

# Alpine: New User Seminar





### CURC Alpine: New User Seminar

#### Instructor:

- Website: www.rc.colorado.edu
- Helpdesk: <u>rc-help@colorado.edu</u>
- Slides: <a href="https://github.com/ResearchComputing/New User Seminar">https://github.com/ResearchComputing/New User Seminar</a>
- Survey: <a href="http://tinyurl.com/curc-survey18">http://tinyurl.com/curc-survey18</a>





### Account Check

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

\*only available during seminar



### Learning Goals

- 1. What is CU Research Computing (CURC)?
- 2. Understand Basic Resources (Alpine cluster)
- 3. Getting an account & logging in
- 4. Navigate the RC system
- 5. Running a job
- 6. Help!



# Things to take note of:

- Confusing, ambiguous, highly nuanced concepts
- Our goal is to help you avoid common mistakes, pitfalls, and frustrations



**Ask Questions!** 

### What is CU Research Computing?



# What is CU Research Computing?

Large-scale, beyond-the-desktop computing resources for the University of Colorado and more!

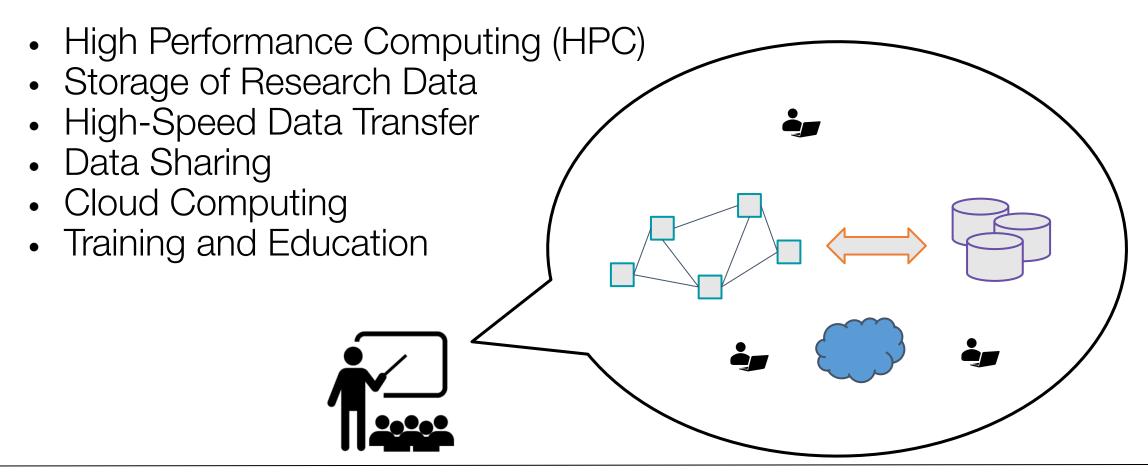








### Resources Include:





### Primarily known for: High Performance Computing (HPC)





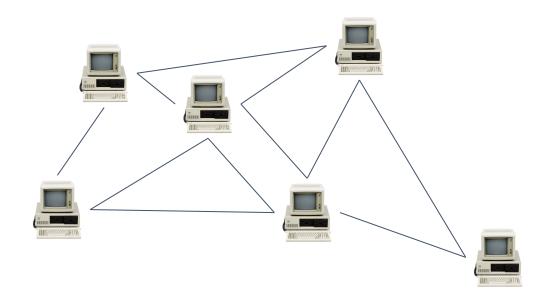
# High Performance Computing (HPC) vs. Traditional Computing

 Traditional computing generally has access to a single processor (perhaps multiple cores)



# High Performance Computing (HPC) vs. Traditional Computing

 HPC is a network (or cluster) of hardware we call "nodes" linked together with high-speed interconnects

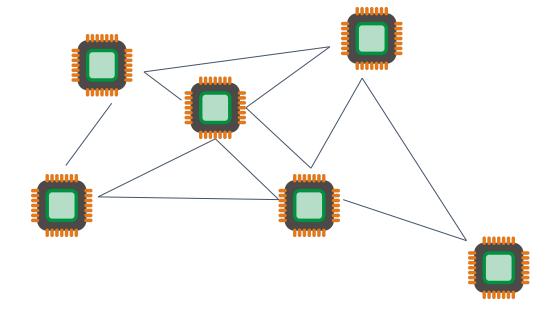




# High Performance Computing (HPC) vs. Traditional Computing

 HPC is a multiprocessor environment that allows users to run jobs on several processors at once (also called parallel processing)

processing).





### What can / use HPC for?

- Solving large problems that require more:
  - Memory than you have on your PC
  - cores/nodes/power thank you have on your PC
- Jobs that require hardware you may not have:
  - High Performance GPU computing
  - Specific Operating System
- Visualization rendering



### Puzzle Analogy

Working on a puzzle by yourself (although enjoyable!) will take

time, even if you're fast!



### Puzzle Analogy

You can speed it up by inviting friends over and enticing them with food

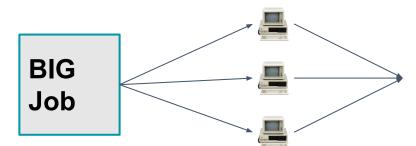


What happens if there are too many people?

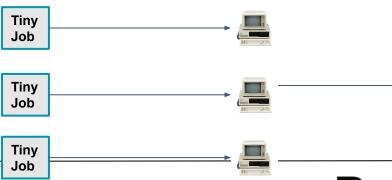


### What can / use HPC for?

- Jobs that would take a long time on local machines can instead be distributed over hardware:
  - Parallelized to split up then joined (if software enabled)



• Broken up into many serial jobs



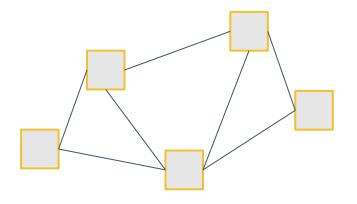


### Research Computing Resources



### HPC Cluster: Alpine

#### **Alpine**



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

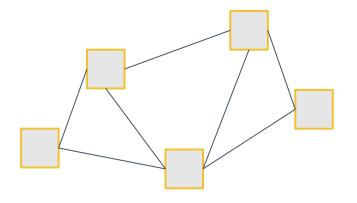
- Alpine is a heterogeneous cluster with pooled resources from the following institutions:
  - CU Boulder
  - Colorado State University
  - Anschutz Medical Campus.





### HPC Cluster: Alpine

#### **Alpine**



 Hardware on Alpine will be purchased and released in stages:

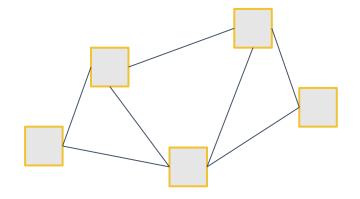
- Alpine (stage 1):
  - 64 General CPU Nodes
    - AMD Milan, 64 Core, 3.83G RAM/Core
  - 8 NVIDIA GPU Nodes
    - 3x NVIDIA A100 (atop General CPU node)
  - 8 AMD GPU Nodes
    - 3x AMD MI100 (atop General CPU node)





### 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





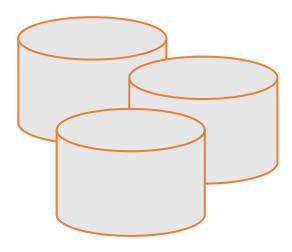
# Storage at CURC

#### Core



- Included with RC account
  - /home
  - /projects
  - scratch space

#### **PetaLibrary**



- Paid Service for:
  - Storage
  - Archive
  - Sharing of research data

#### **Local or Cloud**



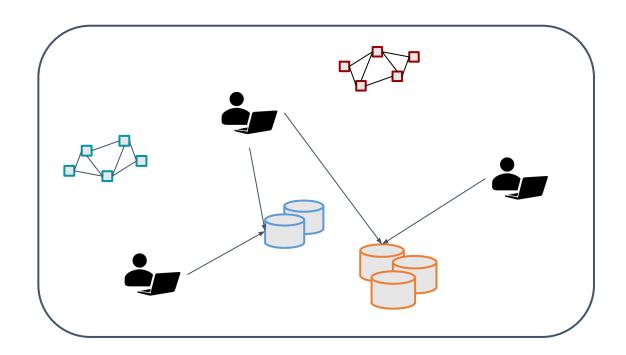
 You can download your data locally or to a variety of other cloud resources





# Data Sharing: Within RC

- Sharing workspaces
  - Project space
  - Scratch Space
  - PetaLibrary Space\*



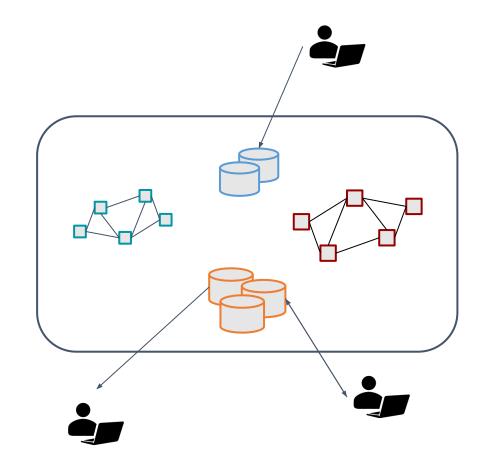
\*If you have purchased PetaLibrary space





# Data Sharing: Outside RC

- Globus (recommended):
  - GUI Web Application
  - Automates large transfers
  - Resumes failed transfers
  - Distributes large transfers across DTNs
  - Endpoints that can shared
- Data Transfer Nodes (DTN)
  - Internal CU network needed
- Command line tools
  - scp, sftp, rsync, rclone





# Accessing Research Computing



### How to Access RC Resources?

- 1. Get an RC account
- 2. Set up two-factor authentication with Duo
- 3. (Inform us of any specific needs)
- 4. Log in
- 5. Create greatness! (responsibly)

### Getting an RC Account

- University of Colorado, Boulder users and affiliates:
  - Request an account through the RC Account request portal
  - https://rcamp.rc.colorado.edu/accounts/account-request/create/organization
- Colorado State University users:
  - Request an CSU eID if you don't have one
  - Fill out account application form
  - Duo authentication
  - Then get an RC user account
  - https://www.acns.colostate.edu/hpc/summit-get-started/
- RMACC Users:
  - Contact your local representative, if known. Email rc-help@colorado.edu
  - We'll guide you through the process





### Demo: Getting an Account

- CU Boulder users and affiliates:
  - Request an account through the RC Account request portal
  - <a href="https://rcamp.rc.colorado.edu/accounts/account-request/create/organization">https://rcamp.rc.colorado.edu/accounts/account-request/create/organization</a>



### Your RC Account

#### Access to:

- 1. Alpine Cluster (also Summit)
- 2. Core Storage
- 3. PetaLibary Storage\*
- 4. Gateways (CU Affiliates)

\*If purchased



### Two Factor Authentication (Duo)

- Provides an extra level of authentication
  - We are outside the firewall!
  - Valuable resources
  - Inviting, high-profile target
  - Lost time investigating/fixing

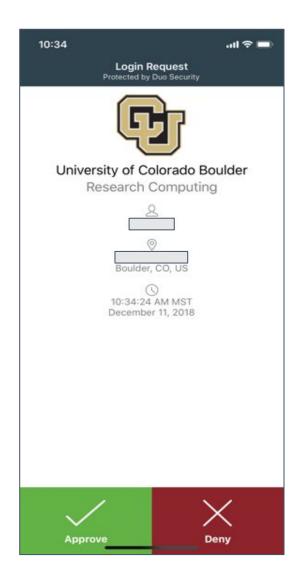
#### Duo

You will receive a Duo invitation when your RC account is created.



### **Duo Authentication**

- 1. Duo smartphone app (recommended)
- Phone Call/Text is an alternatives
- 3. Physical code generator "token" available for \$20







### Linux comfort level check

- •On a scale from (1-10) how familiar/comfortable are you with Linux?
  - The command line
  - Basic commands
  - Linux filesystem
  - Navigating the filesystem



### **Terminal**

- Mac or Linux
  - Terminal application
- Windows
  - PuTTY (recommended)
  - Powershell



- Open OnDemand (alternative for CU affiliates)
  - For those less familiar with Linux (ondemand.rc.colorado.edu/)



### Demo: Logging in via Terminal

To login to an RC login node:

```
$ ssh <username>@login.rc.colorado.edu
```

Supply your IdentiKey password and your Duo app will alert you to confirm the login

If you're using a tutorial account (we provide password):

\$ ssh <tutorial\_user>@tlogin1.rc.colorado.edu





### Demo: logging in with OnDemand

CURC Open OnDemand is a browser based, integrated, single access point for all of your HPC resources at CU Research Computing.

- Visit <a href="https://ondemand.rc.colorado.edu">https://ondemand.rc.colorado.edu</a>.
- CU Boulder only at the moment

# Logging In

- It's important to note that you are NOT logging into any specific resource, Summit, etc.
- When you log in, you land on our login nodes

- From *there*, you can access our other resources:
  - Alpine
  - Summit
  - Blanca



# Navigating Research Computing

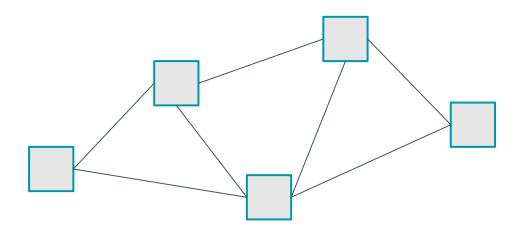


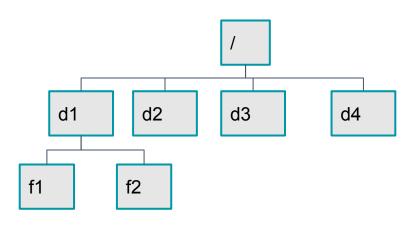
#### Node

File System

- One computing server
- Physical hardware
- Work together in parallel

- The basic tree-like layout
- From most nodes\* you have access to the entire file system





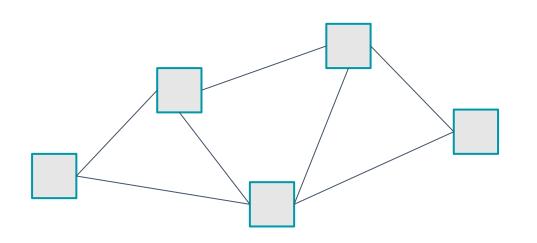


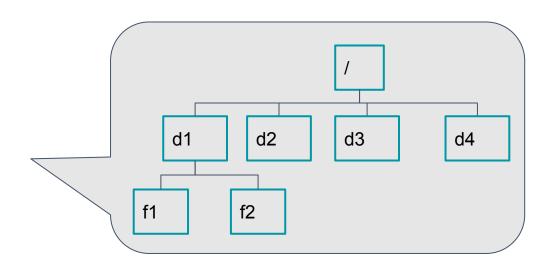
#### Node

**File System** 

- One computing server
- Physical hardware
- Work together in parallel

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# Node Types

Login	Compile	Compute	
Where you log in to	<ul> <li>Where you compile code, install packages</li> </ul>	Where scheduled jobs run	
<ul><li>For editing code, job submission</li><li>No heavy computation</li></ul>	<ul> <li>Explore the Summit software environment</li> <li>Edit code, submit jobs</li> <li>No heavy computation</li> </ul>	Intended for heavy computation	
Ex. edit job script	Ex. Install python libs	Ex. Running Matlab	





### A note on Alpine Compile Nodes

- If you have used Summit in the past, compile nodes work slightly differently:
  - Instead of having dedicated hardware (2 nodes) which are oversubscribed for users to ssh into
  - Alpine's acompile command starts an interactive job which users can compile in which provides the following benefits:
    Users can request specific resources (i.e. more cores to compile with)
    Limits dedicated hardware set aside

    - Can't accidentally run full workflows
  - Because of this you may wait longer for an acompile job





## Demo: Exploring Nodes

- Once logged in, type:
  - \$ acompile

To log in to an Alpine compile (or head) node.

- Once on a compile node, type:
  - \$ module avail

To list currently available software

# Filesystem Structure

/home (2GB)	/projects (250GB)	Scratch (10TB)
<ul> <li>Scripts, Code, Small, important files/directories</li> <li>Not for sharing files or job output</li> </ul>	<ul> <li>Code/files/libraries</li> <li>Software you are installing</li> <li>Sharing files</li> <li>Not for job output</li> </ul>	<ul> <li>Output from running jobs</li> <li>Large files/datasets</li> <li>Sharing files</li> <li>Cluster specific</li> <li>Not for long term storage</li> </ul>
Ex .bashrc	Ex. Shared job scripts	Ex. Data





# Demo: Exploring the Filesystem

 Once logged in use the following commands to navigate to your different workspaces

```
$ cd /home/<user>
$ cd /projects/<user>
$ cd /scratch/alpine/<user>
```

### Using RC Resources

- We have:
  - Logged in
  - Explored nodes
  - Explored filesystem

How do we actually use the computing resources?

# Running a Job



#### Jobs

#### What is a "job"?

- Work for the cluster to perform on
- Has a unique ID

#### 1. Batch jobs

- Submit job script which will be executed when resources are available
  - Create script containing information about the job
  - Submit the job file to a queue

#### 2. Interactive jobs

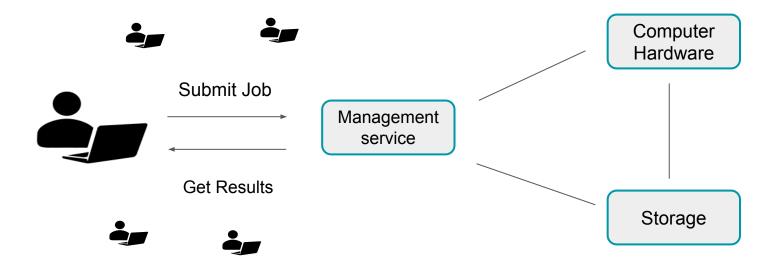
Work interactively at the command line of a compute node





# Job Scheduling

- CURC Clusters are shared resources, jobs are:
  - Submitted to a queue
  - When the required resources become available, the scheduler determines which set of nodes to use
  - Executes your job





#### **SLURM**

- Simple Linux Utility for Resource Management
- Through SLURM users can:
  - Schedule jobs on specific compute resources
  - Run jobs interactively or hands off
  - Query job statistics

## Job Script: 3 main parts

#### Directives

Specify resource requirements

#### 2. Software

- Because jobs run on a different node than from where you submitted...
- ...software that is needed must be loaded via the job script

#### 3. User scripting

the actual user scripting that will execute when the job runs

```
#!/bin/bash

## Directives
#SBATCH --<resource>=<amount>

## Software
module purge

## User Scripting
hostname # example bash command
```



# Slurm Options (directives)

```
#SBATCH <options> sbatch <options>

    Allocation:

                     --account=<account no>

    Partition:

                     --partition=<partition name>

    Sending emails:

                     --mail-type=<type>

    Output file:

                     --output=<file name> (%j gives you job id)

    Number of nodes:

                     --nodes=<nodes>

    Number of tasks:

                     --ntasks=<processes>

    Quality of service:

                     -- qos = < qos >

    Reservation:

                     --reservation=<name>

    Wall time:

                     --time=<wall time>
Job Name:
                     --job-name=<jobname> ...etc...
```

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





## Slurm Options (directives)

- There are MANY slurm directives, most of which are not required
  - See all options at <a href="http://slurm.schedmd.com/sbatch.html">http://slurm.schedmd.com/sbatch.html</a>
- We will focus on the most important ones:
  - Partition: Nodes with the same hardware configuration
  - Wall time: max time your job will run for
  - Node count: # of nodes requested
  - Core count: # of cores requested
  - Output file: name of output file (variable %j holds job id)





### Alpine Partitions

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





- Submit a slurm job with the following instructions:
- 1. The job will be submitted from a bash script named hostname.sh
- 2. The job will run on 1 node
- 3. We will request 1 minute of wall time
- 4. Run on the amilan-ucb partition
- 5. Output should contain job id
- 6. The job should run the Unix "hostname" command



- Set up batch job boilerplate
- Using text editor (vim or nano), create a file called hostname.sh with the following text:

```
#!/bin/bash

## Directives
#SBATCH --<resource>=<amount>

## Software
module purge

## User Scripting
```



#### Directives:

- 1 node
- 1 minute wall time
- "amilan-ucb" partition
- Output should contain job id

#### Number of nodes:

```
--nodes=<nodes>
```

#### Wall time:

```
--time=<wall time>
```

#### Partition:

```
--partition=<partition_name>
```

#### Output file:

```
--output=<file name>
(%j gives you job id)
```





- Software:
  - Do we need any software? (modules)
- User script:
  - What command do we want to run?

```
#!/bin/bash
#SBATCH --nodes=1  # Number of requested nodes
#SBATCH --time=0:01:00  # Max wall time
#SBATCH --partition=amilan-ucb  # Specify Summit haswell nodes
#SBATCH --output=hostname_%j.out  # Rename standard output file
# purge all existing modules
module purge
hostname
```



# Submitting a Job

- 1. Load up the slurm Alpine module (default is still Summit)
  - \$ module load slurm/alpine

- 2. Submit the job:
  - \$ sbatch <script-name>.sh

- 3. Check output
  - \$ cat <output-name>.out



# Review: Learning Goals

- 1. What is CU Research Computing (CURC)?
- 2. Understand Basic Resources (Alpine cluster)
- 3. Getting an account & logging in
- 4. Navigate the RC system
- 5. Running a job
- 6. Help!



# Help! I'm stuck, where do I go?

Documentation: <u>curc.readthedocs.io/</u>

• Trainings with Center for Research Data and Digital Scholarship (CRDDS):

https://www.colorado.edu/crdds/

• Helpdesk: rc-help@colorado.edu

#### Questions



## Survey and feedback

http://tinyurl.com/curc-survey18