Getting things done on the command line

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Announcements: Office Hours

- My office hour will remain Fri 11-12pm, SPH2 434
  - I'll be there tomorrow to sort out administrative issues + setup issues from week 0
  - Others start next week
- Kevin will hold a separate office hour (Hello, Kevin!)
  - Fri 1-2pm, location TBD
- TA office hours
  - Marina: Weds 3-4pm, SPH2 428
  - Shirley & Emma: Thurs 1-2pm, FXB G03*
    - *Kresge 502 on Sept. 20 and Sept. 27
- Syllabus updated

Overview

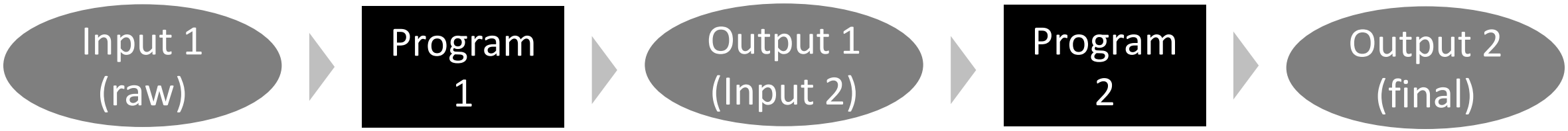
- Command-line philosophy
- File systems
- Utils for…
  - Navigation
  - Organization
  - Inspecting files
  - Data manipulation
- Chaining programs
- Practice

Some terminology

- A "**command line**" is a text-based interface to a computer.
- The MacOS **Terminal** and Windows **Command Prompt** are programs that provide command-line interfaces to Mac and Windows computers.
- Command-line environments are often referred to generically as "**terminals**" or "**consoles**" (a throwback to their antiquated, physical equivalents).
- A "**shell**" is a program that runs inside a terminal to interpret and execute the commands that you type (~the Python interpreter).
- **Bash** is a popular shell used on Unix-based computers.

Why work from the command line?

- Faster than clicking around a graphical user interface (GUI).
- Can answer a lot of basic data questions with command-line tools.
- Convenient for working on a remote computer.
- Command-line “chains” provide practice for designing algorithms.



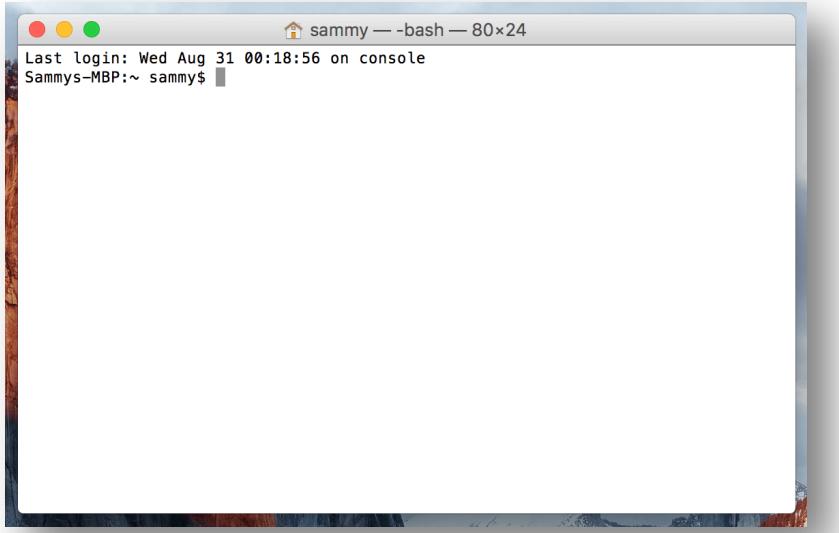
Each command-line program/util is highly optimized for a particular task, e.g. counting lines in a file

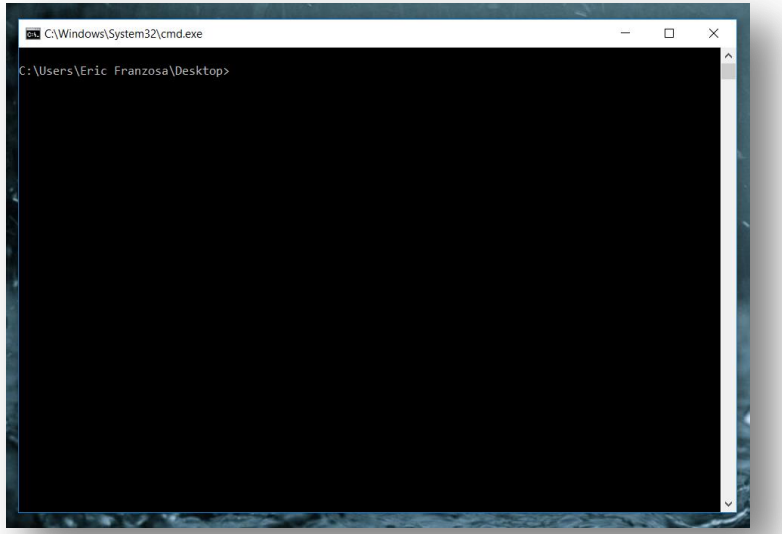
Notes for Windows users

- The standard Windows Command Prompt is an oddball
  - Uses different names for many of the basic commands (I will point these out)
  - Lacks most of the useful, less-basic commands
- Some alternative options to consider (from least to most complex)
  - **GOW** supplements basic programs and adds in some of the missing ones
    - This is what I use
  - **Windows Powershell** is a built-in alternative Command Prompt
    - "Fixes" some inconsistencies, but not all
  - **Cygwin** is an installable alternative Command Prompt
    - Behaves exactly like other terminals, but a bit harder to set up and use
  - The **Linux Subsystem for Windows 10**
    - A full-featured Linux shell within Windows 10 (still a bit experimental)

Opening a Terminal/Command Prompt

- In MacOS, open a Terminal
  - Spotlight → Type “Terminal” → Select **Terminal**
  - *Option-click Terminal in Dock: “Keep in Dock”*
- In Windows 10, open the Anaconda Prompt
  - Start/Search → Type “Anaconda Prompt” → Select **Anaconda Prompt**
  - *Right-click Anaconda Prompt in taskbar: “Pin to Taskbar”*

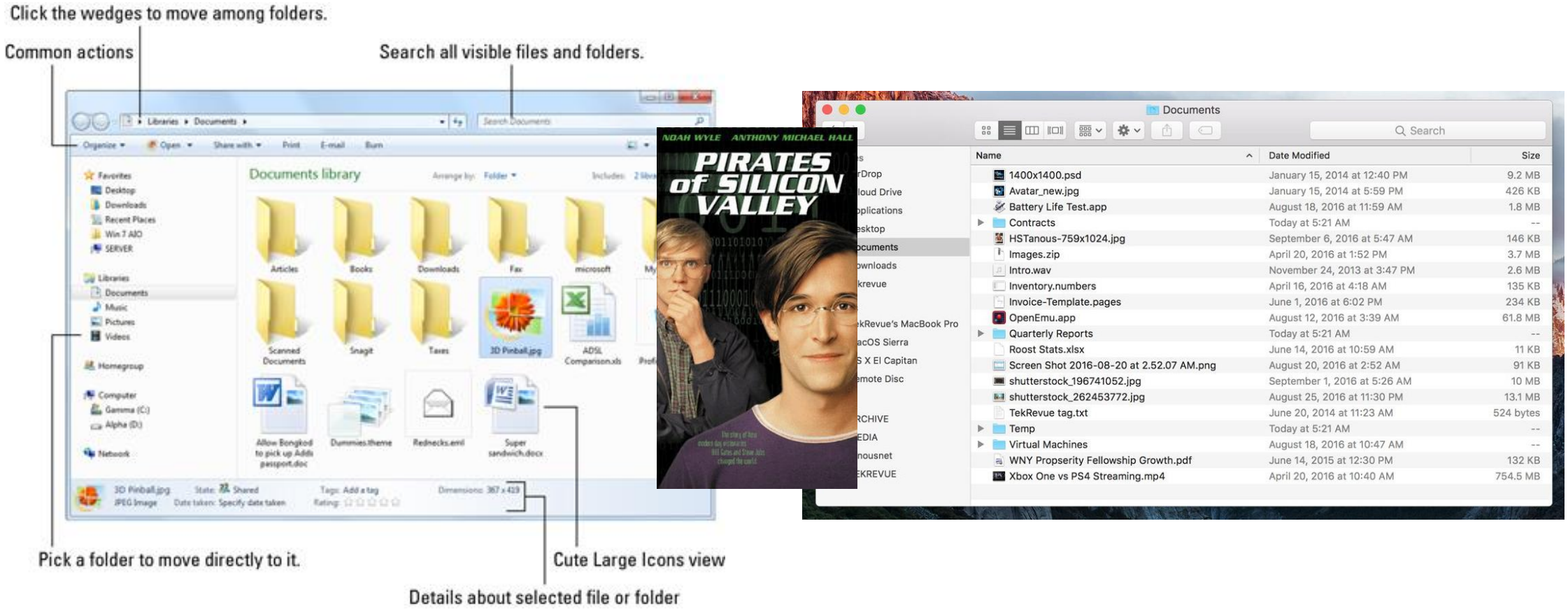




File systems

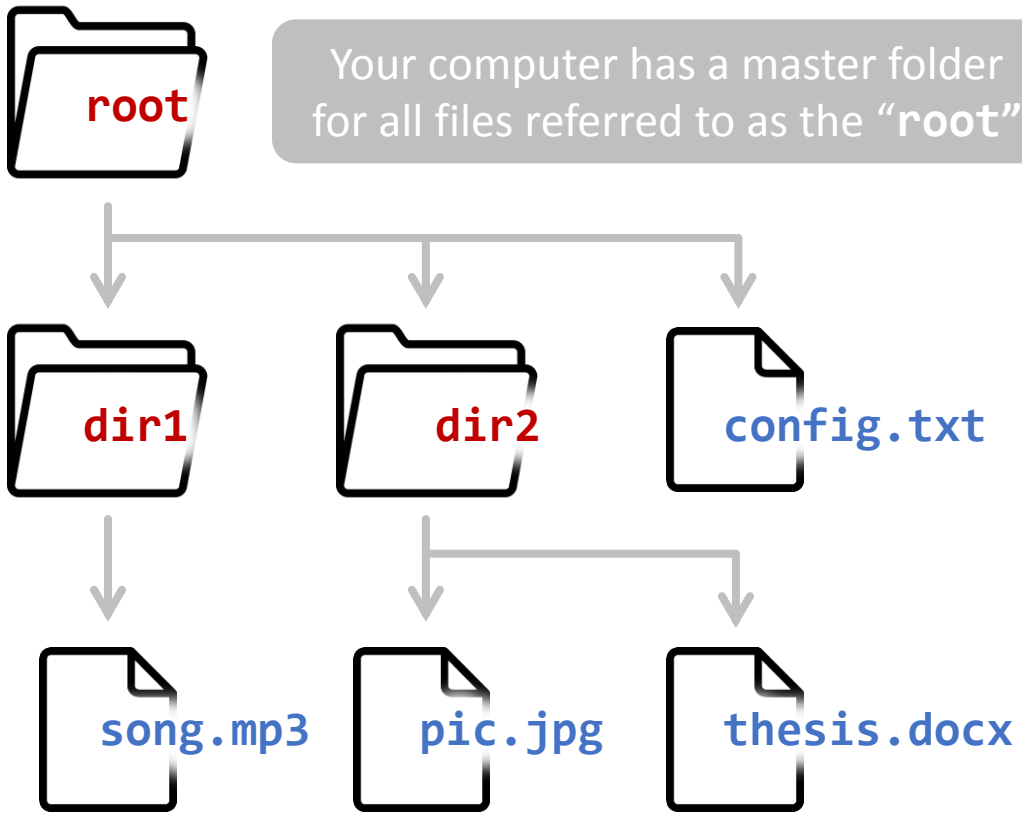
File systems

- The **MacOS Finder** and **Windows Explorer** provide graphical interfaces to Mac/Windows file systems, respectively.



File systems

- A file system is a hierarchical (tree) organization of data on your computer.
- Folders contain files (and other folders) in **parent-child relationships**.



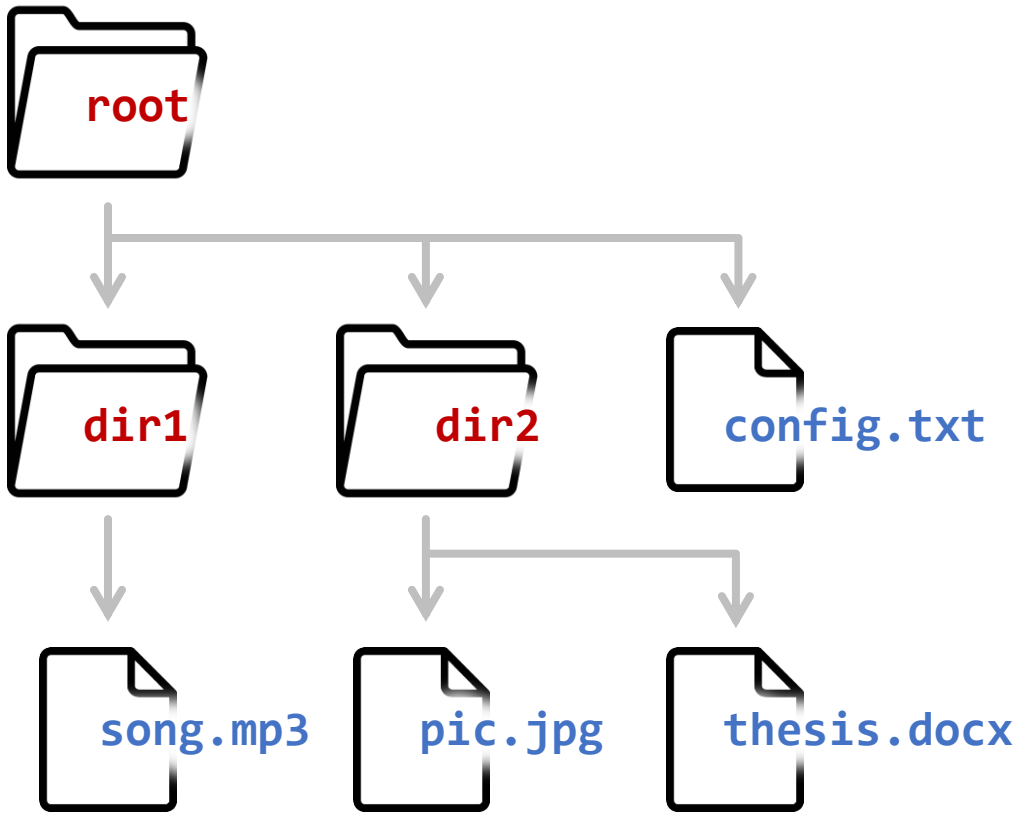
Your computer has a master folder for all files referred to as the "`root`"

The words "folder" and "directory" are used interchangeably

Files are often distinguished from folders by a file extension (`.xyz`): a convenience feature for hinting at file contents and associating them with appropriate programs

File systems

- Another representation of the same data:

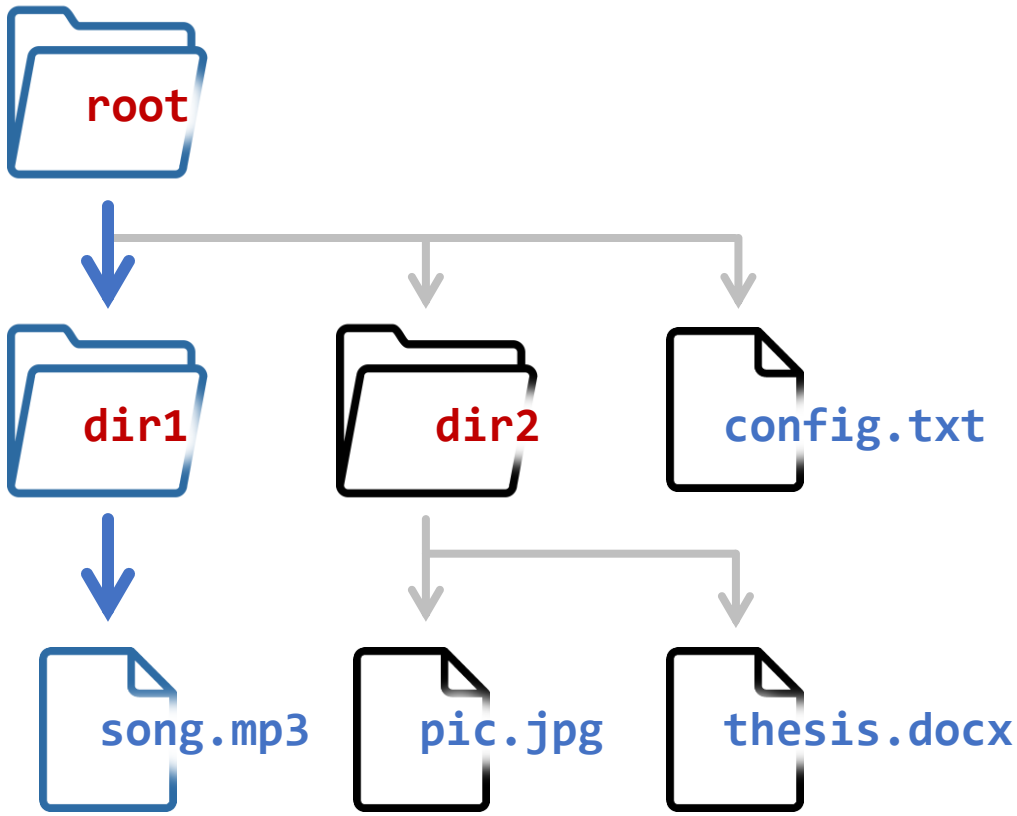


(we'll see that the "tree" command can actually sketch this out for us)

```
root
├─config.txt
├─dir1
│  └─song.mp3
└─dir2
   ├─pic.jpg
   └─thesis.docx
```

Paths

- There is a path in the tree to every folder or file on the computer.
- This path can be represented as a string of text.




```
/dir1/song.mp3
```

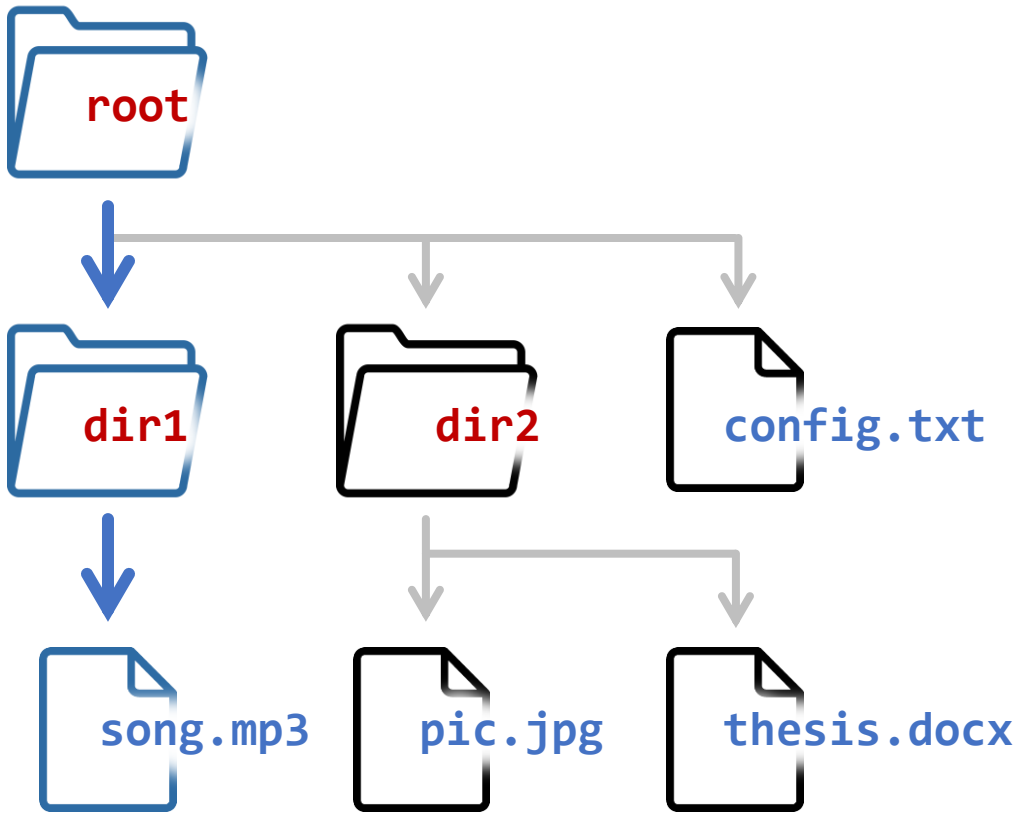
In most operating systems, the root of the hierarchy is represented by "/" (forward-slash) and the same symbol represents parent-child relationships.

```
C:\dir1\song.mp3
```

Windows has a separate root for each hard drive disk (HDD), with the default being "C:". Windows uses "\" (back-slash) for parent-child relationships.

Paths

- Paths that begin at the root are called “absolute paths”.
- Absolute paths are safer; they don’t depend on “frame of reference”.

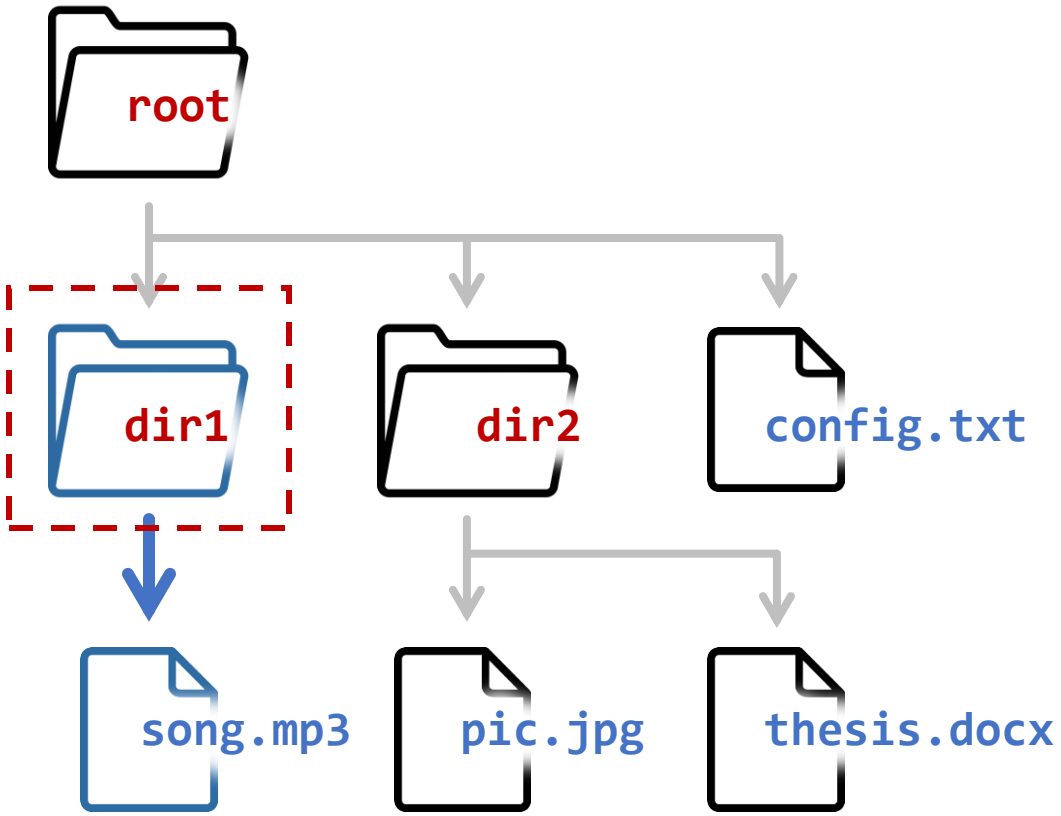



```
/dir1/song.mp3
```

Absolute path to song.mp3

Paths

- All other paths are “relative paths”.
- “Relative” → “Relative to your working directory” (more on that shortly).

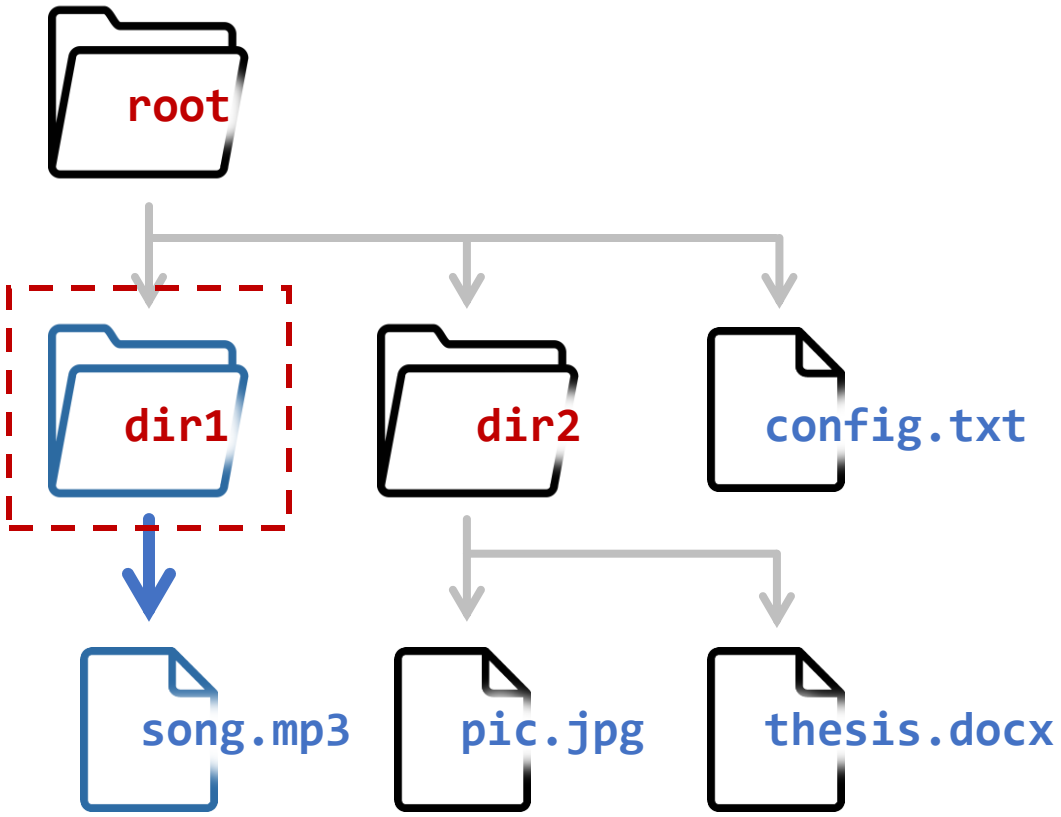


`song.mp3`

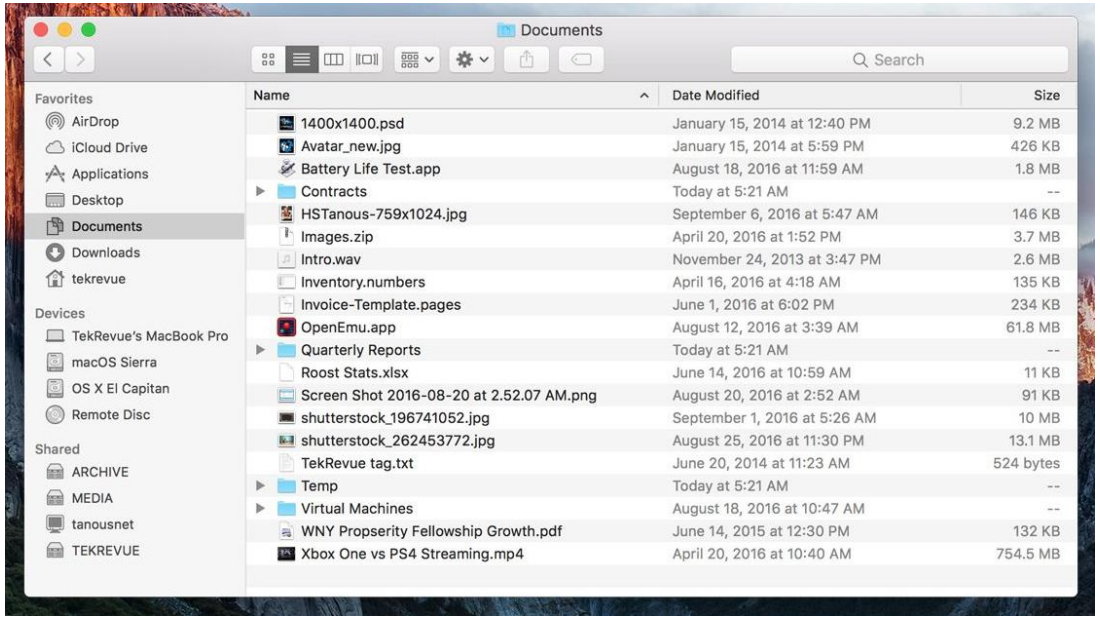
Relative path to song.mp3 if I’m in `dir1/`

Paths

- Relative paths exist because the terminal is “in” a given directory at any specific time (the default is usually your home folder, not the root).



This directory is called the “Working Directory”



Analogous to having finder “open” to `Documents/`

Misc. notes about file systems / paths

- Mac/Linux distinguish between upper vs. lowercase letters (Windows doesn't)
- Your **home folder** is usually a step below the root
  - `/home/franzosa` on Mac/Linux
  - `C:\Users\Franzosa` on Windows
- On Mac/Linux, `~` is a shortcut for the absolute path to your home directory
  - `~/Downloads` is equivalent to `/home/franzosa/Downloads`
- On all systems, `..` is a shortcut for "**my parent folder**"
  - Working in `~/Downloads/`, `..` is equivalent to `/home/franzosa` or `~`
- On all systems, `.` is a shortcut for "**here**" (i.e. the **working directory**)
  - Working in `~/Downloads/`, `.` is equivalent to `~/Downloads`

Getting help & tricks

Command line utilities: `man`

What does it do?
Displays a “manual” page for another tool, detailing expected input data and optional flags

Usage
`$ man less`

Options	What does it do?
Q	[within program] Exits the current man page

*The Windows equivalent is
`$ help PROGRAM` (or) `$ PROGRAM --help`

Command line utilities: man

```
LESS(1)                                   General Commands Manual                                   LESS(1)

NAME
       less - opposite of more

SYNOPSIS
       less -?
       less --help
       less -V
       less --version
       less [-[+]aABcCdeEfFgGiIJKLmMnNqQrRsSuUVwWX~]
            [-b space] [-h lines] [-j line] [-k keyfile]
            [-{oO} logfile] [-p pattern] [-P prompt] [-t tag]
            [-T tagsfile] [-x tab,...] [-y lines] [-[z] lines]
            [-# shift] [+[+]cmd] [--] [filename]...
       (See the OPTIONS section for alternate option syntax with long option names.)

DESCRIPTION
       Less  is  a  program  similar  to more (1), but it has many more features.  Less does not have to read the entire input file before starting, so with large
       input files it starts up faster than text editors like vi (1).  Less uses termcap (or terminfo on some systems), so it can run on a variety  of  terminals.
       There  is even limited support for hardcopy terminals.  (On a hardcopy terminal, lines which should be printed at the top of the screen are prefixed with a
       caret.)

       Commands are based on both more and vi.  Commands may be preceded by a decimal number, called N in the descriptions below.  The number is used by some com-
       mands, as indicated.

COMMANDS
       In the following descriptions, ^X means control-X.  ESC stands for the ESCAPE key; for example ESC-v means the two character sequence "ESCAPE", then "v".

       h or H Help: display a summary of these commands.  If you forget all the other commands, remember this one.

       SPACE or ^V or f or ^F
              Scroll  forward N lines, default one window (see option -z below).  If N is more than the screen size, only the final screenful is displayed.  Warn-
              ing: some systems use ^V as a special literalization character.

       z      Like SPACE, but if N is specified, it becomes the new window size.
```

Command-line shortcuts

- Press the “UP” arrow to cycle through previously executed commands
  - Don’t retype commands unless they are very short
- Press <TAB> to auto-complete program names/paths from a prefix
  - For example, type “`/home/doc`” and press <TAB> to fill “`/home/documents`”
  - Mac/Linux will list auto-complete options (if >1)
  - Windows will cycle through them as you click <TAB> repeatedly

Navigation

(`pwd`, `ls`, `cd`)

Command line utilities: pwd

What does it do?

Prints the current working directory

Usage

```
$ pwd
```

Note: “$” is used to specify the start of a line on a generic command prompt.

*The windows equivalent is `cd`

Command line utilities: `ls`

What does it do?
List files in the current directory

Usage
`$ ls  # list all files in current directory`
`$ ls *.txt # list all text files`

Options	What does it do?
`-l`	List file details
`-h`	Human-readable file sizes (e.g. 3.3MB vs. 3354123)

*The windows equivalent is `dir`

Command line utilities: cd

What does it do?
Changes directories

Usage
`$ cd /home/docs # follow the absolute path to /home/docs`
`$ cd docs # go to subfolder docs in working directory`
`$ cd .. # go to parent folder of working directory`

Organization

(`rm`, `cp`, `mv`, `mkdir`)

Command line utilities: `rm`

What does it do?
Deletes (removes) a file **PERMANENTLY**

Usage
`$ rm file # removes file from the working directory`

Options	What does it do?
`-r`	Force-remove a directory (will fail by default)
`-i`	Confirm each deletion event

*The windows equivalent is `del` for files and `rmdir /S` for folders

Command line utilities: cp

What does it do?
Copy a file

Usage
`$ cp file1 file2  # copy file1 to file2 in working directory`
`$ cp /home/a /home/b # copy a to b (wherever you are)`
`$ cp /home/a ../a  # copy a to my parent folder`

Options	What does it do?
`-i`	Warn before overwriting a file
`-r`	Copy recursively (needed for copying directories)

*The windows equivalent is `copy`

Command line utilities: mv

What does it do?
Move a file to a new location (or rename a file)

Usage
`$ mv file1 file2  # rename file1 as file2 in working directory`
`$ mv /home/a /home/b  # move a to b (wherever you are)`
`$ mv /home/a ../a  # move a to my parent folder`

Options	What does it do?
`-i`	Warn before overwriting a file

*The windows equivalent is `move`

Command line utilities: `mkdir`

What does it do?
Make a directory

Usage
`$ mkdir /home/docs # make the directory docs/ in /home/`
`$ mkdir docs # make docs/ in working directory`
`$ mkdir ../docs # make docs/ in parent directory`

Options	What does it do?
`-p`	Create non-existent parents in the path to new folder

Words of warning

- Manipulating files from the command line is a lot less forgiving than working in the graphical MacOS and Windows file browsers.
- **!!! By default, no warnings/confirmation for deleting/overwriting files !!!**
  - The system will prevent you from deleting “important” file (i.e. files required to keep your computer running, but not “my_thesis.docx”)
- As you are practicing command-line skills, I recommend working within a folder of (e.g.) Dropbox or Google Drive so you can restore deleted files.
- Programmers generally use backups/snapshots and revision control systems (e.g. git/github) to restore work after making mistakes.

Inspecting files

(`less`, `head`/`tail`, `cat`)

No direct Windows equivalents from here on ☹

Command line utilities: `less`

What does it do?
View a file or data stream with navigation options

Usage
`$ less my_file`
`$ cat *.txt | less # 'less' is often used at the end of a chain`

Options	What does it do?
-S	Don't wrap long lines
Q	[while running] Exit the program
←↑→↓	[while running] Arrow keys to navigate in file (PageUp, PageDown work too)
/	[while running] Search for text, use n and N to see next/previous matches

Command line utilities: `head/tail`

What does it do?
Stream the first/last (`tail`/`head`) lines of a data stream (default 10)

Usage	
`$ head my_file`	`# print lines 1-10`
`$ tail my_file`	`# print last 10 lines of file`
`$ head -100 my_file | tail`	`# print lines 91-100`

Options	What does it do?
`-`N	Print N lines instead of default 10

Command line utilities: `cat`

What does it do?
Concatenates (prints) one or more files (often for feeding into another program)

Usage
`$ cat my_file` `# lines of file scroll over screen`
`$ cat my_file | program` `# send contents of file to program`
`$ cat *.txt | program` `# send contents of all text files`

Data manipulation

(grep, cut, sort, uniq, wc, sed)

Command line utilities: grep

What does it do?
Isolate lines of a data stream (file or STDIN) that match a pattern

Usage
`$ grep pattern my_file`
`$ cat *.txt | grep pattern`

Options	What does it do?
`-P`	Richer pattern options (regular expressions); more on these in a later lecture
`-v`	Isolate lines that DO NOT match the pattern (invert the match)
`-i`	Case-insensitive match
`-f`	Specify a file of patterns to match (slow if there are lots of options)

Command line utilities: `cut`

What does it do?
Isolate tab-delimited columns of a data stream. First column is #1 (not #0 as in Python).

Usage
`$ cut -f2 my_file  # isolate the 2nd column of the file`
`$ cut -f2,3 my_file # isolate columns 2 and 3`
`$ cut -f2-5 my_file # isolate columns 2 THROUGH 5`
`$ cut -f3- my_file  # isolate columns 3 to END (python [2:] slice)`

Options	What does it do?
`-f`	Select columns (fields)
`-t'char'`	Break columns on the specified character instead of tab, e.g. `-t','` for .csv file

Command line utilities: `sort`

What does it do?
Sort the lines of a data stream (alphabetically)

Usage
`$ sort my_file`

Options	What does it do?
`-r`	Reverse the sort
`-k` N	Sort on the value of **WHITESPACE**-delimited column N
`-t'`*char*`'`	Specify the delimiter character (e.g. `-t'\t'` for tab)
`-n`	Perform a numeric sort (otherwise `10` comes before `2`)

Command line utilities: `uniq`

What does it do?
Isolate the unique **ADJACENT** lines of a data stream

Usage
`$ sort my_file | uniq # w/o sorting, non-adjacent repeats missed`

Options	What does it do?
`-c`	Count the occurrence of each unique line

Command line utilities: wc

What does it do?
Counts the lines, words, and characters of a data stream

Usage
`$ wc my_file`

Options	What does it do?
`-l`	Only report line count (faster, and often all you want)
`-w`	Only report word count
`-c`	Only report character count

Command line utilities: sed

What does it do?
Edit a data stream, most often used for find/replace operations

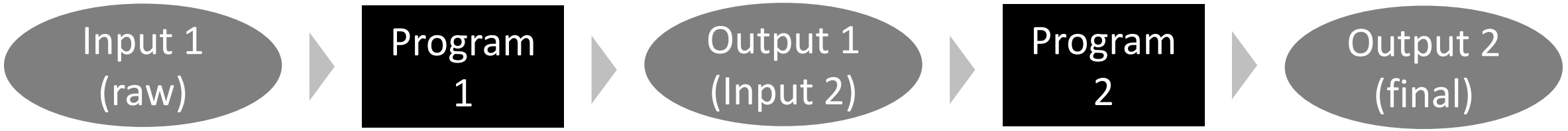
Usage
`$ sed “s/find/replace/g” my_file`
`$ sed “s/apple/banana/g” my_file # replace all instances of “apple” with “banana”`

Options	What does it do?
`-i`	Edit file “in place” (use with caution)
	“*find*” can be a regular expression, and “*replace*” can use captured elements of the pattern (this will make more sense after our regular expressions lecture).

Chains / Pipes

Chaining commands

- We can “chain” the output of one command as the input of the next:



- This is a good model for how we’ll build programs later in the course: with the output of one piece of code feeding into another piece of code.

Chaining commands with pipe, |


```
contralto
dominion
halcyon
intercalate
paradigm
perceptron
raconteur
syntax
```

```
$ head -4 words.txt
```

```
contralto
dominion
halcyon
intercalate
```

```
$ grep “y” words.txt
```

```
halcyon
syntax
```

```
$ head -4 words.txt | grep “y”
```

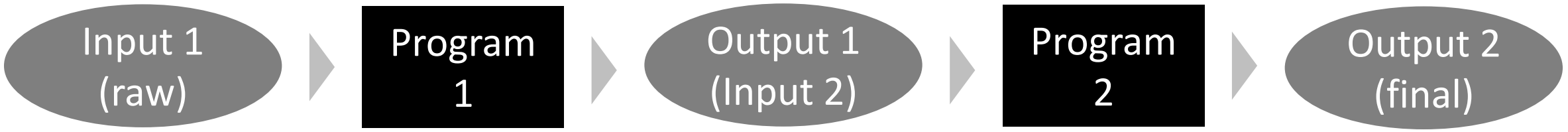
```
halcyon
```

Starting a chain

- Start with first command naming the input file (`my_file.txt`):
  - `grep “Hello” my_file.txt`
- Combine (concatenate) multiple files of the same type:
  - `cat *.txt`
- Another way to provide a single file as STDIN (less common):
  - `grep “Hello” < my_file.txt`

Extending the chain

- Use the pipe '|' to direct STDOUT of program *N* as STDIN of program *N*+1
  - `grep "Hello" my_file.txt | sort`
- Can do this repeatedly
  - `grep "Hello" my_file.txt | sort | uniq | wc -l`

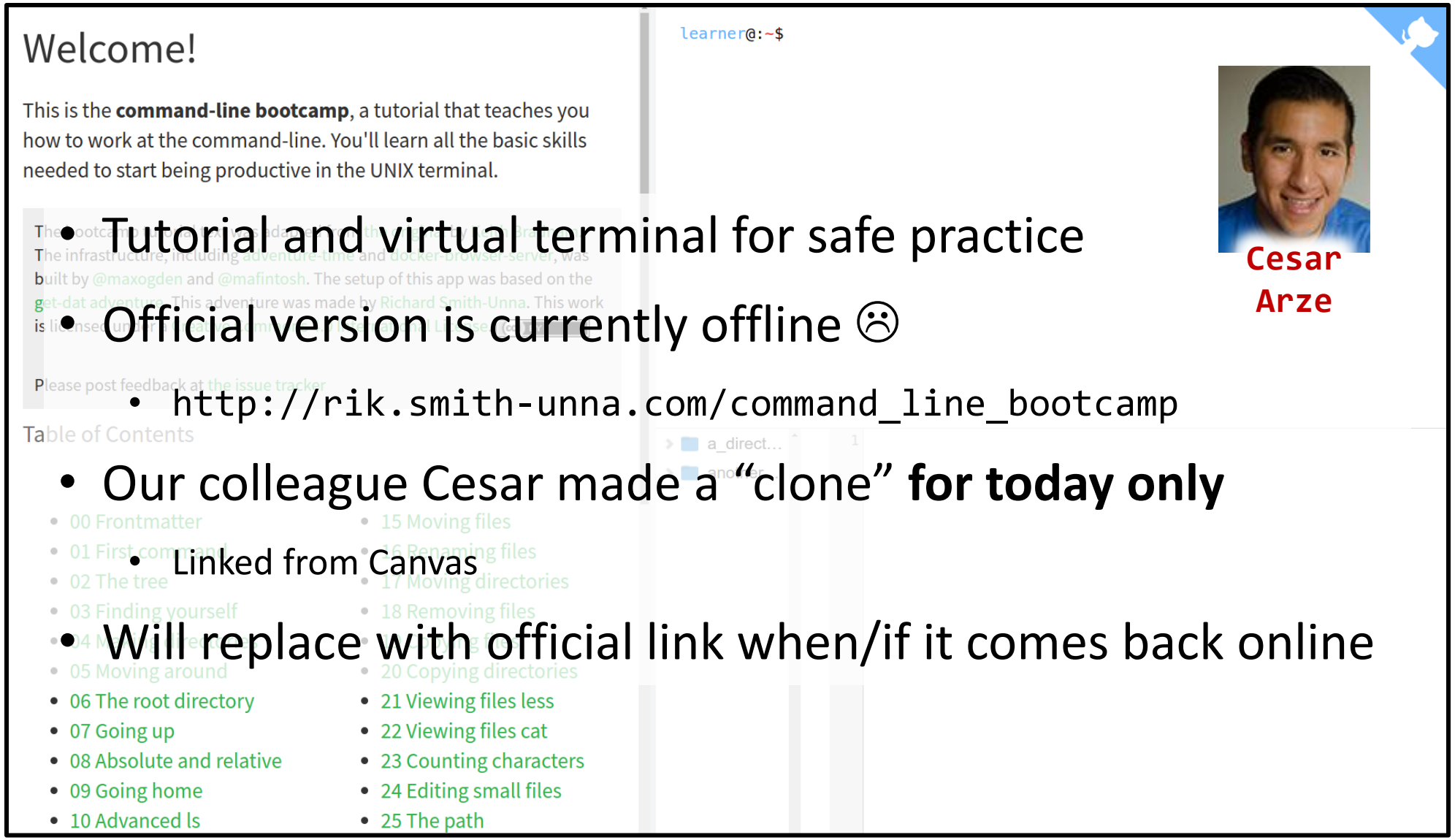


Ending the chain

- Don’t do anything special, results print to screen:
  - `grep “Hello” my_file.txt | sort | uniq | wc –l`
- View the final results in `less`:
  - `grep “Hello” my_file.txt | sort | uniq | wc -l | less`
- Write the results to a file:
  - `grep “Hello” my_file.txt | sort | uniq | wc -l > hello_count.txt`
  - **!!! WARNING: if “`hello_count.txt`” exists, it will be overwritten !!!**

Practice Option I:
command-line bootcamp

Command-line bootcamp



Cesar Arze

- Tutorial and virtual terminal for safe practice
- Official version is currently offline ☹
  - `http://rik.smith-unna.com/command_line_bootcamp`
- Our colleague Cesar made a "clone" **for today only**
  - Linked from Canvas
- Will replace with official link when/if it comes back online

Practice Option II:

Puzzles with `demo.zip`

demo.zip

- Download the archive `demo.zip` from Canvas
- Open a terminal and use `cd` to navigate to `demo.zip`
- Unzip the archive by executing `unzip demo.zip`
- Use the file tree in the corner as a reference

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 1: More words

1. Use `cd` to navigate to the location of `wikipedia_top100.txt`
2. Inspect the contents of the file with `less`
3. Use `wc` to verify that the file contains 100 words
4. Use `mv` to rename the file `more_words.txt`
5. Use `cd` to return to the `demo/` folder

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 2: We the people

1. Use `mkdir` to make a new folder called `gov2/`
2. Use `cd` to enter your new folder
3. Use `cp` to make a copy of `us_constitution.txt` in `gov2/`
    1. Hint: you will use the "`.`" and "`..`" tricks
4. Use `grep` to find lines containing the phrase "United States"
5. Then add a pipe and `wc` to count them
6. Use `cd` to return to the `demo/` folder

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 3: Bug bytes

- Kevin and I do research on the human microbiome
- The file `demo/hmp2012/metadata.tsv` lists metagenomic samples from the first phase of the Human Microbiome Project (HMP)
- Each sample comes from a body site of a particular subject at a given visit

metadata.tsv

#SAMPLE_ID	SUBJECT_ID	VISIT	BODY_SITE
700101852	159591683	2	Supragingival_plaque
700033601	159611913	1	Supragingival_plaque
700032328	159915365	1	Supragingival_plaque
700098450	809635352	1	Posterior_fornix
700016482	159207311	1	Tongue_dorsum
700102585	159227541	2	Stool
700106465	338793263	1	Stool
700101840	159591683	2	Stool
700015965	159591683	1	L_Retroauricular_crease

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 3.1: Bug bytes

- How many samples were there?
  - Use `wc` and subtract 1 to discount the header row
- How many **Stool** samples were there?
  - Solution combines `grep` and `wc`

`metadata.tsv`

#SAMPLE_ID	SUBJECT_ID	VISIT	BODY_SITE
700101852	159591683	2	Supragingival_plaque
700033601	159611913	1	Supragingival_plaque
700032328	159915365	1	Supragingival_plaque
700098450	809635352	1	Posterior_fornix
700016482	159207311	1	Tongue_dorsum
700102585	159227541	2	Stool
700106465	338793263	1	Stool
700101840	159591683	2	Stool
700015965	159591683	1	L_Retroauricular_crease

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 3.2: Bug bytes

- How many unique body sites were surveyed?
  - Solution uses `cut`, `grep`, `sort`, `uniq`, and `wc`
- How many unique subjects participated?
  - Solution uses `cut`, `grep`, `sort`, `uniq`, and `wc`

NOTE: These ones are harder! Feel free to go right to the solutions (end of the slide deck) and build the solution one command at a time.

`metadata.tsv`

```
#SAMPLE_ID      SUBJECT_ID      VISIT   BODY_SITE
700101852       159591683       2       Supragingival_plaque
700033601       159611913       1       Supragingival_plaque
700032328       159915365       1       Supragingival_plaque
700098450       809635352       1       Posterior_fornix
700016482       159207311       1       Tongue_dorsum
700102585       159227541       2       Stool
700106465       338793263       1       Stool
700101840       159591683       2       Stool
700015965       159591683       1       L_Retroauricular_crease
```

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 3.3: Bug bytes

- Which six body sites were sampled the most?
  - Solution uses `cut`, `sort` (twice), `uniq -c`, and `tail`
- How many subjects contributed more than 10 samples?
  - Solution uses `cut`, `sort` (twice), `uniq -c`, and `tail`

metadata.tsv

#SAMPLE_ID	SUBJECT_ID	VISIT	BODY_SITE
700101852	159591683	2	Supragingival_plaque
700033601	159611913	1	Supragingival_plaque
700032328	159915365	1	Supragingival_plaque
700098450	809635352	1	Posterior_fornix
700016482	159207311	1	Tongue_dorsum
700102585	159227541	2	Stool
700106465	338793263	1	Stool
700101840	159591683	2	Stool
700015965	159591683	1	L_Retroauricular_crease

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

Part 3.4: Bug bytes

- How many (subject, body site) pairs were sampled 3 times?
  - Solution uses `cut`, `sort` (twice), `uniq -c`, and `tail`
- How many biological samples had sequencing replicates?
  - I.e. (subject, visit, body site) triples that appear more than once

metadata.tsv

#SAMPLE_ID	SUBJECT_ID	VISIT	BODY_SITE
700101852	159591683	2	Supragingival_plaque
700033601	159611913	1	Supragingival_plaque
700032328	159915365	1	Supragingival_plaque
700098450	809635352	1	Posterior_fornix
700016482	159207311	1	Tongue_dorsum
700102585	159227541	2	Stool
700106465	338793263	1	Stool
700101840	159591683	2	Stool
700015965	159591683	1	L_Retroauricular_crease

```
demo/
├── README.txt
├── hmp2012
│   └── metadata.tsv
├── gov
│   └── us_constitution.txt
└── words
    ├── words.txt
    └── more_words
        └── wikipedia_top100.txt
```

SPOILER ALERT!

(answers to HMP questions follow)

Part 3.1: Bug bytes (solutions)

- Samples:
  - `wc -l metadata.tsv`
  - **ANS = 727 (discounting headers)**
- Stool samples:
  - `grep “Stool” metadata.tsv | wc -l`
  - **ANS = 141**

Part 3.2: Bug bytes (solutions)

- Unique body sites:
  - `grep -v "#" metadata.tsv | cut -f4 | sort | uniq | wc -l`
  - **ANS = 16**
  - *Note: initial grep used to discard the header row*
- Unique subjects:
  - `grep -v "#" metadata.tsv | cut -f2 | sort | uniq | wc -l`
  - **ANS = 103**
- Try building the "body site" solution one command at a time:
  - `grep -v "#" metadata.tsv | less`
  - `grep -v "#" metadata.tsv | cut -f4 | less`
  - `grep -v "#" metadata.tsv | cut -f4 | sort | less`
  - `grep -v "#" metadata.tsv | cut -f4 | sort | uniq | less`
  - `grep -v "#" metadata.tsv | cut -f4 | sort | uniq | wc -l`

Part 3.3: Bug bytes (solutions)

- Six most-sampled body sites:
  - `cut -f4 metadata.tsv | sort | uniq -c | sort | tail -6`
  - **ANS = Posterior_fornix, Anterior_nares, Buccal_mucosa, Supragingival_plaque, Tongue_dorsum, Stool**
- Subjects with 10+ samples:
  - `cut -f2 metadata.tsv | sort | unic -c | sort | tail -22`
  - **ANS = 21**
  - *Note: In this and following examples, we re-run the command with different sized "tails" until we find the find the transition we want. In this case, we are looking for the first time a 10 appears.*

Part 3.4: Bug bytes (solutions)

- (Subject, body site) pairs sampled 3+ times:
  - `cut -f2,4 metadata.tsv | sort | uniq -c | sort | tail -16`
  - **ANS = 15 (including pairs sampled >3 times)**
- Sequencing replicates:
  - `cut -f2,3,4 metadata.tsv | sort | uniq -c | sort | tail -15`
  - **ANS = 14**

Extras

Command line utilities: `column`

What does it do?
"Normalize" the widths of column entries (Excel*ify* your data)

Usage
`$ column -t my_file`

Options	What does it do?
`-s'`*`char`*`'`	Specify the delimiter character (e.g. `-s'\t'` for tab); default = any whitespace

Command line utilities: `diff`

What does it do?

Compare two **TEXT** files and display differing lines

Usage

```
$ diff my_file1 my_file2
```