

### Research Computing New User Seminar

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Slides: <a href="https://github.com/ResearchComputing/New User Seminar">https://github.com/ResearchComputing/New User Seminar</a>









# **Before We Begin**

#### Goals

- Basic resources Research Computing (RC) offers
- 2. How to get an account & log in
- 3. How to navigate Research Computing (RC)
- 4. How to run a job
- 5. Help!



# **Before We Begin**

### Goals

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### Things to take note of

- Confusing, ambiguous, highly nuanced concepts
- Common mistakes or frustrations

**Ask Questions!** 





## **Jargon**

- RC = Research Computing
- HPC = High Performance Computing
- <input> = your input (username, password, etc.), do not include
   <> when you write it

### Why High Performance Computing (HPC)?







### **Personal Computers**

- Personal Data
- Photos
- Games
- Applications...

#### **HPC**

- Behavior analysis
- Climate modeling
- Molecular sciences
- Early universe...

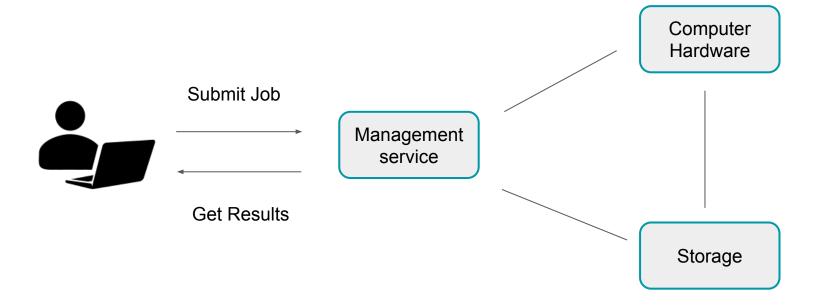








### **High Performance Computing**





### What is Research Computing?

- Provide services for researchers that include:
  - Large scale computing
  - Data storage
  - High speed data transfer
  - Data management support
  - Consulting & Training
- We are likely best known for:
  - Summit Supercomputer
  - PetaLibrary Storage





## **Research Computing Services**

Supercomputing Clusters

Storage

Gateways

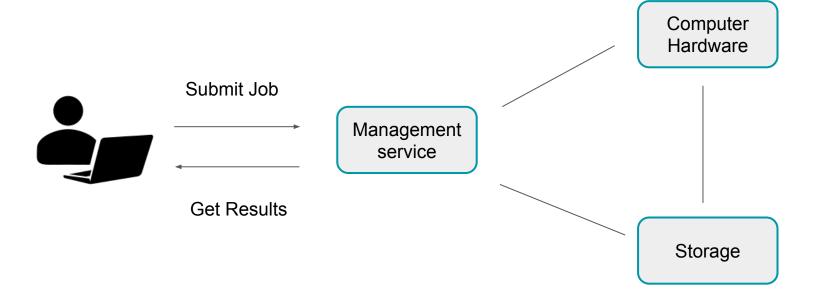
### Research Computing Services

- Supercomputing Clusters
  - Summit, Blanca, (Alpine)

- Storage
  - Core, PetaLibrary

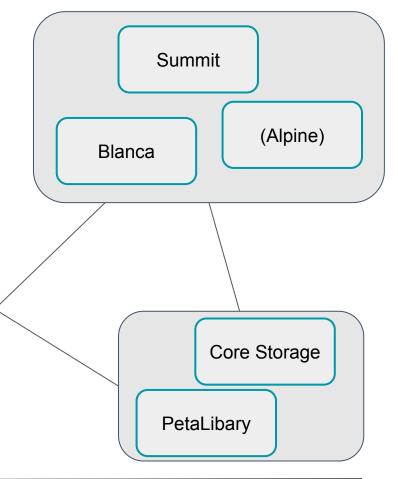
- Gateways
  - JupyterHub, EnginFrame, (CUmulus)

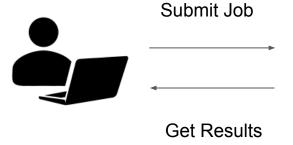
## **High Performance Computing**





# **CU Research Computing**





Research Computing

JNIVERSITY OF COLORADO BOULDER

**Be Boulder.** 

Management service

### **Summit Cluster**

Free-access, NSF-funded supercomputer

- 450+ (mostly) compute nodes
  - Also have memory, and graphics nodes

 Shared between CU, CSU, and Rocky Mountain Advanced Computing Consortium (RMACC)

### **Blanca Cluster**

- Condo computing service
  - Buy-in Cluster
- Compute and Graphics nodes available.

### **PetaLibarary**

- Service for:
  - Storage
  - Archive
  - Sharing of research data.
- Available at a subsidized cost to any researcher affiliated with the University of Colorado Boulder.

### **How to Access RC Resources?**

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





### 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
- CSU 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**

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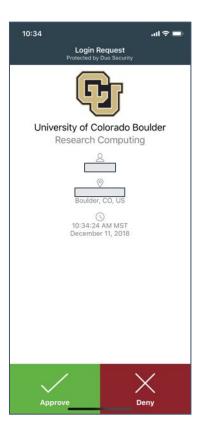
### **Two Factor Authentication**

- 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. Most users use the Duo smartphone app
- 2. "Phone Call" is an alternatives
- 3. Physical code generator "token" available for \$20







### **Terminal**

- Mac or Linux
  - Terminal application

- Windows
  - PuTTY





# **Demo: Logging in**

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

## **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

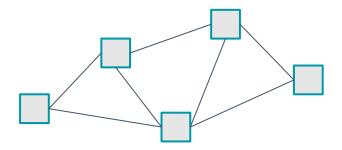
From there, you can access our other resources

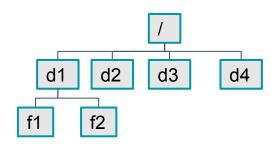
#### **Node**

### File System

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

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







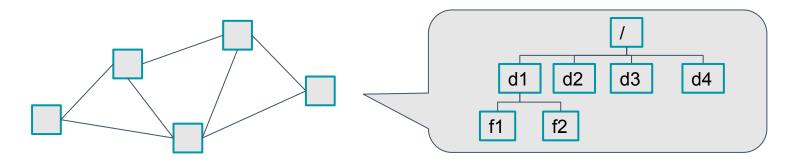


#### **Node**

### File System

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

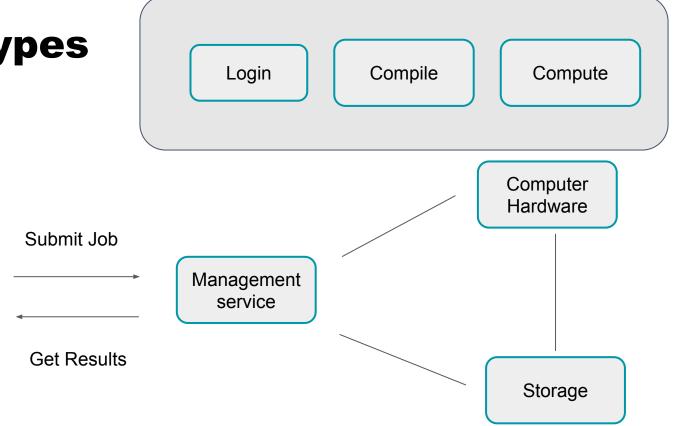
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### **Nodes Types**







### **Nodes**

Login	Compile	Compute
Where you start	Where you compile code, install packages	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>	<ul> <li>Intended for heavy computation</li> </ul>
Ex. edit job script	Ex. Install python libs	Ex. Running Matlab





# **Demo: Exploring nodes**

• Once logged in:

ssh scompile

To log in to a compile (or head) node.

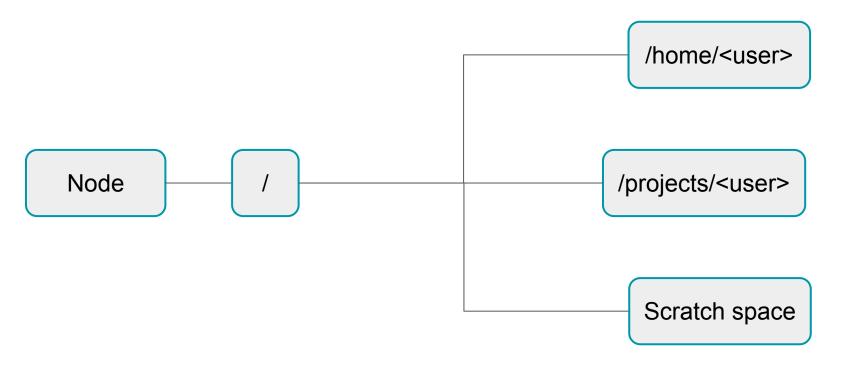
module avail

To check currently available software





# File system map





### **File Structures**

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





# **Demo: Exploring the Filesystem**

Once logged in:

```
cd /home/<user>
cd /projects/<user>
cd /scratch/summit/<user>
```

To navigate to your different directories





# **Using Research Computing**

- We have logged on
- We have explored nodes and filesystem
- But how do we actually use the computing resources?

## The fundamental "job"

What is a "job"?

Jobs are scripted packages of work for the cluster to perform on

### 1. Batch jobs

- Submit job script which will be executed when resources are available
  - Create or modify a 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**

- On a supercomputer, jobs are scheduled rather than just run instantly
  - Shared system
  - Jobs are put in a queue until resources are available

- Simple Linux Utility for Resource Management (SLURM)
  - Keeps track of what nodes are busy/available, and what jobs are queued or running
  - Tells the resource manager when to run which job on the available resources



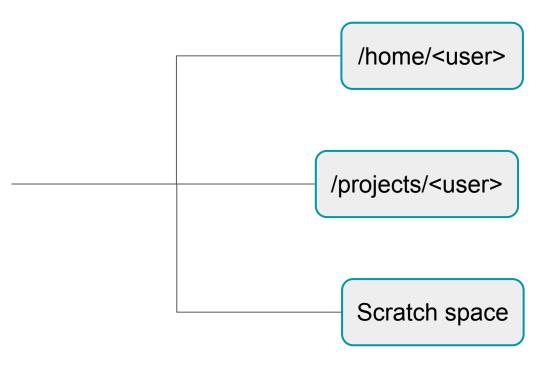


# Your first job

Where to put it?

How to write it?

How to run it?





# Job Script: 3 main parts

#### Directives

Specify resource requirements

#### Software

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

### User scripting

the actual user scripting that will execute when the job runs





## Directive Options http://slurm.schedmd.com/sbatch.html

#SBATCH <options> sbatch <options>

Allocation: --account=<account no>

Partition: --partition=<partition name>

Sending emails: --mail-type=<type>

Email address: --mail-user=<user>

Number of nodes: --nodes=<nodes>

Number of tasks: --ntasks=<processes>

Quality of service: --dos=<dos>

Reservation: --reservation=<name>

Wall time: --time=<wall time>

Job Name: --job-name=<jobname>

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





### **Writing a Job: Hostname**

Submit a slurm job with the following instructions:

- 1. The job will be submitted from a bash script named hostname summit.sh
- 2. The job should run the Unix "hostname" command
- 3. The job will run on 1 node
- 4. We will request 1 minute wall time
- 5. Run using "testing" QOS
- 6. Run on the shas-testing partition
- 7. Output should contain job #





### **Demo: Writing Hostname**



### **Demo: Writing Hostname**

```
#!/bin/bash
#SBATCH --nodes=1
                                        # Number of requested nodes
#SBATCH --time=0:01:00
                                        # Max wall time
#SBATCH --gos=testing
                                        # Specify QOS
#SBATCH --partition=shas-testing
                                        # 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 module (probably not needed)
  - module load slurm/summit

- 2. Submit the job:
  - sbatch hostname\_summit.sh

3. Check output



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

We've got your back:

Documentation: <a href="https://curc.readthedocs.io/en/latest/">https://curc.readthedocs.io/en/latest/</a>

Trainings:

https://www.colorado.edu/crdds/what-we-do/education-training

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

### Review

#### Goals

- 1. Basic resources RC offers
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### **Questions**

