NCGR NISE-Bioinformatics

Contents

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Chapter 1

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This document is available at https://inbre.ncgr.org/nise-bioinformatics

Chapter 2

Getting Started

Welcome to the Virtual Bioinformatics New Mexico INBRE Summer Experience (NISE)! We look forward to working with you this summer to dig into recent and ancient pandemics. We'll explore pandemics at different levels, looking at pathogens (genetics, evolution, transmission), disease (testing, outcomes, interventions, vaccination and immunity, risk factors), and societal factors (equity, policies, economy, mental health). You will each complete a 3 country research project and present it during the final week. We will help and support you along the way.

2.1 Computer requirements

You will need to meet or exceed the following computer requirements: Windows 7, Mac (High Sierra or later), or Linux CPU 1 Ghz; 8G RAM or More; Mic and Camera. You should also have access to stable internet. Please make sure you have Zoom, Discord (you will need a free account), a browser, and access to microsoft word and powerpoint or google docs and slides. You will also need a terminal app to connect to our server (which one you will use will depend on what platform you are working on; we can help you with this once the internship is underway). If you have any concerns, please reach out to us.

You will need to install the following software on your local computer.

1. Zoom

Install the correct version for your OS. Don't plan to use the web version, as this does not have enough features.

2. MobaXterm (Windows Users Only. Mac or Linux users will use their native terminal)

- Download the “Home” “Installer” edition. Be careful not to install the portable or professional editions.
- Before installing, extract the installer zip folder to any location on your computer.
- Now run the installer and follow the prompts.

4. Filezilla
5. Jalview

2.2 Connecting to the linux server

1. Open your terminal.
2. Type the following on your command line, substituting in your username for .

```
ssh -p2406 <username>@inbre.ncgr.org
```

3. Enter your password.

If you have trouble connecting, please contact Ethan Price at inbre@ncgr.org.

Chapter 3

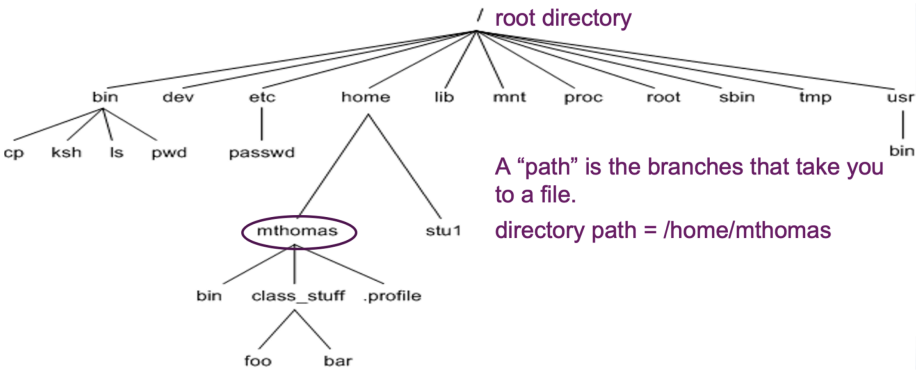
Linux

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

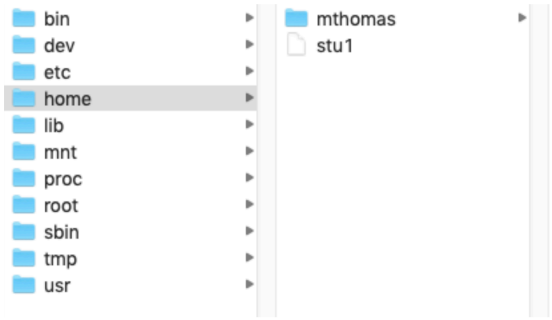
3.1 A little shell... aka the $ prompt is the command line interface

- 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)

3.2 Directory Structure



In a Finder window, you would see this:



3.3 Find the shell in system you’ll use to log into the NCGR’s server

- For **Windows**: search for MobaXterm from the start menu.
  - It may be useful to drag the terminal icon to the **desktop** for easier access in the future.
- 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 into the **Dock** for easier access in the future.

3.4 Log on to logrus server

Enter the following command to log on to logrus:

- substitute **your** personal username in for "user"

```
ssh -p2406 user@inbre.ncgr.org
```

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.

3.5 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 ~]$

Command **output** is shown after the "##" in this document.

3.6 Part I: Basic Topics

3.6.1 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
```

3.6.2 Listing options

using the ls command

- **l**ong list:

```
ls -l
```

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

- **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
```

3.6.3 Navigation

1) "**c**hange **d**irectory" to the directory you made

- where ~ is shorthand for your home directory

```
cd ~/linuxc
```

```
pwd
```

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

3.6.4 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
```

3.6.5 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.

To perform a command from the list by number:

```
!17
```

To perform the last command you made:

```
!!
```

3.6.6 Files: creating by redirecting standard out

redirect operator >

To send output to a file instead of standard out:

- standard out is just 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!

3.6.7 File name completion with tab

To autocomplete remainder of file name instead of typing it all in:

- cat h…(press tab)
  - cat history
- prevents typos and saves time

3.6.8 Files: moving files from one filename to another

mo**v**ing "mv" command

Syntax: mv sourcefilename destinationfilename

```
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
```

3.6.9 Files: copying files from one filename to another

co**p**ying "cp" command

Syntax: cp sourcefilename destinationfilename

1) Change back to the linuxc directory:

```
cd ~/linuxc
```

2) Make a "back up" copy of a file in your working directory:

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

3) Check if the newly copied file is there:

```
ls
```

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

3.6.10 Files: securely copying files between your laptop and logrus

secure **cop**y "scp" command

- a secure way to copy files to/from a server while you're working on an outside network
  - like from your home or starbucks to logrus and vice versa

Syntax: scp [options] sourcepath destinationpath

1) Create a file to copy

```
touch scp_test.txt
```

2)

- **Mac** users
  - open a **local** terminal
  - do **not** connect it to logrus
- **Windows** users
  - open a new MobaXterm session (shell)

3) Run the scp command from your **local** terminal window:

- to **download** the file **to your computer** from logrus
- the last period means that the destination is your working directory

```
scp -P 2406 <user>@inbre.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) Check to see if the file you copied from logrus is on **your** computer!

5) Now **upload** a file **to logrus** from your computer

- Again, run the scp command from your **local** terminal window:

```
scp -P 2406 scp_test.txt <user>@inbre.ncgr.org:~/linuxc
```

6) Check to see if the file you copied from your computer is on **logrus**!

3.6.11 Files and directories: removing files is deleting files

removing "rm" command

Syntax: rm [options] filename

```
rm -i newfile_bu.txt
```

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

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

```
yes
```

```
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.

3.6.12 Tool box: How to abort a command/process

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
```

If you can't execute commands, then CTRL c

```
## ^C
```

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

3.7 PART II: Advanced Topics

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

Syntax: ln -s FileYouWantToLink/PointTo NameYouWantToGiveIt

```
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 Aug 17 22:50 newfile.txt
```

3.7.2 Understanding a fasta file format

Fasta files (.fasta or .fa) contain one or more sequences, each preceded by a **header** starting with ">".

Show only the **first 10 lines** of a file with "head" command:

```
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
```

Now show only the **last 10 lines** of a file using the "tail" command:

```
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.

Use the pipe operator to redirect "cat" output to "head":

- The symbol "|" denotes a pipe

```
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
```

3.7.3 Understanding fastq (fq) file format

Fastq files contain sequence reads and associated **meta data**.

```
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
```

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?

3.7.4 Using grep (global regular expression print) to extract metrics

Grep will output the lines containing a provided expression.

Syntax: grep [options] "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/
## >MT019530.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/
## >MT019531.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/
## >MT019532.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/
## >MT019533.1 |Severe acute respiratory syndrome coronavirus 2 isolate BetaCoV/Wuhan/
## >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 WHUO
## >MN988669.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV WHUO
## >MN938384.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-
## >MN975262.1 |Severe acute respiratory syndrome coronavirus 2 isolate 2019-nCoV_HKU-
## >MN908947.3 |Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, co
```

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 c to halt the overflow of output.

We can add in the pipe operator to 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
```

wc: prints newline, word, and byte counts for each file:

```
## 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
```

3.7.5 Working with compressed files

Powerful Z commands (zcat)

- p. 1 of 2

Let's copy another file:

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

3.7.6 Start ^ and end $ symbols

Powerful Z commands (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
```

3.7.7 Files: parsing and creating data-subsets

p.1 of 5

Be sure you are in linuxc directory (as usual)

AWK command

- **A**ho, **W**einberger and **K**ernighan
  - 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:

How many fields does the 1st row of table1.txt have?

Let's look at the 1st row of table1.txt:

1, Justin Timberlake, Title 545, Price $7.30

How many fields does it have?

3.7.8 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,
```

3.7.9 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
```

3.7.10 Files: parsing and creating data-subsets

p. 4 of 5: Conditional awk

Time to really watch for syntax errors!

1) Statements inside the curly brackets {statement} are called a block.
2) 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**.
3) The whole awk command is inside ' '.

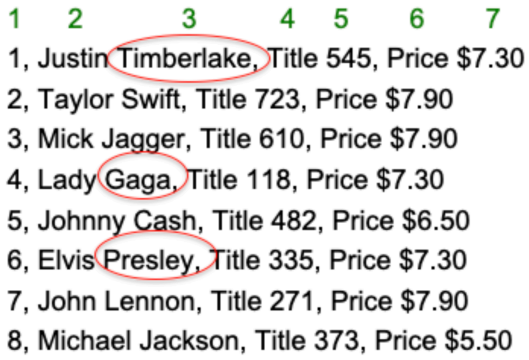
- For example:
  - awk '$7==“$7.30”{print $3}' table1.txt
- The condition is:
  - if $7==“$7.30”
  - meaning if the element at column 7 is equal to “$7.30”, then execute statement(s) in the block {print $3}.

3.7.11 Revisiting table1 and *previous* awk command

p. 5 of 5

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

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



3.7.12 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 from table1.txt, and save the changes to a new file.

You can do this with sed.

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

Use cat to display the contens of the new file:

```
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
```

3.7.13 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 variablename in filenameexpression; do command ${variablename}; done

```
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

3.7.14 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.

3.8 Exercises

1. Using awk, print to output the first names of artists with album prices over $7.50 from ta- ble1.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 home- work_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.

3.9 PART III

1) Log on to logrus server

2) Enter the following command to log on to the server:

```
ssh -p2406 user@inbre.ncgr.org
```

- Don't forget to substitute **your** personal username in

3) Make a new directory under **your home directory**:

```
mkdir fastq_files
```

4) Enter into the new directory:

```
cd fastq_files
```

5) Move the fastq file from yesterday to the present working directory:

```
mv ~/linuxc/SP1.fq .
```

```
ls -ltr
```

```
## total 0
## lrwxrwxrwx 1 elavelle elavelle 28 Aug 17 22:50 SP1.fq -> /home/fds/unix_basics/SP1.f
```

6) How can we count the number of records in a fastq file?

```
grep -c "@cluster" SP1.fq
```

```
## 250
```

7) If you want to determine the number of lines in a file, you can use the "wc" command.

```
cat SP1.fq | wc -l
```

```
## 1000
```

8) Why does the first command output 250 and the second 1000?

3.10 More Exercises

1. With one command, send a copy of table1.txt in the linuxc directory to your home directory with the name table1_bu.txt
2. Print to standard output the last line of table1.txt
3. Use a loop to count the number of lines in all files in the linuxc directory.
4. Print to standard output the last names of music artists with album prices less than or equal to $7.30
5. Create a file with only the accession numbers of the sequences contained in the covid.fasta file (with no additional spaces or symbols).

3.11 Jeopardy

https://jeopardylabs.com/play/linux-commands-how-to

Chapter 4

Our World in Data (parsing)

4.1 Practice parsing

Let's practice with a small file. Make sure you are in a **screen**.

1. Make a directory under your home directory called "parse".
2. Go into that directory.
3. Copy the file "pandemics.csv" from this directory: "/home/data/nise" to the directory you just made.
4. Take a look at the file.
5. Sort by year an put it into a new file called "sort.pandemic.csv" Note that you will need to change the delimiter to a comma (-t), tell it to sort numerically (-n), and tell it which column to sort (-k) sort -t, -n -k3 pandemics.csv > sort.pandemics.csv
6. Pull out all the instances that mention plague Note that grep is case sensitive by default so you might want to use the -i flag to make it case insensitive in case the is inconsistent
7. Pull out all the instance of the flu
8. Let's count the number of each type of pathogen (column 2). You could do this with a series of grep commands but with a big file you might not know all the possible pathogens and it would get tedious. So let's do this in a step-wise fashion and make sure each piece is as expected, then pipe

it into the next step.
a. First pull out column 2 using awk or cut
b. Get the unique values (make sure you "sort" before you "uniq" or you will only deredundify adjacent identical values).
c. Get the count (hint: add -c to the uniq step)

9. Grab and count the organisms for the instances that mention plague

Hint: It is the same as #8 except you need to grab the plague lines first. When you put a command after the pipe it will read in the output of the previous command so only use the file name on the first command.

Click for All Answers

Note that there are often several ways to do things in linux and not all methods are shown.

```
1. mkdir ~/parse

2. cd ~/parse

3. cp /home/data/nise/pandemics.csv . [Don't forget the space and period at the end; tl

4. cat pandemics.csv [you could also use more, less, head, tail, or other commands]

5. sort -t, -nk 3 pandemics.csv > sort.pandemics.csv

6. grep -i plague sort.pandemics.csv

7. grep -i flu sort.pandemics.csv

8. awk -F, '{print $2}' sort.pandemics.csv | sort | uniq -c
     [Note that you can also use: "cut -d, -f2 pandemics.csv" for the first step]

9. grep -i plague sort.pandemics.csv | awk -F, '{print $2}' | sort | uniq -c
```

4.2 Our World in Data

Now let's use the data from "Our World In Data". For things that are new, we have added some in-line answers but before you reveal the answer, try it yourself first using the hints provided.

10. Make sure you are still in the parse directory.
11. Link to the file "owid-covid-data.csv". It is in this directory: "/home/data/nise/".

Click for Answer

```
ln -s /home/data/nise/owid-covid-data.csv .
```

12. How many rows are in the file? Use wc -l (wc = word count, -l = lines)

Click for Answer

```
wc -l owid-covid-data.csv
```

13. How many columns? There is a special variable, NF, in awk, which prints the number of fields

Note: this will print the number of fields in each row. You can hit ctrl-c if you don't want to go through the whole file

Click for Answer

```
awk -F, '{print NF}' owid-covid-data.csv
```

14. Let's look at hospital_beds_per_thousand (column 60). We also need to get the location (country) from column 3 and the date from column 4. We'll pipe it into less so that we can scroll through it (to get out of less, hit "q").

Click for Answer

```
cut -d, -f 3,4,60 owid-covid-data.csv | less
```

15. There are lots of dates for each country. Let's do the same search but limit it to early in the pandemic (2020-03-11), which is the day that the World Health Organization declared COVID-19 to be pandemic. Put it into a file called "beds.2020-03-11.csv" so we don't have to keep generating it.

16. What country had the least beds per thousand on 2020-01-03 and which has the most? Hint: Sort by the number of beds and pipe it into less.

Note: Some lines have missing data and will sort at the top of the file so you will have to scroll down.

17. How many beds were there in the United States on 2020-01-03?

Hint: There is a "United States" and a "United States Virgin Islands". To avoid getting the latter, have the match end with a comma. Also, require grep to start the match at the beginning of the line (^). It is good practice to be specific when using grep.

Click for Answer

```
grep "^United States," beds.2020-03-11.csv
```

18. How many beds were there in your three countries on 2020-01-03?

If your countries don't have data on that date, go back to the original file and see if you can find data for any date.

Hint: we'll use the extended version of grep which will allow us to search all 3 at once. Use the -E flag and put the things you are searching for in double quotes, seperated by pipes.

Click for Answer

```
grep -E "^Sweden,|^Norway,|^Denmark," beds.2020-03-11.csv
```

19. Create a file that has only the United States data for beds with the same three columns we have been using. Call it usbeds.csv. We'll use this file for the questions below.

20. Get the number of beds in the United States for each day in 2020. Note: Since these numbers don't change, this is kind of silly but it will give you the skills to grab other variables across a date range.
21. Get the number of beds in the United States for the first COVID wave (March through September 2020).

Hint: Use sed to remove the dashes then awk with $2>=20200301&&$2<=20200930.

Click for Answer

```
sed 's/-//g' usbeds.csv | awk '$2>=20200301&&$2<=20200930{print}'
```

22. BONUS: Get the average number of beds in the United States for the first COVID wave (March through September 2020). This is a tough one. See if you can understand the code.

Click for Answer

```
sed 's/-//g' usbeds.csv | sed 's/-//g' |awk -F, '$2>=20200301&&$2<=20200930{SUM+=$3;CNT+=1}END{pr
```

Click for All Answers

```
11. pwd [If you aren't in that directory you can: "cd ~/parse"]

10. ln -s /home/data/nise/owid-covid-data.csv .

12. wc -l owid-covid-data.csv

13. awk -F, '{print NF}' owid-covid-data.csv

14. cut -d, -f 3,4,60 owid-covid-data.csv | less

15. cut -d, -f 3,4,60 owid-covid-data.csv | grep 2020-03-11 > beds.2020-03-11.csv

16. sort -t, -n -k3 beds.2020-03-11.csv | less

    Least: Mali,2020-03-11,0.1
```