do not contain the word temp?

- (A) find /data -name '*.dat' | grep ose | grep -v temp
- (B) find /data -name ose.dat | grep -v temp
- (C) grep -v temp $(find /data -name '*ose.dat')
- (D) None of the above.