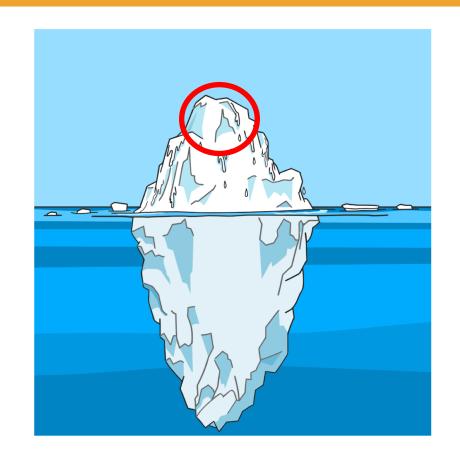
# High Performance Computing (HPC) Crash Course

Brandon Reyes

For help email: <u>rc-help@colorado.edu</u>

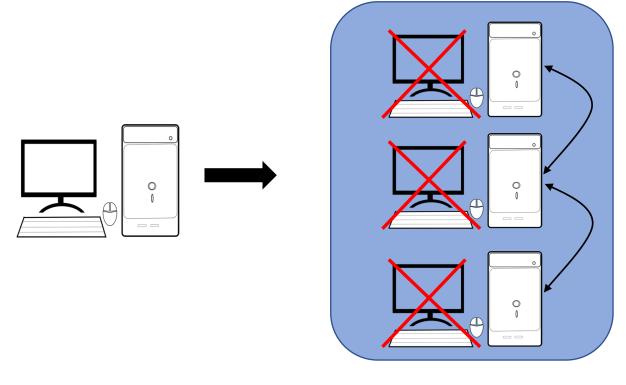
### WHAT DO WE WANT TO ACHIEVE?

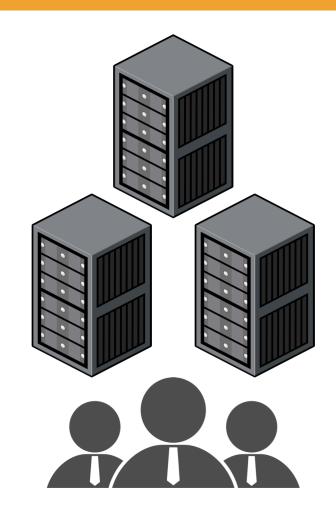
- Goal: Obtain an overview of a common workflow on an HPC system
- Audience: Individuals who are new to HPC systems



# WHAT IS AN HPC SYSTEM?

Let's keep it simple!





# SOME PERKS OF AN HPC SYSTEM

Perks	HPC System
Common software and programming languages are easily available (modules)	
Large storage, RAM, and number of CPUs or GPUs (+ multiple nodes)	
Independent tasks or parallel applications can be completed significantly faster	

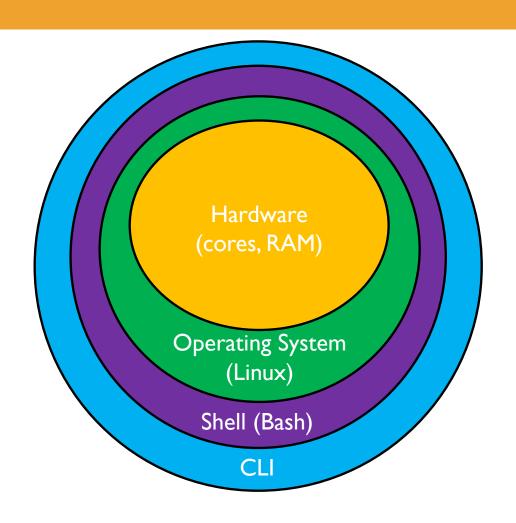
# **ALPINE STATS**

### Partitions available on Alpine:

Partition	Description	# of nodes	cores/node	RAM/core (GB)
amilan	AMD Milan (default)	184	64	3.74
ami100	GPU-enabled (3x AMD MI100)	8	64	3.74
aa100	GPU-enabled (3x NVIDIA A100)	8	64	3.74
amem <sup>1</sup>	High-memory	4	48	21.486
csu	Nodes contributed by CSU	77	32 or 48	3.74
amc	Nodes contributed by AMC	20	64	3.74

# COMMAND-LINE INTERFACE (CLI)

- Text-based interaction with operation system
- A simple HPC workflow will use the CLI to:
  - Access HPC
  - Work with folders (directories) and files
    - View or edit files (text editor)
  - Submit our code to the HPC system
  - Help us monitor the HPC jobs



### WHAT DOES A CLI LOOK LIKE?

### Real world CLI

**Documentation CLI** 

\$ Is

### ACCESSING AN HPC SYSTEM

- Create a Research Computing account
- Set up <u>Duo 2-factor Authentication</u>
- Open a terminal



\$ ssh username@login.rc.colorado.edu

• ssh is a secure way to access a computer over a network



\$ module load slurm/alpine

Allows one to submit jobs to Alpine (more on this later)

# PARALLEL APPLICATION

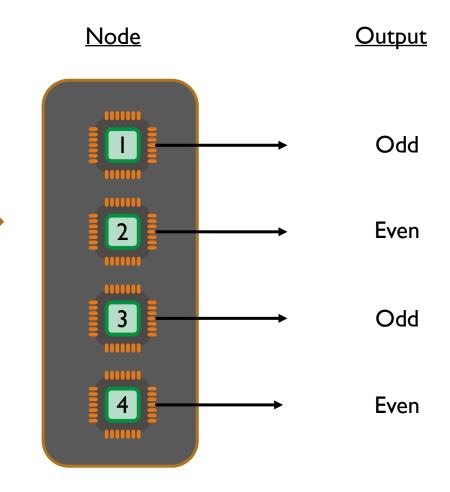
Parallel Application Pseudocode

I # assign work to core2 if core number is even:

3 print("Even")

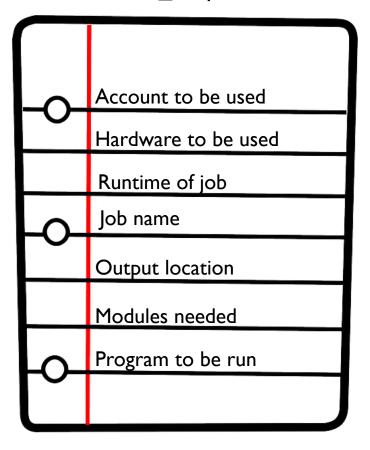
4 else:

5 print("Odd")

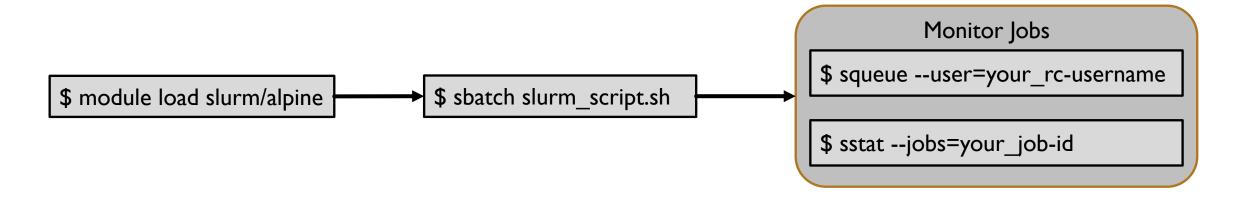


# SLURM JOB SCRIPTS

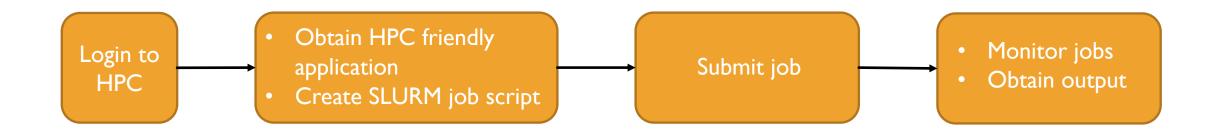
slurm\_script.sh



## SUBMITTING A SLURM SCRIPT

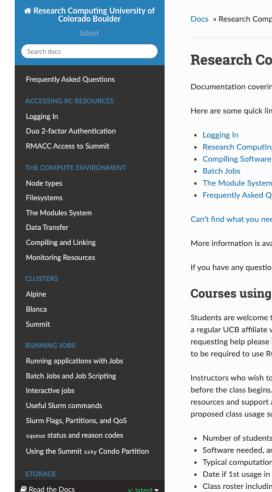


## OVERVIEW OF HPC WORKFLOW



### **FURTHER HELP**

- Documentation
  - curc.readthedocs.io
- rc-help@colorado.edu



**Docs** » Research Computing User Guide

C Edit on GitHub

### **Research Computing User Guide**

Documentation covering the use of Research Computing resources.

Here are some quick links into the documentation to get you started.

- Logging In
- Research Computing Filesystems
- Batch Jobs
- The Module System
- Frequently Asked Questions (FAQ)

Can't find what you need? Provide feedback on the CURC docs!

More information is available at https://www.colorado.edu/rc.

If you have any questions, please contact rc-help@colorado.edu.

#### **Courses using RC Resources**

Students are welcome to use RC resources on their own for class projects and can request access as a regular UCB affiliate via the link off the RC homepage at: https://www.colorado.edu/rc. When requesting help please indicate that the work is for a class project and any deadlines. If students are to be required to use RC resources for a class, see below.

Instructors who wish to lead a class using RC resources must contact us at rc-help@colorado.edu before the class begins. This is to ensure that our resources can meet your needs and if adequate resources and support are available. Early in the process we will need to know details about the proposed class usage such as:

- Number of students
- · Software needed, and if it will be installed by instructor/TA
- Typical computational work (number of jobs or sessions, length, number of CPUs)
- Date if 1st usage in class/lab
- · Class roster including TAs and auditors.

# Thank You!

### WHEN SHOULD YOU USE AN HPC SYSTEM?

- Your calculation consumes more memory (RAM) than you have
- You need to run a large number of tasks that are independent
  - Your application can be run in parallel (more on this later)

### WHAT DOES A CLI LOOK LIKE?

### Real world CLI

# root@abe5c26dbf5d:/home# ls HOMEWORK data\_analysis.py Presentations hello\_world.cpp README.txt slurm\_script.sh

### **Documentation CLI**

/home \$ Is
HOMEWORK data\_analysis.py
Presentations hello\_world.cpp
README.txt slurm\_script.sh

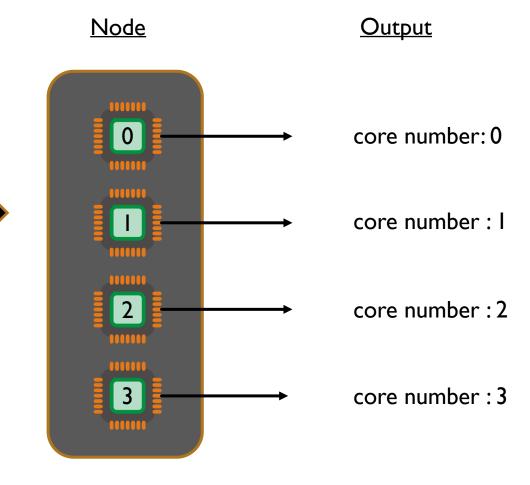
### Access to a CLI:

- macOS and Ubuntu (Linux)
  - Start up a terminal
- Windows
  - PuTTY (terminal emulator)

### PARALLEL APPLICATION

### Parallel Application Pseudocode

```
1 # get parallel library
2 Load_MPI(...)
3
4 # get core number
5 core = MPI_get_core_number(...)
6
7 # print core number
8 print("core number:" core)
```

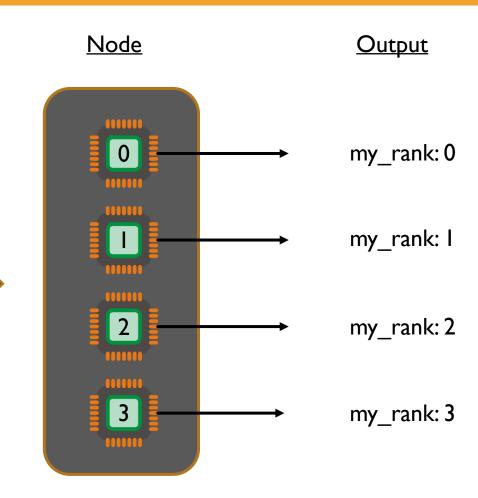


### PARALLEL CONCEPT

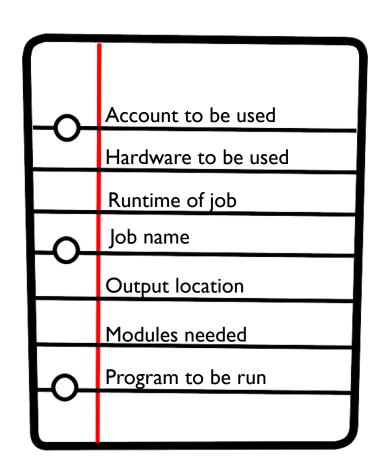
### **Parallel Application**

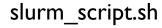
### MPI Hello World

```
#include <iostream>
#include <mpi.h>
int main(int argc, char **argv)
   // initialize MPI
   MPI_Init(&argc , &argv);
   // Get the rank of the running process
   int my_rank;
   MPI_Comm_rank(MPI_COMM_WORLD, &my_rank);
   // print the rank
    std::cout << " my_rank: " << my_rank << std::endl;</pre>
   //finalize MPI
   MPI_Finalize();
    return 0;
```



# SLURM JOB SCRIPTS





```
#!/bin/bash
    #SBATCH --account=...
   #SBATCH --partition=amilan
    #SBATCH --nodes=1
    #SBATCH --ntasks=4
    #SBATCH --time=01:00:00
10
    #SBATCH --job-name=hello-world
12
    #SBATCH --output=hello-world.%j.out
14
    module purge
16
    module load gcc
    module load openmpi
   mpirun -np 4 ./hello_world.exe
```

### SUBMITTING A SLURM SCRIPT

