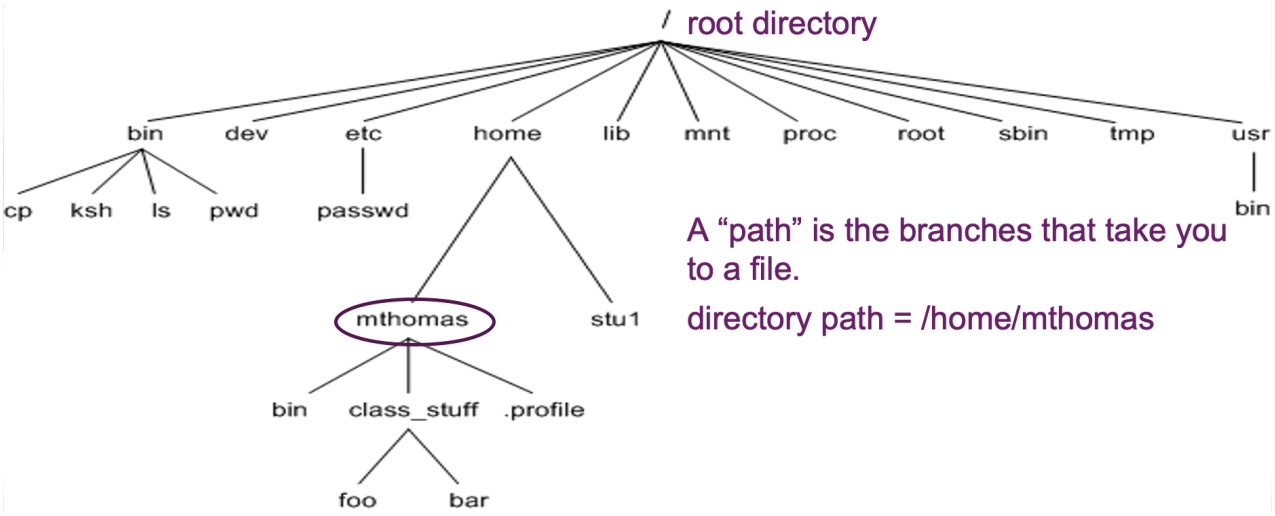
Linux operating system (OS) and Bourne-Again SHell (bash) command-language basics

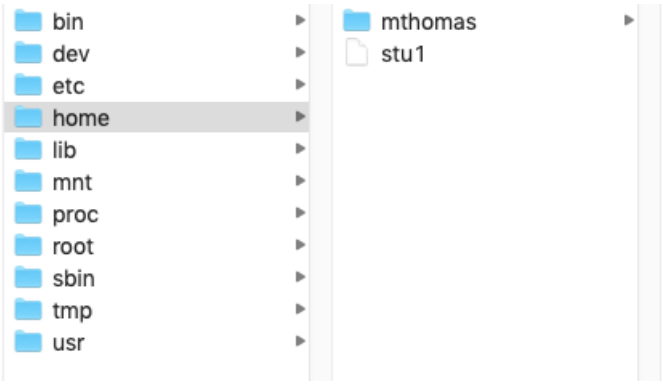
A little shell... aka the $ prompt is the *command line interface*

- A shell is a user interface to the operating system.
  - CLI (Command Line Interface)
  - GUI (Graphical User Interface)
- Bourne-Again SHell (bash) is a Unix shell and *command language*
- Each command drives a program or script by talking to the Operating System (Linux)

Directory Structure



In a Finder window, you would see this



Find the shell in system you'll use to log into the NCGR's server.

For Windows: search for MobaXterm from the start menu. For Mac: search for "terminal" in the bar located in the Launchpad (rocket icon in the taskbar). It may be useful to drag the terminal icon to the desktop (in Windows) or into the Dock (in Mac) for easier access in the future.

Log on to logrus server Enter the following command to log on to logrus: **ssh -p 44111 <username>@gateway.training.ncgr.org** Substitute your personal username in for <username>

Notes:Because we're logging in remotely, the -p option is required to specify port 44111.
If you're prompted to confirm the connection, say "yes", then enter your password

Now that I logged on, where am I?

You're at the *command line interface* of the logrus analysis server!
To the left of the command prompt, you should see something like this: [[eprice@logrus ~]$

Please note words to the right of the colon are a comment to the command.
Command output is shown after the "##" in this document.

PART I: Basic Topics

Understanding directories

print working directory (pwd), mkdir (make directory), and list contents (ls)

```
pwd

## /home/eprice
```

This is your "home" directory.

Now, create a dir under your home directory for this linux class.

```
mkdir  linuxc
```

```
ls
```

```
##  linuxc
```

Listing options

using the ls command

ls -l :**l**ong list

```
ls  -l
```

```
##  total  4
##  drwxrwxr-x  2  eprice  eprice  4096  Aug  17  22:50  linuxc
```

ls -ltr :**l**ong list, by **t**ime, **r**everse order -old to new

```
ls  -ltr
```

```
##  total  4
##  drwxrwxr-x  2  eprice  eprice  4096  Aug  17  22:50  linuxc
```

Navigation

1) "change" to your new directory, where ~ is shorthand for your home directory

```
cd  ~/linuxc
```

```
pwd
```

```
##  /home/eprice/linuxc
```

Files: creating with touch command

1) Create a file

```
touch  newfile.txt
```

```
ls  -l
```

```
##  total  0
##  -rw-rw-r--  1  eprice  eprice  0  Aug  17  22:50  newfile.txt
```

2) Change to your home dir

```
cd ~

pwd

## /home/eprice
```

History command

lists the commands you have entered

```
history

## 17 ls -ltr
## 18 cd ../linuxc ## 19 ls
-ltr
## 20 history
```

Scroll through recent commands with the up and down arrows.

!17 :handy - performs that command

!! :performs the last command

Files: creating by redirecting standard out

> :redirect operator. Send to a file instead of standard out, which is the terminal.

```
history > history.txt

ls -l

## total 4
## -rw-rw-r-- 1 eprice eprice 0 Aug 17 22:50 history.txt
## drwxrwxr-x 2 eprice eprice 4096 Aug 17 22:50 linuxc

cat history.txt

## 17 ls -ltr
## 18 cd ../linuxc
## 19 ls -ltr
## 20 history
## 21 ls -ltr
## 20 history > history
```

Now you have a file with your commands!

File name completion with tab

cat h <hit tab> :the file name will complete if it is unique

Files: moving "mv" command

Syntax: mv <source filename> <destination filename>

```
mv  history.txt  history_file.txt
ls  -l
##  total  4
##  -rw-rw-r--  1  eprice eprice    0  Aug  17  22:50  history_file.txt
##  drwxrwxr-x  2  eprice  eprice  4096  Aug  17  22:50  linuxc
```

Files: copying "cp" command

Change back to the linuxc directory

```
cd ~/linuxc
```

Syntax: cp <source filename> <destination filename>

```
cp ~/linuxc/newfile.txt newfile_bu.txt
```

Makes a "back up" copy in your working directory. How do you check it's there?

```
ls
```

```
## newfile_bu.txt
## newfile.txt
```

Secure Copy (scp): from laptop to logrus while on an outside network (e.g. Starbucks)

1) Create a file to copy

```
touch scp_test.txt
```

2) Mac users: open a local terminal (do not connect it to logrus)

2) Windows users: open a new MobaXterm session (shell)

Syntax: scp [options] <source path> <destination path>

3) Run the scp command from your local terminal window to download the file:

```
scp -P 44111 <user>@gateway.training.ncgr.org:~/linuxc/scp_test.txt .
```

Note: When you designate a port with secure copy (scp), you use a capital P

You will be prompted for your logrus password if not using MobaXterm

4) Now check that the file is on your own computer!

5) Using local terminal (the same one used to download), try uploading the file to logrus:

```
scp  -P  44111  scp_test.txt  <user>@gateway.training.ncgr.org:~/linuxc
```

Files and directories: removing "rm" command

The syntax for the remove command is: rm <filename>.

```
rm -i newfile_bu.txt

## rm: remove regular empty file newfile_bu.txt?
```

Enter "yes" or "y" in response to the question

```
ls -l

## total 0
## -rw-rw-r-- 1 eprice eprice 0 Aug 17 22:50 newfile.txt
```

At this point everyone should have the above in their linuxc class directory.

Tool box: How to abort a command/process

<control-key> c : Hold "control" key then hit "c" key then release. Control-key often referred to as CTRL.

Let's say you type a command and nothing happens, it *hangs*. This can happen when the syntax doesn't make sense. Good time for <CTRL> c

```
cat
## ^C
```

You should be returned to your prompt: [<username>@logrus linuxc]$

PART II: Advanced Topics

Files: Symbolic links and the soft link (-s)

Syntax: ln -s <file you want to link/point to> <name you want to give it>

```
ln -s /home/eprice/covid.fasta covid.fasta

ls -l

## total 0
## lrwxrwxrwx 1 eprice eprice 26 Aug 17 22:50 covid.fasta -> /home/eprice/covid.fasta ## -rw-rw-r-- 1 eprice eprice 0 Aug 17 22:50 newfile.txt
```

Understanding a fasta file format

Fasta files (.fasta or .fa) contain one or more sequences, each preceeded by a header starting with ">".
To show only first 10 lines of a file, use the pipe operator to redirect it to "head":

```
head covid.fasta
```

```
## >NC_045512.2 |Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, co
## ATTAAAGGTTTATACCTTCCCAGGTAACAAACCAACCAACTTTCGATCTCTTGTAGATCT
## GTTCTCTAAACGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACT
## CACGCAGTATAATTAATAACTAATTACTGTCGTTGACAGGACACGAGTAACTCGTCTATC
## TTCTGCAGGCTGCTTACGGTTTCGTCCGTGTTGCAGCCGATCATCAGCACATCTAGGTTT
## CGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTCCCTGGTTTCAACGAGAAAAC
## ACACGTCCAACTCAGTTTGCCTGTTTTACAGGTTCGCGACGTGCTCGTACGTGGCTTTGG
## AGACTCCGTGGAGGAGGTCTTATCAGAGGCACGTCAACATCTTAAAGATGGCACTTGTGG
## CTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAACTTGAACAGCCCTATGTGTTCATCAA
## ACGTTCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGCAGAACT
```

To show the last 10 lines of a file, use "tail":

```
tail covid.fasta
```

```
## TATTGACGCATACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAGAAGGC
## TGATGAAACTCAAGCCTTACCGCAGAGACAGAAGAAACAGCAAACTGTGACTCTTCTTCC
## TGCTGCAGATTTGGATGATTTCTCCAAACAATTGCAACAATCCATGAGCAGTGCTGACTC
## AACTCAGGCCTAAACTCATGCAGACCACACAAGGCAGATGGGCTATATAAACGTTTTCGC
## TTTTCCGTTTACGATATATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTACATAGC
## ACAAGTAGATGTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAGTGTGTAACATTA
## GGGAGGACTTGAAAGAGCCACCACATTTTCACCGAGGCCACGCGGAGTACGATCGAGTGT
## ACAGTGAACAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAAT
## TTTAGTAGTGCTATCCCCATGTGATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAA
## AAAAAAAAAAAAAAAAAAAAAA
```

The pipe operator will redirect output of a command to another command.

```
cat covid.fasta | head
```

```
## >NC_045512.2 |Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, co
## ATTAAAGGTTTATACCTTCCCAGGTAACAAACCAACCAACTTTCGATCTCTTGTAGATCT
## GTTCTCTAAACGAACTTTAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAGTGCACT
## CACGCAGTATAATTAATAACTAATTACTGTCGTTGACAGGACACGAGTAACTCGTCTATC
## TTCTGCAGGCTGCTTACGGTTTCGTCCGTGTTGCAGCCGATCATCAGCACATCTAGGTTT
## CGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTCCCTGGTTTCAACGAGAAAAC
## ACACGTCCAACTCAGTTTGCCTGTTTTACAGGTTCGCGACGTGCTCGTACGTGGCTTTGG
## AGACTCCGTGGAGGAGGTCTTATCAGAGGCACGTCAACATCTTAAAGATGGCACTTGTGG
## CTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAACTTGAACAGCCCTATGTGTTCATCAA
## ACGTTCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGCAGAACT
```

```
cat covid.fasta | tail
```

```
## TATTGACGCATACAAAACATTCCCACCAACAGAGCCTAAAAAGGACAAAAAGAAGAAGGC
## TGATGAAACTCAAGCCTTACCGCAGAGACAGAAGAAACAGCAAACTGTGACTCTTCTTCC
## TGCTGCAGATTTGGATGATTTCTCCAAACAATTGCAACAATCCATGAGCAGTGCTGACTC
## AACTCAGGCCTAAACTCATGCAGACCACACAAGGCAGATGGGCTATATAAACGTTTTCGC
## TTTTCCGTTTACGATATATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTACATAGC
## ACAAGTAGATGTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAGTGTGTAACATTA
## GGGAGGACTTGAAAGAGCCACCACATTTTCACCGAGGCCACGCGGAGTACGATCGAGTGT
## ACAGTGAACAATGCTAGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAAT
## TTTAGTAGTGCTATCCCCATGTGATTTTAATAGCTTCTTAGGAGAATGACAAAAAAAAAA
## AAAAAAAAAAAAAAAAAAAAAA
```

Understanding fastq (fq) file format

```
ln -s /home/fds/unix_basics/SP1.fq SP1.fq
```

```
ls -ltr
```

```
## total 0
## -rw-rw-r-- 1 eprice eprice 0 Aug 17 22:50 newfile.txt
## lrwxrwxrwx 1 eprice eprice 26 Aug 17 22:50 covid.fasta -> /home/eprice/covid.fasta ## lrwxrwxrwx 1 eprice eprice
Aug 17 22:50 SP1.fq -> /home/fds/unix_basics/SP1.fq
```

Fastq files contain sequence reads and associated meta data.

Tail the last 4 lines

```
tail -n 4 SP1.fq
```

```
## @cluster_834:UMI_TTAAGG
## AGGGTGGGGGATCACATTTATTGTATTGAGG
## +
## =A=@AB===>4?A=??EEB?EB@C?ECB=A?
```

A fastq file has 4 lines per record:

- The header; starts with "@"
- The sequence
- Throwaway line; begins with "+"
- Phred-scaled quality scores

What is the difference between this and a fasta file?

Using grep (global regular expression print) to extract metrics

Grep will output the lines containing a provided expression.

Syntax: grep "<expression>" <filename>

```
grep ">" covid.fasta
```

```
## >NC_045512.2 |Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, co
## >MT627325.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT622319.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568634.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568635.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568636.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568637.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568638.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568639.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568640.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT568641.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407649.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407650.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407651.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407652.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407653.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407654.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407655.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407656.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407657.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407658.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT407659.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT534630.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT510727.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT510728.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079843.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079844.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079845.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079846.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079847.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079848.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079849.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079850.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079851.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079852.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079853.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT079854.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT446312.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT412134.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT396241.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT039874.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT281577.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
```

```
## >MT291826.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291827.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291828.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291829.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291830.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291831.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291832.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291833.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291834.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291835.2 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT291836.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT259226.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT259227.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT259228.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT259229.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT259230.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT259231.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253696.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253697.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253698.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253699.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253700.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253701.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253702.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253703.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253704.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253705.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253706.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253707.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253708.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253709.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT253710.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT226610.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT121215.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT135041.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT135042.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT135043.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT135044.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT123290.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT123291.2 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT123292.2 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT123293.2 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT093631.2 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT049951.1 |Severe acute respiratory syndrome coronavirus 2 isolate SARS-CoV-2/huma
## >MT039873.1 |Severe acute respiratory syndrome coronavirus 2 isolate HZ-1, complete
## >MT019529.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/I
```

```
## >MT019530.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/I
## >MT019531.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/I
## >MT019532.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/I
## >MT019533.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/I
## >MN996527.1 |Severe acute respiratory syndrome coronavirus 2 isolate WIV02, complete
## >MN996528.1 |Severe acute respiratory syndrome coronavirus 2 isolate WIV04, complete
## >MN996529.1 |Severe acute respiratory syndrome coronavirus 2 isolate WIV05, complete
## >MN996530.1 |Severe acute respiratory syndrome coronavirus 2 isolate WIV06, complete
## >MN996531.1 |Severe acute respiratory syndrome coronavirus 2 isolate WIV07, complete
## >MN988668.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV WHU01
## >MN988669.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV WHU02
## >MN938384.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-S
## >MN975262.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-S
## >MN908947.3 |Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, com
```

Adding the "-c" option counts the number of lines containing a match (not the number of matches!).

```
grep -c ">" covid.fasta
```

```
## 102
```

The "-v" option reverses the grep search, which is the first step towards finding the total length of sequences.

```
grep -v ">" covid.fasta
```

Use <CTRL> c to halt the overflow of output.

We can add in the pipe operator redirect our output to the "wc" command. The output shows the number of newline characters, followed by line count and total character count.

```
grep -v ">" covid.fasta | wc
```

```
##   50812   50812 3096018
```

Let's trim out the newline characters with "tr -d" before doing the word count:

```
grep -v ">" covid.fasta | tr -d '\n' | wc
```

```
##       0       1 3045206
```

Working with compressed files

with powerful Z commands (zcat) p. 1 of 2

Let's copy another file:

```
cp /home/fds/unix_basics/table1.txt.gz /home/<user>/linuxc
```

```
zcat table1.txt.gz
```

```
## 1, Justin Timberlake, Title 545, Price $7.30
## 2, Taylor Swift, Title 723, Price $7.90
## 3, Mick Jagger, Title 610, Price $7.90
## 4, Lady Gaga, Title 118, Price $7.30
## 5, Johnny Cash, Title 482, Price $6.50
## 6, Elvis Presley, Title 335, Price $7.30
## 7, John Lennon, Title 271, Price $7.90
## 8, Michael Jackson, Title 373, Price $5.50
```

```
zgrep "Jagger" table1.txt.gz
```

```
## 3, Mick Jagger, Title 610, Price $7.90
```

!! = last command
:s = substitute /word1/with word2

```
!!:s/Jagger/John
```

```
## 5, Johnny Cash, Title 482, Price $6.50
## 7, John Lennon, Title 271, Price $7.90
```

Start ^ and end $ symbols

with zgrep p. 2 of 2

Display all the lines that **start** with 8:

```
zgrep "^8" table1.txt.gz
```

```
## 8, Michael Jackson, Title 373, Price $5.50
```

Display all the lines that **end** with 50:

```
zgrep "50$" table1.txt.gz
```

```
## 5, Johnny Cash, Title 482, Price $6.50
## 8, Michael Jackson, Title 373, Price $5.50
```

Files: parsing and creating data-subsets p. 1 of 5

(be in the linuxc directory as usual)

AWK (Aho, Weinberger and Kernighan the authors of the language)
General syntax:

awk 'pattern {action}' input-file :output goes to standard out=terminal
awk 'pattern {action}' input-file > output-file :or send to an output file

Exercise: Let's look at the 1st row of table1.txt
1, Justin Timberlake, Title 545, Price $7.30

How many fields does it have?

Files: parsing and creating data-subsets p. 2 of 5

```
gunzip table1.txt.gz

cat table1.txt

## 1, Justin Timberlake, Title 545, Price $7.30
## 2, Taylor Swift, Title 723, Price $7.90
## 3, Mick Jagger, Title 610, Price $7.90
## 4, Lady Gaga, Title 118, Price $7.30
## 5, Johnny Cash, Title 482, Price $6.50
## 6, Elvis Presley, Title 335, Price $7.30
## 7, John Lennon, Title 271, Price $7.90
## 8, Michael Jackson, Title 373, Price $5.50

awk '{print $1 $3 $5}' table1.txt

## 1,Timberlake,545,
## 2,Swift,723,
## 3,Jagger,610,
## 4,Gaga,118,
## 5,Cash,482,
## 6,Presley,335,
## 7,Lennon,271,
## 8,Jackson,373,
```

Files: parsing and creating data-subsets p. 3 of 5

Using field separator command -F

```
cat table1.txt

## 1, Justin Timberlake, Title 545, Price $7.30
## 2, Taylor Swift, Title 723, Price $7.90
## 3, Mick Jagger, Title 610, Price $7.90
## 4, Lady Gaga, Title 118, Price $7.30
## 5, Johnny Cash, Title 482, Price $6.50
## 6, Elvis Presley, Title 335, Price $7.30
## 7, John Lennon, Title 271, Price $7.90
## 8, Michael Jackson, Title 373, Price $5.50

awk -F, '{print $3}' table1.txt
```

```
##  Title 545
##  Title 723
##  Title 610
##  Title 118
##  Title 482
##  Title 335
##  Title 271
##  Title 373
```

Files: parsing and creating data-subsets p. 4 of 5

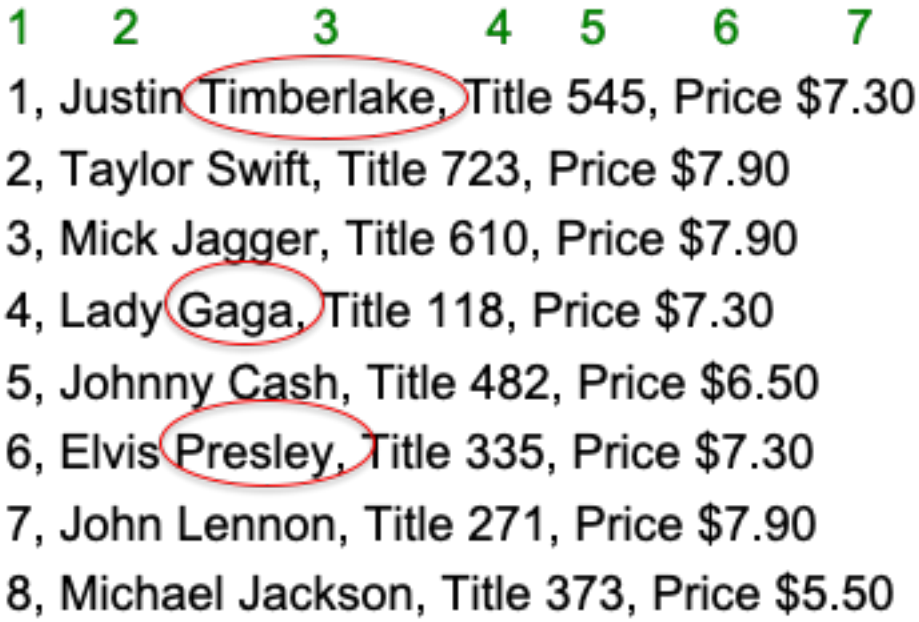
Conditional awk - time to really watch for syntax errors!

Statements inside the curly brackets {statement} are called a block.
If you put a conditional expression in front of a block with with ==, the statement inside the block will be executed only if the condition is true.
The whole awk command is inside ' '. For example:
awk '$7=="$7.30"{print $3}' table1.txt
The condition is if $7=="$7.30", meaning if the element at column 7 is equal to $7.30, execute statement(s) in the block {print $3}.

Revisiting table1 and *previous* awk command p. 5 of 5

Conditional awk - time to really watch for syntax errors!

awk '$7=="$7.30" {print $3}' table1.txt




```
awk '$7=="$7.30"{print $3}' table1.txt
```

```
## Timberlake,
## Gaga,
## Presley,
```

Files: Stream EDitor (sed)

text substitution

Syntax
sed s/pattern/replacement

Examples

```
echo "it's a trap" | sed s/ra/ar/
```

```
## it's a tarp
```

Say you want to change all price occurrences of $7.90 to $8.90 in table1.txt
You can do this with sed.

```
sed 's/7.90/8.90/' table1.txt > table2.txt
```

cat also displays file contents.

```
cat table2.txt
```

```
## 1, Justin Timberlake, Title 545, Price $7.30
## 2, Taylor Swift, Title 723, Price $8.90
## 3, Mick Jagger, Title 610, Price $8.90
## 4, Lady Gaga, Title 118, Price $7.30
## 5, Johnny Cash, Title 482, Price $6.50
## 6, Elvis Presley, Title 335, Price $7.30
## 7, John Lennon, Title 271, Price $8.90
## 8, Michael Jackson, Title 373, Price $5.50
```

The Bash "for" Loop

Suppose we want to run a command for a group of files in a directory. We can use a for loop to target all of them at once.

Syntax: for <variable_name> in <filename_expression>; do <command> ${<variable_name>}; done

For example the command:

```
for file in *; do echo ${file}; done
```

```
## covid.fasta
## newfile.txt
## SP1.fq
## table1.txt
## table2.txt
```

- The part up to the first semicolon targets every file in the working directory with the "*" wildcard
- The second part will sequentially echo each file in the working directory
- The third part is required to terminate the loop

Help with command syntax

If you forget details of a certain command, documentation can easily be found with a web search. There is also cheat sheet on the weebly site under Supplemental Documents.

Exercises

1. Using awk, print to output the first names of artists with album prices over $7.50 from table1.txt. Then redirect this output to a file named homework_1.txt
2. Using sed, replace all commas with semicolons in table1.txt. Save this to a file named homework_2.txt
3. Piping history to grep, show all commands you've used with the expression "ls". Save this to a file named homework_3.txt
4. Piping cat to wc -l on the history text file made during the tutorial, count the number of lines in it.
5. Using scp, download table1.txt to your own machine. Check it's there, then upload it back to logrus.

Supplementary Materials

Please find more information on the topics below plus a Unix cheat sheet on the class weebly website:

https://ncgrfallworkshop2021.weebly.com/supplemental-materials.html