Lesson 2: Files and Directories

Challenge 1

Many ways to do the same thing - absolute vs relative paths

Starting from a filesystem location of /Users/amanda/data/, which of the following commands could Amanda use to navigate to her home directory, which is/Users/amanda?

- 1. cd .
- **2**. cd /
- 3. cd /home/amanda
- **4.** cd ../..
- **5.** cd ~
- 6. cd home
- 7. cd ~/data/..
- 8. cd
- 9. cd ..

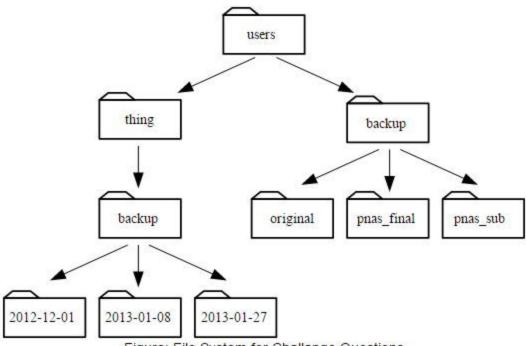


Figure: File System for Challange Questions

Challenge 2

Relative path resolution

Using the filesystem diagram below, if pwd displays /Users/thing, what will 1s ../backup display?

- 1. ../backup: No such file or directory
- **2**. 2012-12-01 2013-01-08 2013-01-27
- **3.** 2012-12-01/ 2013-01-08/ 2013-01-27/

4. original pnas final pnas sub

File System for Challenge Questions

Challenge 3

1s reading comprehension

Assuming a directory structure as in the above Figure (File System for Challenge Questions), if pwd displays /Users/backup, and -r tells 1s to display things in reverse order, what command will display:

pnas sub/ pnas final/ original/

- 1. ls pwd
- 2. ls -r -F
- 3. ls -r -F /Users/backup
- 4. Either #2 or #3 above, but not #1.

Challenge 4

Exploring more 1s arguments

What does the command 1s do when used with the -s and -h arguments?

Answer: -s size ; -h human readable

http://explainshell.com/

Answer: Try `man Is` to get help about `Is`. You read about what `-s` and `-h` do.

Lesson 3: Creating Things

Challenge 1

Renaming files

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?

```
    cp statstics.txt statistics.txt
    mv statstics.txt statistics.txt
    mv statstics.txt .
    cp statstics.txt .
```

Challenge 2

Moving and Copying

What is the output of the closing 1s command in the sequence shown below?

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

1. proteins-saved.dat recombine
2. recombine
3. proteins.dat recombine
4. proteins-saved.dat
```

Challenge 3

Organizing Directories and Files

Jamie is working on a project and she sees that her files aren't very well organized:

```
$ ls -F
analyzed/ fructose.dat raw/ sucrose.dat
```

The fructose.dat and sucrose.dat files contain output from her data analysis. What command(s) covered in this lesson does she need to run so that the commands below will produce the output shown?

```
$ ls -F
analyzed/ raw/
$ ls analyzed
fructose.dat sucrose.dat
```

To get the necessary output she could run 'mv *.dat analyzed'

Move 2 dat files to analyzed folder

Challenge 4

Copy with Multiple Filenames

What does cp do when given several filenames and a directory name, as in:

```
$ mkdir backup
$ cp thesis/citations.txt thesis/quotations.txt backup
```

Answer: `cp` will copy both files in `thesis` to `backup`

What does op do when given three or more filenames, as in:

```
$ ls -F
intro.txt methods.txt survey.txt
$ cp intro.txt methods.txt survey.txt
```

Answer:

`cp` throws an error because it doesn't know where to put the `*.txt` files

Challenge 5

Listing Recursively and By Time

The command <code>ls -R</code> lists the contents of directories recursively, i.e., lists their sub-directories, sub-sub-directories, and so on in alphabetical order at each level. The command <code>ls -t</code> lists things by time of last change, with most recently changed files or directories first. In what order does <code>ls -R</code> <code>-t</code> display things?

Answer: 'Is -R -t' will list directories by time and recursively

Lesson 4: Pipes and filters

Using wildcards

When run in the molecules directory, which is command will produce this output?

ethane.pdb methane.pdb

1. ls *t*ane.pdb
2. ls *t?ne.*

3. ls *t??ne.pdb
4. ls ethane.*

Challenge 2:

What does sort -n do?

If we run sort on this file:

10 2 19 22 6

the output is:

If we run sort -n on the same input, we get this instead:

Explain why -n has this effect.

Answer:

'sort' with out '-n' will assume that what you are sorting are characters.

When sorting characters, "10" comes before "2" because "1" come before "2". In other words, you can think of sort as sorting on the first character and then

on the second character, etc. So "300000" would come before "8" because "3" comes before "8". With the `-n` flag, sort considers 10 a number rather than a character string and sorts the numbers as you'd expect.

Challenge 3:

What does < mean?

What is the difference between:

wc -1 < mydata.dat

and:

wc -1 mydata.dat

Answer: They both take in `mydata.dat` as input, but one command take it as an argument and the other takes it as standard input.

Challenge 4:

What does >> mean?

What is the difference between:

echo hello > testfile01.txt

and:

echo hello >> testfile02.txt

Hint: Try executing each command twice in a row and then examining the output files.

Answer:

'echo hello > testfile01.txt' will always overwrite 'testfile01.txt' while 'echo hello >> testfile02.txt' will create the file if it doesn't exist and append to the file otherwise.

Challenge 5

Piping commands together

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

```
    wc -1 * > sort -n > head -n 3
    wc -1 * | sort -n | head -n 1-3
    wc -1 * | head -n 3 | sort -n
    wc -1 * | sort -n | head -n 3
```

Challenge 6:

Why does uniq only remove adjacent duplicates?

The command uniq removes adjacent duplicated lines from its input. For example, if a file salmon.txt contains:

```
coho
coho
steelhead
coho
steelhead
steelhead
then uniq salmon.txt produces:
coho
steelhead
coho
steelhead
```

Why do you think uniq only removes *adjacent* duplicated lines? (Hint: think about very large data sets.) What other command could you combine with it in a pipe to remove all duplicated lines?

Answer:

Removing adjacent duplicates is completely in-line with the Unix philosophy: build small programs that do things really well and combine them to do bigger things. Combining `uniq` and `sort` will return only the unique fish in the list.

Uniq - Discard all but one of successive identical lines from INPUT (or standard input), writing to OUTPUT (or standard output).

Challenge 7:

Pipe reading comprehension

A file called animals.txt contains the following data:

```
2012-11-05, deer

2012-11-05, rabbit

2012-11-05, raccoon

2012-11-06, rabbit

2012-11-06, deer

2012-11-06, fox

2012-11-07, rabbit

2012-11-07, bear
```

What text passes through each of the pipes and the final redirect in the pipeline below?

```
cat animals.txt | head -n 5 | tail -n 3 | sort -r > final.txt
```

Answer final.txt should contain:

2012-11-06,rabbit 2012-11-06,deer 2012-11-05,raccoon

Challenge 8:

Pipe construction

For the file animals.txt from the previous exercise, the command:

```
$ cut -d , -f 2 animals.txt
```

produces the following output:

deer
rabbit
raccoon
rabbit
deer
fox

rabbit

bear

What other command(s) could be added to this in a pipeline to find out what animals the file contains (without any duplicates in their names)?

Answer: `cut -d , -f 2 animals.txt | sort | uniq`

Lesson 5: Loops

Challenge 1:

Variables in Loops

Suppose that 1s initially displays:

```
fructose.dat glucose.dat sucrose.dat
```

What is the output of:

```
for datafile in *.dat
do
ls *.dat
done
```

Now, what is the output of:

```
for datafile in *.dat
do
ls $datafile
done
```

Why do these two loops give you different outputs?

Answer:

You can try this out using the following commands

```
touch fructose.dat glucose.dat sucrose.dat for datafile in *.dat; do ls *.dat; done
```

it prints

•••

fructose.dat glucose.dat sucrose.dat

```
fructose.dat glucose.dat sucrose.dat fructose.dat glucose.dat sucrose.dat
```

because each time `ls *.dat* displays all the files with a `.dat` extension.

```
for datafile in *.dat; do ls $datafile; done
```

prints

•••

fructose.dat glucose.dat sucrose.dat

•••

because each iteration of the loop prints one item in `*.dat` which expands to the three `.dat` files.

Challenge 2:

Saving to a File in a Loop - Part One

In the same directory, what is the effect of this loop?

```
for sugar in *.dat
do
    echo $sugar
    cat $sugar > xylose.dat
done
```

- 1. Prints fructose.dat, glucose.dat, and sucrose.dat, and the text from sucrose.dat will be saved to a file called xylose.dat.
- 2. Prints fructose.dat, glucose.dat, and sucrose.dat, and the text from all three files would be concatenated and saved to a file called xylose.dat.

- 3. Prints fructose.dat, glucose.dat, sucrose.dat, and xylose.dat, and the text from sucrose.dat will be saved to a file called xylose.dat.
- 4. None of the above.

Challenge 3:

Saving to a File in a Loop - Part Two

In another directory, where 1s 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
```

- All of the text from fructose.dat, glucose.dat and sucrose.dat would be concatenated and saved to a file called sugar.dat.
- 2. The text from sucrose.dat will be saved to a file called sugar.dat.
- 3. All of the text from fructose.dat, glucose.dat, sucrose.dat andmaltose.txt would be concatenated and saved to a file called sugar.dat.
- 4. All of the text from fructose.dat, glucose.dat and sucrose.dat would be printed to the screen and saved to a file called sugar.dat

Challenge 4:

Doing a Dry Run

Suppose we want to preview the commands the following loop will execute without actually running those commands:

```
for file in *.dat
do
    analyze $file > analyzed-$file
done
```

What is the difference between the two loops below, and which one would we want to run?

```
# Version 1
for file in *.dat
do
    echo analyze $file > analyzed-$file
done
# Version 2
for file in *.dat
do
    echo "analyze $file > analyzed-$file"
done
```

Answer:

Version 1 would echo analyze \$file and save the result to the file analyzed-\$file. We would not see anything on the screen

Version 2 is the one we want and it would print the expanded string "analyze \$file > analyzed-\$file" to the console for each iteration of the for loop.

Challenge 5:

Nested Loops

Suppose we want to set up up a directory structure to organize some experiments measuring the growth rate under different sugar types *and* different temperatures. What would be the result of the following code:

```
for sugar in fructose glucose sucrose

do

for temperature in 25 30 37 40

do

mkdir $sugar-$temperature

done

Done
```

Answer:

First, a sugar is extracts from [fructose, glucose, sugar]. For this sugar four directories are made that have the pattern \$sugar-\$temperature where \$temperature is on of the 4 temps given. This is repeated for each sugar so that 12 new directories are made.

Lesson 6: Shells Scripts

Challenge 1:

Variables in shell scripts

In the molecules directory, imagine you have a shell script called script.sh containing the following commands:

```
head -n $2 $1
tail -n $3 $1
```

While you are in the molecules directory, you type the following command:

```
bash script.sh '*.pdb' 1 1
```

Which of the following outputs would you expect to see?

- 1. All of the lines between the first and the last lines of each file ending in .pdb in themolecules directory
- 2. The first and the last line of each file ending in .pdb in the molecules directory
- 3. The first and the last line of each file in the molecules directory
- 4. An error because of the quotes around *.pdb

Challenge 2:

List unique species

Leah has several hundred data files, each of which is formatted like this:

```
2013-11-05, deer, 5

2013-11-05, rabbit, 22

2013-11-05, raccoon, 7

2013-11-06, rabbit, 19

2013-11-06, deer, 2

2013-11-06, fox, 1
```

```
2013-11-07, rabbit, 18
2013-11-07, bear, 1
```

Write a shell script called species.sh that takes any number of filenames as command-line parameters, and uses cut, sort, and uniq to print a list of the unique species appearing in each of those files separately.

Challenge 3:

Find the longest file with a given extension

Write a shell script called longest.sh that takes the name of a directory and a filename extension as its parameters, and prints out the name of the file with the most lines in that directory with that extension. For example:

```
$ bash longest.sh /tmp/data pdb
```

would print the name of the .pdb file in /tmp/data that has the most lines.

Challenge 4:

Why record commands in the history before running them?

If you run the command:

```
history | tail -n 5 > recent.sh
```

the last command in the file is the history command itself, i.e., the shell has addedhistory to the command log before actually running it. In fact, the shell *always* adds commands to the log before running them. Why do you think it does this?

Challenge 5:

Script reading comprehension

Joel's data directory contains three files: fructose.dat, glucose.dat, and sucrose.dat. Explain what a script called example.sh would do when run as bash example.sh *.dat if it contained the following lines:

```
# Script 1
echo *.*

# Script 2
for filename in $1 $2 $3
do
```

```
cat $filename
done
# Script 3
echo $0.dat
```

Lesson 7: Finding Things

Challenge 1

Using grep

```
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:

```
    grep "of" haiku.txt
    grep -E "of" haiku.txt
    grep -w "of" haiku.txt
    grep -i "of" haiku.txt
```

Challenge 2

find pipeline reading comprehension

Write a short explanatory comment for the following shell script:

```
wc -l $(find . -name '*.dat') | sort -n
```

Challenge 3

Matching ose.dat but not temp

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 /datawhose names end in ose.dat (e.g., sucrose.dat or maltose.dat), but do *not* contain the word temp?

- 1. find /data -name '*.dat' | grep ose | grep -v temp
- 2. find /data -name ose.dat | grep -v temp
- 3. grep -v "temp" \$(find /data -name '*ose.dat')
- 4. None of the above.

Challenge 4

Little Women

You and your friend, having just finished reading *Little Women* by Louisa May Alcott, are in an argument. Of the four sisters in the book, Jo, Meg, Beth, and Amy, your friend thinks that Jo was the most mentioned. You, however, are certain it was Amy. Luckily, you have a file LittleWomen.txt containing the full text of the novel. Using a for loop, how would you tabulate the number of times each of the four sisters is mentioned? Hint: one solution might employ the commands grep and wc and a 1, while another might utilize grep options.