

Intro to Unix and the Command Line, Part 1

Background, file hierarchy, file management programs

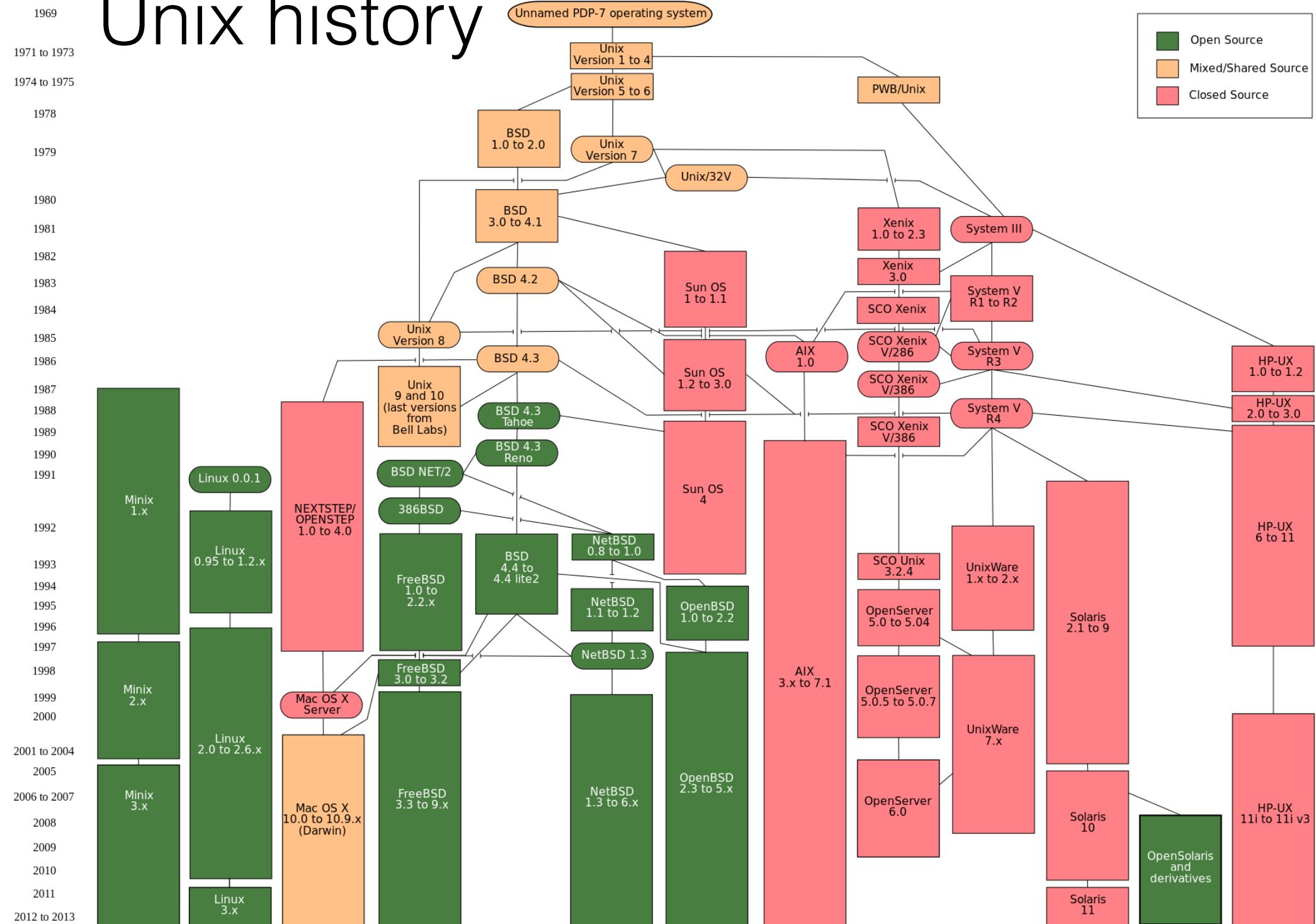
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UNIX

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Unix history



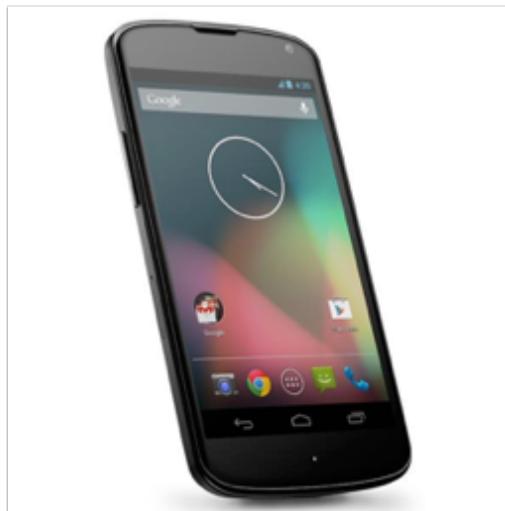
What computers can run Unix?



Apple OS X Macs



Wireless internet routers

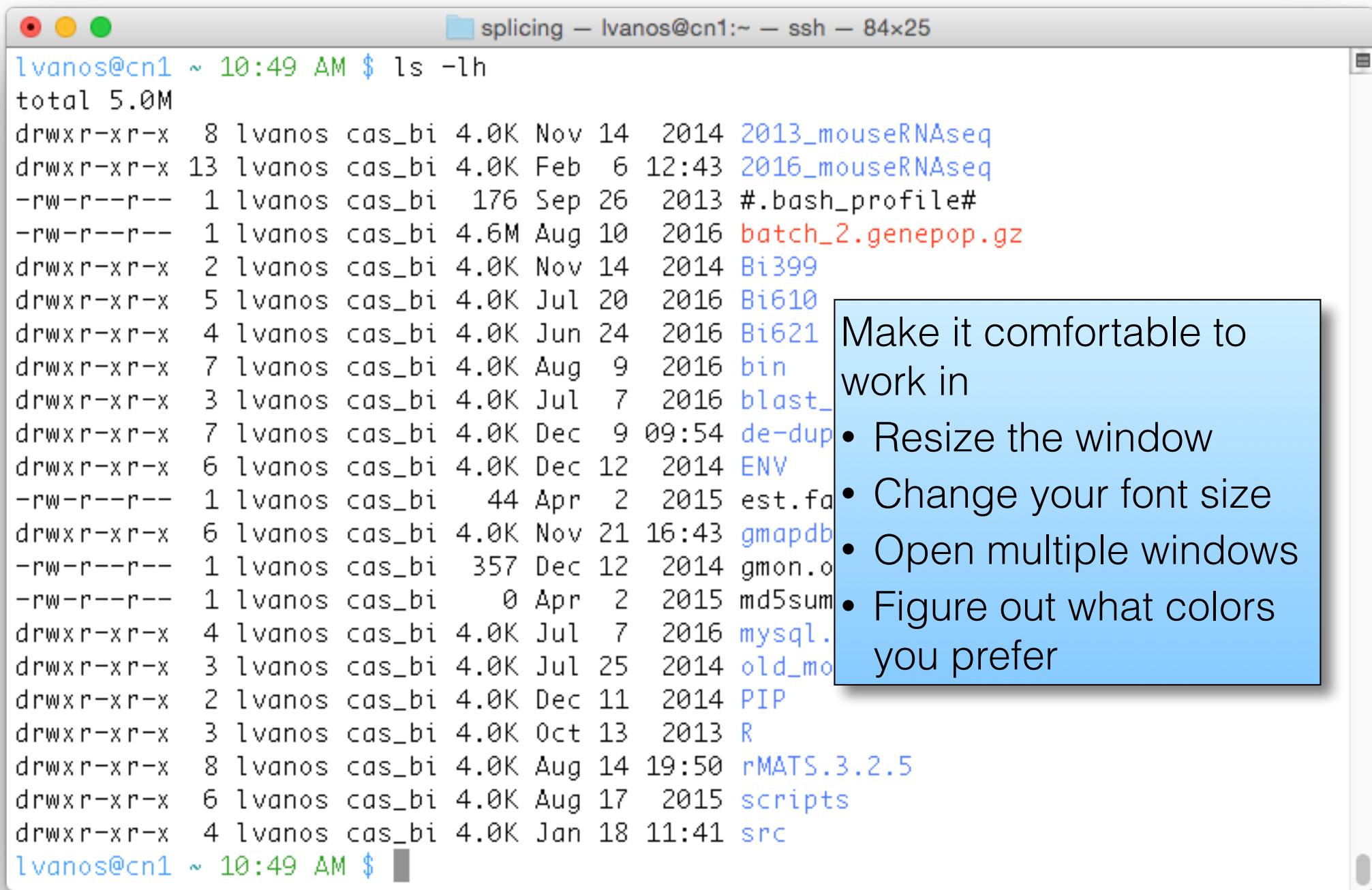


Google's Android phones



Airplane
entertainment
systems

The terminal window



A screenshot of a terminal window titled "splicing" with the command "ls -lh" running. The output shows a list of files and directories in the current directory. A blue callout box on the right side of the terminal window contains the text "Make it comfortable to work in" and a bulleted list of tips.

```
lvanos@cn1 ~ 10:49 AM $ ls -lh
total 5.0M
drwxr-xr-x 8 lvanos cas.bi 4.0K Nov 14 2014 2013_mouseRNAseq
drwxr-xr-x 13 lvanos cas.bi 4.0K Feb  6 12:43 2016_mouseRNAseq
-rw-r--r--  1 lvanos cas.bi 176 Sep 26 2013 #.bash_profile#
-rw-r--r--  1 lvanos cas.bi 4.6M Aug 10 2016 batch_2.genepop.gz
drwxr-xr-x  2 lvanos cas.bi 4.0K Nov 14 2014 Bi399
drwxr-xr-x  5 lvanos cas.bi 4.0K Jul 20 2016 Bi610
drwxr-xr-x  4 lvanos cas.bi 4.0K Jun 24 2016 Bi621
drwxr-xr-x  7 lvanos cas.bi 4.0K Aug  9 2016 bin
drwxr-xr-x  3 lvanos cas.bi 4.0K Jul  7 2016 blast_
drwxr-xr-x  7 lvanos cas.bi 4.0K Dec  9 09:54 de-dup
drwxr-xr-x  6 lvanos cas.bi 4.0K Dec 12 2014 ENV
-rw-r--r--  1 lvanos cas.bi  44 Apr  2 2015 est.fa
drwxr-xr-x  6 lvanos cas.bi 4.0K Nov 21 16:43 gmapdb
-rw-r--r--  1 lvanos cas.bi 357 Dec 12 2014 gmon.o
-rw-r--r--  1 lvanos cas.bi    0 Apr  2 2015 md5sum
drwxr-xr-x  4 lvanos cas.bi 4.0K Jul  7 2016 mysql.
drwxr-xr-x  3 lvanos cas.bi 4.0K Jul 25 2014 old_mo
drwxr-xr-x  2 lvanos cas.bi 4.0K Dec 11 2014 PIP
drwxr-xr-x  3 lvanos cas.bi 4.0K Oct 13 2013 R
drwxr-xr-x  8 lvanos cas.bi 4.0K Aug 14 19:50 rMAT5.3.2.5
drwxr-xr-x  6 lvanos cas.bi 4.0K Aug 17 2015 scripts
drwxr-xr-x  4 lvanos cas.bi 4.0K Jan 18 11:41 src
lvanos@cn1 ~ 10:49 AM $
```

Make it comfortable to work in

- Resize the window
- Change your font size
- Open multiple windows
- Figure out what colors you prefer

Obtain a cheat sheet

Break out your Google-fu and find you one like

Basic UNIX commands

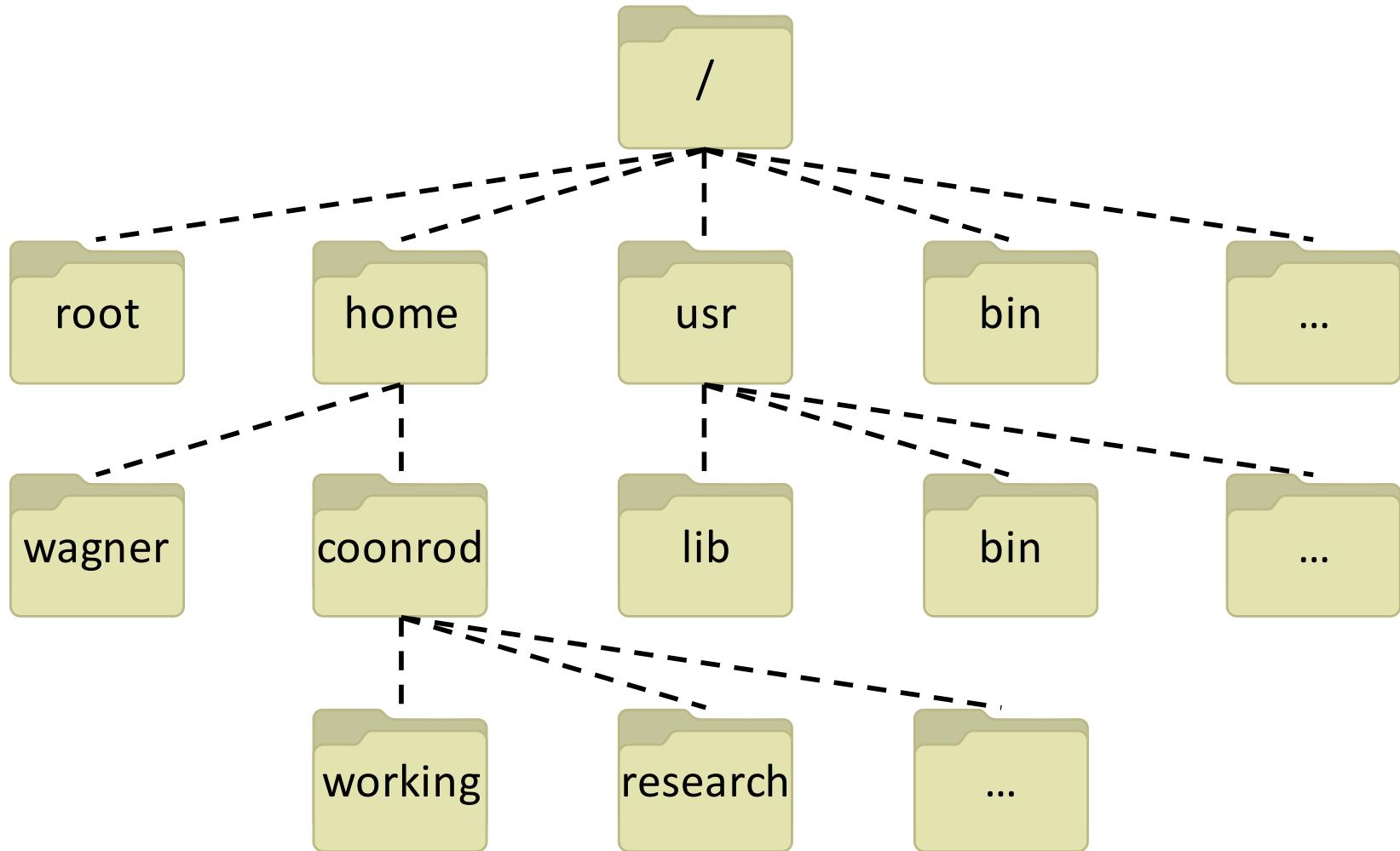
Note: not all of these are actually part of UNIX itself, and you may not find them on all UNIX machines. But they can all be used on **turing** in essentially the same way, by typing the command and hitting return. Note that some of these commands are different on non-Solaris machines - see [SunOS differences](#).

If you've made a typo, the easiest thing to do is hit **CTRL-u** to cancel the whole line. But you can also edit the command line (see the guide to [More UNIX](#)). UNIX is case-sensitive.

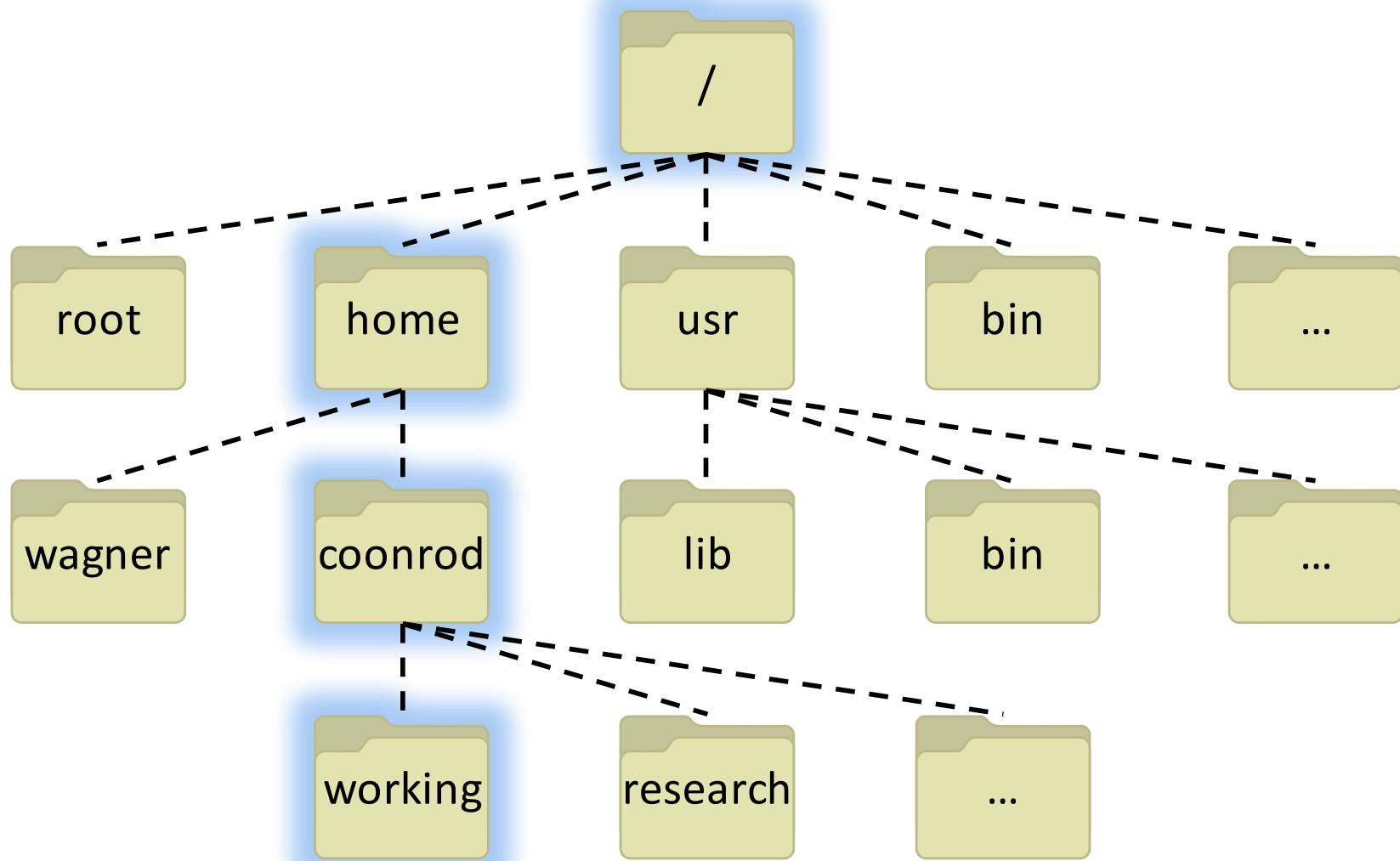
Files

- **ls** --- lists your files
ls -l --- lists your files in 'long format', which contains lots of useful information, e.g. the exact size of the file, who owns the file and who has the right to look at it, and when it was last modified.
ls -a --- lists all files, including the ones whose filenames begin in a dot, which you do not always want to see.
There are many more options, for example to list files by size, by date, recursively etc.
- **more filename** --- shows the first part of a file, just as much as will fit on one screen. Just hit the space bar to see more or **q** to quit. You can use **/pattern** to search for a pattern.
- **emacs filename** --- is an editor that lets you create and edit a file. See the [emacs page](#).
- **mv filename1 filename2** --- moves a file (i.e. gives it a different name, or moves it into a different directory (see below))
- **cp filename1 filename2** --- copies a file
- **rm filename** --- removes a file. It is wise to use the option **rm -i**, which will ask you for confirmation before actually deleting anything. You can make this your default by making an [alias](#) in your .cshrc file.

In Unix, everything is a file organized in a hierarchy



Every file can be identified by a unique *path*



/home/coonrod/working

Interlude: navigating the file system

```
$ #all commands will be preceded by a "$"  
#any comments will be preceded by a "#"  
  
#How to navigate the file system  
$ pwd          #present working directory  
/Users/leslievanos  
  
$ ls           #list the contents of your current directory  
batch\_1.loc      genos          sample\_01.fq  
batch\_2.fst\_2-3.tsv  lengths.txt    stacks/  
contigs.fa        python/         test.txt  
example.sh\*       s_1_sequence.txt  trimmed\_reads.fq  
  
$ cd python/    #change directory to python/  
$ ls  
helloworld.py\*
```

Structure of a command

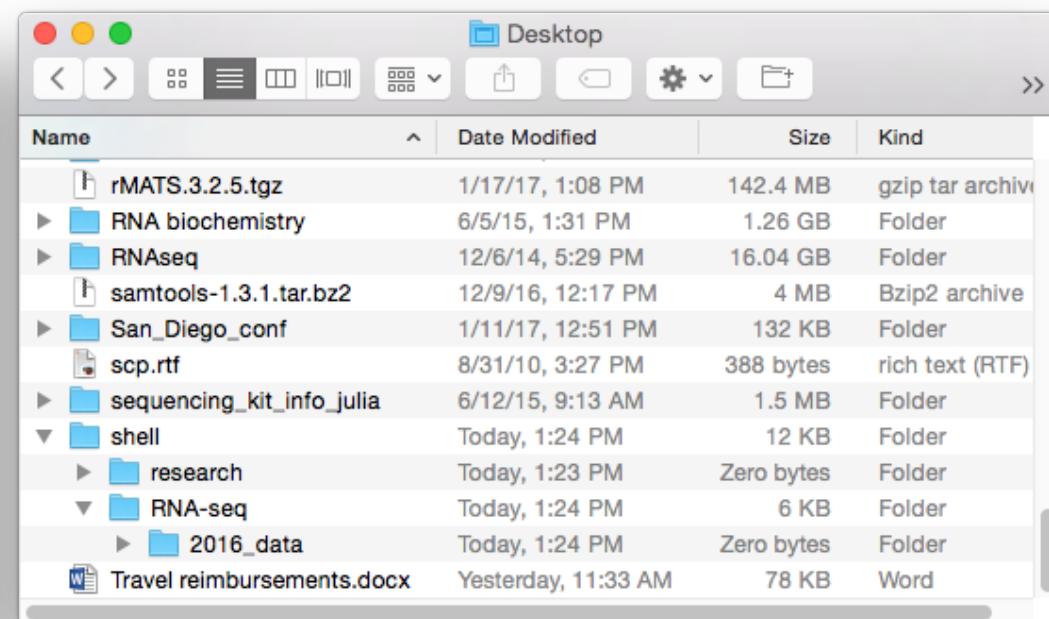
```
$ command -options arguments
```

Paths, continued

This shell view of the nested directories
Users, leslievanos, Desktop, shell, RNA-seq, and 2016_data...

```
RNA-seq - ivanos@cn1:/research/bi610 - bash - 71x20
[01:22:47:~] $ cd Desktop/
[01:22:56:Desktop] $ mkdir shell
[01:23:05:Desktop] $ cd shell/
[01:23:09:shell] $ mkdir research
[01:23:14:shell] $ ls
research/
[01:23:14:shell] $ mkdir RNA-seq
[01:23:21:shell] $ ls
RNA-seq/ research/
[01:23:25:shell] $ cd RNA-seq/
[01:23:40:RNA-seq] $ mkdir 2016_data
[01:24:00:RNA-seq] $ ls -lah
total 0
drwxr-xr-x+ 3 leslievanos staff 102B Feb 10 13:24 .
drwxr-xr-x+ 4 leslievanos staff 136B Feb 10 13:23 ../
drwxr-xr-x+ 2 leslievanos staff 68B Feb 10 13:24 2016_data/
[01:24:03:RNA-seq] $ pwd
/Users/leslievanos/Desktop/shell/RNA-seq
[01:24:04:RNA-seq] $
```

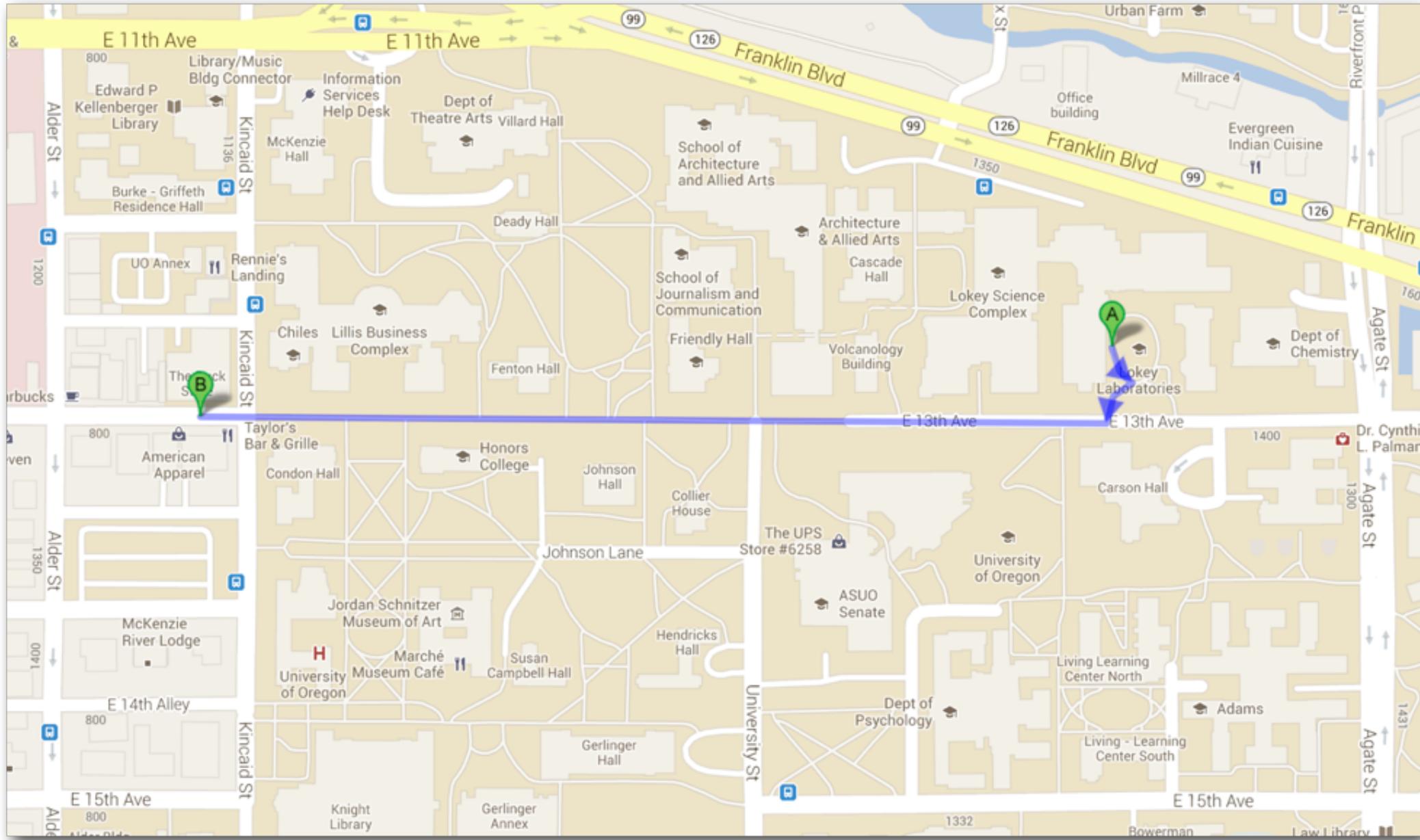
...is equivalent to this GUI view of the same directories



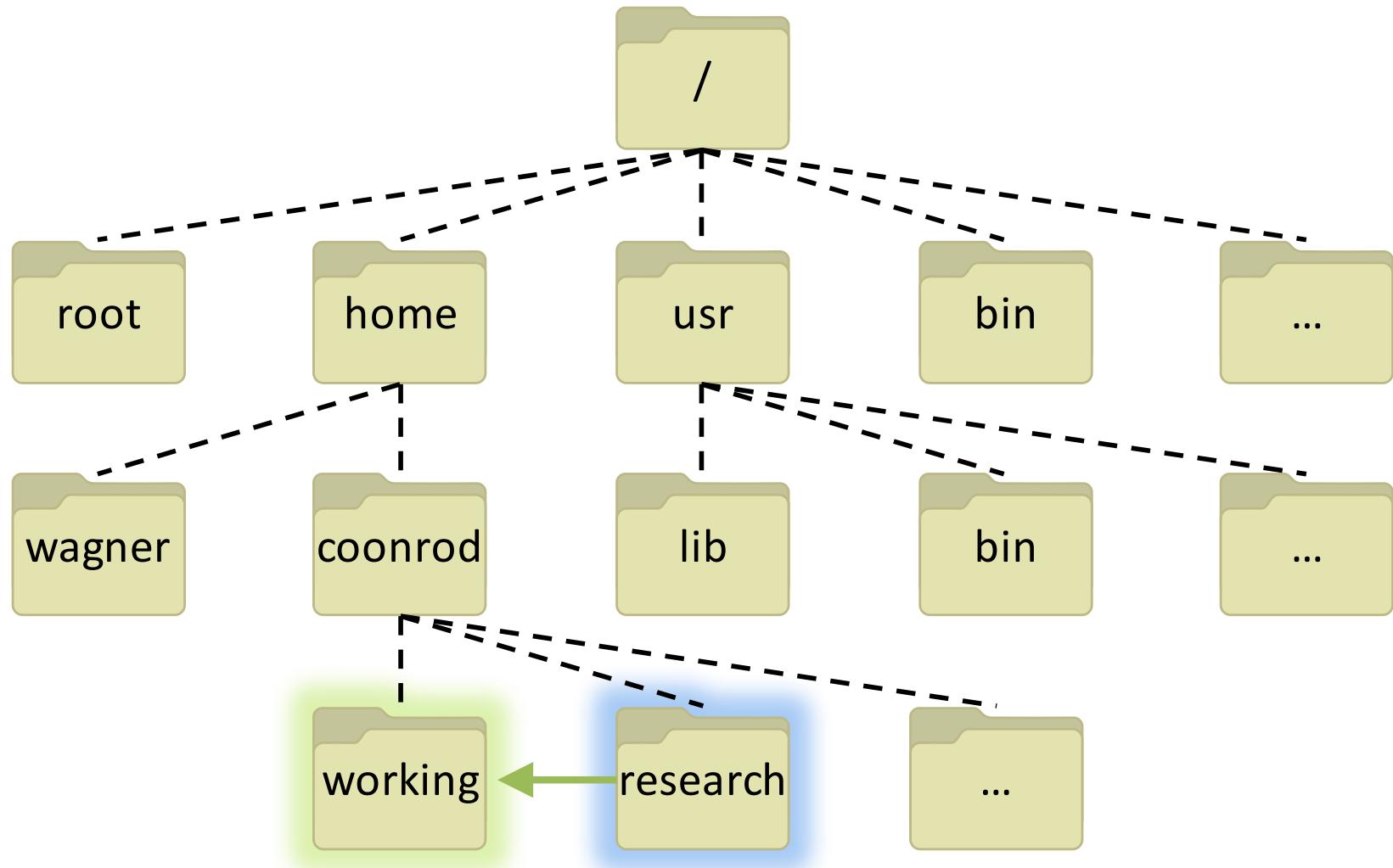
...and the RNA-seq directory is uniquely identified by its path:
/Users/leslievanos/Desktop/shell/RNA-seq

Absolute and relative paths

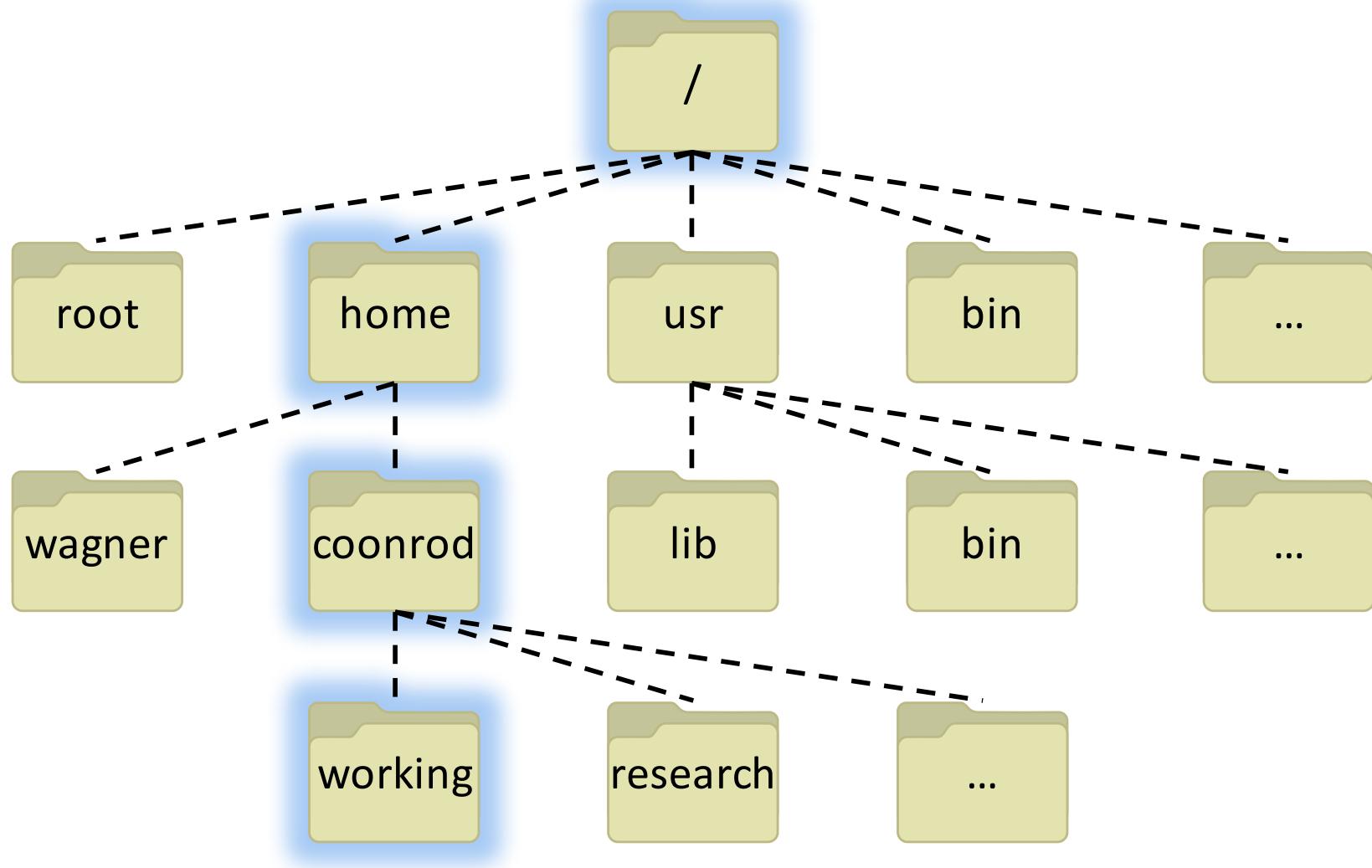
How do I get to the UO bookstore?



Navigating the file system

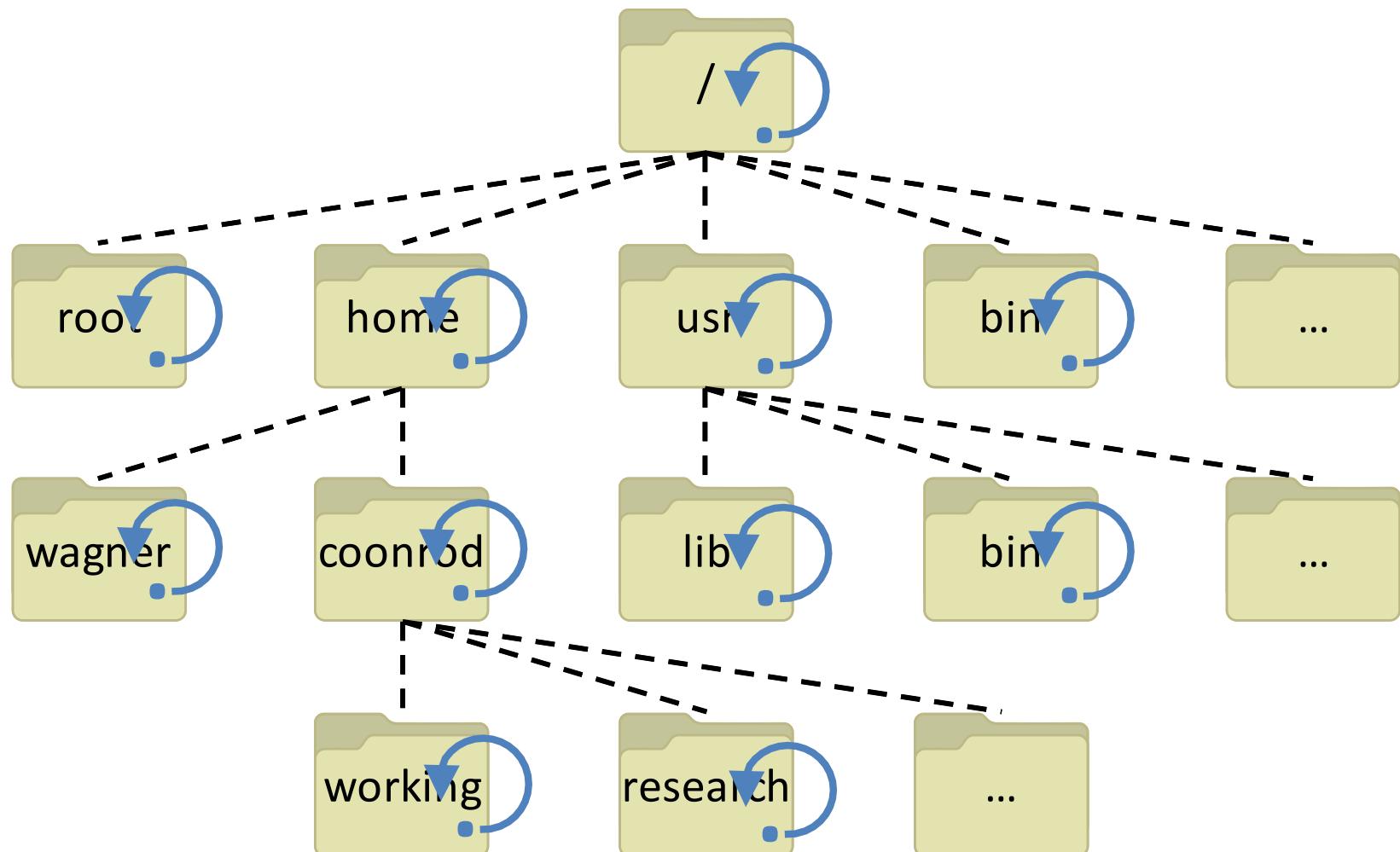


Navigating the file system: Absolute paths



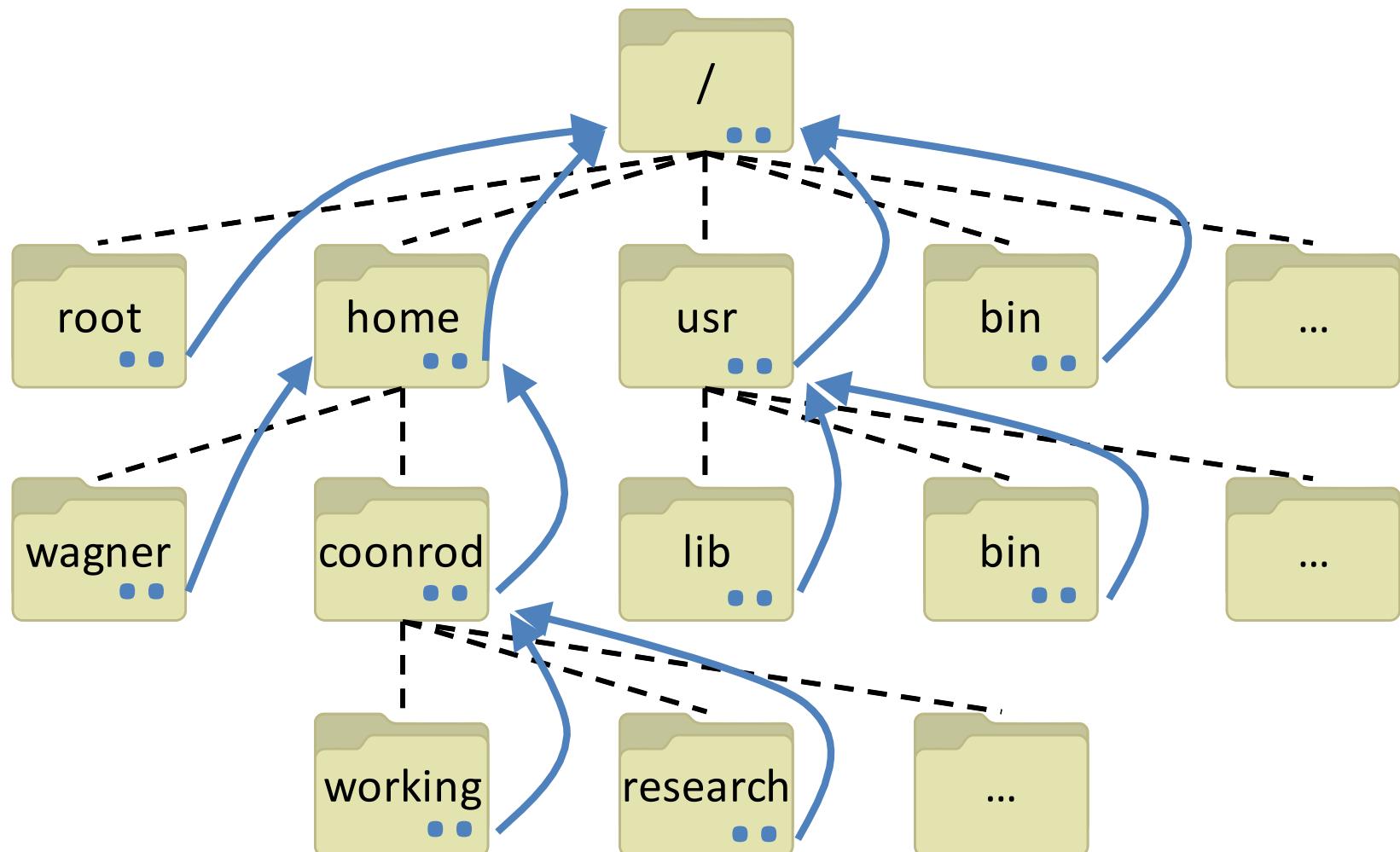
```
$ cd /home/coonrod/working
```

Special files: 'dot'



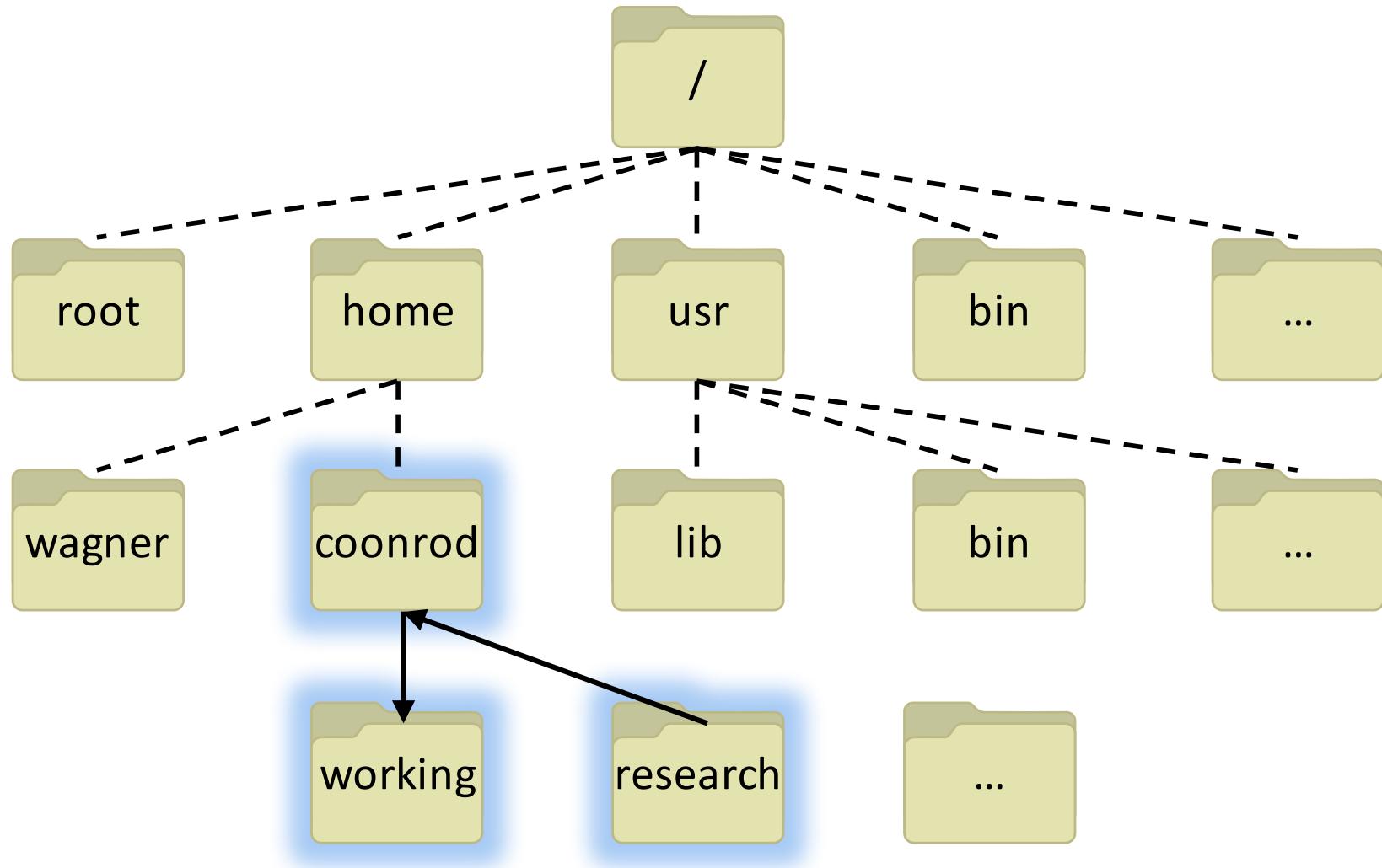
```
$ cd .
```

Special files: 'dot dot'



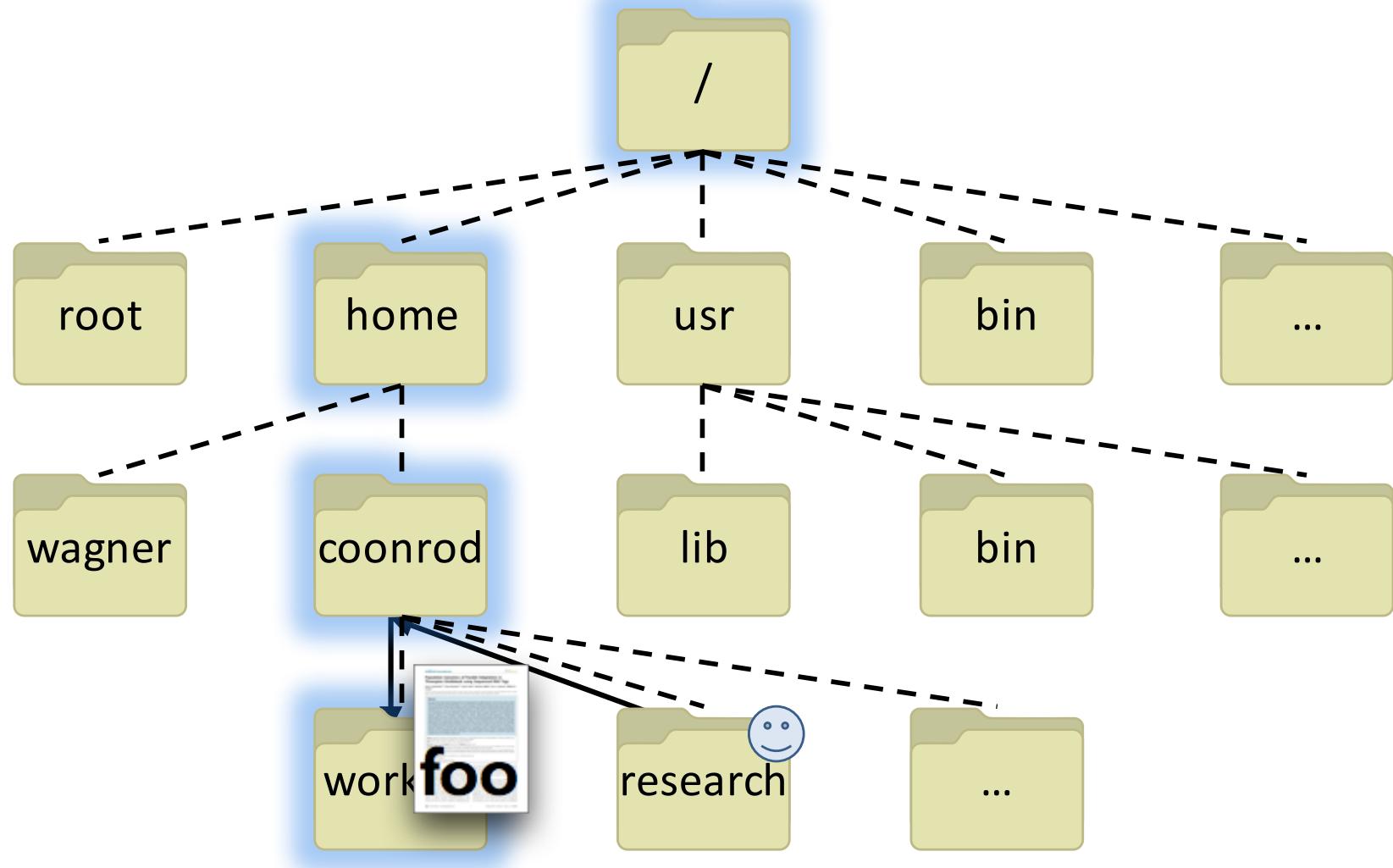
\$ cd ..

Navigating the file system: Relative paths



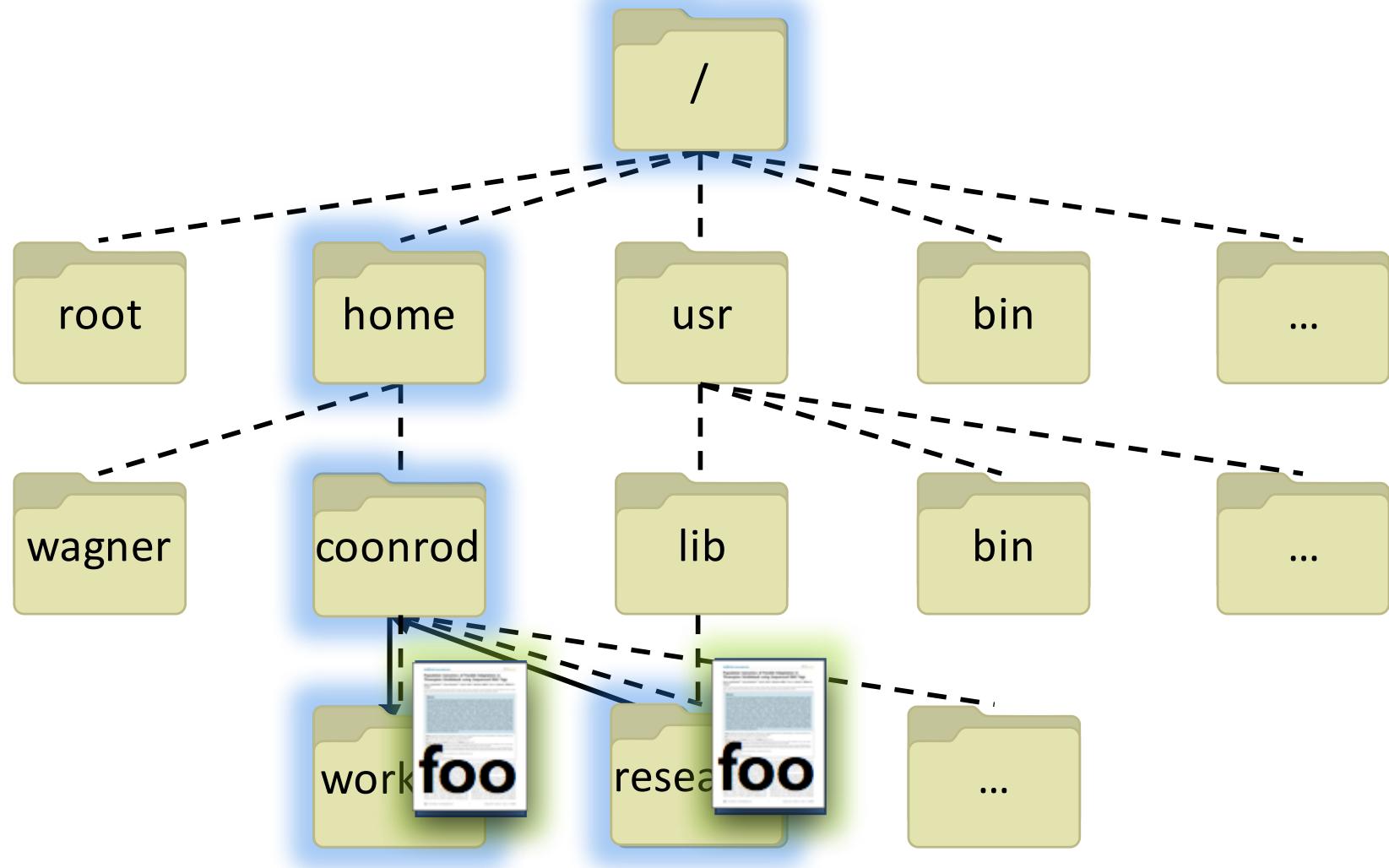
```
$ cd ../working
```

Navigating the file system: Absolute vs relative paths



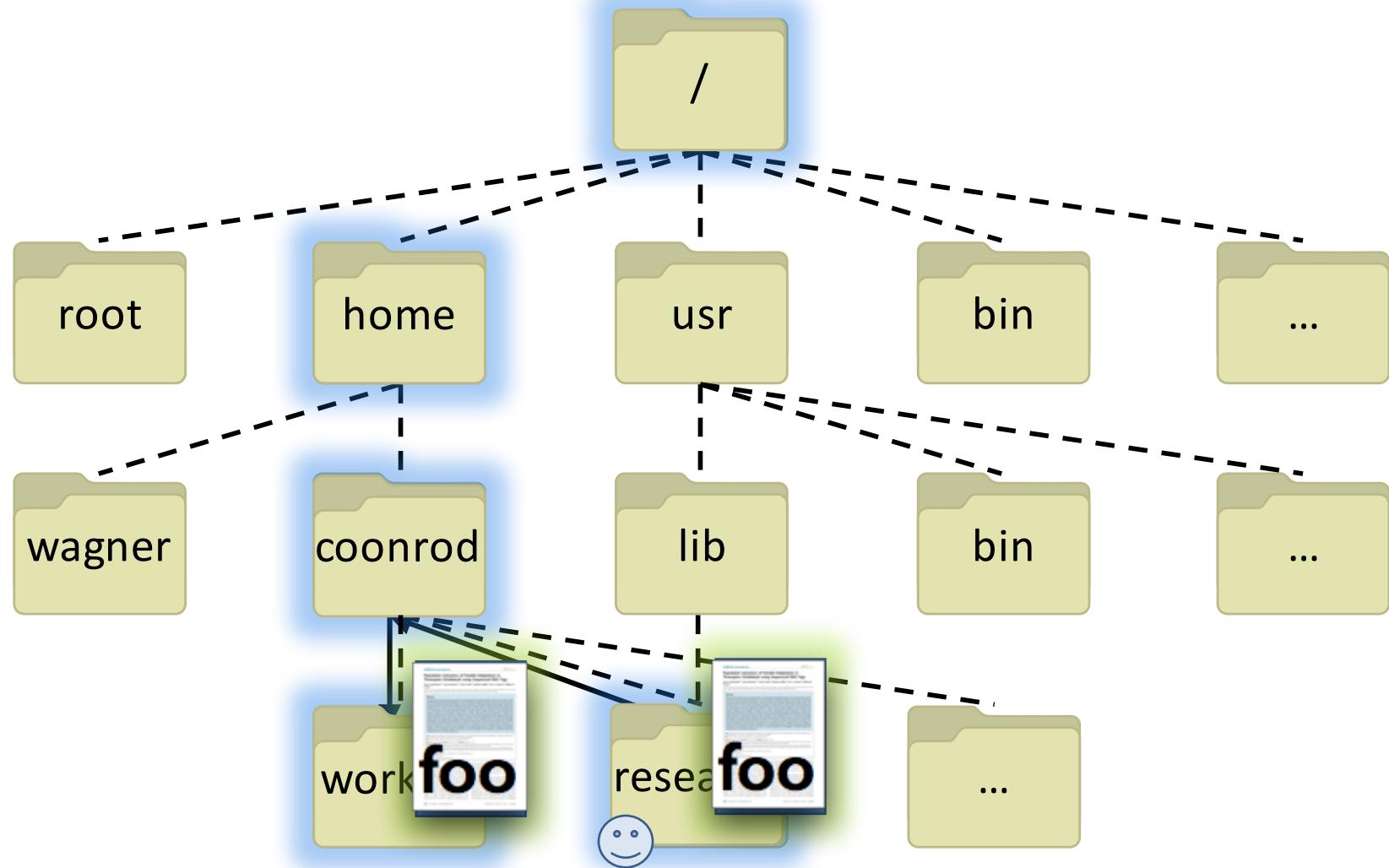
Absolute path: /home/coonrod/working/foo
Relative path: ../../working/foo

Navigating the file system: Files with the same name?



Absolute path: /home/coonrod/working/foo
Absolute path: /home/coonrod/reseach/foo

Navigating the file system: Files with the same name?



Relative path: ./foo

Relative path: ../working/foo

Interlude: creating files and folders

```
$ cd ~          #tilde: shortcut to your home dir
$ mkdir temp    #make directory called temp
$ cd temp       #change directories into temp
$ touch test.txt #create an empty file called test.txt

$ ls            #list the contents of your current directory
test.txt

$ rm test.txt   #removes the file test.txt
#(Note - it doesn't ask first!!)
$ ls

$ cd ..         #moves up one directory
$ ls
temp
$ rmdir temp    #removes directory temp
```

Interlude: navigating the file system

```
$ cd ~          #tilde: shortcut to your home dir  
$ cd -          #dash: shortcut to the last dir you were in  
$ cd            #what does this do?  
$ cd ..         #move up one directory  
$ cd ../..      #move up two directories  
$ cd /          #move to the root directory  
  
#not sure where you're at? Don't forget  
$ pwd  
  
#list the contents of a directory you're not currently in  
$ ls /usr/bin/  
  
#remember, command -options -arguments  
$ ls -lah /usr/bin/
```

Are you typing? You're doing it wrong

- Use tab-completion
 - Tab once to complete uniquely
 - Tab twice to see all possible completions
- Up-arrow
 - Previous commands can be found by pressing the “up-arrow” key
 - “Down-arrow” to find commands you haven’t typed yet
- `history`

How do you find out what options are available for a command?

- use the man pages
 - `man` command
 - `ls` example

<code>ls -l</code>	<code>ls -a</code>	<code>ls -lh</code>	<code>ls -F</code>
Provides a <i>long</i> listing	Includes <i>all</i> files, including hidden files	Displays the <i>long</i> listing with <i>human</i> readable numbers	Denotes directories, executables, etc., with special characters

- Notice, Leslie has an alias set up for `ls -F` (more on this later)

Many ways to view a file

more	less	head	tail	cat
View text file one screen at a time	Same as more, but allows backwards movement	View the first 10 lines of a file	View the last 10 lines of a file	Spit out the whole file at once
Space-bar: scroll q: quit	Arrow keys: scroll Space-bar: end of file q: quit	-n num Controls the number of lines	-n num Controls the number of lines	

Explore the file hierarchy on ACISS

- You should have already signed up for your account
- Connect to ACISS
 - `ssh <user>@login.aciss.uoregon.edu`
 - Password is your uoregon password
 - Mac/Linux: terminal
 - Windows: Cygwin or use virtual machine
(Windows 10 anniversary update: Bash?)
- <http://aciss-computing.uoregon.edu/>

ICA1 – Explore the file hierarchy on ACISS

1. What is the absolute path to your home directory?
2. Move to the directory `/etc`
 - a. What is the first line of the file ‘hosts’ in the directory `/etc`?
 - b. What is the relative file path to get to `/var/log` from here?
 - c. What is the absolute path?
3. Move to the directory `/var/log`
 - a. What is the contents of line 73 of the `dmesg` file?
 - b. Without changing directories, what is the second line of the `cpuinfo` file in the `/proc` directory?
 - i. What is the command to read this file with a relative path?
 - ii. An absolute path?
4. Move back to the root – what directories do you see?
5. Move back home – what are three ways to move from home to the root?
6. What do the following options do (use `man command`)?
 - a. `-1` when using `ls`
 - b. `-i` when using `rm`
 - c. `-I` when using `rm`
 - d. `-r` when using `rm`
 - e. `-S` when using `less`
 - f. `--number` when using `cat`

Hint: typing /pattern while in the man page will search for “pattern”

Moving and copying files

- On your own computer, create a directory called `shell`
- Download `s_1_sequence.txt` from Canvas and place it in your newly created `shell` directory
- Use the `man` page for `cp` to make a copy of your file `s_1_sequence.txt` called `s_1_seq.txt`
- Use the `man` page for `mv` to rename your file `s_1_seq.txt` to `s_1_seq.fastq`
- Use the `rm` command to remove `s_1_sequence.txt`