**Objectives**

Questions

* How can I save and re-use commands?

Objectives

* Write a shell script that runs a command or series of commands for a fixed set of files.
* Run a shell script from the command line.
* Write a shell script that operates on a set of files defined by the user on the command line.
* Create pipelines that include shell scripts you, and others, have written.

Video notes

1. change directory to **molecules** folder, type:

pwd

cd Desktop/data-shell/molecules

ls

2. create a new shell script, type:

nano middle.sh

(this takes me to shell script editors)

3. Edit shell script that works only for **octaine.pdb** file, type:

head -n 15 octane.pdb | tail -n 5

press ctrl & O, it asks “File Name to Write: middle.sh”, hit enter

then press ctrl & X to exit.

(it takes you back to terminal.)

ls

(the list shows “nano middle.sh” file)

4. Execute the **middle.sh** command, type:

bash middle.sh

5. Edit shell script that could work for any file, type:

nano middle.sh

head -n 15 “$1” | tail -n 5

(“1” means the first file name or other argument on command line)

bash middle.sh octaine.pdb

or type:

bash middle.sh pentane.pdb

6. Edit shell script by making head/tail more flexible, type:

nano middle.sh

head -n “$2” “$1” | tail -n “$3”

bash middle.sh pentane.pdb 15 5

7. add comments to the shell script (to help understand scripts), type:

# Select lines from the middle of the file.

# Usage: bash middle.sh filename end\_line num\_line

nano middle.sh

8. sort the files by word count

(1) Create a new nano file:

nano sorted.sh

(2) edit the shell script:

# sort files by their length

# Usage: bash sorted.sh one\_or\_more\_filenames

wc -l “$@” | sort -n

(3) use the script:

bash sorted.sh \*.pdb ../creatures/\*.dat

(sorted all .pdb files in **molecules** folder and all .dta files in **creatures** folder)

9. Find most recent 5 lines of history code, put in a shell script

history | tail -n 5 > redo-figure-3.sh

nano redo-figure-3.sh

(takes you to nano editor, and show the most recent 5 lines of code)

10. change directory, type:

pwd

cd ..

pwd

ls

cd north press tab 2012 press tab (now in north-pacific-gyre/2012-07-03/)

11. Calculate stats for data files

(1) create shell script, type:

nano do-stats.sh

(2) edit shell script, type:

# Calculate stats for data files.

for datafile in “$@”

do

echo $datafile

bash goostats $datafile stats-$datafile

done

(3) Do the analysis

bash do-stats.sh NENE\*[AB].txt

Quizzes

**Question 1**

Graphical user interface, text, application, email

Description automatically generated

My answer:

# Produce Unique Filenames

# Usage: bash species.sh Filename

cut -d , -f 2 "$@" | sort | uniq

**Question 2**

**Graphical user interface, text, application, email

Description automatically generated**

My answer:

Script 1 asks to show any files that contain the**.** symbol. The command bash script1.sh \*.pdb gives the same results: it just gives all the files that contain **.** symbol. That gives all the files in the **data-shell/molecules** directory.

Script 2 asks to print out variables 1, 2, 3. The command bash script2.sh \*.pdb prints out the three variables contents **cubane.pdb**, **ethane.pdb**, and **methane.pdb**.

Script 3 asks to print out any file names that end in .pdb. The command bash script3.sh \*.pdb gives all variables that end in .pdb, that is: **cubane.pdb ethane.pdb methane.pdb octane.pdb pentane.pdb propane.pdb.pdb.**