Alpine Job Submission

Research Computing
UNIVERSITY OF COLORADO **BOULDER**

Be Boulder.

HPC Job Submission

Instructor: Instructor

RC Homepage: https://www.colorado.edu/rc/

RC Docs: https://curc.readthedocs.io/en/latest/

RC Helpdesk: rc-help@colorado.edu

Course Materials:
https://github.com/ResearchComputing/Supercomputing_Spinup

Survey: http://tinyurl.com/curc-survey18

Adapted from presentations by RC members Andrew Monaghan, Aaron Holt, John Blaas, and Mea Trehan: 1, 2, 3, 4.

Outline

- General Information
  - Alpine resources

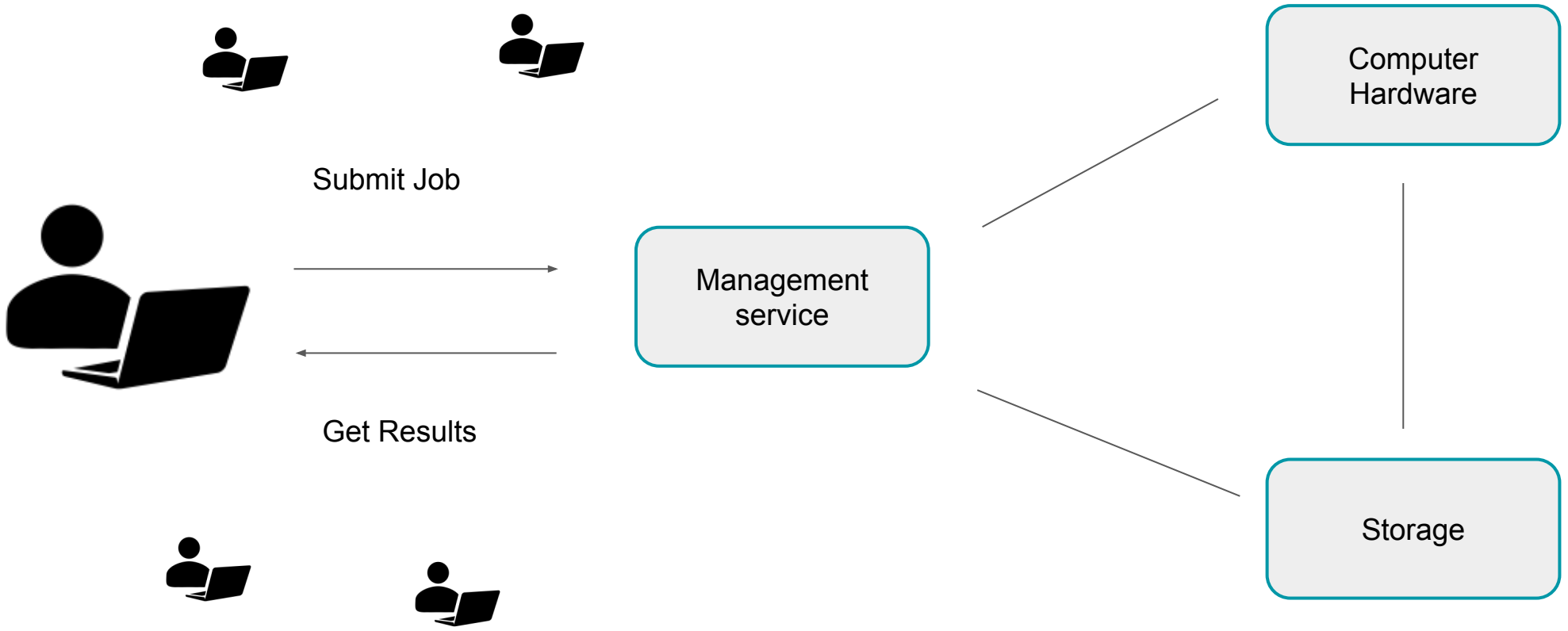
- Examples of submitting jobs to the supercomputer!
  - Traditional job submission (terminal)
    - Simple batch jobs: hello world, running programs
    - GPU Jobs
    - Advanced batch jobs: mpi, serial-parallel
    - Interactive jobs

RC account check

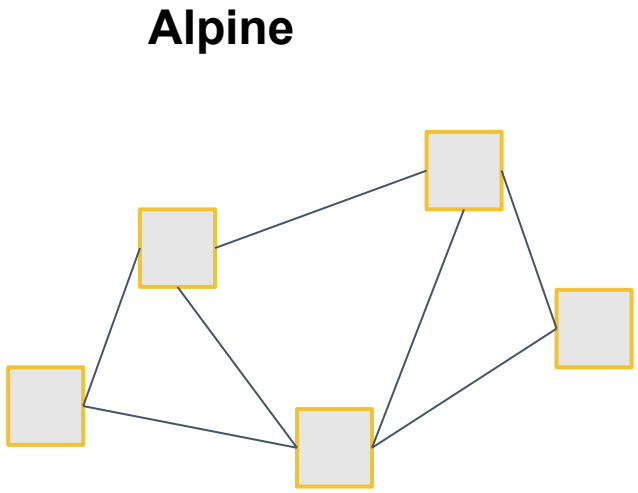
Does anyone ***not*** have a **CU Research Computing account** who would like to use a temporary account*?

**only available during seminar*

HPC - High Performance Computing



HPC Cluster: Alpine

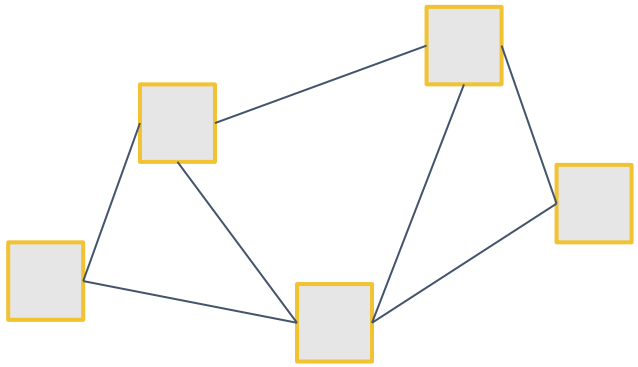


- Alpine is the 3rd-generation HPC cluster at CURC, following:
  - Janus
  - RMACC Summit

- Alpine is a heterogeneous cluster with pooled resources from the following institutions:
  - CU Boulder
  - Colorado State University
  - Anschutz Medical Campus.

HPC Cluster: Alpine

Alpine

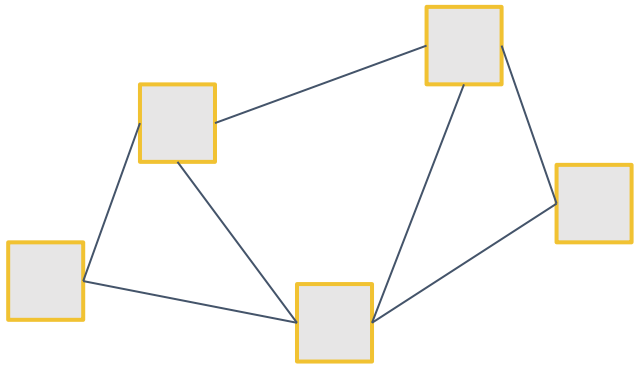


- Hardware on Alpine is purchased and released in stages:

- Alpine (stage 1):
  - 64 General CPU Nodes
    - *AMD Milan, 64 Core, 3.83G RAM/Core*
  - 8 NVIDIA GPU Nodes
    - *3x NVIDIA A100 (atop General CPU node)*
  - 8 AMD GPU Nodes
    - *3x AMD MI100 (atop General CPU node)*

HPC Cluster: Alpine

Alpine



- Interconnect
  - **CPU nodes**: HDR-100 InfiniBand (200Gb inter-node fabric)
  - **GPU nodes**: 2x25 Gb Ethernet +RoCE
    - nvlink compatibility in progress
  - **Scratch Storage**: 25Gb Ethernet +RoCE
- Operating System
  - RedHat Enterprise Linux version 8 operating system

Submitting Jobs via Terminal

RC Access: Logging in

- If you have an RC account already, login as follows from a terminal:

```
$ ssh <username>@login.rc.colorado.edu
# Where username is your identikey
```

- Logging in with a temporary account:

```
$ ssh user<XXXX>@tlogin1.rc.colorado.edu
# Where user<XXXX> is your temporary username, RC will provide pw
```

Working on RC Resources

- When you first log in, you will be on a login node. Your prompt:

```
[user@loginNN ~]$
```

- The login nodes are lightweight virtual machines primarily intended to serve as ‘gateways’ to RC resources. In order to get a better view of the software available on Alpine start a compile job.

```
[user@loginNN ~]$ acompile
```

- Navigate to a workspace of your choice (e.g. scratch) and download the material for this workshop:

```
[user@shas0137 ~]$ git clone
https://github.com/ResearchComputing/Supercomputing_Spinup.git
[user@shas0137 ~]$ cd Supercomputing_Spinup
[user@shas0137 ~]$ export SPINUP_ROOT=$(pwd)
```

Working Directory

- Navigate to the “job_submission” directory

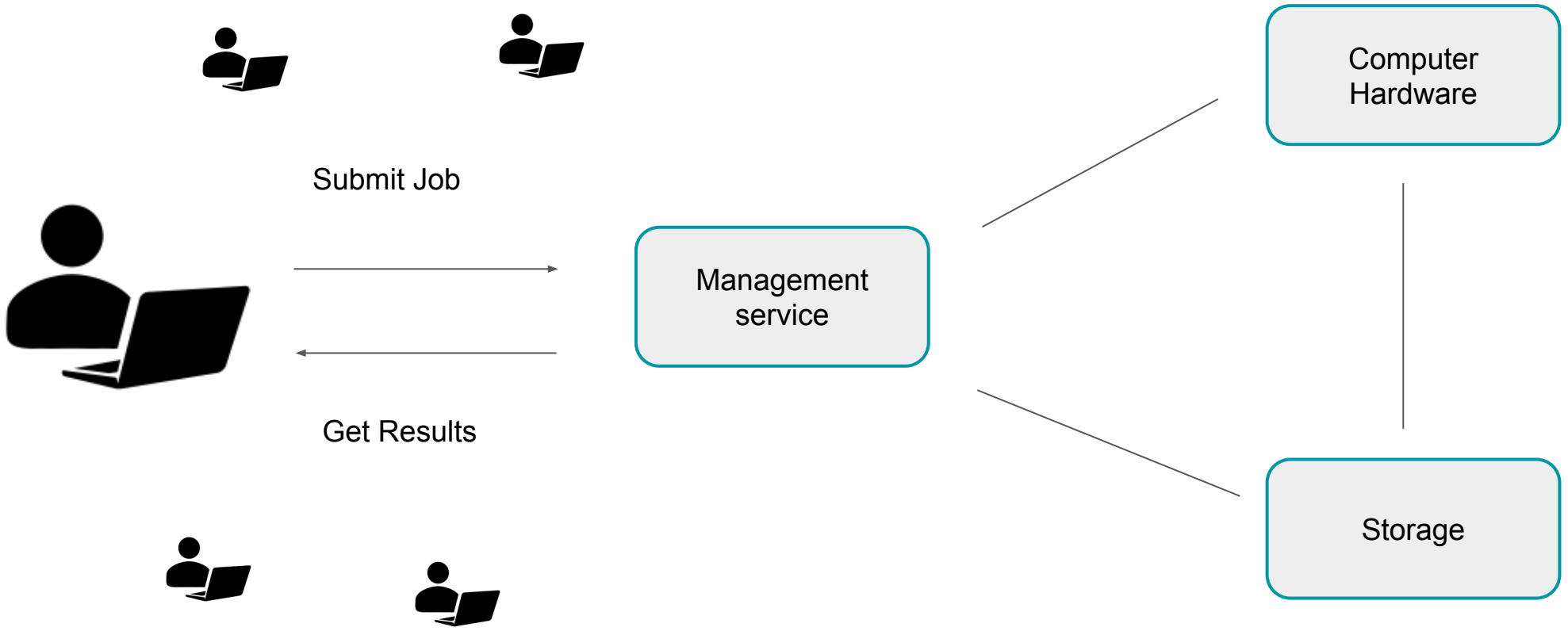
```
[user@loginNN ~]$ cd $SPINUP_ROOT/job_submission
```

- This is the “working directory” we will be working with in this course/tutorial, keep in mind as we submit/create jobs

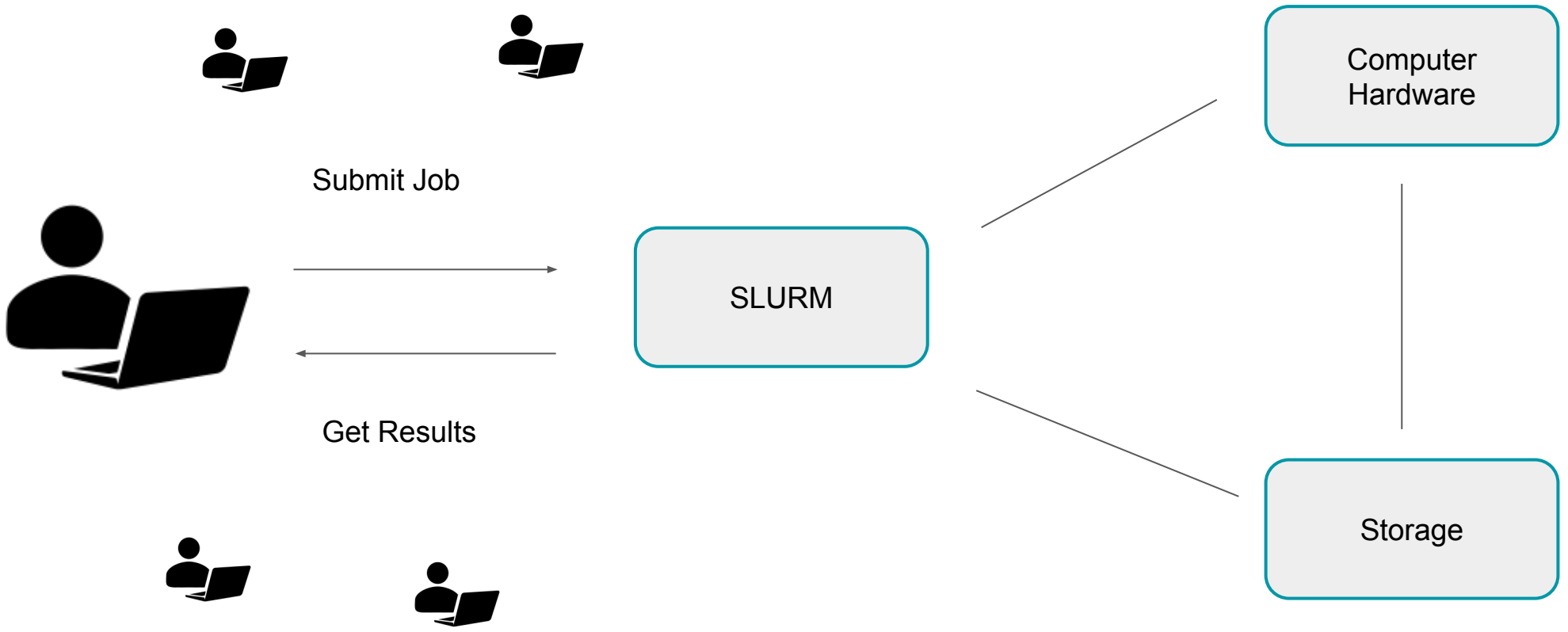
Jobs

- Because our clusters are shared resources with many users trying to utilize available compute with their applications, we need a system to divide compute in a simple and fair system.
- SLURM
  - **S**imple **L**inux **U**tility for **R**esource **M**anagement
- Through SLURM, users can grab allotments of compute resources called Jobs
- 2 Types of Jobs
  - **Batch Jobs**
  - **Interactive Jobs**

HPC - High Performance Computing



HPC - High Performance Computing



Batch Jobs

- **Batch Jobs** are jobs your submit to the scheduler where they are run later without supervision.
  - By far the most common job on Summit
  - Requires a job script
  - "batch of cookies"

- A job script is simply a script that includes **SLURM directives** (resource specifics) ahead of any commands.

Submit your first batch job

- First, load up the **slurm Alpine module** (default is still Summit)

```
$ module load slurm/alpine
```

- sbatch: command to submit a batch job
- Submit your first job! :

```
$ cd $SPINUP_ROOT/job_submission
$ sbatch alpine_scripts/test.sh
```

- The SLURM Script contains the parameters needed to define a job but additional flags can be used to temporarily replace any set parameters.

```
$ sbatch --partition=amilan-<institution> alpine_scripts/test.sh
```

http://slurm.schedmd.com/sbatch.html

Anatomy of a job script

```
#!/bin/bash

## Directives (HPC Resources)
#SBATCH --<resource>=<amount>

## Software
module load <software>

## User scripting
<command>
```

Anatomy of a job script

- open `alpine_scripts/test.sh` (nano or vim)

```
#!/bin/bash

## Directives
#SBATCH --ntasks=1                          # Number of requested tasks/cores
#SBATCH --time=0:01:00                      # Max run time
#SBATCH --partition=amilan-ucb              # Specify Alpine CPU node
#SBATCH --output=test_%j.out                # Rename standard output file

## Software
module purge                               # Purge all existing modules

## User commands
echo "This is a test of user $USER"
```

Job Options

Specified at command line or in job script as…
`#SBATCH <options>` …where options include:

- **Partition:** `--partition=<partition_name>`
- Sending emails: `--mail-type=<type>`
- Email address: `--mail-user=<user>`
- **Number of nodes:** `--nodes=<nodes>`
- **Number of cores:** `--ntasks=<number-of-tasks>`
- Quality of service: `--qos=<qos>`
- Allocation: `--account=<account_name>`
- Wall time: `--time=<wall time>`
- Job Name: `--job-name=<jobname>`
- **Output:** `--output=<name>`

More on slurm commands: https://slurm.schedmd.com/quickstart.html

FYI: You do NOT actually type <> above – this designates something specific you as a user must enter about your job

Alpine Partitions

- Partitions specify the type of compute node that you wish to use
  - Specify with the `--partition` flag

```
#SBATCH --partition=amilan-ucb
```

Partition	Description	# of nodes	RAM/core (GB)	cores/node	GPUs/node
amilan-<institution>	General Compute Node: AMD Milan	64	3.83	64	0
ami100-<institution>	GPU Node: 3x AMD MI100	8	3.83	64	3
aa100-<institution>	GPU Node: 3x Nvidia A100	8	3.83	64	3

Institutions:

- **ucb**: University of Colorado, Boulder
- **csu**: Colorado State University
- **amc**: Anschutz Medical Campus

Quality of Service

- Quality of Service specifies additional constraints Job
  - On Alpine, this means if your job needs to run longer than 1 day
  - Specify with the `--qos` flag
  - Doesn't need to be set otherwise

```
#SBATCH --qos=long
```

QoS	Description	Max wall time	Max jobs/user	Max nodes/user
normal	Default QoS	Derived from partition	n/a	256
long	For jobs needing longer wall times	7 D	n/a	20

Writing your first job script

Your turn!

- Create a job script and submit it as a batch job with the following instructions:

1. Navigate to the job_submission directory
2. Create file alpine_scripts/sleep.sh
3. The job should contain the following commands:

```
echo "Running on host" `hostname`
echo "Starting Sleep"
sleep 30
echo "Ending Sleep. Exiting Job!"
```

Details on job script parameters are in the next slide

Job details of sleep.sh

1. The job will run on **1 core on 1 node**
2. We will request a **1 minute wall time**
3. Run on the **amilan-ucb partition**
4. Set the output file to be named **"./output/sleep.%j.out"**
5. Contains the following **commands** ->

```
echo "Running on host" `hostname`
echo "Starting Sleep"
sleep 30
echo "Ending Sleep. Exiting Job!"
```

* Bonus: Email yourself when the job ends

```
$ sbatch alpine_scripts/sleep.sh
```

Job Output

- Once a job completes its execution, the standard output of the script will be redirected to an output file.
  - Great for debugging!
  - Could be different from output generated by your application
  - File is created in directory job was run unless specified in your --output directive.
  - If the directive --output is not provided then a generic file name will be used (slurm_xxxxxx.out).

```
$ cat output/sleep.xxxxxx.out  # where xxxxxx is your Job Id
```

Solution can be found in "./solutions" subdirectory

Checking your jobs (1)

- `squeue`: Monitor your jobs status **in queue and while running**:
  - By Default shows all jobs in queue
  - Narrow this down with:

```
$ squeue -u <username>
$ squeue -p <partition>
```

- sacct: Check back on usage statistics of **previous Jobs**
  - By default only checks all jobs from the start of the current day.
  - Narrow this down with:

```
$ sacct -u <username>
$ sacct --start=MM/DD/YY -u <username>
$ sacct -j <job-id>
```

Checking your jobs (2)

- Another method of checking details of your job while running is with `scontrol`
- Advanced command usually used by system administrators, but you can use it too!

```
$ scontrol show job <job number>
```

- seff: Utility to **check efficiency post-job**

```
$ module load slurmtools
$ seff <job number>
```

Software and Jobs

- Okay so running a job is easy, but how do I run a job with my software?

- LMOD
  - Module system on CURC systems
  - Modifies your environment to make your desired software visible to your terminal.

```
$ module load matlab
$ ml matlab #shorthand version!
```

Software and Jobs (2)

- More LMOD commands:

```
$ module purge              #Unloads all current modules
$ module unload matlab      #Unloads matlab
$ module spider matlab      #Searches for matlab in module tree
```

- What if my software isn't available through LMOD?
  - Software must be installed locally if not available through LMOD
  - RC User support is happy to assist,*installs are best effort*
  - For more assistance contact rc-help@colorado.edu

Example 1: Serial R Code

Running an external program

- Let's run R on an R script
- Batch script calls and runs programs/R_program.R
  - Let's take a look at the R program

- Let's examine the batch script alpine_scripts/R.sh
  - Note how R is loaded
  - R program can be run with "Rscript <script>"

- Go ahead and submit the batch script:

```
$ sbatch alpine_scripts/R.sh
```

Example 2: Serial Matlab Code

Launch Matlab!

- Create a job script and submit it as a batch job with the following instructions:

1. Name it alpine_scripts/matlab.sh
2. Load the matlab module (module load matlab)
3. The job should contain the following commands:

```
cd programs
matlab –nodisplay –nodesktop –r "matlab_tic;"
```

Details on job script parameters are in the next slide

Job details of matlab.sh

1. The job will run on **1 core of 1 node**
2. We will request a **2 minute wall time**
3. Run on the **amilan-ucb partition**
4. Set the output file to be named **"./output/matlab.%j.out"**
5. Contains the following commands:

```
cd programs
matlab -nodisplay -nodesktop -r "matlab_tic;"
```

*Bonus: Email yourself when the job ends

```
$ sbatch alpine_scripts/matlab.sh
```

GPU Jobs

GPU Jobs

- On Alpine the `--gres` slurm directive is ***required*** to use GPU accelerators on a GPU node.

- At a minimum, one would specify:
  - A GPU partition (e.g. `--partition=aa100-ucb` for an nvidia GPU node)
  - `--gres=gpu` in a job to specify that they would like to use a single gpu on their specified partition
    - You can request up to 3 accelerators on Alpine (e.g. `--gres=gpu:3`)

GPU Job Script Example

```
#!/bin/bash

## Directives
#SBATCH --ntasks=1                          # Number of requested tasks/cores
#SBATCH --time=0:01:00                      # Max run time
#SBATCH --partition=aa100-ucb               # Specify Alpine NVIDIA A100 node
#SBATCH --gres=gpu:2                        # Request 2 GPUs from the node
```

Advanced Job Scripts

Running an mpi job

- For cases where you have a code that is parallelized, meaning it can run across multiple cores.
- Number of tasks always > 1. E.g.,

```
#SBATCH --ntasks=4
```

- Will always need to load a compiler and mpi. E.g.,

```
module load intel impi
```

- Executable preceded with mpirun, srun, or mpiexec. E.g.,

```
mpirun -np 4 python yourscript.py
```

- Examine and run the example 'submit_python_mpi.sh'

```
$ sbatch --partition=amilan-ucb submit_python_mpi.sh
```

Running serial jobs in parallel

- Not all code is designed to run with MPI (nor always makes sense to do so)

- RC has a couple different tools that lets users run serial programs in parallel
  - RC LoadBalancer
  - GNU Parallel

- Example in: `scripts/python_loadbalance.sh`

Interactive Jobs

Interactive jobs

- Sometimes we want our job to run in the background
- Sometimes we want to work on program in real time
    - Great for testing, debugging

- We can get access to a compute node interactively with `sinteractive`

- For example, let's run the R job we previously ran as a batch job, but this time let's do it interactively

Running an interactive job

- To work with R interactively, we request time from Alpine
- When the resources become available the job starts
- Commands to run:

```
$ sinteractive --time=00:10:00
```

- Once we receive a prompt, then:

```
$ module load R
$ cd programs
$ Rscript R_program.R
```

- Once we finish we must exit! (job will time out eventually)

```
$ exit
```

Thank you!

- Survey: http://tinyurl.com/curc-survey18
- Contact information: rc-help@Colorado.edu

- Slurm Commands: https://slurm.schedmd.com/quickstart.html