



# Alpine: New User Seminar



Research Computing  
UNIVERSITY OF COLORADO **BOULDER**

# CURC Alpine: New User Seminar

Instructor: Trevor Hall

- Website: [www.rc.colorado.edu](http://www.rc.colorado.edu)
- Helpdesk: [rc-help@colorado.edu](mailto:rc-help@colorado.edu)
- Slides: [https://github.com/ResearchComputing/New\\_User\\_Seminar](https://github.com/ResearchComputing/New_User_Seminar)
- Survey: <http://tinyurl.com/curc-survey18>

# RMACC Cyber Infrastructure Portal



- <https://ask.cyberinfrastructure.org/c/rmacc/65>
- This forum provides opportunity for RMACC members to converse amongst themselves and with the larger, global research computing community.
- The “go to” general Q&A platform for the global research computing community - researchers, facilitators, research software engineers, CI engineers, sys admins and others.

# Learning Goals

1. Understand Basic CURC Resources & the Alpine cluster
2. Getting an account & logging in
3. Navigate the RC system
4. Running a job
5. Help!

# Things to take note of:

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

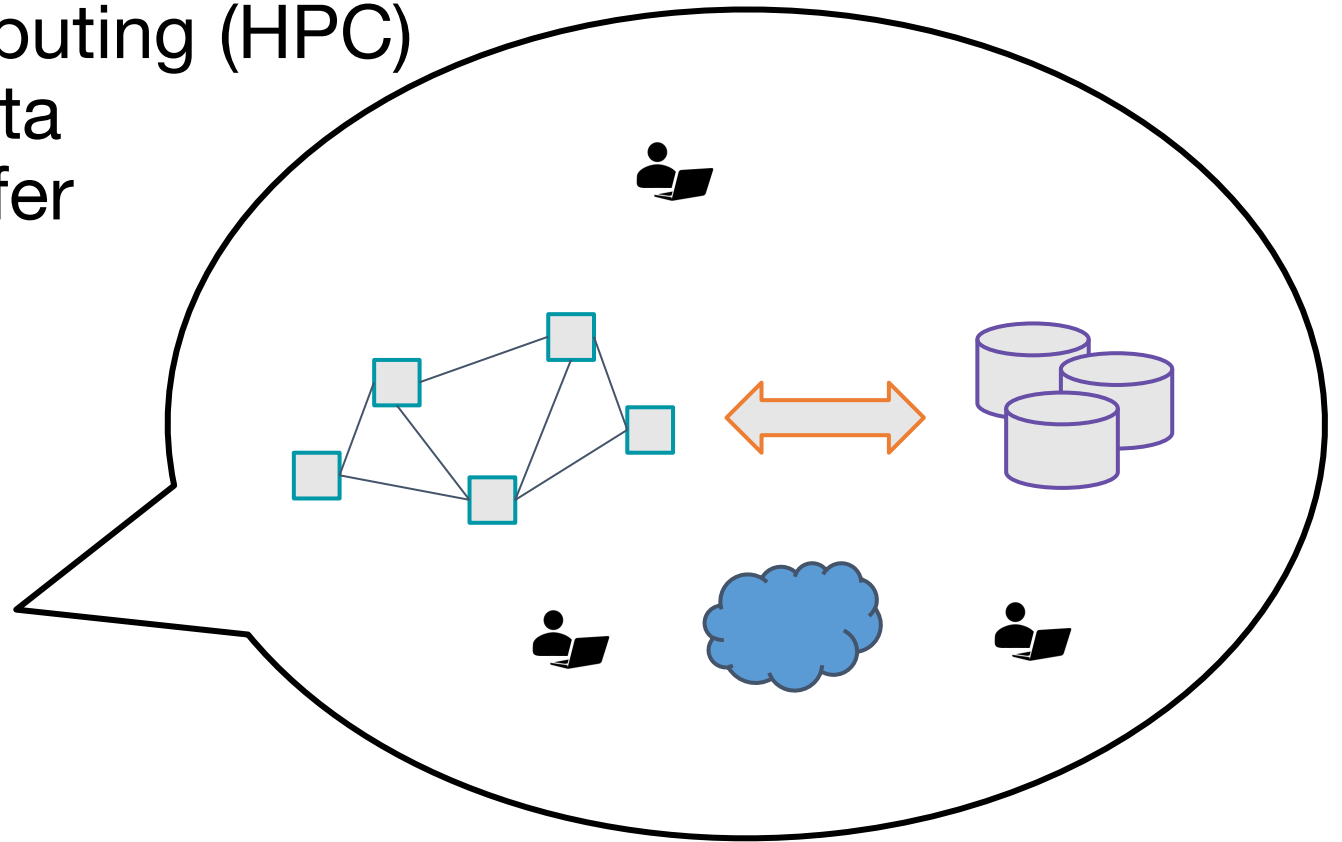


**Ask Questions!**



# Resources Include:

- High Performance Computing (HPC)
- Storage of Research Data
- High-Speed Data Transfer
- Data Sharing
- Cloud Computing
- Training and Education
- Secure Research



# 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)



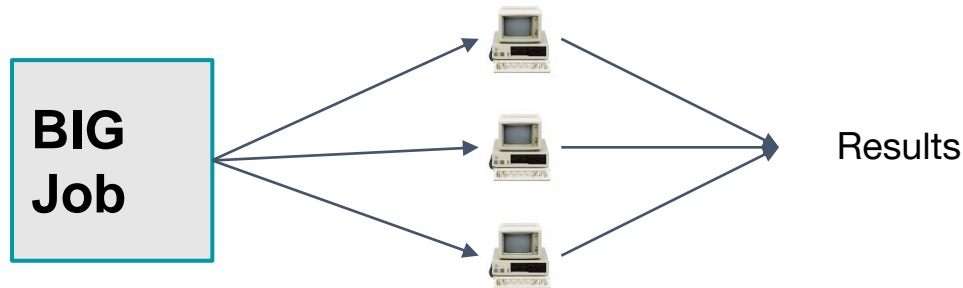


# What can / use HPC for?

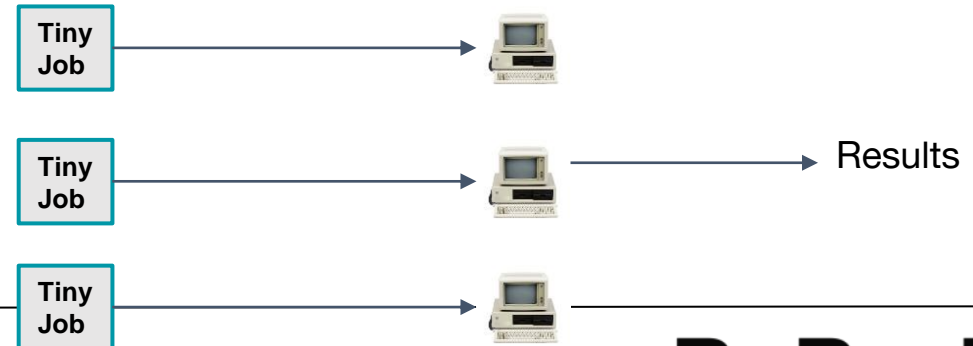
- Solving large problems that require more:
  - Memory than you have on your PC
  - cores/nodes/power than you have on your PC
- Jobs that require hardware you may not have:
  - High Performance GPU computing
  - Specific Operating System
- Visualization rendering

# 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)



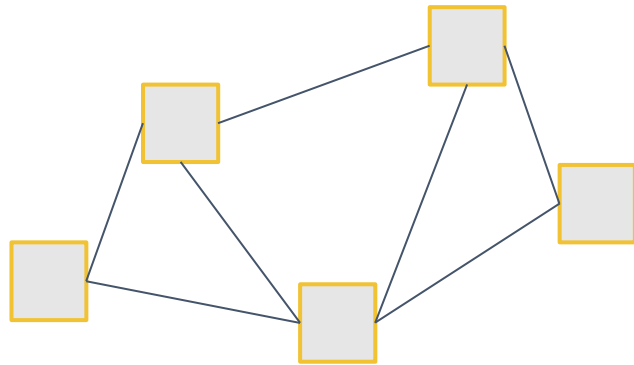
- Broken up into many serial jobs



# Research Computing Resources

# HPC Cluster: Alpine

Alpine

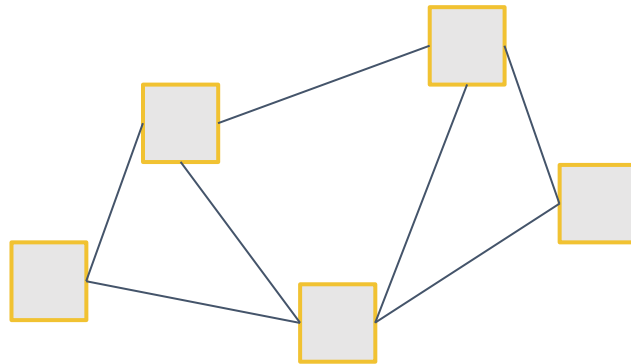


- Alpine is the 3rd-generation HPC cluster at CURC, following:
  - Janus
  - RMACC Summit
- Alpine is a heterogeneous cluster with hardware currently provided by CU Boulder, CSU, and Anschutz
- Access available to CU Boulder, CSU, AMC and RMACC users



# HPC Cluster: Alpine

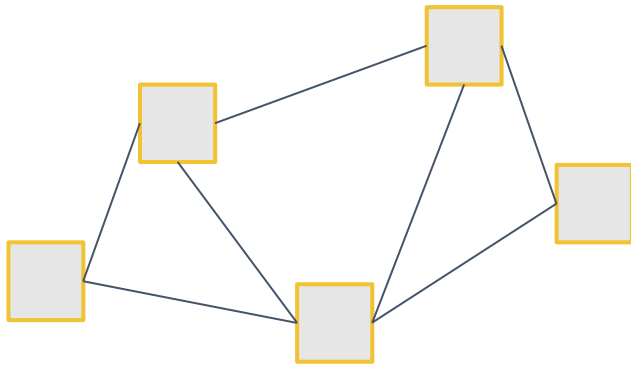
Alpine



- Hardware on Alpine will continue to be purchased and released in stages:
- Alpine (stage 3):
  - 184 General CPU Nodes
    - *AMD Milan, 64 Core, 3.74G RAM/Core*
  - 8 NVIDIA GPU Nodes
    - *3x NVIDIA A100 (atop General CPU node)*
  - 8 AMD GPU Nodes
    - *3x AMD MI100 (atop General CPU node)*
  - 12 AMD High-Memory Nodes
    - *AMD Milan, 48 Core, 21.5G RAM/Core*
  - Additional Hardware contributed by CSU, AMC
    - *Nodes which boost priority for CSU/AMC users*

# HPC Cluster: Alpine

Alpine



- Interconnect

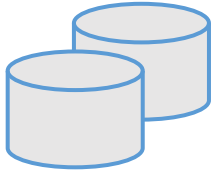
- **CPU nodes:** HDR-100 InfiniBand (200Gb inter-node fabric)
- **GPU nodes:** 2x25 Gb Ethernet +RoCE
- **Scratch Storage:** 25Gb Ethernet +RoCE

- Operating System

- RedHat Enterprise Linux version 8 operating system

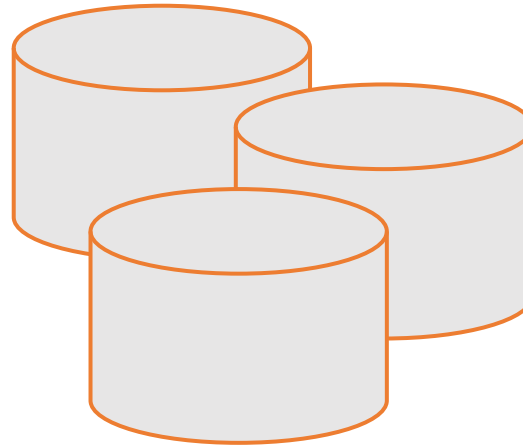
# Storage at CURC

## Core



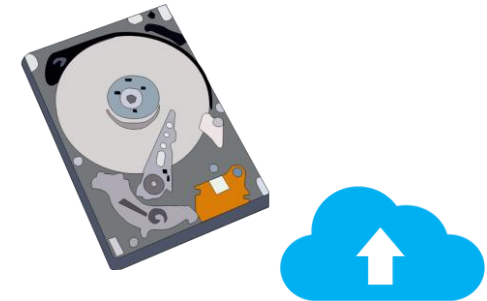
- Included with RC account
  - /home
  - /projects
  - scratch space

## PetaLibrary



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

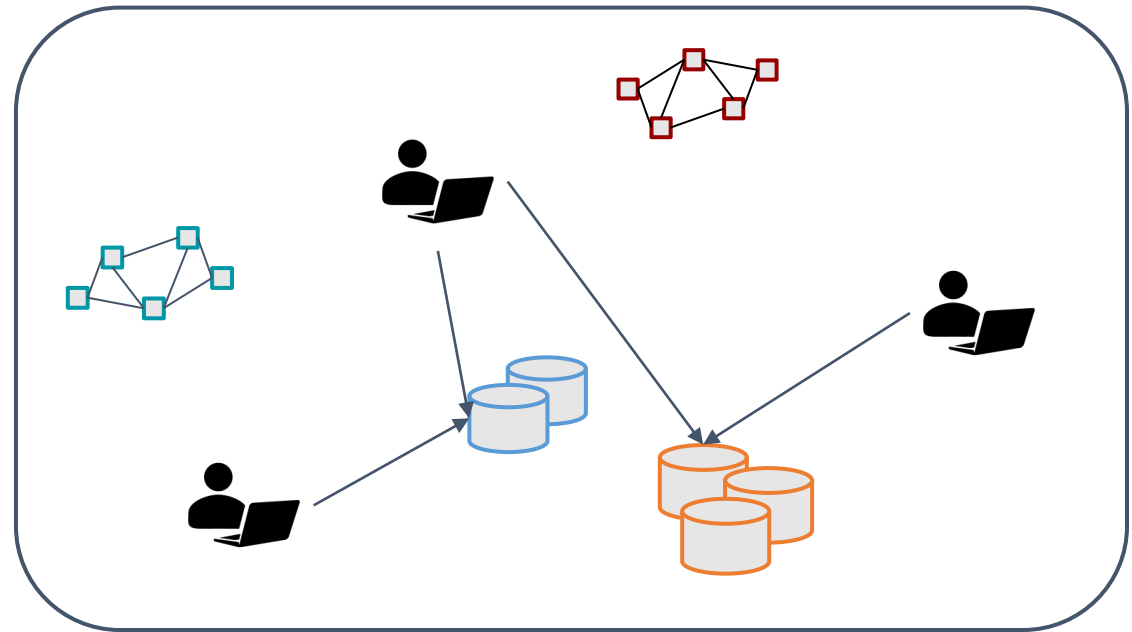
## Local or Cloud



- You can download your data locally or to a variety of other cloud resources
- Cloud Foundations at Research Computing

# Data Sharing: Within RC

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

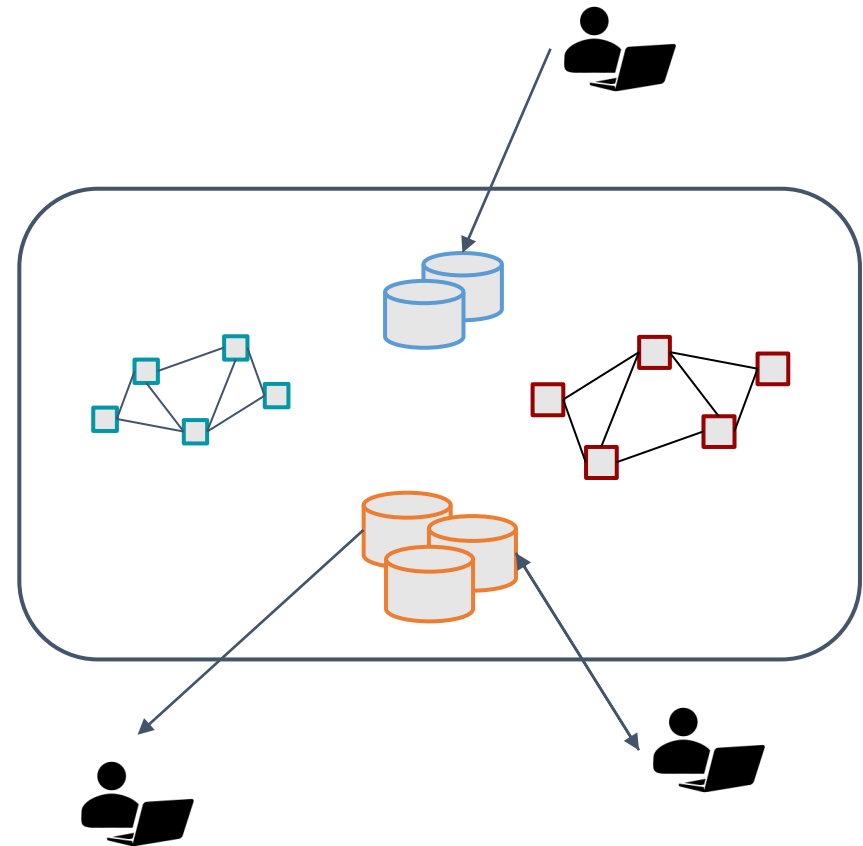


\*If you have purchased PetaLibrary space



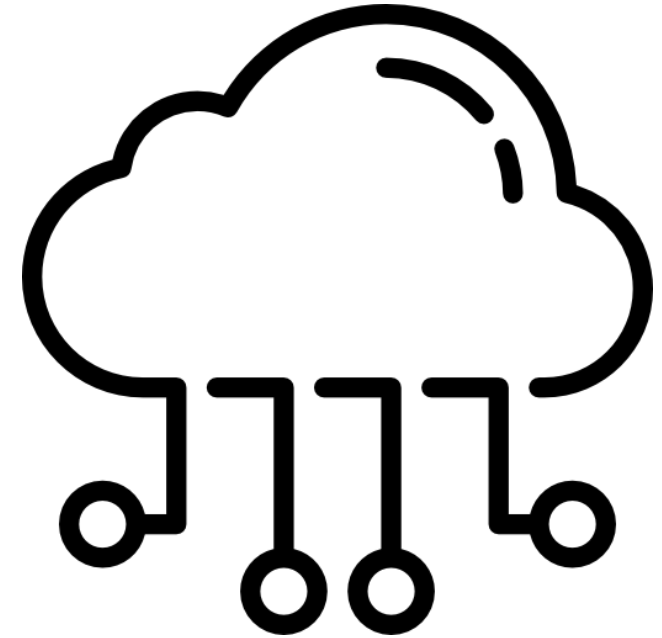
# Data Sharing: Outside RC

- 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 (VPN)
- Command line tools
  - scp, sftp, rsync, rclone



# Cloud Computing

- CURC supports both AWS and on-premise cloud via CUMulus
  - For use cases not well-supported by HPC
- Can be used as an alternative to HPC
- Can be used to enhance HPC
  - Automatic job submission, high availability, etc.



Request a CUMulus application by contacting the RC helpdesk at [rc-help@colorado.edu](mailto:rc-help@colorado.edu)

# 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
- <https://it.colostate.edu/research-computing-and-cyberinfrastructure/compute/get-started-with-alpine/>

- **RMACC Users:**

- Create an [ACCESS-CI](#) Account in the ACCESS user portal
- Email us at [rc-help@colorado.edu](mailto:rc-help@colorado.edu) and request an account. Please include the following information: your ACCESS username, your institutional affiliation, your role, your department, your first and last name, your preferred email address for communication

# Demo: Getting an Account

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

# Your RC Account

## Access to:

1. Alpine Cluster
2. Core Storage
3. PetaLibrary Storage\*
4. Open OnDemand
5. Approximately 2,000 Service Units (SUs) per month

\*If purchased

# Your RC Account

## How can I use more computational time?:

- Trailhead Allocation (Default)
  - ~2,000 SUs / Month
- Ascent Allocation
  - 250,000 SUs
- Peak Allocation
  - >250,000 SUs

Request an allocation at

<https://curc.readthedocs.io/en/latest/clusters/alpine/allocations.html?highlight=alpine%20allocation#comparing-trailhead-auto-allocation-ascent-allocation-and-peak-allocation-tiers>

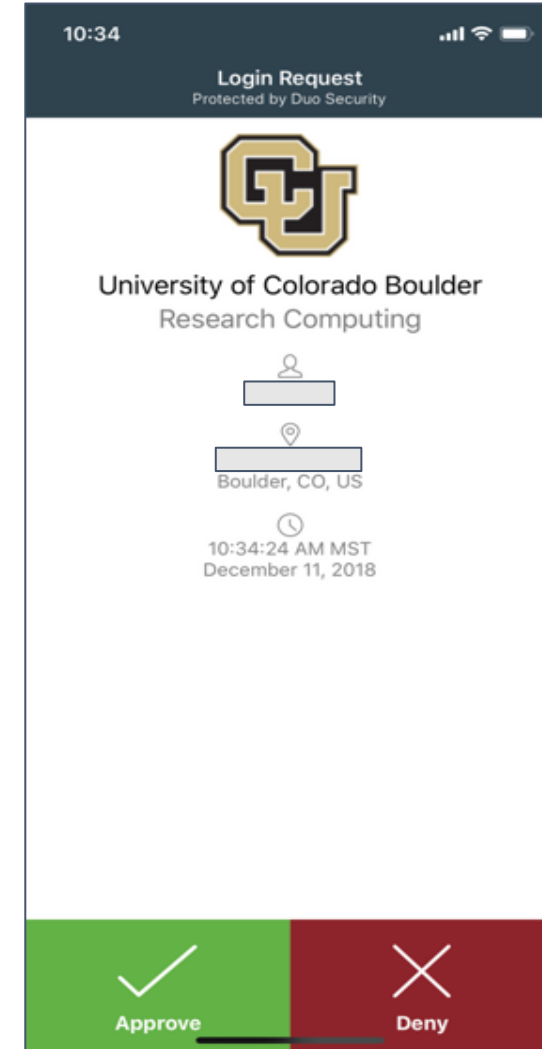


# Two Factor Authentication (Duo)

- 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)**
2. 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
  - Powershell
- Open OnDemand (*alternative for CU affiliates*)
  - For those less familiar with Linux ([ondemand.rc.colorado.edu/](https://ondemand.rc.colorado.edu/))

```
[user0083@tlogin1 ~]$ pwd  
/home/user0083  
[user0083@tlogin1 ~]$ █
```

# 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

\*CU and CSU exclusive

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# 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.

- CU Boulder: Visit <https://ondemand.rc.colorado.edu>.
- Other RMACC Institutions: Visit <https://ondemand-rmacc.rc.colorado.edu/>

# Logging In

- It's important to note that you are ***NOT*** logging into any specific resource, Alpine, Blanca, etc.
- When you log in, you land on our ***login nodes***
- From ***there***, you can access our other resources:
  - Alpine
  - Blanca
  - Petalibrary

# Navigating Research Computing

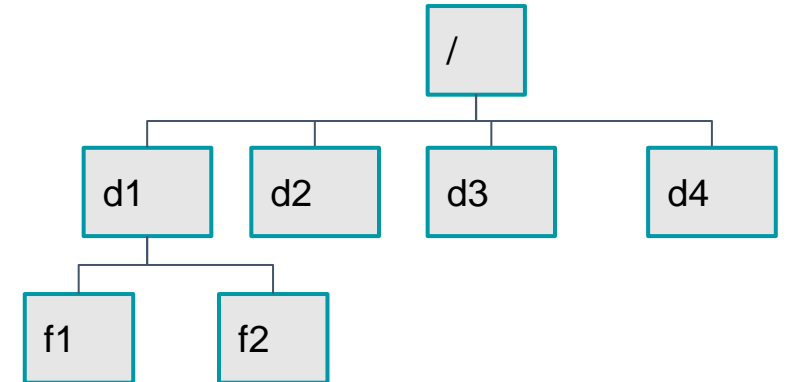
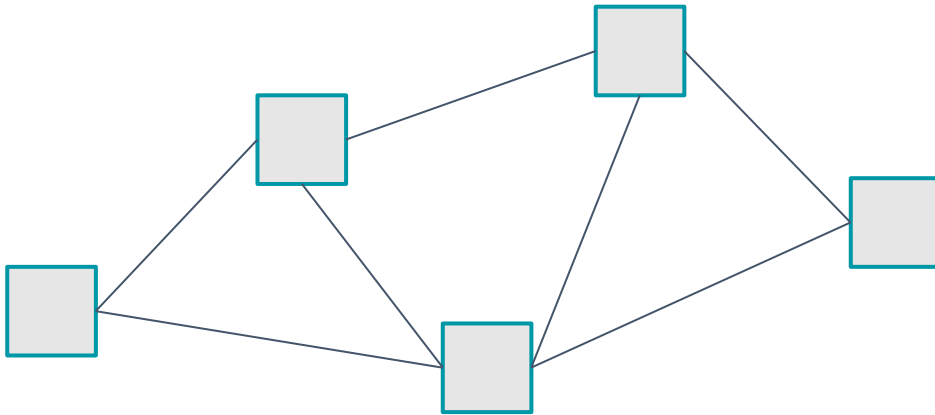


## Node

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

## File System

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

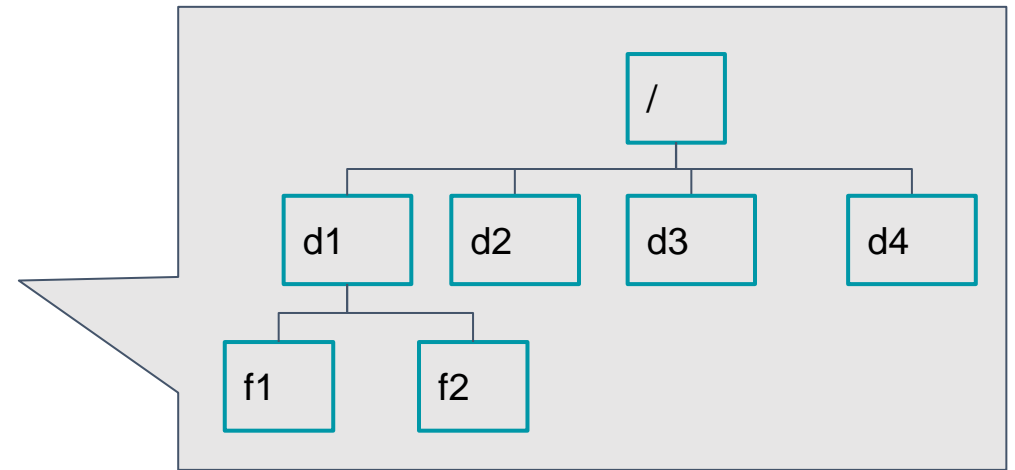
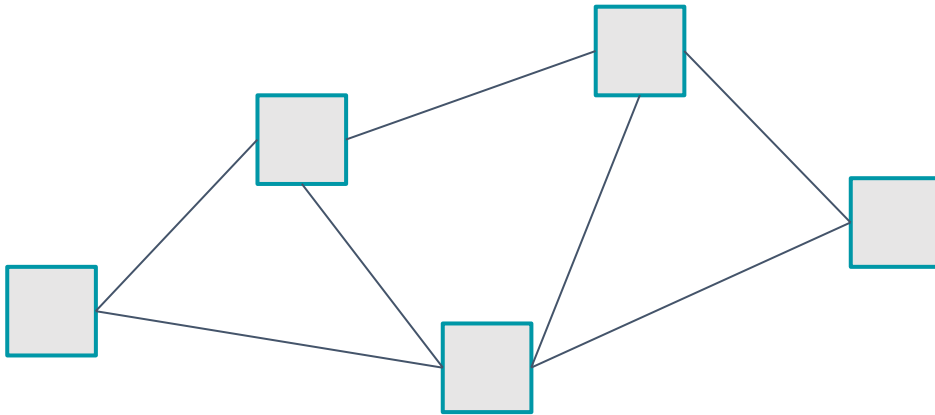


## Node

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# Node Types

## Login

- Where you log in to
- For editing code, job submission
- No heavy computation

Ex. edit job script

## Compile

- Where you compile code, install packages
- Explore the Alpine software environment
- Edit code, submit jobs
- No heavy computation

Ex. Install python libs

## Compute

- Where scheduled jobs run
- Intended for heavy computation

Ex. Running Matlab

# 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

# Alpine Compile Nodes

- `$ module load slurm/alpine`
- `$ acompile`
  - starts a job with default: 1 core, 3.74GB RAM, for 60 minutes\*
- `$ acompile --help`
  - `--time=<time-limit>` # set minimum runtime
  - `--ntasks=<number-of-cores>` # default 1, max 4
  - `--gpu=<nvidia|amdgpu>` # request gpu to compile with
  - `--x11` # enable
  - `graphical forwarding`

\*only a single `acompile` job can be open at a time

# 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)

- Scripts, Code, Small, important files/directories
- Not for sharing files or job output

Ex .bashrc

## /projects (250GB)

- Code/files/libraries
- Software you are installing
- Sharing files
- Not for job output

Ex. Shared job scripts

## /scratch/alpine (10TB)

- Output from running jobs
- Large files/datasets
- Sharing files
- Cluster specific
- Not for long term storage

Ex. Data

# 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

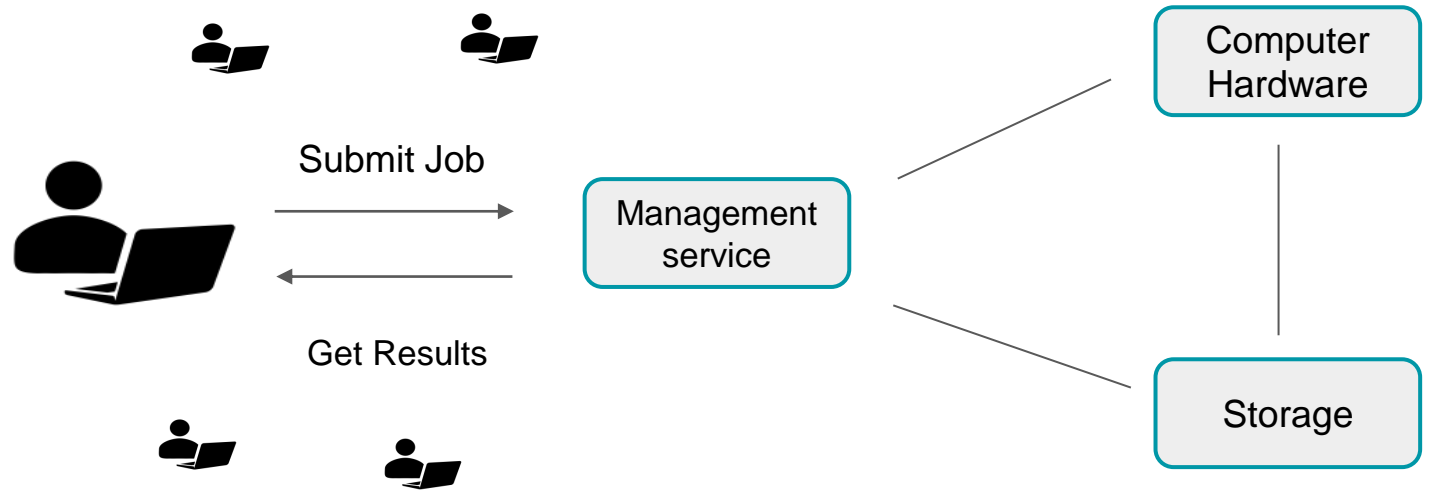
- Submit job script which will be executed when resources are available
  - Create script containing information about the job
  - Submit the job file to a queue

## 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

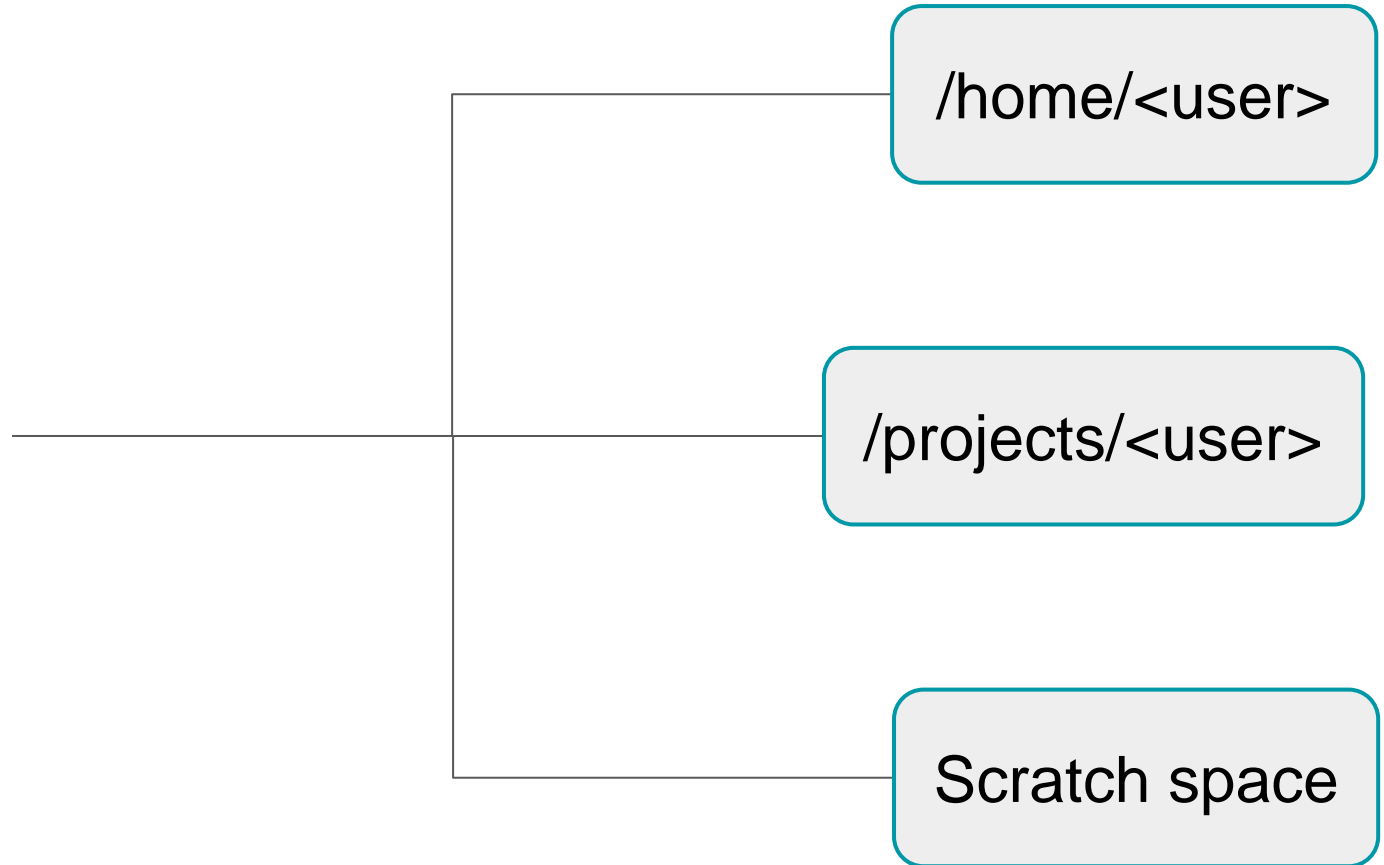


# SLURM

- **S**imple **L**inux **U**tility for **R**esource **M**anagement
- Through SLURM users can:
  - Schedule jobs on specific compute resources
  - Run jobs interactively or hands off
  - Query job statistics

# Your first job

- Where to write it?
- How to write it?
- How to run it?



# Job Script: 3 main parts

## 1. Directives

- Specify resource requirements

## 1. Software

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

## 1. 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 <http://slurm.schedmd.com/sbatch.html>
- We will focus on some common options:
  - **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

# Alpine Partitions

Partition	Description	# of nodes	RAM/core (GB)	cores/node	GPUs/node
amilan	General Compute Node: AMD Milan	64	3.74	64	0
ami100	GPU Node: 3x AMD MI100	8	3.74	64	3
aa100	GPU Node: 3x Nvidia A100	8	3.74	64	3
amem	High-memory node	4	21.5	48	0

# Review: Learning Goals

1. Understand Basic Resources (Alpine cluster)
2. Getting an account & logging in
3. Navigate the RC system
4. Running a job
5. Help!

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

- **Documentation:** [curc.readthedocs.io/](http://curc.readthedocs.io/)
- **Trainings with Center for Research Data and Digital Scholarship (CRDDS):** <https://www.colorado.edu/crdds/>
  - **Coming up:**
    - [Supercomputing Spin Up: Part 1 -- Working with Linux](#) (1/25)
    - [Supercomputing Spin Up: Part 2 – Job Scheduling](#) (1/31)
    - [Setting up Your Research Software on Alpine](#) (1/31)
- **Helpdesk:** [rc-help@colorado.edu](mailto:rc-help@colorado.edu)
- **Consult Hours (now!)**

# Helpdesk Tickets

To: [rc-help@colorado.edu](mailto:rc-help@colorado.edu)

Dear Research Computing,

Help! My code won't run!  
Help!

Help please,  
Trevor

To: [rc-help@colorado.edu](mailto:rc-help@colorado.edu)

Dear Research Computing,

I am running into issues running my Python script. I am using a conda environment called `my_python_env` with the pytorch software, and I am receiving the following error. I am not sure how to troubleshoot. My job ID is 620350. Let me know what I can try!

sbatch: error: Batch job submission failed: Invalid partition name specified.

Thanks,  
Trevor

# Questions

CURC User Policies: <https://curc.readthedocs.io/en/latest/additional-resources/policies.html?highlight=policies#curc-user-policies>

# Survey and feedback

<http://tinyurl.com/curc-survey18>