



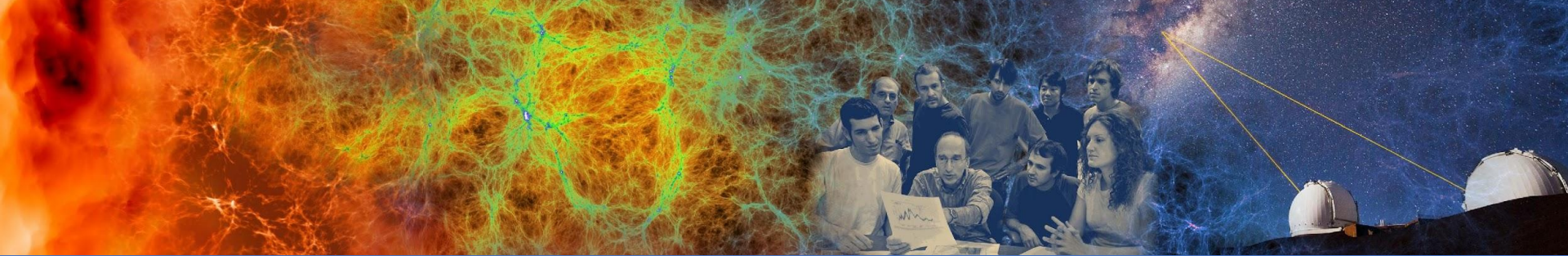
# Using Perlmutter

Introduction to HPC Bootcamp  
Aug 8, 2023

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NERSC

# Outline

- **Connecting and transferring files to Perlmutter**
  - **Daniel Fulton**, HPC System Software Engineer, Computational Systems Group
- **Jupyter at NERSC**
  - **Rollin Thomas**, Senior Computing Engineer, Programming Environment and Models Group
- **File systems, compile and run jobs**
  - **Helen He**, HPC Consultant, User Engagement Group



# Connecting and Transferring Files to Perlmutter



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# Connecting to Perlmutter

Users primarily interact with Perlmutter via text **login shell** (e.g. `/bin/bash`)

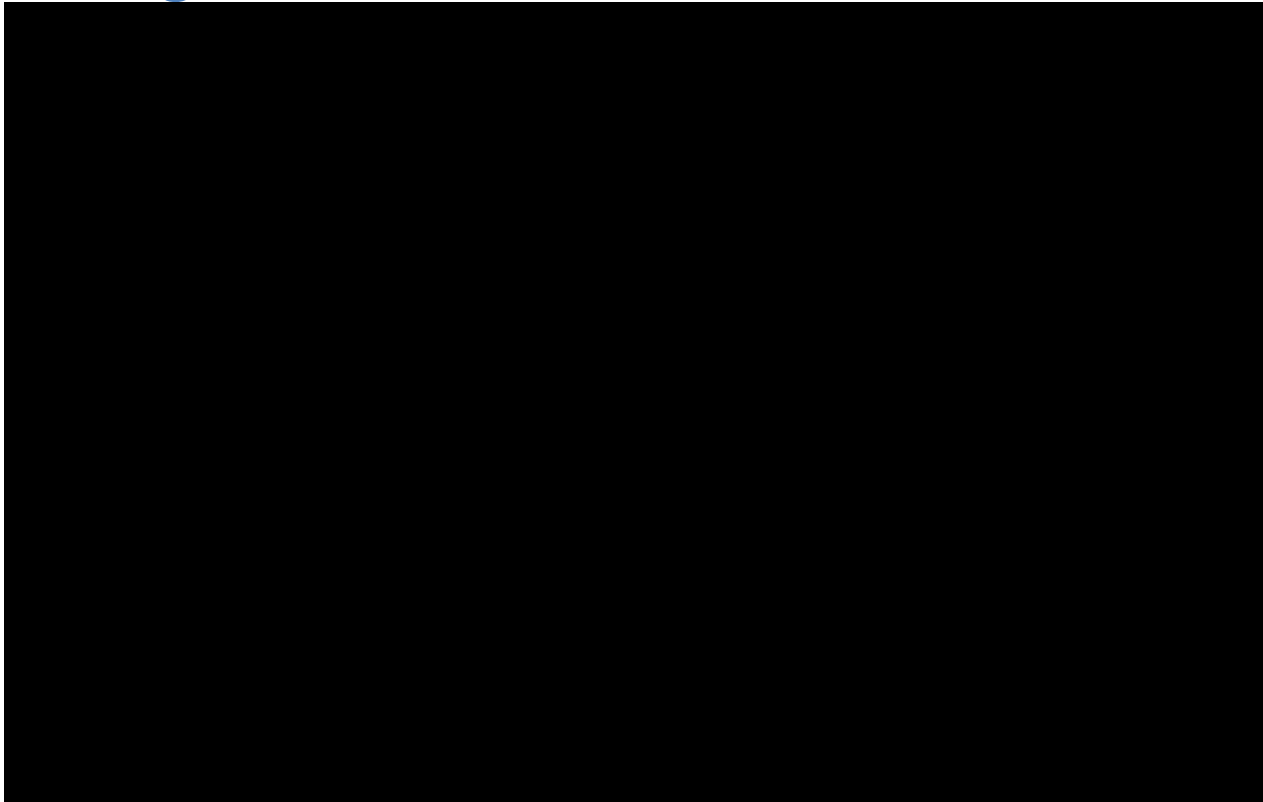
- Terminal emulator + SSH
  - Windows: Native **Powershell** or 3rd party **putty**, **cmdr**
  - Mac: Native **Terminal.app** or 3rd party **iTerm 2**
  - Linux: Any native terminal (**Gnome Terminal**, **Terminator**, **Konsole**)
- NERSC Jupyterhub web portal (<https://jupyter.nersc.gov>)
- NoMachine (NX) remote desktop client

All connections to NERSC systems require an authorized NERSC user account and authentication via one of the following:

- Your NERSC user password + One Time Password
- 24-hour sshproxy key (obtained with password+OTP)

See <https://docs.nersc.gov/connect/> and Slack [#perlmutter\\_support](#)

# Connecting to Perlmutter with SSH





# Connecting to Perlmutter: 24 hour keys

The screenshot shows a web browser window displaying the NERSC Documentation page titled "Connecting to NERSC". The browser's address bar shows the URL `docs.nersc.gov/connect/`. The page has a teal header with the NERSC logo and a search bar. A left sidebar lists various documentation categories, with "Connecting" selected. The main content area is titled "Connecting to NERSC" and includes a sub-section "Login Nodes". This section explains that opening an SSH connection results in a connection to a login node and provides instructions on how to connect. It includes two terminal snippets for SSH commands: `ssh <user>@perlmutter.nersc.gov` and `ssh <user>@saul.nersc.gov`. A "Table of contents" on the right lists other topics like "Connect to NERSC Computational Systems", "SSH", and "Troubleshooting".

NERSC Documentation

- Home
- Getting Started
- Tutorials
- Accounts
- Iris
- Systems
- Storage Systems
- Connecting
- Multi-Factor Authentication
- Federated Identity
- NoMachine / NX, X Windows Accelerator
- Environment
- Policies
- Development
- Developer Tools
- Running Jobs
- Applications
- Analytics
- Machine Learning
- Performance
- Services
- Science Partners

## Connecting to NERSC

### Login Nodes

Opening an [SSH connection](#) to NERSC systems results in a connection to a login node. Typically systems will have multiple login nodes which sit behind a load balancer. New connections will be assigned a random node. If an account has recently connected the load balancer will attempt to connect to the same login node as the previous connection.

### Connect to NERSC Computational Systems

Please make sure you have configured [Multi-Factor Authentication \(MFA\)](#) prior to login.

To access Perlmutter via `ssh` you can do the following:

```
ssh <user>@perlmutter.nersc.gov
```

or

```
ssh <user>@saul.nersc.gov
```

If you have configured [sshproxy](#) then you can run the following:

```
ssh -i ~/.ssh/nersc <user>@perlmutter.nersc.gov # or 'ssh -i ~/.ssh/nersc <user>@saul.nersc.gov'
```

#### Table of contents

- Login Nodes
- Connect to NERSC Computational Systems
- X11 Forwarding
- SSH
  - Connecting with SSH
  - Password-less logins and transfers
  - SSH certificate authority
  - Key fingerprints
    - Perlmutter
    - DTN[01-04]
    - NoMachine/NX
  - Host Keys
    - Perlmutter
- Troubleshooting
  - "Access Denied", "Permission Denied" or "Too many authentication failures"
  - Host authenticity
  - Host identification changed
  - SSH connection disconnects periodically
  - Other SSH connection failures

# Connecting to Perlmutter: SSH Shortcuts

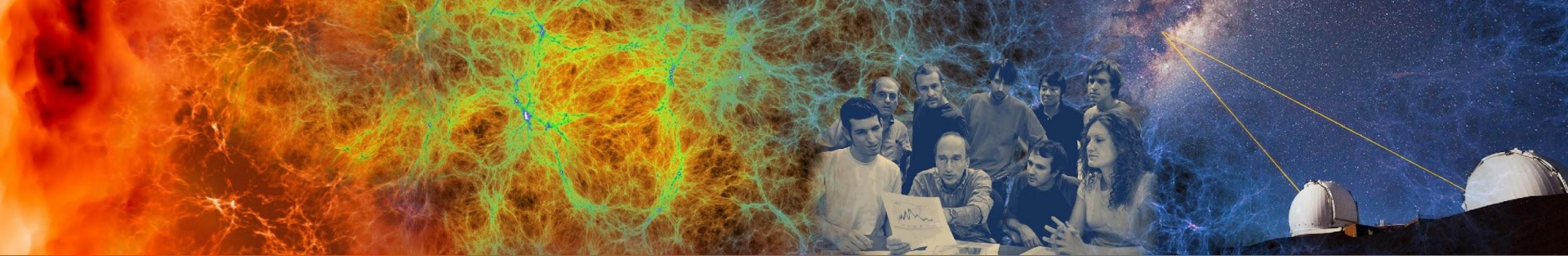


# Transferring Data to Perlmutter

Great, now how do I get my files to onto the supercomputer?!

- For this workshop:
  - On NERSC internal filesystems (CFS): `mv`, `cp`, or `rsync`  
`cp /path/to/original /path/to/new/copy`
  - From your laptop: `scp`, `rsync`, drag and drop with Jupyter  
`scp /path/on/laptop user@perlmutter.nersc.gov:/path/on/pm`
  - From Github: `git clone`  
`git clone https://www.github.com/ns/myrepo.git`
- Other interesting use cases:
  - For large scientific data: Globus
  - When Globus doesn't work: `rsync`
  - Download from trusted URLs: `wget`, `curl`
  - Large, live, scientific data: come talk to us





# Jupyter at NERSC



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# About Me (Rollin)

Grew up moving between Indiana, Tennessee, and Ohio

Wanted to work on computers and astronomy

Learned that physics would be a good foundation for that

Went to Purdue and got a Physics degree there

Almost quit, but a computational physics class helped me understand physics better

Got rejected from 10+ internships but got one at University of Oklahoma working on supernovae

Went to OU, got a PhD doing supernova simulations w/Fortran using Seaborg at NERSC

I kept avoiding writing my dissertation by optimizing my code

Got rejected from 12+ fellowships but got an interview at LBL w/Saul Perlmutter + friends

Worked on a few supernova cosmology experiments at LBL, more coding, less physics

Moved to NERSC to broaden my impact on science: New user communities, Python, Jupyter, ...

# About Jupyter



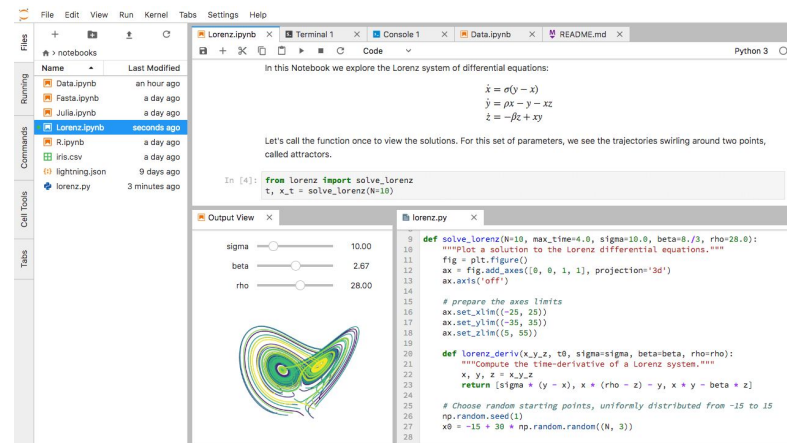
Open source, literate computing ecosystem built on “notebooks” and programming interfaces / user applications for interacting with and executing them

Notebooks (JSON documents) can contain:

- Live code
- Equations
- Visualizations
- Narrative text
- Interactive widgets

Jupyter is used for:

- Data cleaning and data transformation
- Numerical simulation
- Statistical modeling
- Data visualization
- Machine learning
- Workflows and analytics frameworks

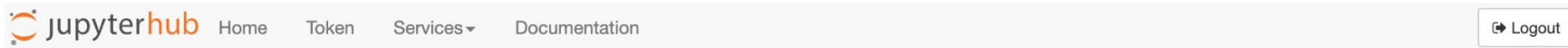


# Jupyter at NERSC

→ <https://jupyter.nersc.gov> ←

# Hub Home Page or “Console”

All these options get you running Jupyter on Perlmutter but give you different ways to use its resources.



	Login Node	Shared GPU Node	Exclusive CPU Node	Exclusive GPU Node	Configurable Job
Perlmutter	<a href="#">start</a>	<a href="#">start</a>	<a href="#">start</a>	<a href="#">start</a>	<a href="#">start</a>
Resources	Use a login node shared with other users, outside the batch queues.	Use a single GPU on a node within a job allocation using default settings.	Use your own node within a job allocation using defaults.	Use a single GPU on a node within a job allocation using defaults.	Use multiple compute nodes with specialized settings.
Use Cases	Visualization and analytics that are not memory intensive and can run on just a few cores.	Work that fits on a single GPU, and uses at most a quarter of a GPU node's CPU cores and host memory.	Visualization, analytics, machine learning that is compute or memory intensive but can be done on a single node.	Visualization, analytics, machine learning that is compute or memory intensive but can be done on a single node.	Multi-node analytics jobs, jobs in reservations, custom project charging, and more.

Use Jupyter on one of  
Perlmutter's 40 login nodes

*Immediate start, no charging,  
but more limited resources*

Single-click launch of Jupyter on one  
of Perlmutter's 4500+ compute nodes

*Scheduled, charged, and time-limited,  
but with GPUs and/or a whole node just  
to yourself*

Customized launch of Jupyter  
on Perlmutter compute nodes

*Scheduled, charged,  
time-limited, but you control  
settings directly*



# About Using Jupyter This Week



We've *reserved* compute nodes for the bootcamp this week:

Day	Reservation Name	Start Time	End Time
Tuesday	<a href="#">intro_hpc_aug8</a>	10:30 AM	5:00 PM
Wednesday	<a href="#">intro_hpc_aug9</a>	1:30 PM	3:30 PM
Thursdsay	<a href="#">intro_hpc_aug10</a>	1:00 PM	10:00 PM

This lets your notebook server launch faster on compute nodes.

But you have to tell Perlmutter to launch your notebook server on the reserved nodes. How do you do this...?

***... use the “Configurable Job” option.***

Outside of reservation hours, you can explore the other single-click options.

# Running a Notebook Server Using One Whole Node

## Server Options

Select Account: m4388

Select QOS: regular

Select Reservation: ???

Leave everything else the same

Use this setup if you want either:

- To use all 4 GPUs on a node, and/or
- All of the CPU cores on a node

Account ("\_g" suffix will be added as needed):

m4388

Constraint:

gpu

QOS:

regular

cpus-per-task (node has 128 cpus):

128

gpus-per-task (node has 4 GPUs):

4

nodes (maximum of 4 for jupyter QOS):

1

ntasks-per-node:

1

Reservation:

reservation\_name

time (time limit in minutes):

360

Start

# Running a Notebook Server Using a Single GPU

## Server Options

Account ("\_g" suffix will be added as needed):

m4388

Constraint:

gpu

QOS:

shared

cpus-per-task (node has 128 cpus):

32

gpus-per-task (node has 4 GPUs):

1

nodes (maximum of 4 for jupyter QOS):

1

ntasks-per-node:

1

Reservation:

reservation\_name

time (time limit in minutes):

360

Start

Select **Account**:

m4388

Select **QOS**:

shared

Lower **cpus-per-task** to:

32 (you can just type 32)

Lower **gpus-per-task** to:

1

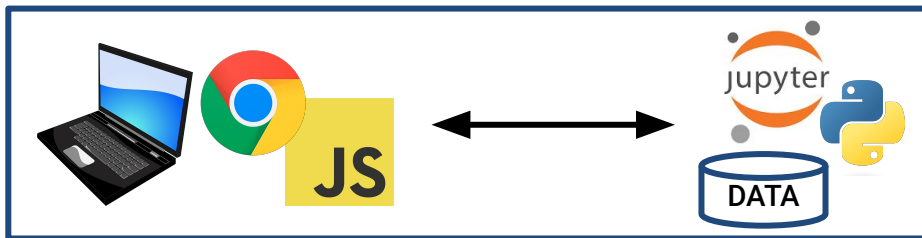
Select **Reservation**:

???

Leave everything else the same

Use this setup if you want just one GPU

# Laptop Jupyter vs HPC Jupyter (I)

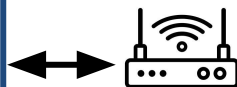


Laptop

A little compute  
A little data  
All in one place



Laptop



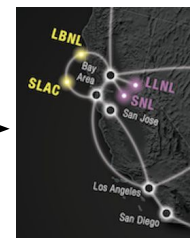
Router



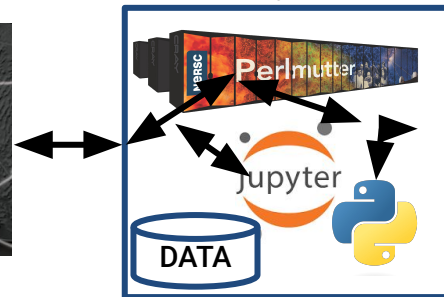
ISP



Internet



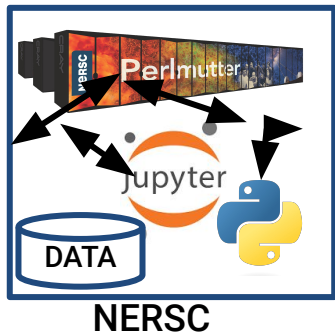
Esnet



NERSC

Lots of compute  
Lots of data  
But way over here

# Laptop Jupyter vs HPC Jupyter (II)



**Laptop:** Home directory is “right there” on your laptop  
**Perlmutter:** Home directory is served over (an incredible) network  
Many filesystems are served to Perlmutter over network

**Great, but, ... there’s no free lunch:**

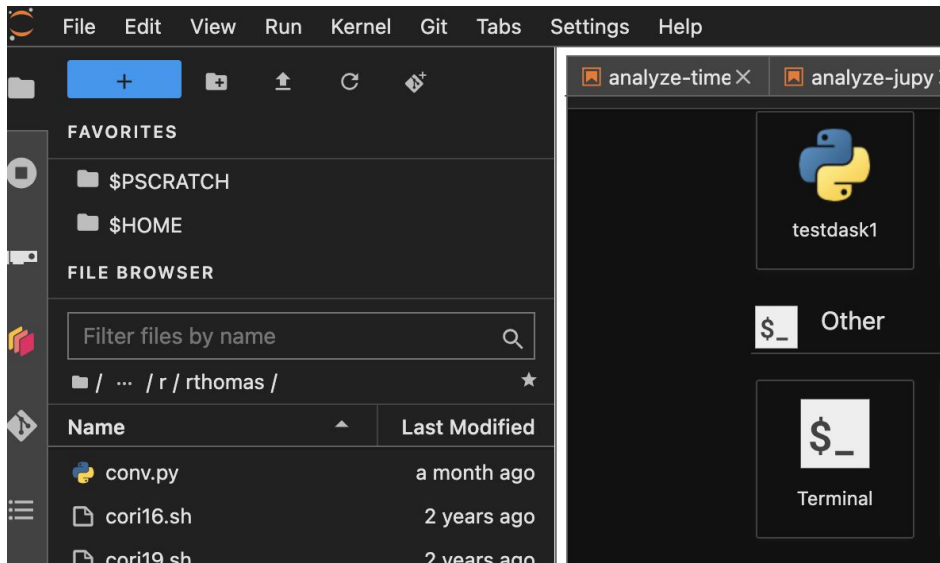
- File system has to look consistent across all those nodes
- I/O has to be coordinated from app to node to network to disk & back
- We use Cray’s “Data Virtualization Service,” and it’s being tuned

**Sometimes another user’s file system usage pattern in a running job grabs ahold of DVS and won’t let go!**

**For Jupyter on compute nodes: Things can slow down, look sluggish, or you may get “gateway timeout” messages. Don’t panic, it’ll recover**

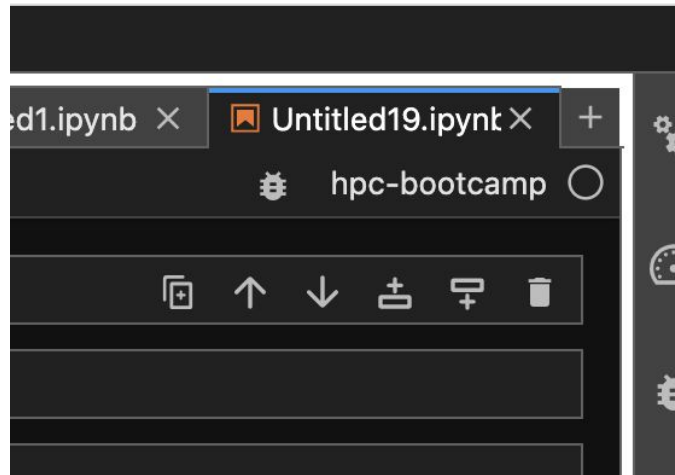


# Demo if Time Allows



## To open a terminal panel:

- Click the “+” in the top left corner
- Scroll down
- Select “Terminal” from under “Other”



## Select your kernel at the top right

- Most projects can use “hpc-bootcamp”
- Several others you may want to use

# Things to Remember:

Remember to use the “Configurable Job” option during reservation hours:

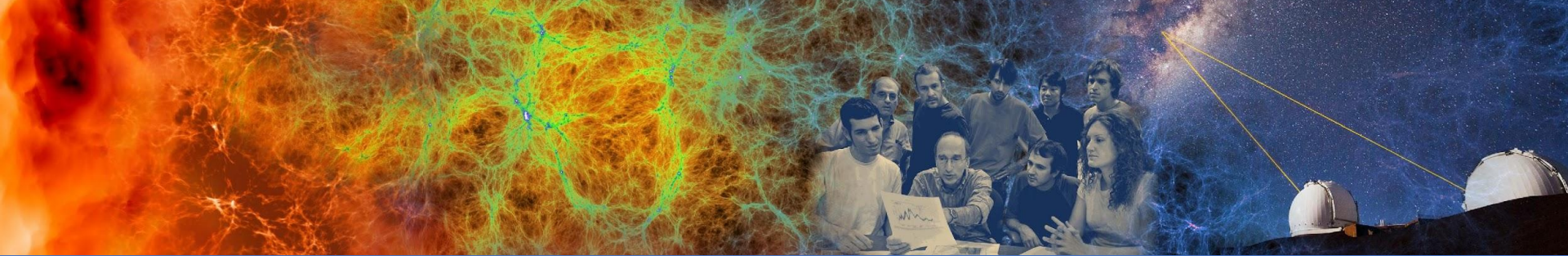
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Outside of reservation hours, you can explore the other single-click options.

NERSC Jupyter documentation: <https://docs.nersc.gov/services/jupyter/>

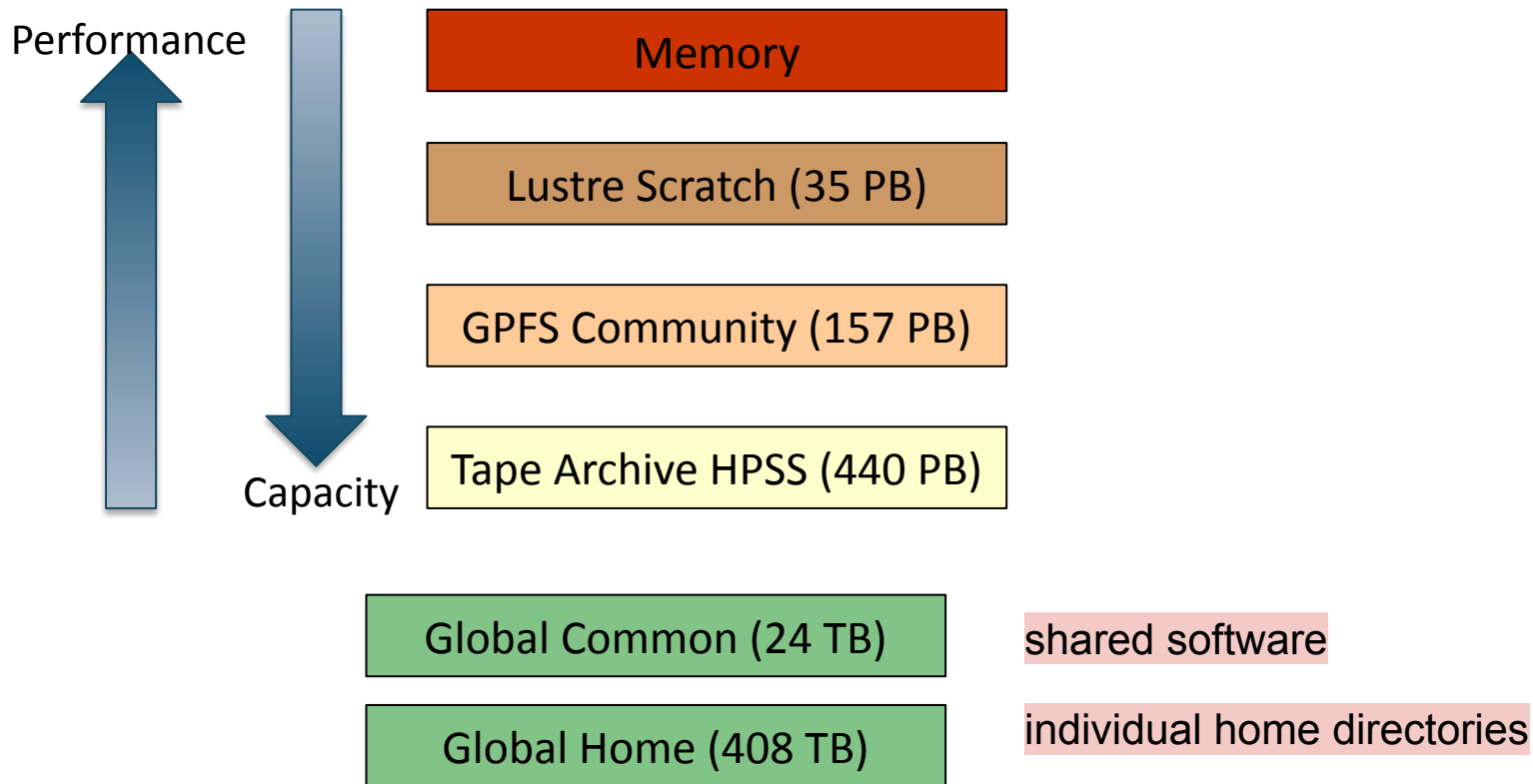
Have fun!

Any questions?



# File Systems, Compile and Run Jobs

# Simplified NERSC File Systems



# Perlmutter File Systems

## Global Home

- Permanent, relatively small storage
- NOT tuned to perform well for parallel jobs
- Snapshot backups
- **Perfect for storing data such as source codes, shell scripts**
- **cd \$HOME**

## Community File System (CFS)

- Permanent, larger storage
- Medium performance for parallel jobs
- Snapshot backups
- **Perfect for sharing data within research group**
- **cd \$CFS**

## Scratch

- Large, temporary storage
- Optimized for read/write operations, NOT storage
- Not backed up
- Purge policy (8 weeks)
- **Perfect for staging data and performing computations**
- **cd \$SCRATCH**



# Where should I work on my bootcamp project

- Materials for each project are available in the m4388 project area on Perlmutter CFS at `$CFS/m4388/Project*-<name>`, such as `Project2-ClimRR`
- Students who work on Project X Group Y will work in a shared directory in `$CFS/m4388/Project*-Group*`, such as `Prj2-GroupC`
- To copy over the entire project to your group working directory
  - `cd $CFS/m4388/Prj2-GroupC`
  - `cp -r $CFS/m4388/Project2-ClimRR .` (notice the last dot)
- Any student could also do individual work in their own scratch directory
  - `cd $SCRATCH`
  - `cp -r $CFS/m4388/Project2-ClimRR .` (notice the last dot)

# Programming Environment and Compile

- Some users use JupyterHub to login and mostly using Python for data analytics. There is a “terminal” kernel in JupyterHub.
- Many users also directly login to Perlmutter with SSH from a terminal, and work on scientific applications written in C/C++ and Fortran
  - These codes need to be compiled first, then run the generated executable on compute nodes
- There are multiple compilers available on Perlmutter
  - The default is GCC compiler
- Compiler wrappers are used to compile, such as
  - `cc -o mycode.exe mycode.c`
  - `CC -o mycode.exe mycode.cc`
  - `ftn -o mycode.exe mycode.f90`

# Jobs at NERSC

- Most are **parallel jobs** (10s to 100,000+ cores)
  - Meaning a job is run with multiple MPI tasks, each task tackle a subproblem, such as a subdomain
- Also a number of “**serial**” jobs
  - Typically “pleasantly parallel” simulation or data analysis
- Production runs execute in batch mode
- Our batch scheduler is **SLURM**
- Typical run times are a few to 10s of hours
  - Limits are necessary because of MTBF and the need to accommodate 9,000 users’ jobs

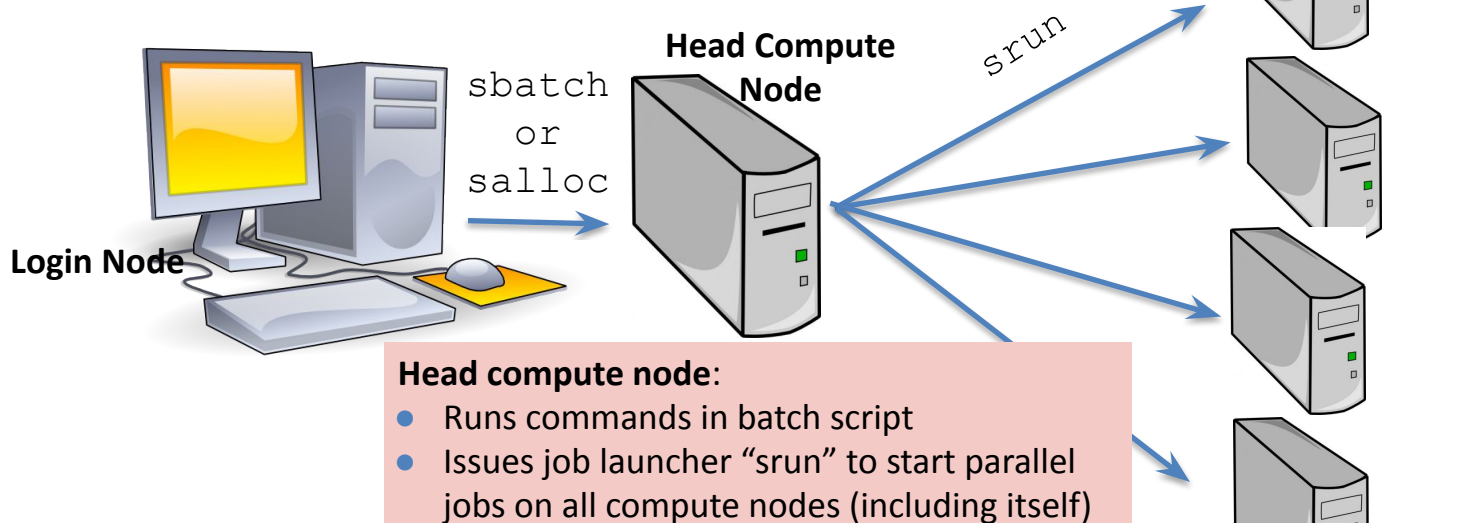
# Login Nodes and Compute Nodes

- Login nodes
  - Edit files, compile codes, submit batch jobs, etc.
  - Run short, serial utilities and applications
- Compute nodes
  - Execute your application
  - Dedicated resources for your job
  - Perlmutter has CPU and GPU compute nodes

# Launching Parallel Jobs with Slurm

## Login node:

- Submit batch jobs via sbatch or salloc
- Do not run big executables on login nodes





# My First “Hello World” Program

```
/* C Example, mpi-hello.c */
#include <stdio.h>
#include <mpi.h>

int main (argc, argv)
    int argc;
    char *argv[];
{
    int rank, size;

    MPI_Init (&argc, &argv);    /* starts MPI */
    MPI_Comm_rank (MPI_COMM_WORLD, &rank);    /* get current process
id */
    MPI_Comm_size (MPI_COMM_WORLD, &size);    /* get number of
processes */
    printf( "Hello world from process %d of %d\n", rank, size);
    MPI_Finalize();
    return 0;
}
```

**To compile:**

`% cc -o mpi-hello mpi-hello.c`

# Run “Hello World” Program

```
my_batch_script:
(request 2 CPU nodes for 10 min, run in debug queue)

#!/bin/bash
#SBATCH -q debug
#SBATCH -N 2
#SBATCH -t 10:00
#SBATCH -C cpu

# run with 8 MPI tasks (this is a comment)
srun -n 8 -c 64 -cpu-bind=cores ./mpi-hello
```

**To run via batch queue**

**% sbatch my\_batch\_script**

**To run via interactive batch**

**login% salloc -N 2 -q interactive -C cpu -t 10:00**

**<Wait for session prompt. Land on a compute node>**

**compute% **srun -n 8 -c 64 -cpu-bind=cores ./mpi-hello****

# Monitor Your Batch Jobs

- **squeue**
  - By default squeue displays jobs from all users
- **sqs**
  - sqs is a NERSC wrapper on squeue.
  - By default sqs displays jobs from current user

# Compile and Run Demo



# Commands Used in Compile and Run Demo

```
% pwd
% cd $SCRATCH
% cp -r $CFS/m4388/sample_compile_run .
% cd sample_compile_run
% ls
  mpi-hello.c mpi-hello.cc  mpi-hello.f90  submit_job.sh
% more mpi-hello.c
% cc -o mpi-hello mpi-hello.c
(or % CC -o mpi-hello mpi-hello.cc
  or % ftn -o mpi-hello mpi-hello.f90)
% more submit_job.sh
% sbatch submit_job.sh
% sqs
% squeue |more
% more slurm-*.out
% salloc -N 2 -C cpu -t 10:00 -q interactive
  <wait for allocation>
% srun -n 8 -c 64 --cpu-bind=cores ./mpi-hello
```

# If You Have Any Questions

- This week and next week:
  - Ask trainers, peer mentors, group members for help
  - Ask in Intro to HPC Bootcamp Slack channel
- Longer term (your NERSC account is valid through 01/16/2024):
  - Join NERSC user Slack channel
  - Submit a ticket via NERSC Help Portal
  - Check NERSC Docs: <https://docs.nersc.gov/>





Thanks for your attention!

