PLEASE FILL IN THIS → side of the classroom first!

If you are using one of the Gilman desktops...

- Sign in on a desktop
- Double click the desktop folder "SSH & Secure File Transfer"
- Double click on "putty.exe"
- Sign into the server
- Chill

If you need help, raise your hand or put an ORANGE sticky note on your monitor

Advanced UNIX

BCBGSO Workshop

March 3rd, 2018

Presenter: Carla Mann

Thanks!

- BIG thanks to Jennifer Chang for inspiration for slides and materials
- Organizers: Urminder Singh and Paul Villanueva
- Funding/Support/Volunteers: BCBGSO
- Tech support: Biology IT, especially Levi Baber

Our many, MANY volunteers:

Ashish Jain Bekah Starks Sagnik Banerjee

Sharmistha Chakrabortty Yulu Chen Basil Khuder

Avani Khadilkar Weija Su Hylia Gao

Alvin Chon

Materials

 All exercise activities from this workshop are available at: https://github.com/cmmann/20180302-unix-adv

 Supporting materials are available at: https://github.com/cmmann/20180302-UNIX-ADVANCED-

You can download this PowerPoint and follow along on your computer.

 You will probably benefit quite a bit from downloading (and using) the cheat sheet!

Set-Up

Mac/Linux:

Open terminal

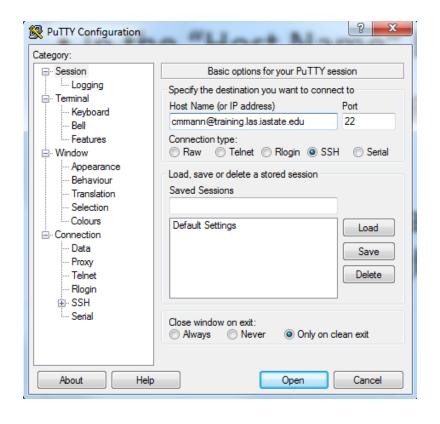
ssh <yournetid>@training.las.iastate
.edu

Windows:

Open Putty.exe

Enter

<yournetid>@training.las.iastate
.edu
into the Host Name box



Overview

Lesson 0: Quick Review of Basic UNIX

Lesson 0.5: Setup

Lesson 1: Text Editing with nano

Lesson 2: Shell Scripting

Lesson 3: Condo and Slurm

Lesson 4: Data Exploration with grep

Lesson 5: Regular Expressions (if we get to it)

Lesson 0: Quick Review

When describing a path to an/application:

```
this/is/path/to/the/file.txt
```

- For our purposes:
 - "folder" and "directory" refer to the same thing
 - "terminal", "console", and "console window" all refer to the place you will type commands
- In PowerPoint, commands you will type in the terminal will look like this
- Keys you press will look like this: [Ctrl] or [command]
- If you should press keys at the same time: [Ctrl] + [C]
- A name or value that is user-dependent or variable will look this>
- Don't use spaces in names; use dashes [-] instead

cd: change directory

ls: list directory contents

man <command>: show manual page for command

Lesson 0.5: Setup

Once logged in, use this command to clone the materials into your workspace:

```
git clone
https://github.com/cmmann/20180303-unix-
adv.git
```

If you are prompted for a username/password, check to make sure you typed the URL correctly!

Lesson 1: Text Editing

Overview:

Lesson 1.1: Text Editors in UNIX

Lesson 1.2: nano

Lesson 1.1: Text Editors in UNIX

Multiple ways of editing text in files in UNIX

Vim is a VERY powerful text editor, but has a steep learning curve

 Very worthwhile to learn, but we could spend an entire workshop on it, so we're not going to mess with it today

"Friendliest" Unix text editor is nano

*If you already know how to use Vim, feel free to use it!

Lesson 1.2: Text Editing with nano

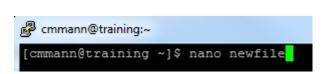
Command:

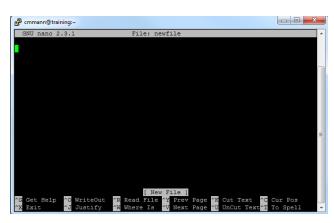
nano <filename>

What it does:

If <filename> exists, nano will open the file and you can read and manipulate it

If <filename > does not exist, nano will create a new file called <filename > and open it for you





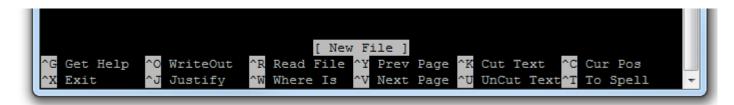
Lesson 1.2: Text Editing with nano

nano is kind enough to give you a list of controls at the bottom of the editing window

You can easily type in the nano window just as you would in Notepad, TextEdit, or any other text editor

To exit out of a nano window, type [Ctrl]+[x]

nano will ask if you want to save changes; type [y] or [n]



Goals:

- 1. Navigate to adv-unix/exercise1/
- Use nano to open "exercise1.txt"
- **3. Edit** the text of "3. What is the capital of Assyria?" to read "3. What is your favorite color?"
- Answer the questions in the file (the answers don't really matter, just your ability to edit the file)
- **5. Exit** (save when prompted)

Goals:

- 1. Navigate to adv-unix/exercise1/
- Use nano to open "exercise1.txt"
- 3. Edit the text of "3. What is the capital of Assyria?" to read "3. What is your favorite color?"
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Exit (save when prompted)

Lesson 2: Shell Scripting

Overview:

Lesson 2.0: What is a shell?

Lesson 2.1: Creating a shell script

Lesson 2.3: Executing a shell script

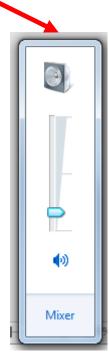
Exercise 2: Completed throughout the lesson

Lesson 2.0: What is a shell?

A shell is an interface for accessing an operating system's services

Shells can be GUIs (graphical user interface) or CLIs (command-line interface)





Lesson 2.0: What is a shell?

There are multiple 'flavors' of command-line interfaces: DOS, POSIX, CMD.EXE, many others

We are going to use a command-line shell called Bash:

To enable Bash scripting on your terminal, enter:

bash

And as simply as that, the server now knows what to use to interpret commands

Lesson 2.0: Shell Scripting

Every command you type into your terminal can be saved into a file

This file is called a shell script

That file can then be executed, or run, from the terminal

The commands in the file will be read line-by-line and executed, as if you had typed them in the terminal

Lesson 2.1: Creating a Shell Script

When creating a shell script, we first need to create a file

This file should end in ".sh", which signifies that it is a shell script

Note that the computer doesn't require the ".sh" extension to recognize this (it uses something different) – this is a human convention so you know the file contains a shell script

Exercise 2:

Create a file, using nano, called "hello.sh"

Lesson 2.1: Creating a Shell Script

WE know the script should be executed with bash – Unix doesn't. How do we tell UNIX what tools to use?

By starting off the file with a hashbang and a file path! This tells UNIX to use certain a certain shell to run the script

In our case, we're using bash. So the first line of hello.sh, and EVERY SHELL SCRIPT YOU WRITE (that will be interpreted with bash), will be:

#!/bin/bash

Exercise 2: Go ahead and add this header to hello.sh

Lesson 2.1: Comments

Scripts can be complicated

Keep track of what scripts are doing with comments

In .sh files, any text following '#' is ignored by bash

#So this is ignored
But only #this last bit is ignored

Exercise 2:

#Using a comment, add your name and the date to your hello.sh script

Lessor

It is good

Will you st



"Always code as if the guy who ends up maintaining your code will be a violent psychopath who knows where you live"

-Martin Golding

s well

ig 6 months

Lesson 2.1: Creating a Shell Script

We are going to create a simple script within hello.sh that prints "hello" to the console upon execution.

You can print to the console using the command "echo":

echo "what you want to say"

Lesson 2.1: Creating a Shell Script

You can do the same thing, within the script

Exercise 2:

In your hello.sh file, type:

```
echo "hello world!"

or
echo "Hello, world!"

(if you want to be grammatically correct)
```

Then exit and save the file.

You can execute scripts you've written (that are in your present working directory) by typing:

./scriptname.sh

This tells the server the path to the command it's executing

But we execute other commands by typing just ls or cd or echo

Why can't we just execute the file by typing it's name?

Security.

What happens if somebody comes into your directory and creates an executable file called ls that contains:

```
#!/bin/bash
echo "sucks to be you"
rm -rf /
```

(Don't create this file or run rm -rf /)

Security.

What happens if somebody comes into your directory and creates an executable file called ls that contains:

```
#! /bin/bash
echo "sucks to be you"
rm -rf /
```

This way, you can be sure that you're using the genuine ls command.

So how do we execute hello.sh?

So how do we execute hello.sh?

What happens when you run the script?

So how do we execute hello.sh?

What happens when you run the script?

```
[cmmann@training:~

[cmmann@training ~]$ ./hello.sh
bash: ./hello.sh: Permission denied
[cmmann@training ~]$
```

See what happens with:

bash hello.sh

```
[cmmann@training ~]$ ./hello.sh
bash: ./hello.sh: Permission denied
[cmmann@training ~]$ ls -l hello.sh
-rw-r---. 1 cmmann domain users 40 Mar 1 22:44 hello.sh
[cmmann@training ~]$ bash hello.sh
hello, world!
[cmmann@training ~]$
```

Why is the script executing, even though we don't have permission!?!?

Fun fact: The execute permission is not a *security* feature – instead, it's a flag to the system that a script is executable, and the system now knows to look for a #! header line to know what program to use to *interpret* the instructions in your script.

So when we run a script with ./hello.sh, we are executing *hello.sh*, which the system does not recognize as executable

When we run the script with bash hello.sh, we are executing bash, which is reading hello.sh and then executing the commands it has read

The difference between the two:

In scenario 1, hello.sh is telling the system what to do.

In scenario 2, bash is reading hello.sh, and then bash is telling the system what to do.

bash has executable permissions, so it can 'boss' the system around, but hello.sh currently doesn't, so it can't.



Try changing the permissions on hello.sh to make it executable for you, the owner

How would you change the Execute permission for hello.sh? chmod ??? hello.sh

Remember: read = 4, write = 2, execute = 1

Exercise 2:

Try changing the permissions on hello.sh to make it executable for you, the owner

How would you change the execute permission for hello.sh?

chmod ??? hello.sh

Remember: read = 4, write = 2, execute = 1

Try executing the script now:

./hello.sh

```
[cmmann@training ~]$ ls -l hello.sh
-rw-r--r-. 1 cmmann domain users 40 Mar 1 22:44 hello.sh
[cmmann@training ~]$ chmod u+x hello.sh
[cmmann@training ~]$ ls -l hello.sh
-rwxr--r-. 1 cmmann domain users 40 Mar 1 22:44 hello.sh
[cmmann@training ~]$ ./hello.sh
hello, world!
[cmmann@training ~]$ bash hello.sh
hello, world!
```

If Execute permission isn't providing security, then what is?

If Execute permission isn't providing security, then what is?

Read and Write permissions!

Try changing permission of hello.sh so that you have Write and Execute, but not Read:

If Execute permission isn't providing security, then what is?

Read and Write permissions!

Try changing permission of hello.sh so that you have Write and Execute, but not Read:

```
[cmmann@training ~]$ ls -l hello.sh
-rwxr--r-. 1 cmmann domain users 40 Mar 1 22:44 hello.sh
[cmmann@training ~]$ chmod 344 hello.sh
[cmmann@training ~]$ ls -l hello.sh
--wxr--r-. 1 cmmann domain users 40 Mar 1 22:44 hello.sh
[cmmann@training ~]$ ./hello.sh
[cmmann@training ~]$ ./hello.sh
/bin/bash: ./hello.sh: Permission denied
[cmmann@training ~]$ bash hello.sh
bash: hello.sh: Permission denied
```

Why don't they work?

Why don't they work?

Because without Read permission, the system can't read the commands in the file, regardless of how it's called!

So Read (and to a lesser extent, Write) permissions are the true 'security' features of permissions

Exercise 2:

Goal:

Lesson 3: Condo and Slurm

Overview:

Lesson 3.1: High Performance Computing

Lesson 3.2: Condo

Lesson 3.3: Slurm

Lesson 3.4: Slurm Job Script generation

Lesson 3.5: Slurm commands

Also known simply as "HPC"

High Performance Computing most generally refers to the practice of aggregating computing power in a way that delivers much higher performance than one could get out of a typical desktop computer or workstation in order to solve large problems in science, engineering, or business.

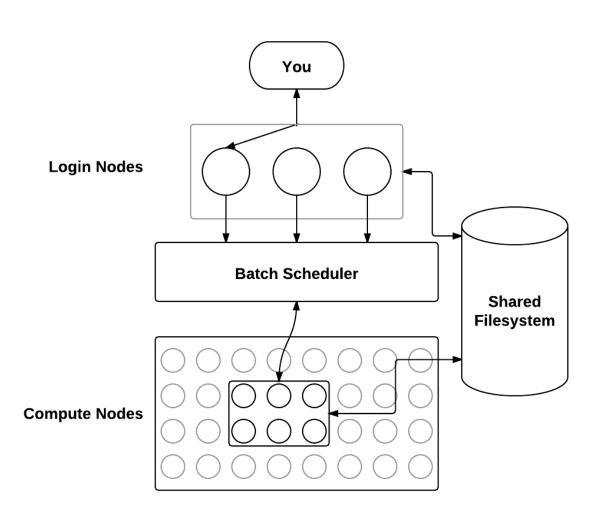
https://insidehpc.com/hpc-basic-training/what-is-hpc/



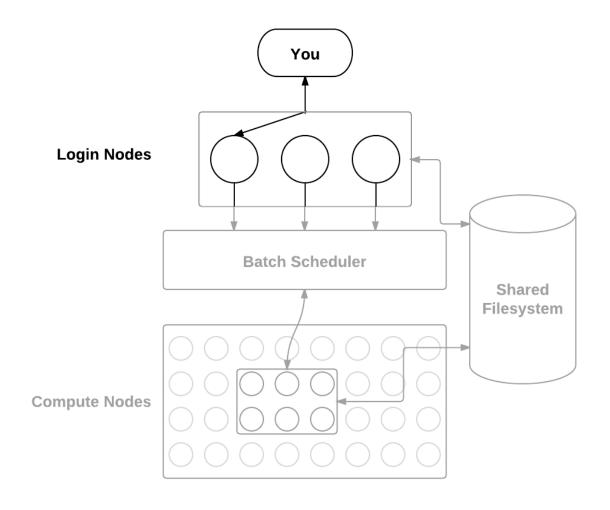
Typically, an HPC resource consists of a "cluster" of computational nodes, so sometimes you will hear HPC referred to as a "cluster"

http://www.ticra.com/products/software/grasp/mpi-hpc-linux-cluster

- Many people can simultaneously use an HPC cluster
- An HPC resources can perform several computationally intensive jobs at once by distributing those jobs across several computational nodes

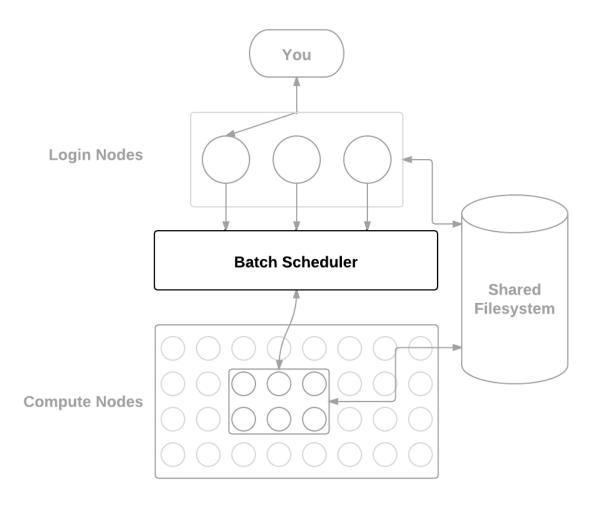


Users
 communicate
 with the server
 through SSH, and
 connect to a
 "head" or "login"
 node

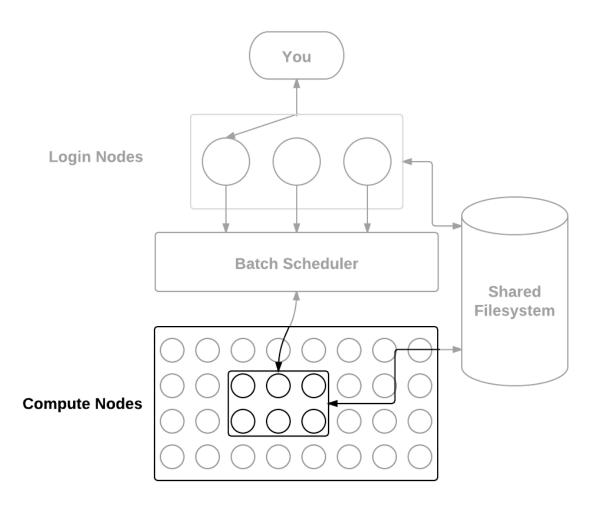


The user submits

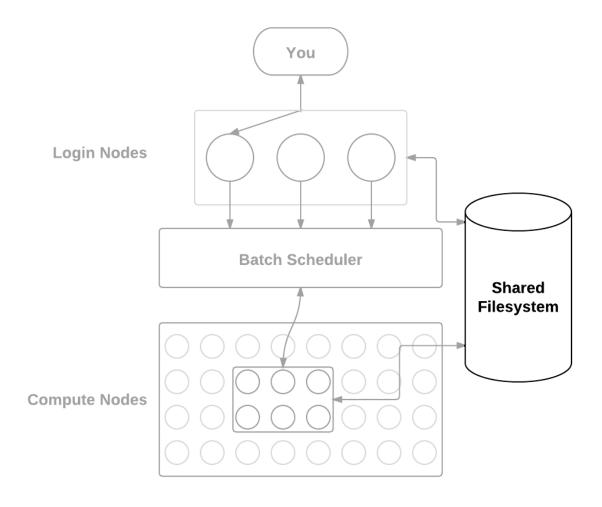
 a job through the
 head node to a
 "scheduler"



 The scheduler distributes jobs across the "compute" nodes in the cluster, so that jobs can be performed as efficiently as possible



 Once the compute nodes have finished performing a job, the results are stored where the user can access them



Lesson 3.2: Condo

- Condo is one of ISU's frequently utilized HPC resources
- Further information: https://www.hpc.iastate.edu/guides/condo-2017

ITS has very good guides on IT resources

Lesson 3.2: Condo

- NEVER DO LARGE OPERATIONS DIRECTLY IN YOUR CONSOLE/ON THE HEAD NODE
- This means you shouldn't run large jobs directly in your terminal when connected to an HPC cluster
- When SSH'd into the HPC cluster, the environment you're in is only meant to handle task scheduling
- You submit jobs to the compute nodes through Slurm scripts

Lesson 3.3: Slurm

 Simple Linux Utility for Resource Management

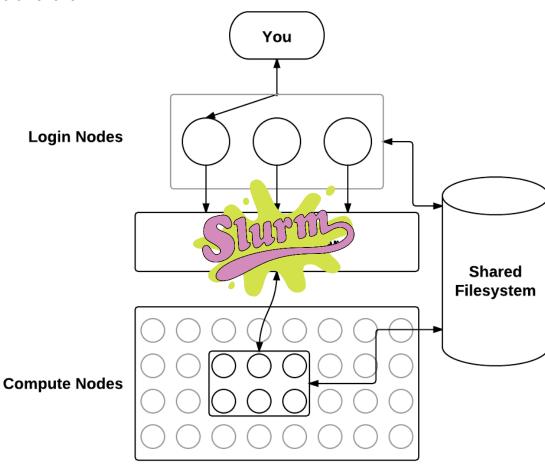
 The name is indeed referencing Slurm "soda" from the TV show Futurama





Lesson 3.3: Slurm

 Slurm is the batch scheduler that ISU uses for distributing jobs on our HPC resources



Lesson 3.3: Slurm

- HPC jobs are submitted through the console, in the form of scripts
- Each of these scripts will have special instructions for Slurm, and Slurm will handle them appropriately

```
#!/bin/bash

# Copy/paste this job script into a text file and submit with the command:
# sbatch thefilename

#SBATCH --time=1:00:00  # walltime limit (HH:MM:SS)
#SBATCH --nodes=1  # number of nodes
#SBATCH --ntasks-per-node=16  # 16 processor core(s) per node
#SBATCH --job-name="Sample Job"
#SBATCH --mail-user=cmmann@iastate.edu  # email address
#SBATCH --mail-type=BEGIN
#SBATCH --mail-type=BEGIN
#SBATCH --mail-type=FAIL
#SBATCH --output="2018samplejob.txt"  # job standard output file (%j replaced by job id)
#SBATCH --error="2018sampleerror.txt"  # job standard error file (%j replaced by job id)
# LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE
```

 ITS has set up a wonderful tool for automatically generating Slurm scripts

https://www.hpc.iastate.edu/guides/condo-2017/slurm-job-script-generator-for-condo

We will be able to use Slurm on our training server;
 you can get access to condo through your lab:

https://www.hpc.iastate.edu/guides/condo-2017/who-can-use-condo

Slurm Job Script Generator for Condo

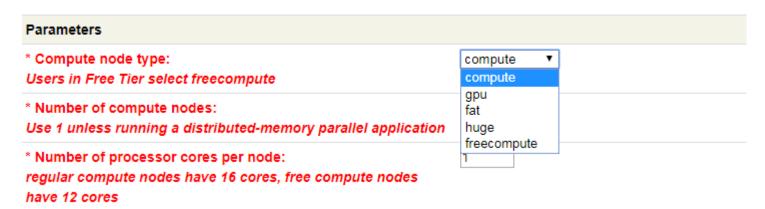
* indicates a required field

Parameters	
* Compute node type:	compute ▼
Users in Free Tier select freecompute	
* Number of compute nodes:	1
Use 1 unless running a distributed-memory parallel application	
* Number of processor cores per node:	1
regular compute nodes have 16 cores, free compute nodes	
have 12 cores	
fat node has 32 cores, huge node has 40 cores, GPU node has	
12 cores	
* Walltime limit:	1 hours 00 mins 00 secs
Maximum time the job may run. Shorter jobs may start running	
sooner.	
Max memory per compute node:	64 MB ▼
Default memory is 8000 MB per processor core requested for	
the regular compute nodes (1 GB == 1024 MB)	
Job name:	testJob
Default is the job script name. Displayed by the squeue	
command.	
Receive email for job events:	□ BEGIN □ END □ FAIL
BEGIN: when job starts, END: when job ends, FAIL: if job fails	my.email@iastate.edu
	EMAIL
Job standard output file:	testJob.output
Default is "slurm-%j.out", where %j is the job ID.	•
Job standard error file:	testJob.error
Default is same file as the job standard output file.	

Compute node type:

Allows you to select the node type for your job

You will mostly use "compute" or "freecompute"; gpu, fat, and huge are more expensive and for processing truly ridiculous amounts of information (like TB, as opposed to GB)



Number of compute nodes:

Allows you to select how many nodes will process your job

More nodes = faster completion = more \$

* Number of compute nodes:

Use 1 unless running a distributed-memory parallel application

Number of processor cores per node:

Allows you to select how many processors in each node will be utilized

More processors = faster completion = more \$

* Number of processor cores per node: regular compute nodes have 16 cores, free compute nodes have 12 cores fat node has 32 cores, huge node has 40 cores, GPU node has 12 cores

Walltime limit:

Limits how long a job will run

A job will immediately be canceled if it runs into its walltime limit

Shorter walltimes tend to be prioritized (to finish as many jobs as quickly as possible)

• Pro-tip (Thanks, Sagnik!):

If you're running a script for the first time, allocate 1-2min of walltime, instead of several hours or days

Check to make sure your script actually runs before requesting more than a few minutes of HPC time!

Max memory per compute node:

Limits how much memory each node you are utilizing will use

MB ▼

More memory = faster completion = more \$

Max memory per compute node:

Default memory is 8000 MB per processor core requested for the regular compute nodes (1 GB == 1024 MB)

Job name:

A name you can provide to more easily identify your jobs

Job name:

Default is the job script name. Displayed by the squeue command.

testJob

Receive email for job events:

You can provide an email address to optionally receive emails to inform you when your job starts, when it ends, and if it fails due to an error of some kind

Receive email for job events:

BEGIN: when job starts, END: when job ends, FAIL: if job fails

BEGIN END FAIL
my.email@iastate.edu
EMAIL

Job standard output file:

If your job would output information to the console, this is the name of the file it will output to

Job standard output file:

Default is "slurm-%j.out", where %j is the job ID.

testJob.output

Job standard error file:

If your job fails due to an error, the error message/log will be output to this file

Job standard error file:

Default is same file as the job standard output file.

testJob.error

As you specify options, the page will dynamically generate a script header containing your parameters

Job Script

```
#!/bin/bash

# Copy/paste this job script into a text file and submit with the command:

# sbatch thefilename

#SBATCH --time=1:00:00  # walltime limit (HH:MM:SS)

#SBATCH --nodes=1  # number of nodes

#SBATCH --ntasks-per-node=1  # 1 processor core(s) per node

#SBATCH --mem=64M  # maximum memory per node

#SBATCH --job-name="testJob"

#SBATCH --output="testJob.output"  # job standard output file (%j replaced by job id)

#SBATCH --error="testJob.error"  # job standard error file (%j replaced by job id)

# LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE
```

Below this section, you can write code to execute some function/run a program

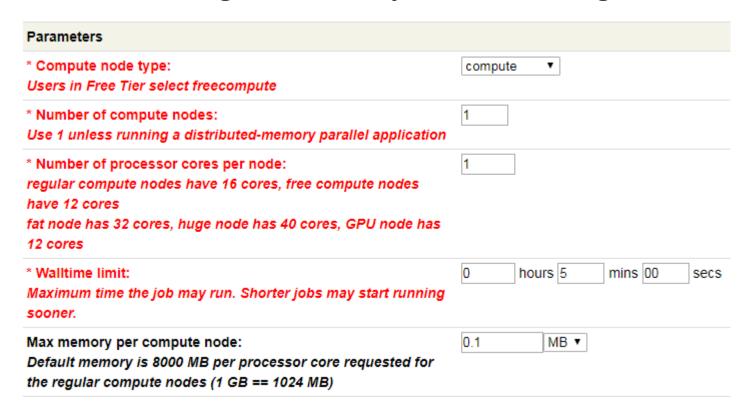
Lesson 3.4: Slurm Job Script Generation

When creating Slurm commands, you can:

- 1. Open your script file with nano
- Copy the header script to your clipboard ([Ctrl] + [c] or [command] + [c])
- 3. Then **Left click** or **[command]** + **click** to paste the header directly into the console

Lesson 3.4: Slurm Job Script Generation

- We are not on condo
- We are on a training server
- Use these settings for Slurm jobs on training server:



Exercise 3 Prelude

- Use https://www.hpc.iastate.edu/guides/condo-2017/slurm-job-script-generator-for-condo to generate Slurm headers for your file
- Name a standard output file and a standard error
- Copy the Job Script
- Create a copy of the file called slurm-test.sh; call this copy <yourname>-slurm-test.sh
- Open <yourname>-slurm-test.sh and paste your Slurm Job Script header above the code in <yourname>-slurm-test.sh
- Change "0.1M" to "1K"

Lesson 3.5: Slurm Commands

3.51: Submit a Slurm script

3.52: Check the job queue

3.53: Cancel a Slurm job

3.54: Check job stats

Lesson 3.51: Submit a Slurm script

Command: sbatch <slurmscript.sh>
What it does:

sbatch submits a script to Slurm, which reads the parameters in the #SBATCH lines and then allocates resources and distributes jobs accordingly

```
training.las.iastate.edu - PuTTY

[cmmann@training 20180303-unix-adv]$ sbatch carla-slurm-test.sh

Submitted batch job 18

[cmmann@training 20180303-unix-adv]$ sbatch carla-slurm-test1.sh

Submitted batch job 19
```

Your job will be assigned a job ID; you can use this job ID to check job stats, cancel jobs, etc.

Lesson 3.52: Check the job queue

Command: squeue -options

What it does:

View information on jobs in the Slurm queue

Options:

-u <user>: View information only on jobs submitted by a particular user

```
[cmmann@training 20180303-unix-adv]$ squeue

JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)

17 training carlaSlu cmmann PD 0:00 1 (Resources)

16 training carlaSlu cmmann R 0:56 1 localhost
```

Lesson 3.53: Cancel a Slurm job

Command: scancel <jobid>

What it does:

Immediately stops running <jobid>, or removes <jobid> from the Slurm queue

```
[cmmann@training 20180303-unix-adv]$ squeue
            JOBID PARTITION
                                 NAME
                                          USER ST
                                                        TIME NODES NODELIST (REASON)
               21 training carlaSlu
                                        cmmann PD
                                                        0:00
                                                                  1 (Resources)
                                                                  1 localhost
                  training carlaSlu
                                        cmmann R
                                                        0:06
[cmmann@training 20180303-unix-adv]$ scancel 21
[cmmann@training 20180303-unix-adv]$ squeue
            JOBID PARTITION
                                 NAME
                                          USER ST
                                                        TIME
                                                              NODES NODELIST (REASON)
                   training carlaSlu
                                                        0:14
                                                                   1 localhost
                                        cmmann
```

Exercise 3

1. Submit < yourname > - slurm - test.sh to Slurm for processing.

The code should take exactly 30 seconds to run, once it reaches the head of the queue.

- 2. Use squeue to view the Slurm queue
- 3. Try to cancel SOMEONE ELSE's job. What happens?
- 4. View your output file. What did the code in
- <yourname>-slurm-test.sh do?

Lesson 4:

Overview:

Lesson 4.0: Review Text Output

Lesson 4.1: Word Count

Lesson 4.2: Piping

Lesson 4.3: Sort

Lesson 4.4: Uniq

Lesson 4.5: Grep

Exercise 4: Hello

Lesson 4.0: Text Output

Commands:

```
cat <filename.txt>
head <filename.txt>
tail <filename.txt>
less <filename.txt>
```

What they do:

cat outputs the entirety of <filename.txt> to the console (don't try this with large files!!)

head outputs the first 10 lines of the file

tail outputs the last 10 lines of the file

less lets you scroll around a file

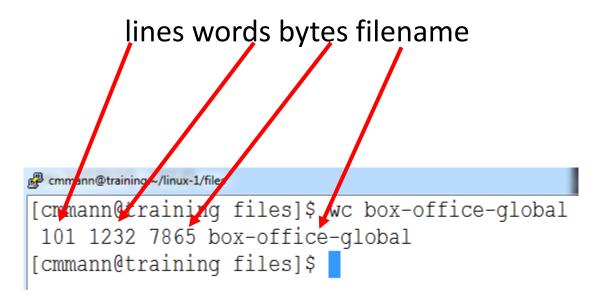
Lesson 4.1: Word Count

Command:

wc <filename>

What it does:

Outputs the number of:



Lesson 4.1: Word Count

Options:

- -1: output ONLY the number of LINES and filename
- -w: output ONLY the number of WORDS and filename
- -m: print the number of characters in the file and filename

Lesson 4.1: Word Count

So that's cool, but these options all put out the filename as well

How do we get around that?

Many, many possible ways, but we're going to use piping for now

Lesson 4.2: Piping

We can take the output of one command, and directly feed it to another command – all in one line, using the []] key (this is generally directly below the backspace key)

```
command1 | command2
```

Example:

```
[cmmann@training files]$ wc bill-of-rights
10 482 2797 bill-of-rights
[cmmann@training files]$ cat bill-of-rights | wc -l
10
```

Lesson 4.3: sort

Command:

```
sort <file>
```

What it does:

Sorts <file> alphabetically by line

Options:

 -n : sort numerically (if there are no numbers, it will default to alphabetic sort

-r: sort in reverse alphabetical order

-u : sort only unique items

Lesson 4.4: uniq

Command:

uniq

What it does:

Finds unique occurrences of text input

Options:

-c : count the occurrences of each line

-d : print only duplicated lines

-u : print only unique lines

Lesson 4.4: uniq

uniq must be called on something that is already sorted!

It works by comparing adjacent items in a list and discarding if they are identical.

Generally called after sort:

```
cat hello.txt | sort | uniq
```

Lesson 4.5: Grep

Stands for "Global Regular Expression Print"

EXTREMELY POWERFUL search tool

Finds text matching highly variable criteria and prints the lines containing that text

Can search multiple files, and find the files that match

Lesson 4.5: Grep

Command:

```
grep -options <pattern> <files>
```

What it does:

```
grep searches <files> for content matching
<pattern>
```

```
[cmmann@training:~/linux-1/files] $ grep 'Avatar' *office*
box-office-domestic:2 Avatar Fox $760,507,625 2009
box-office-global:1 Avatar Fox $2,788.0 $760.5 27.3% $2,027.5
72.7% 2009
```

Lesson 4.6: Piping and Grep

We can also feed text directly to grep, and have it search that:

Command:

```
<intext> | grep -options <pattern>
```

What it does:

```
grep searches <intext> for content matching
<pattern>
```

Lesson 4.7: Grep All Files in A Directory

We can also search for content within a directory:

```
grep -R <pattern> <directoryname/>
```

For this, we have to use the $-\mathbb{R}$ Recursive option!

Lesson 4.8: Grep Options

Grep has many, many options:

- -c : count how many LINES on which the pattern occurs
- −○ : show only the part of a line that matches a pattern; this will show all matches in the line
- -v : invert match so select things that DON'T match
 <pattern>
- -i : case insensitive matching
- -1: list the files with a match
- -⊥: list the files that don't have a match

Exercise 4: Hello

- 1. Navigate to ~/20180303-adv-unix/exercise4/
- 2. Open "exercise4.sh"
- 3. Edit the file to perform the exercises.
- 4. Execute the file!

Hint:

If you aren't sure if you're getting the correct answers, you can run exercise4answers.sh.

Lesson 5: Regular Expressions

Overview:

Lesson 5.1: What are Regular Expressions?

Lesson 5.2: egrep

Lesson 5.3: Matching words with egrep

Lesson 5.4: Fuzzy Matching

Lesson 5.5: Number Matching

Lesson 5.6: Operators

Lesson 5.7: Matching X Letters

Lesson 5.8: Example

Lesson 5.9: Continuing Education

Lesson 5.1: Regular Expressions

Also called 'regex' or 'regexp'

UNBELIEVABLY POWERFUL tool for defining search patterns

Consists of 'codes' that denote various conditions

These conditions can be used to very narrowly find things, or very, very broadly find things

Lesson 5.2: Regular Expressions

In UNIX, frequently used with grep

The option "-E" tells grep that the pattern is a regular expression!

It is very important that you remember the "-E" option, otherwise grep will try to match your exact pattern, instead of what it represents.

Lesson 5.2: egrep

Alternatively, you can use egrep:

```
egrep <'regexppattern'> <file>
```

This behaves exactly as "grep -E", and will be used through the rest of the slides.

Lesson 5.3: Matching Words

We can still match words while grepping regular expressions:

will still find any instance of the letters 'cat' in a file

But grep allows us to search for words similar to 'cat'...

The regexp to find words containing 'cat' or 'cot' would be: '[c][ao][t]'

The brackets encase 'character' slots

What would '[fw][i][s][h]' match?

The regexp to find words containing 'cat' or 'cot' would be: '[c][ao][t]'

The brackets encase 'character' slots

What would '[fw][i][s][h]' match?

If we only wanted to match the 'word' cat or cot, and not, we can bracket '[c][ao][t]' with spaces:

'[][c][ao][t][]'

Note that many, many systems use Regular Expressions, and some have slightly different usage.

For many systems, you can specify a match to 'whitespace' (spaces and tabs) using "\s", but this does not work in bash.

This bracket system, though, is rather cumbersome. Instead, we could specify:

'\b[c][ao][t]'

In this context, '\b' means to match the beginning of a word.

The '\' before the 'b' is an *escape* character – it signals that we don't want to *literally* match the letter 'b', but the condition that 'b' represents.

We can use a '-' to represent a span of characters:

```
'[a-c][o][g]' would recognize 'aog', 'bog', 'cog'
'[l-z][o][g]' would only recognize 'log', 'mog', 'nog' etc.
```

Lesson 5.5: Number Matching

We can also match numbers:

What number(s) will the following match? '[0-3][5-8][345]'

Lesson 5.5: Number Matching

We can also match numbers:

What number(s) will the following match? '[0-3][5-8][345]'

Lesson 5.6: Operators

'[cd][ao][tg]' would match 'cat' or 'dog'

(But also 'cag', 'dat', and any combination of those letters)

What regular expression would you use to find words containing "trap" or "tarp"?

'[cd][ao][tg]' would match 'cat' or 'dog'

(But also 'cag', 'dat', and any combination of those letters)

What regular expression would you use to find words containing "trap" or "tarp"?

But what if we wanted to match 'trap' or 'tarp', but not 'trrp' or 'taap'?

We can use operators to specify this!

If you want to match this OR that:

```
egrep 'this|that' <file>
```

When using regular expressions, grep understands that "|" means "OR"

If you to find things that are NOT something, you use:

```
egrep -v 'something' <file>
```

What if you want to match the character '|'?

We use escape characters again!

```
egrep '\|'
```

What if we want to find something more complicated, like a zip code?

What is the form of a zip code?

How could we potentially match that?

But that's rather cumbersome. Instead, we can specify a specific number of times to look for a set of characters:

In regexp, you can use a number in brackets AFTER the thing that you want to repeat

We can put more than just a number in there:

```
a { n, } : will match the letter 'a' n OR MORE times
```

What will 'a { 2 , } ' match? aardvark, armadillo, aaaah

We can put more than just a number in there:

```
a { n, } : will match the letter 'a' n OR MORE times
```

What will 'a { 2 , } ' match? aardvark, armadillo, aaaah

We can also specify a range of times to match:

a { n, m} : will match 'a' at least n times, but not more than m times.

What will 'a { 2, 3 } ' match? aardvark, armadillo, aaaah

We can also specify a range of times to match:

a { n, m} : will match 'a' at least n times, but not more than m times.

What will 'a { 2, 3 } ' match? aardvark, armadillo, aaaah

We can also specify more matches:

a*: match 'a' 0 or more times

a+: match 'a' 1 or more times

a? : match 'a' once if it happens, but matching it is optional

We can match EXTREMELY complicated things

Real world example: PDB files

In my day job, I want to find the coordinates of atoms in PDB files.

These lines take the form:

ATOM	1	N	SER A	44	0.312	28.338	23.824	1.00109.80	N
ATOM	2	CA	SER A	44	-1.014	28.655	23.237	1.00113.84	С
ATOM	3	C	SER A	44	-1.893	27.385	23.044	1.00115.10	С
ATOM	4	0	SER A	44	-1.573	26.307	23.566	1.00111.94	0
ATOM	1589	03'	A B	9	4.770	39.279	56.136	1.00228.34	0
ATOM	1590	C2 '	A B	9	2.693	40.521	56.600	1.00214.10	C
ATOM	1591	02 '	A B	9	3.406	41.227	57.593	1.00219.27	0
ATOM	1592	C1'	ΑВ	9	1.906	41.493	55.715	1.00207.15	C

So these lines look similarly, but they have different numbers and characters spaced differently.

And the rest of the file looks NOTHING like this.

How could I pull out ONLY these lines?

ATOM	1	N	SER A	44	0.312	28.338	23.824	1.00109.80	N
ATOM	2	CA	SER A	44	-1.014	28.655	23.237	1.00113.84	C
ATOM	3	C	SER A	44	-1.893	27.385	23.044	1.00115.10	C
ATOM	4	0	SER A	44	-1.573	26.307	23.566	1.00111.94	0
ATOM	1589	03'	A B	9	4.770	39.279	56.136	1.00228.34	0
ATOM	1590	C2 '	A B	9	2.693	40.521	56.600	1.00214.10	C
ATOM	1591	02 '	A B	9	3.406	41.227	57.593	1.00219.27	0
ATOM	1592	C1'	A B	9	1.906	41.493	55.715	1.00207.15	C

We could try:

egrep 'ATOM' 1R2X.pdb, but...

```
REMARK 290
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY TRANSFORMATIONS
REMARK 290 THE FOLLOWING TRANSFORMATIONS OPERATE ON THE ATOM HETATM
REMARK 290 RECORDS IN THIS ENTRY TO PRODUCE CRYSTALLOGRAPHICALLY
```

ATOM	1	N	SER A	44	0.312	28.338	23.824	1.00109.80	N
ATOM	2	CA	SER A	44	-1.014	28.655	23.237	1.00113.84	C
ATOM	3	С	SER A	44	-1.893	27.385	23.044	1.00115.10	C
ATOM	4	0	SER A	44	-1.573	26.307	23.566	1.00111.94	0
ATOM	1589	03'	ΑВ	9	4.770	39.279	56.136	1.00228.34	0
ATOM	1590	C2 '	ΑВ	9	2.693	40.521	56.600	1.00214.10	С
ATOM	1591	02 '	ΑВ	9	3.406	41.227	57.593	1.00219.27	0
ATOM	1592	C1'	ΑВ	9	1.906	41.493	55.715	1.00207.15	C

We can specify that we only want to match 'ATOM' if it starts at the beginning of the line:

```
egrep '^ATOM' 1R2X.pdb
```

The character '^' is a special character called an 'anchor' that means to match the beginning of the line

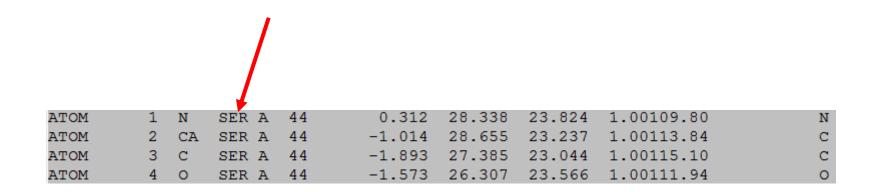
But what if I ONLY want the protein atom coordinates?

```
28.338
                                                     23.824
                                                              1.00109.80
ATOM
              N
                   SER A
                           44
                                    0.312
                  SER A
                          44
                                   -1.014
                                            28.655
                                                     23.237
                                                              1.00113.84
                                                                                      C
ATOM
              CA
ATOM
                   SER A
                           44
                                   -1.893
                                            27.385
                                                     23.044
                                                              1.00115.10
                                                                                      C
                                            26.307
                                                     23.566
                                                              1.00111.94
ATOM
                   SER A
                          44
                                   -1.573
```

```
ATOM
       1589
                                     4.770
                                             39.279
                                                      56.136
                                                               1.00228.34
              03'
                     A B
                            9
MOTA
       1590
              C2 '
                                     2.693
                                             40.521
                                                      56.600
                                                               1.00214.10
                     A B
MOTA
       1591
              02 '
                     A B
                            9
                                     3.406
                                             41.227
                                                      57.593
                                                               1.00219.27
                                                              1.00207.15
ATOM
       1592
              C1'
                     A B
                                     1.906
                                             41.493
                                                      55.715
```

We make a really *complicated* regexp:

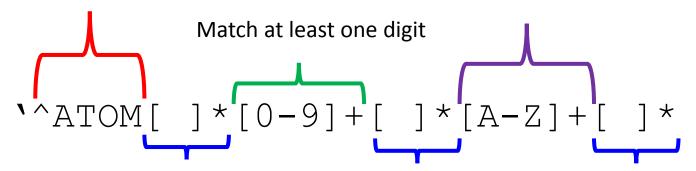
```
egrep '^ATOM[]*[0-9]+[]*[A-Z]+[]*[A-Z]+[
```



What is this doing?

Match ATOM at the beginning of the line

Match at least one letter



Match any number of spaces

Match exactly 3 letters

Lesson 5.9: Regexp Continuing Education

There are many, many more options available to use with regexp in bash

We could spend an entire workshop on this alone. (We're not going to today, though.)

If you want to learn more, visit:

http://tldp.org/LDP/Bash-Beginners-Guide/html/sect 04 01.html#sect 04 01 02

Exercise 5: Real Life Stuff

- 1. Open and edit exercise5.sh
- 2. Complete the exercises within.
- 3. Run exercise5.sh

Closing

Thanks for coming!

Please take this survey so that we can improve the workshop for future attendees:

https://goo.gl/forms/cumiG8DvCOzOmDuC2