

EEB 177 Lecture 4

Topics

- ▶ Advanced shell commands
- ▶ Permissions

Office Hours

Tues 2-3 Thurs 1-2

Terasaki 2149

Preliminaries

- ▶ Start **nano**: `$ nano` and save the file “classwork-Tuesday-1-21.txt” to your class-assignments directory
- ▶ push this to your remote repository
- ▶ you can write answers to today’s exercises in this file.

working with csv files in the shell

We can use several commands you have learned already plus the `cut` command to easily manipulate csv files.

First, take a look at `Pacifici2013_data.csv` using your text editor. Then move to the containing directory and use a unix command to view the first line (only) of that file.

What is the delimiter in this file?

```
head -n 1 Pacifici2013_data.csv
```

We can use `cut` to extract specific fields by specifying the delimiter with `-d` and the desired columns with `-f` argument.

```
head -n 1 Pacifici2013_data.csv | cut -d ';' -f 1-4
```

If we wanted to list rows of data without the header, we can pipe the results of cut to tail (remember tail -n +2 will show the contents of a file or stream starting from the second line).

```
cut -d ";" -f 2 Pacifici2013_data.csv | head -n 5 |  
tail -n +2
```

Challenge

Show the Order of the first 5 species in the data set. Append this to your class-exercises files for today.

(hint: you will need `cut`, `|`, `tail`, and `head`)

Challenge

use what you know plus the `uniq` command to count the number of unique families in this file. **hint:** you will need to sort your data before you apply `uniq`. Append the line “There are X unique families:” (fill in the value for x) to your exercise file. Then append the list of unique families to your exercise file.

Reformatting a csv file

We will now work through example 1.6.2 to create a data file with the following fields: Order, Family, Genus, Scientific_Name and AdultBodyMass_g with the following properties

- ▶ no headers
- ▶ data are sorted by size from large to small
- ▶ delimiter is a space

We will need to introduce the `tr` command to translate characters.

sorting and outputting the file

sort in reverse order of body mass

```
tail -n +2 ../data/Pacifici2013_data.csv | cut -d ";"  
-f 2-6 | tr -s ";" " " | sort -r -n -k 6
```

create the file BodyM.csv

```
tail -n +2 ../data/Pacifici2013_data.csv | cut -d ";"  
-f 2-6 | tr -s ";" " " | sort -r -n -k 6 > BodyM.csv
```

grep review

. Grep is a powerful pattern matching command that can be combined with the regular expressions you used in lab.

Useful grep options: - `-c` to count lines - `-w` to match words - `-i` to make case insensitive - `-n` to show line number of match.

use wc to the number of species in BodyM.csv

use `grep` to find all of the wombats (Vombatidae) in this list

```
grep Vombatidae BodyM.csv
```

how could you count these lines?

how could you count these lines? `grep -c Vombatidae`
`BodyM.csv`

use grep to find all of the genus Bos in this list.

try searching for Bos. What is going on?

use the -w command to find whole words

```
grep -w Bos BodyM.csv
```

-i makes the search case insensitive

```
grep -i Bos BodyM.csv
```

Other grep options

-B X finds x lines before -A X finds X lines after
find the 3 lines before all occurrences of Bos.

Other grep options

`-n` shows the line number of the match.

```
grep -n "Gorilla gorilla" BodyM.csv
```

finding all lines that do not match

-v returns everything that does not match the grep pattern

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-v returns everything that does not match the grep pattern

How many lines do not match gorilla?

```
grep Gorilla BodyM.csv | grep -v gorilla
```

finding files with `find`

`find` allows you to search for **files** with specified attributes.

use the wildcard `.*` to find everything in your sandbox directory.

```
find .
```

```
.
```

```
./temp.txt
```

```
./cep-taxa.txt
```

```
./gitignore
```

```
./junk
```

```
...
```


if you pass find a path it will give all files and folders in that directory

```
find ../data/
```

```
../data
```

```
../data/toremove.txt
```

```
../data/Gesquiere2011_data.csv
```

```
../data/Saavedra2013_about.txt
```

```
...
```

if you pass find a path it will give all files and folders in that directory

```
find ../data/
```

```
../data
```

```
../data/toremove.txt
```

```
../data/Gesquiere2011_data.csv
```

```
../data/Saavedra2013_about.txt
```

```
...
```

count all of the files and folders within ../data/

find options

You can search for a specific file with `-name`

```
find ../data/ -name "n30.txt"
```

This can be helpful when you don't know exactly where you left a file.

```
find /home/eeb-177-student/Desktop/ -name  
"classwork-Tues-1-17.txt"
```

```
/home/eeb-177-student/Desktop/eeb-177/class-assignments/cla
```

find gets even more powerful with wildcards.

for example, to find all of the files with about in the data directory....

```
find /home/eeb-177-student/Desktop/eeb-177/CSB/unix/  
-iname "*about*"
```

```
/home/eeb-177-student/Desktop/eeb-177/CSB/unix/data/Saavedr  
/home/eeb-177-student/Desktop/eeb-177/CSB/unix/data/Marra20  
/home/eeb-177-student/Desktop/eeb-177/CSB/unix/data/Pacific
```

note that -iname ignores the case in the file names

find the path to all of your classwork files and append these to your classwork file for today.

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```
find /home/eeb-177-student/Desktop/ -iname "*class*"
```

```
>>
```

```
/home/eeb-177-student/Desktop/eeb-177/class-assignments/classwork
```

specifying the depth of the search

to restrict the depth in the folder hierarchy of the search, use the `-maxdepth N` option.

What will this line do?

```
$ find ../data -maxdepth 1 -name "*.txt" | wc -l
```

How many text files are there in `../data` if you do not restrict the depth?

You can exclude certain files with not

```
find ../data/ -not -name "*about*" | wc -l
```


Permissions

In Unix, each file and directory has an attribute that determines who can read (r), write (w), execute (x), or do nothing (-) to a file. There are three categories of file users

- ▶ owner
- ▶ group (set of users)
- ▶ everyone else

you can see permissions with `ls -l`

permissions structure

chmod and chown

These commands change permissions and ownership (u, g, or o for user, group or other).

```
touch permissions.txt ls -l
```

```
-rw-rw-r-- 1 eeb-177-student eeb-177-student 0 Jan 24 07:51
```

```
chmod u=rwx permissions.txt
```

```
ls -l
```

```
-rwxrw-r-- 1 eeb-177-student eeb-177-student      0 Jan 24 0
```

notice that the user may now execute this file.

you can also add and remove permissions for a user with + and -.

```
chmod g+w,u+x permissions.txt
```

```
ls -l permissions.txt
```

```
-rwxrw-rw-
```

Add write permissions for all users.

Remove read, write, and execute permission from others

Writing a shell script

Lets illustrate some ideas about paths, scripts, and permissions by writing a simple shell script. You are going to write a program in your text editor that will execute a series of shell commands that you have already learned.

open up gedit and type the following lines:

open gedit in your class-assignments folder and save the following file as dir.sh:

```
#!/bin/bash
ls -la
echo "Above are the directory listings for this folder"
pwd
echo "right now it is :
date
```

save this file as **dir.sh**

Paths

there are two standard locations for programs– `/usr/bin` and `/bin`
use `ls` to see what is in them

The shell searches these directories (and others that have been added to the path) whenever you type a command.

Type `echo $PATH` to see your current path.

which will tell you the directory to a command. Try `which cat`

Creating a scripts directory and adding it to the path

we want a single working copy of each program on our machines so we need to make sure the shell searches for our programs...

- ▶ go to your home directory
- ▶ create a directory called `scripts`
- ▶ to add the `scripts` directory to the path, open the `.profile` file in `gedit`
- ▶ add this line (exactly) `export PATH="$PATH:$HOME/scripts"`



exit and save

Now we have created a program we would like to run and created a path to the `scripts` directory. What else do we need to do?

hint: where is `dir.sh` right now?

the shebang (#!)

#! is called the shebang—it means that all following contents of script will be sent to the program following the shebang

#! /bin/bash sends it all to bash

remember, new scripts are not executable w/o changing permissions

checking permissions

- ▶ `cd ~/scripts`
- ▶ check permission with `ls -l`
- ▶ add permission to execute with `chmod u+x`

try running your program from different directories. Does it work?
Why?

exercise

Add your scripts directory to your remote repository. You will need to

- ▶ `git init` in your scripts directory
- ▶ add your script
- ▶ commit your script
- ▶ create a remote repo on github
- ▶ copy and paste the command lines from the remote repo after you create it.

```
git remote add origin
https://github.com/michaelalfaro/eeb-177-scripts.git
git remote add origin
https://github.com/michaelalfaro/eeb-177-scripts.git
git push -u origin master
```

you will be using your scripts directory throughout the quarter, so make sure this repo is working

