Shell

### Introduction

Learning Goals

Explain how the shell relates to the keyboard, the screen, the operating system, and users' programs.

Shell

Explain when and why command-line interfaces should be used instead of graphical interfaces.

### Files and Directories

- Explain the similarities and differences between a file and a directory.
- Iranslate an absolute path into a relative path and vice versa.
- Onstruct absolute and relative paths that identify specific files and directories.
- Second steps in the shell's read-run-print cycle.
- Identify actual command, flags, and filenames in command-line call.
- **()** Demonstrate the use of tab completion, and explain its advantages.
- whoami
- ø pwd
- /
- ls
- Is -F
- Is -F data
- Is -F /data

- cd data
- cd ..
- Is -F -a
- Is

north-pacific-gyre/2012-07-03

Is no tab

### Creating Things

- Create a directory hierarchy that matches a given diagram.
- Oreate files in that hierarchy using an editor or by copying and renaming existing files.
- Solution Display the contents of a directory using the command line.
- Oelete specified files and/or directories.
- mkdir thesis
- cd thesis
- nano draft.txt
- rm draft.txt
- rm thesis
- rmdir thesis

- rm -r thesis
- mv thesis/draft.txt thesis/quotes.txt
- mv thesis/quotes.txt .
- cp quotes.txt thesis/quotations.txt

Create a workspace on your desktop so that it's easy to find, and easy to explore with your GUI filesystem tool (Explorer, Finder, Nautilus, ...)

\$ cd

- \$ cd Desktop
- \$ mkdir swc
- \$ cd swc

A bug in recent versions of nano on Windows causes the Git Bash terminal windows to be blanked when nano exits – annoying.

A work-around for the issue is to open another Git Bash window and run nano there. Of course you will have to cd in both windows as you move around the file system.

An alternative is to download and install the Notepad++ editor and ask one of the helpers or instructors to help you add Notepad++ to your PATH – the list of directories that the shell looks in to find the programs you ask it to run.

### Creating Things

- Create a directory hierarchy that matches a given diagram.
- Oreate files in that hierarchy using an editor or by copying and renaming existing files.
- Solution Display the contents of a directory using the command line.
- Oelete specified files and/or directories.
- mkdir thesis
- cd thesis
- nano draft.txt
- rm draft.txt
- rm thesis
- rmdir thesis

- rm -r thesis
- mv thesis/draft.txt thesis/quotes.txt
- mv thesis/quotes.txt .
- cp quotes.txt thesis/quotations.txt

What command(s) could you run so that the commands below will produce the output shown? (and do it)

Shell

\$ ls
analyzed raw
\$ ls analyzed
fructose.dat glucose.dat sucrose.dat

### Pipes and Filters

- Redirect a command's output to a file.
- Process a file instead of keyboard input using redirection.
- Sonstruct command pipelines with two or more stages.
- Explain what usually happens if a program or pipeline isn't given any input to process.
- Sexplain Unix's "small pieces, loosely joined" philosophy.
  - cd molecules
  - wc \*.pdb
  - \*, ?
  - wc -l
  - wc –help
  - wc -l \*.pdb > lengths
  - cat lengths
  - sort lengths

- sort lengths > sorted-lengths
- head -1 sorted-lengths
- sort lengths | head -1
- cd north-pacific-gyre/2012-07-03
- wc -l \*.txt
- wc -l \*.txt | sort | head -5
- Is \*Z.txt

We're going to start working with Nelle Nemo's Great Pacific Garbage Patch files, so everybody needs a copy of her directories and files so that you can pretend that you are Nelle.

Use Mercurial to grab the files from Bitbucket and put them in a nnemo directory in your SWC workspace:

```
$ cd
$ cd Desktop/swc
$ hg clone https://bitbucket.org/douglatornell/swc-nelle-files nnemo
```

You can copy and paste the hg clone command from the Etherpad. We'll learn what it means in the Version Control with Mercurial section later today.

### Pipes and Filters

- Redirect a command's output to a file.
- Process a file instead of keyboard input using redirection.
- Sonstruct command pipelines with two or more stages.
- Explain what usually happens if a program or pipeline isn't given any input to process.
- Sexplain Unix's "small pieces, loosely joined" philosophy.
  - cd molecules
  - wc \*.pdb
  - \*, ?
  - wc -l
  - wc –help
  - wc -l \*.pdb > lengths
  - cat lengths
  - sort lengths

- $\bullet~{\rm sort~lengths}>{\rm sorted-lengths}$
- head -1 sorted-lengths
- sort lengths | head -1
- cd north-pacific-gyre/2012-07-03
- wc -l \*.txt
- wc -l \*.txt | sort | head -5
- Is \*Z.txt

### Loops - Part 1

- Write a loop that applies one or more commands separately to each file in a set of files.
- Trace the values taken on by a loop variable during execution of the loop.
- Explain the difference between a variable's name and its value.
- Explain why spaces and some punctuation characters shouldn't be used in files' names.
  - for ... do ... done
  - varname, \$varname

echo

• "\$varname"

### Loops - Part 2

- Demonstrate how to see what commands have recently been executed.
- 2 Re-run recently executed commands without retyping them.
  - Is \*[AB].txt
  - Up-Arrow
  - history

- Ctrl-A, Ctrl-E
- Ctrl-R
- Otrl-C

### Exercise

In your analyzed directory, what is the effect of this loop?

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

- Prints fructose.dat, glucose, and sucrose, and copies sucrose to create xylose.
- Prints fructose, glucose, and sucrose, and concatenates all three files to create xylose.
- Prints fructose, glucose, sucrose, and xylose, and copies sucrose to create xylose.
- One of the above.

### Shell Scripts

- Write a shell script that runs a command or series of commands for a fixed set of files.
- Q 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.
- Oreate pipelines that include user-written shell scripts.
- bash myscript.sh
- \$1, \$2, ... \$n, \$\*

- # comment
- history | tail -4 > script.sh



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 number of lines, directory, and name of the file with the most lines in that directory with that extension. For example:

Shell

\$ bash longest.sh more-molecules pdb

would print the number of lines, directory, and name of the .pdb file in more-molecules that has the most lines.

## **Finding Things**

Use grep to select lines from text files that match simple patterns.

Shell

- ② Use find to find files whose names match simple patterns.
- Use the output of one command as the command-line parameters to another command.
- Explain what is meant by "text" and "binary" files, and why many common tools don't handle the latter well.