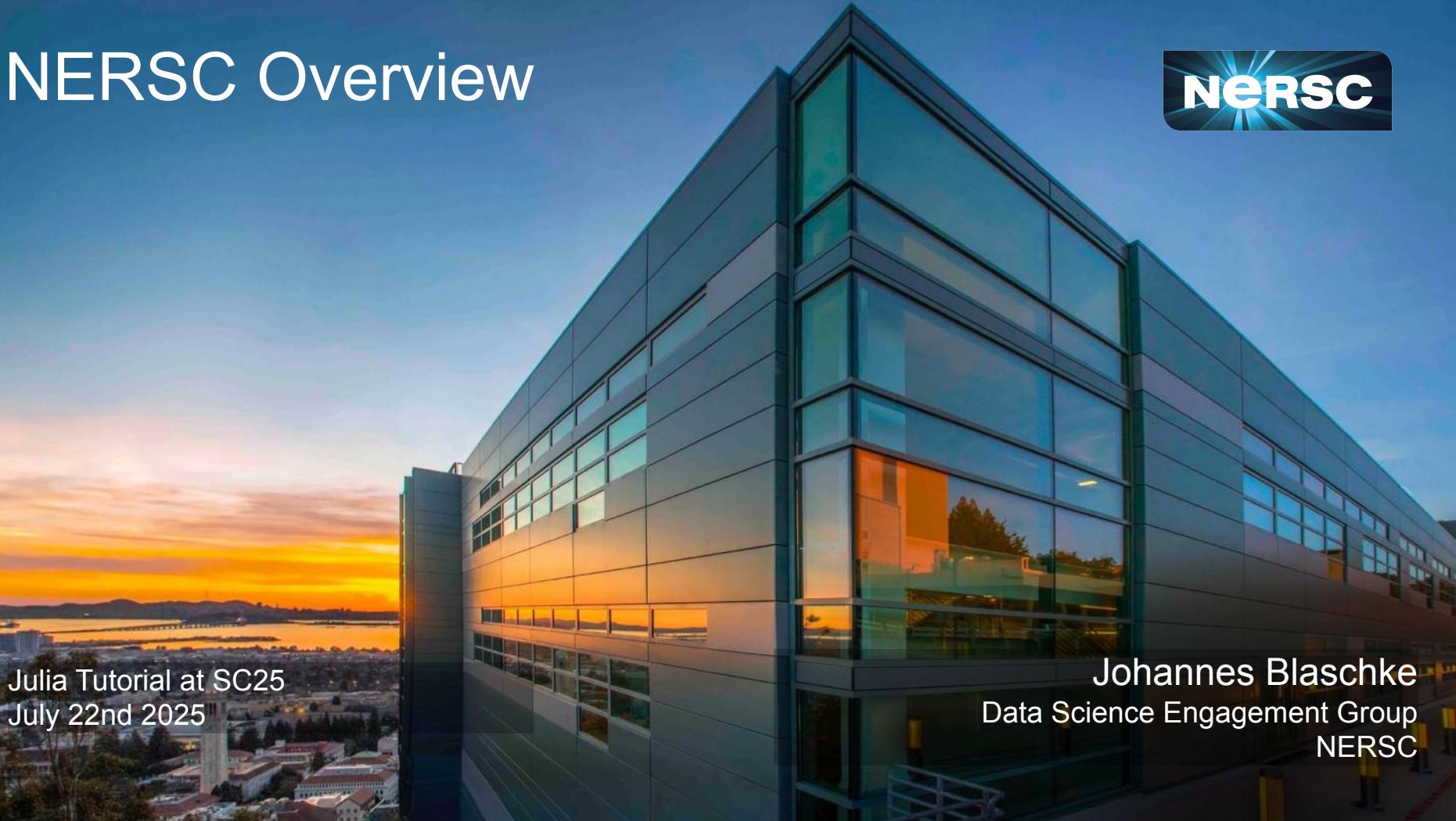


NERSC Overview



Julia Tutorial at SC25
July 22nd 2025

Johannes Blaschke
Data Science Engagement Group
NERSC

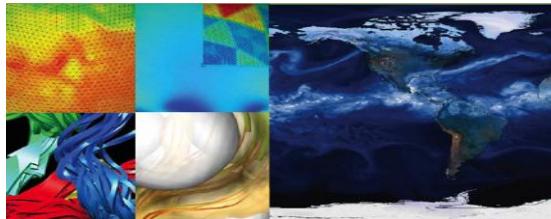
NERSC: Mission HPC for DOE Office of Science Research



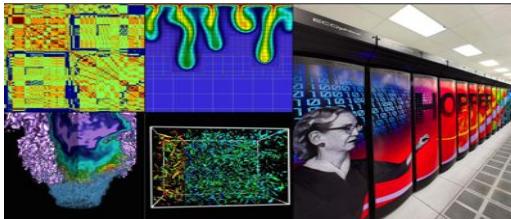
U.S. DEPARTMENT OF
ENERGY

Office of
Science

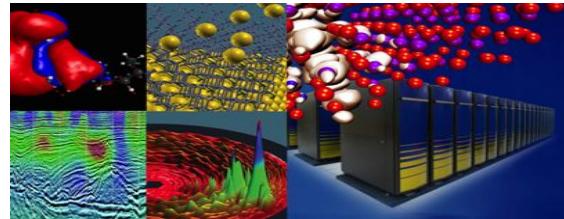
Largest funder of physical science
research in the U.S.



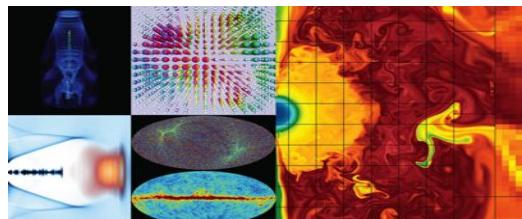
Biological and Environmental Research



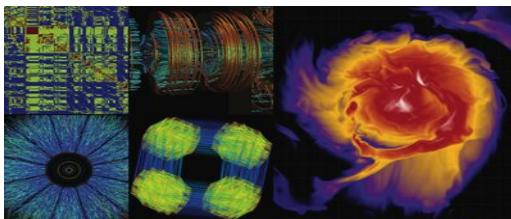
Computing



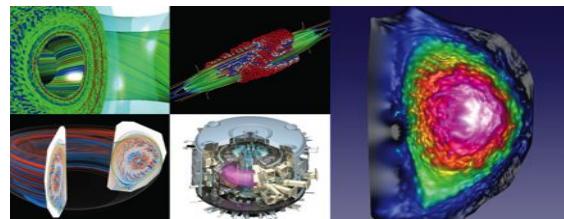
Basic Energy Sciences



High Energy Physics



Nuclear Physics

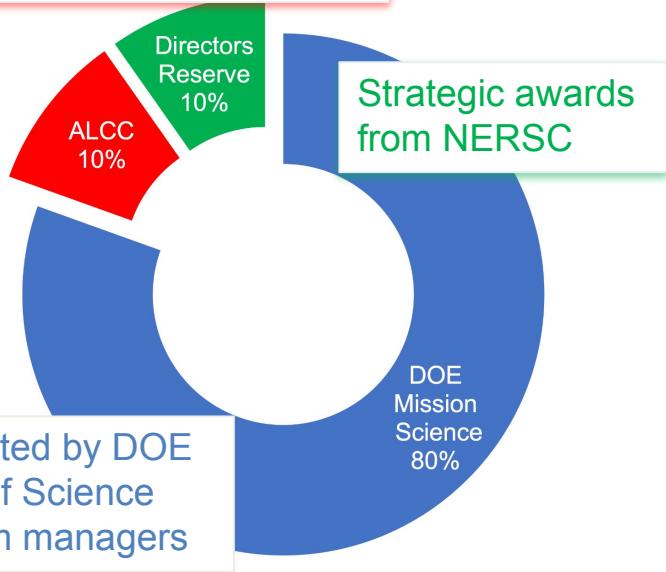


Fusion Energy, Plasma Physics

NERSC Directly Supports Office of Science Priorities

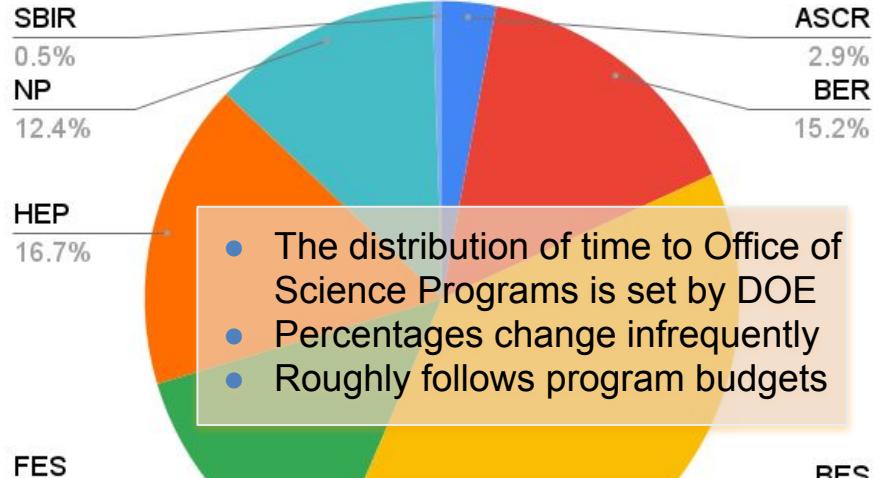
2023 Allocation Breakdown (Hours Millions)

Competitive awards run by DOE Advanced Scientific Computing Research Office



Distributed by DOE Office of Science program managers

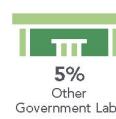
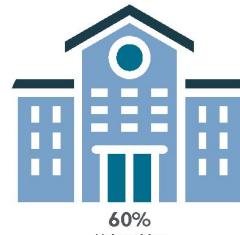
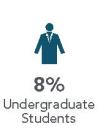
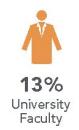
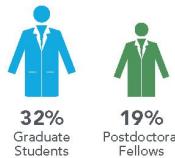
Strategic awards from NERSC



NERSC Turns 50 This Year!



~10,000 Annual Users from ~800 Institutions + National Labs



CDC 6600 at LLNL 1974

Success Is Depth and Breadth of Scientific Impact

An Accelerating Universe

Saul Perlmutter, Berkeley Lab

Perlmutter's Nobel winning team is believed to have been the first to use supercomputers to analyze and validate observational data in cosmology, contributing to the discovery of the accelerating expansion of the universe.



Oscillating Neutrinos

Sudbury Neutrino Observatory (SNO)

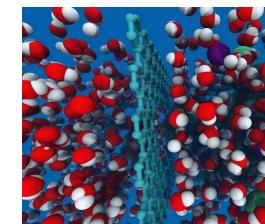
Data from SNO was transferred to NERSC and analyzed in what became known as the "West Coast Analysis" leading to the discovery of neutrino oscillations and a Nobel Prize.



New Approach to Water Desalination

Jeff Grossman, MIT

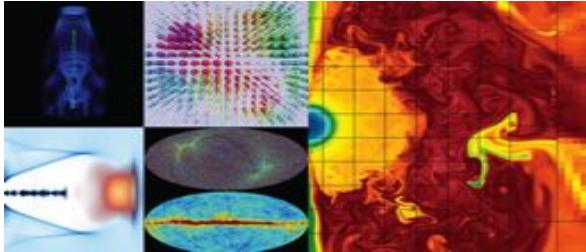
One of Smithsonian Magazine's Top 5 Most Surprising Milestones of 2012 was the computationally driven discovery of an approach to desalination of water that is more efficient and less expensive than existing systems.



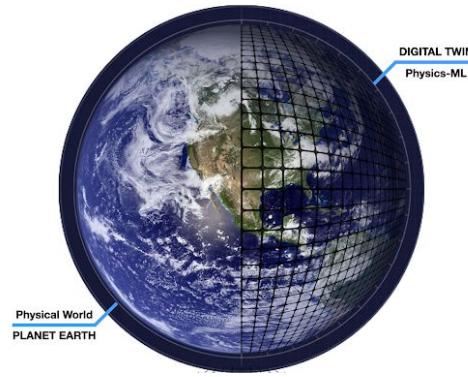
NERSC has been acknowledged in 8,790 refereed scientific publications & high profile journals since 2020

- Nature [47]
- Nature Family of Journals [463]
- Proc. of the National Academy of Sciences [222]
- Science [36]
- Monthly Notices of the Royal Astron. Society [397]
- Physical Review* [4,170]
- Astrophysical Journal [792]
- Physics of Plasmas [685]

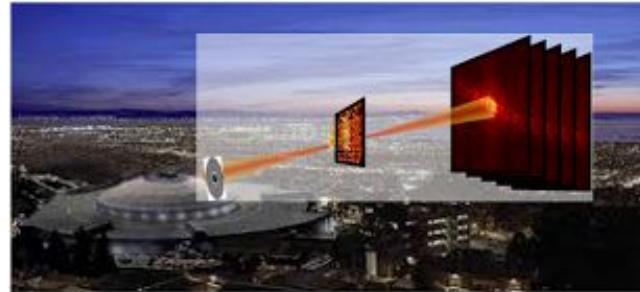
We Accelerate Scientific Discovery for Thousands of Office of Science Users with 3 Advanced Capability Thrusts



Large-scale applications
for simulation, modeling
and data analysis



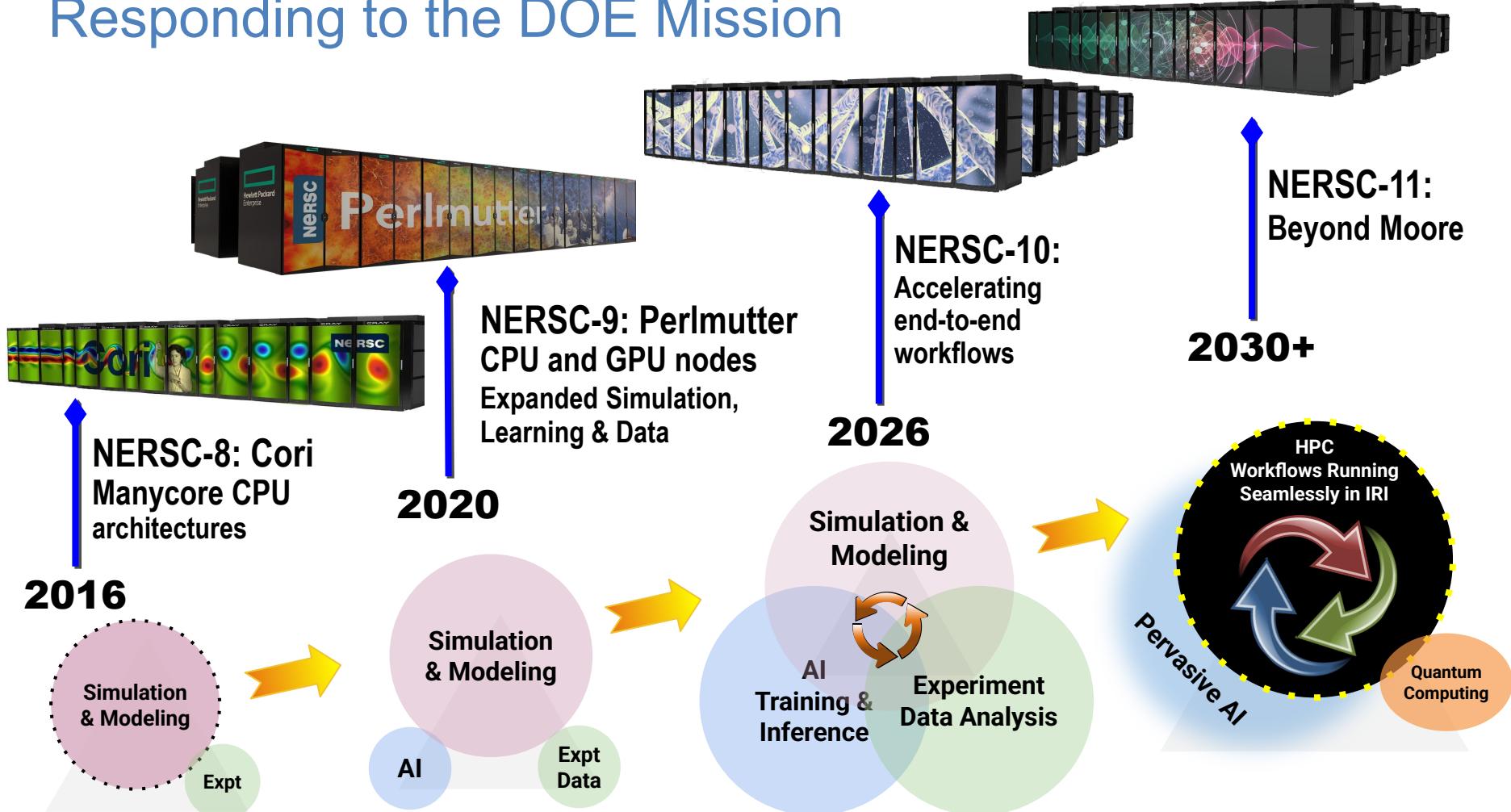
Complex experimental
and AI driven workflows



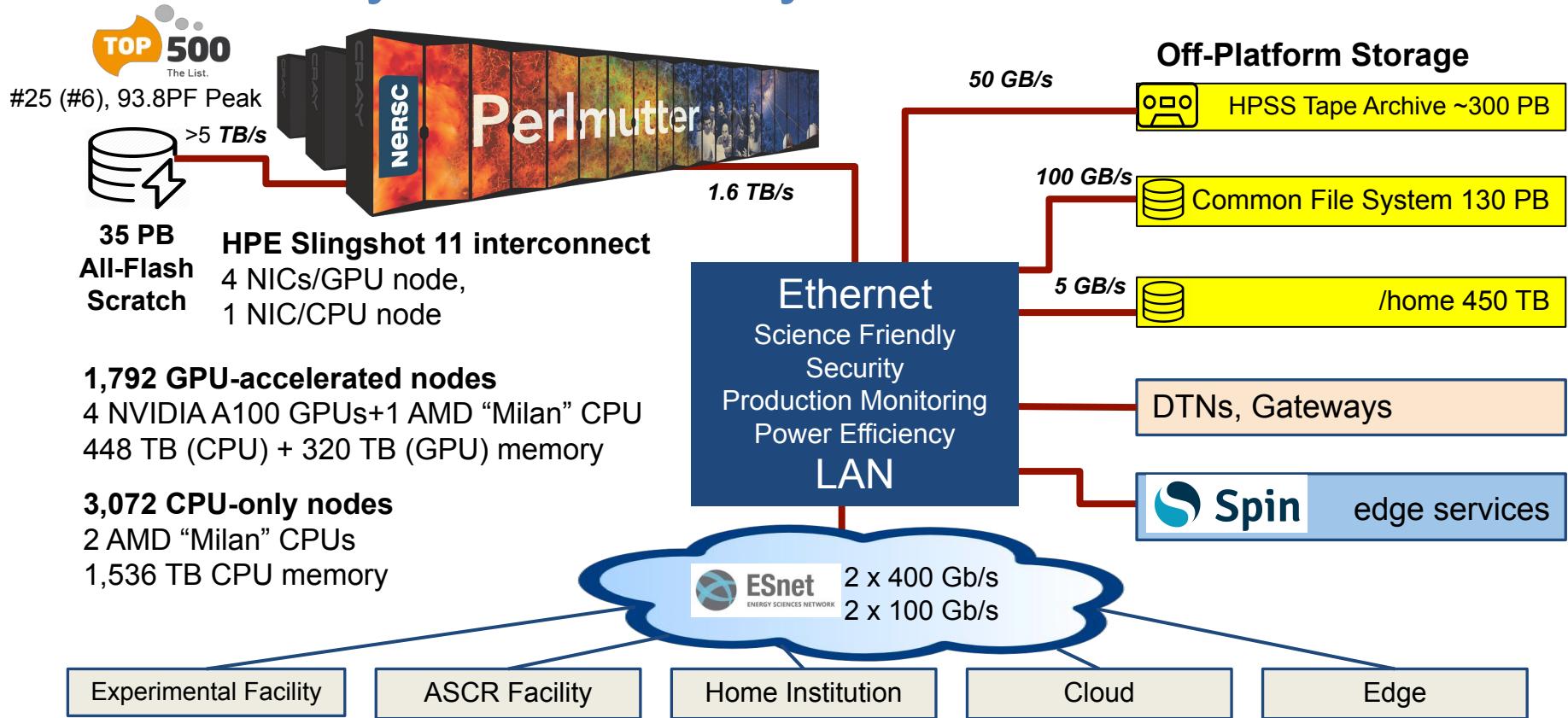
Time-sensitive and
interactive computing

The NERSC workload is diverse with growing emphasis on integrated research workflows

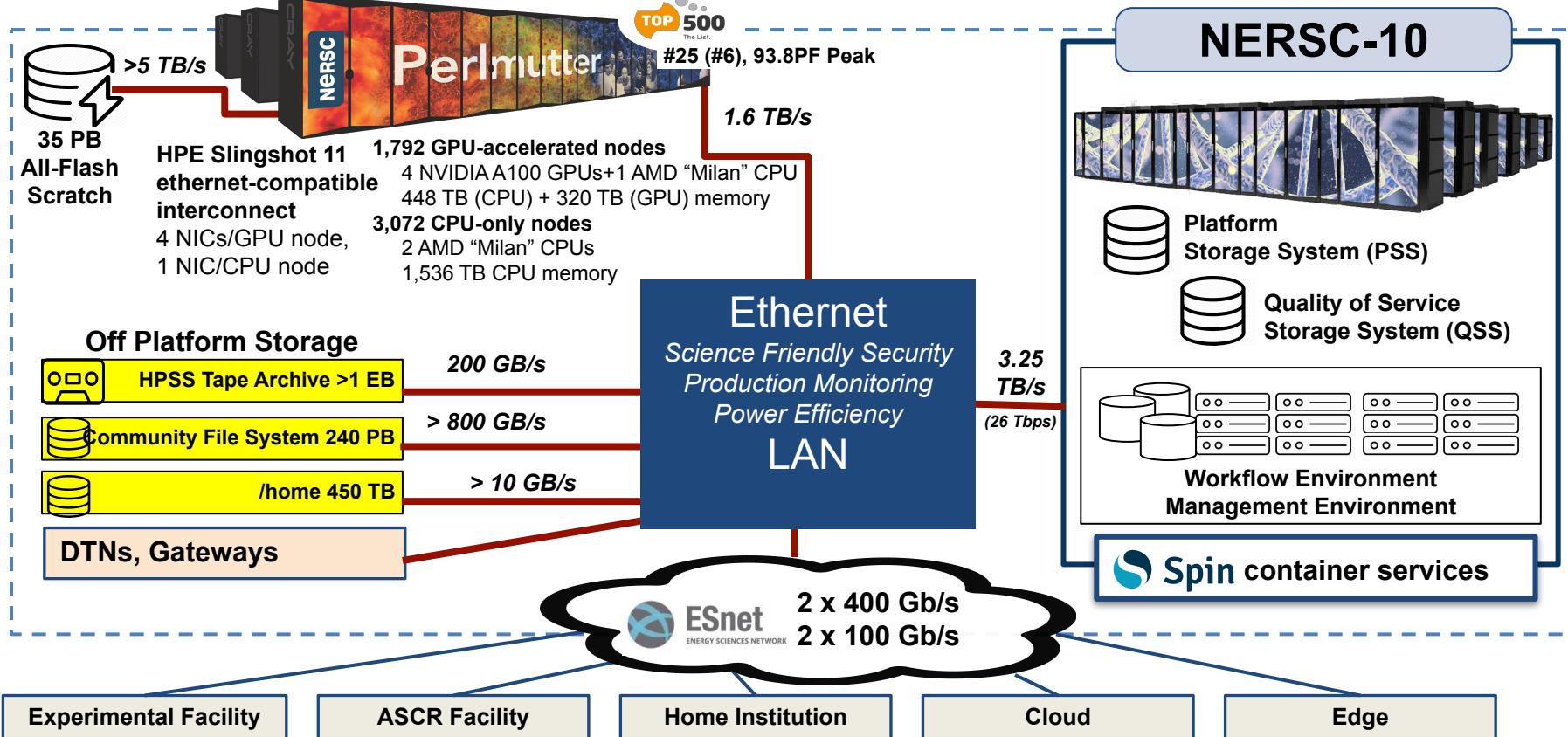
Responding to the DOE Mission



NERSC Systems Ecosystem



NERSC Ecosystem in 2027



Perlmutter system configuration

NVIDIA "Ampere" GPU Nodes

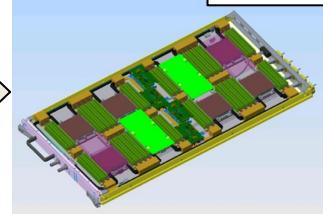
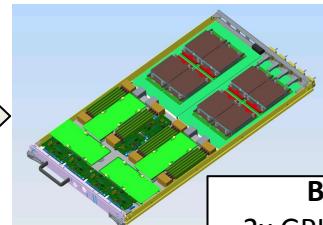
4x GPU + 1x CPU
40 GiB HBM + 256 GiB DDR
4x 200G "Slingshot" NICs

AMD "Milan" CPU Node

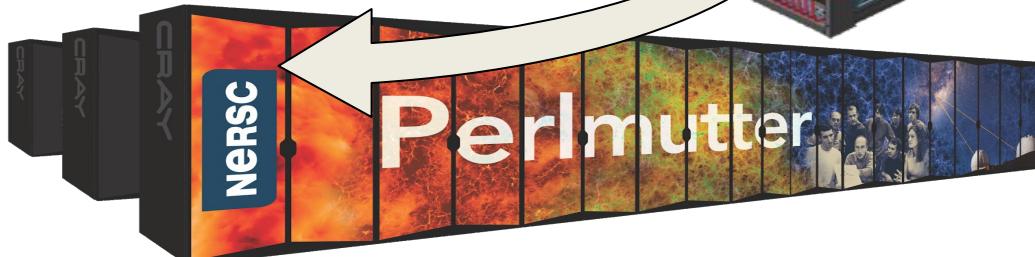
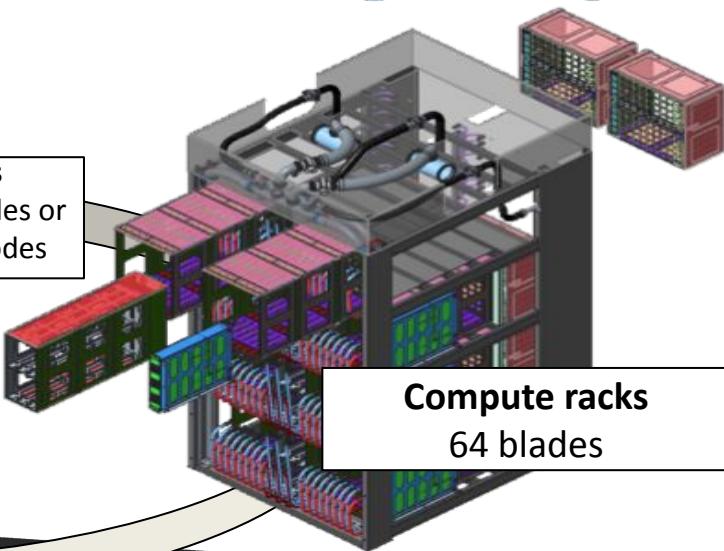
2x CPUs
> 256 GiB DDR4
1x 200G "Slingshot" NIC

Centers of Excellence
Network
Storage
App. Readiness
System SW

Perlmutter system
GPU racks
CPU racks
~6 MW



Blades
2x GPU nodes or
4x CPU nodes

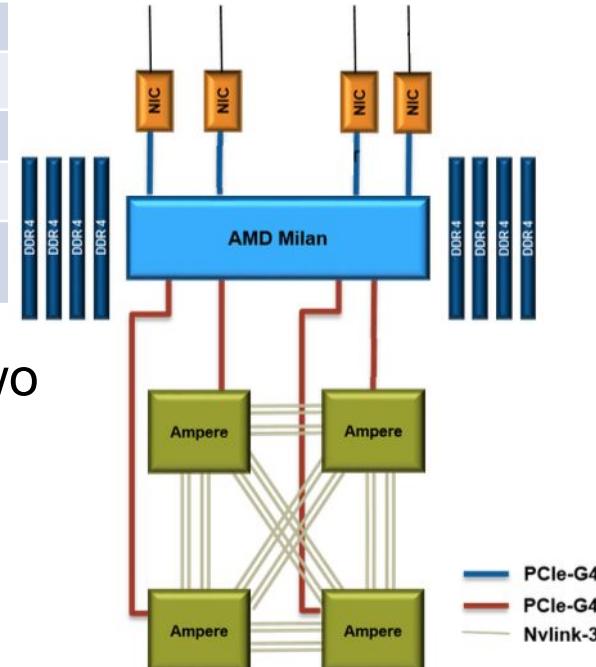


Perlmutter Node Configuration

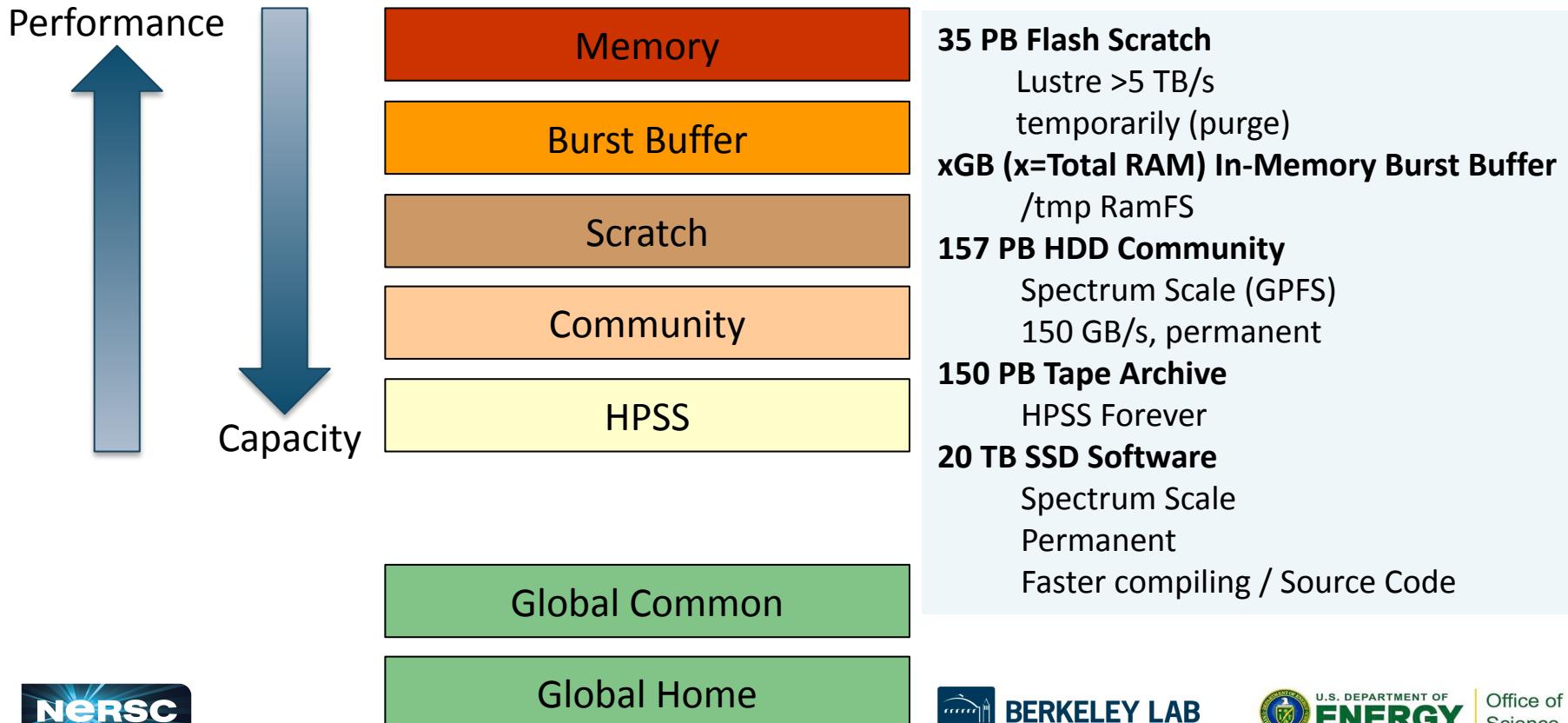
Partition	Nodes	CPU	RAM	GPU	NIC
GPU	1536	1x AMD EPYC 7763	256GB	4x NVIDIA A100 (40GB)	4x HPE Slingshot 11
	256	1x AMD EPYC 7763	256GB	4x NVIDIA A100 (80GB)	4x HPE Slingshot 11
CPU	3072	2x AMD EPYC 7763	512GB	–	1x HPE Slingshot 11
Login	40	1x AMD EPYC 7713	512GB	4x NVIDIA A100 (40GB)	–
Large Memory	4	1x AMD EPYC 7713	1TB	4x NVIDIA A100 (40GB)	1x HPE Slingshot 11

- Each Milan CPU has 64 2.45 GHz cores with two hardware threads
- Access is managed via Slurm partitions
- Login nodes are GPU-enabled

GPU Node Architecture:



Simplified NERSC File Systems



Global File Systems

Global Home

- Permanent, relatively small storage
- Mounted on all platforms
- NOT tuned to perform well for parallel jobs
- Quota cannot be changed
- Snapshot backups (7-day history)
- **Perfect for storing data such as source code, shell scripts**
- **Addressed using \$HOME**

Community File System (CFS)

- Permanent, larger storage
- Mounted on all platforms
- Medium performance for parallel jobs
- Quota can be changed
- Snapshot backups (7-day history)
- **Perfect for sharing data within research group**
- **Addressed using \$CFS**

Local File Systems

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**
- **Addressed using \$SCRATCH**

Burst Buffer

- Temporary storage
- High-performance in-memory file system
- **Perfect for getting good performance in I/O-constrained codes**
- **Not shared between nodes**

There are many different ways to access NERSC. To use our resources, you need to either:

1. Log into the login nodes and interact with Slurm (covered here)
2. Use services (eg. Jupyter) that expose web interfaces (covered later)
3. Interact via our REST API – called the “Superfacility API”
(see: <https://docs.nersc.gov/services/sfapi/>)

Connecting with SSH

- To access Perlmutter, use:

saul.nersc.gov

perlmutter.nersc.gov



```
blaschke@laptop:~$ ssh <user>@saul.nersc.gov  
blaschke@laptop:~$ ssh <user>@perlmutter.nersc.gov
```

- To be able to open GUI applications on the login nodes use: `ssh -Y`



```
blaschke@laptop:~$ ssh -Y <user>@saul.nersc.gov
```

Connecting with SSH

After successfully logging on, you will be greeted by the terms of use, and the command-line input prompt:

For past outages, see: <https://my.nersc.gov/outagelog-cs.php>
blaschke@perlmutter:login17:~

From here you can interact with
perlmutter...

17

Submitting Jobs

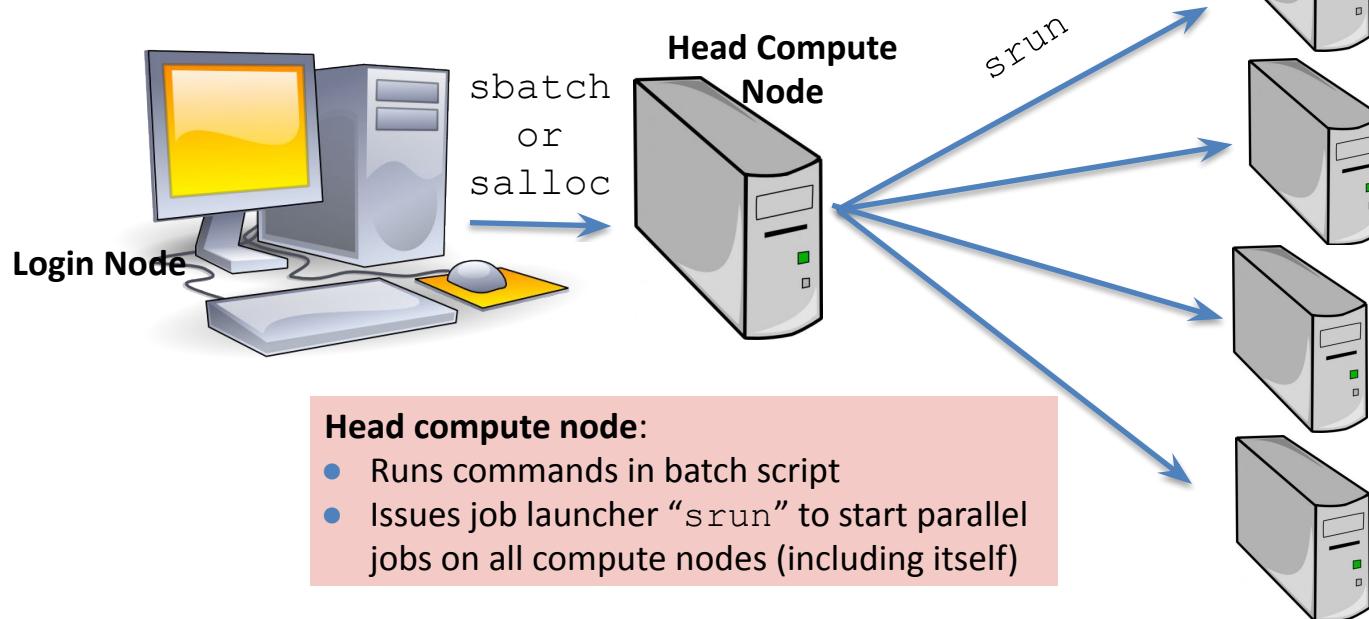
- Jobs can be submitted to queueing system through sbatch or salloc:
 - `sbatch <my_job_script>`
 - `salloc <options>`
- The above methods list details about resources needed for a job and for how long
- Eg.: a request for a cpu node to be allocated for 5 mins:
 - `salloc -N 1 -C cpu -q debug -t 5 -A <project>`



Submitting Jobs

Login node:

- Submit batch jobs via `sbatch` or `salloc`



*figure courtesy Helen (2020 NERSC Training)

My First “Hello World” Job Script

debug queue

2 nodes

10 min “walltime”

run on haswell partition

use SCRATCH file system

run 64 processes in parallel



my_batch_script.sh

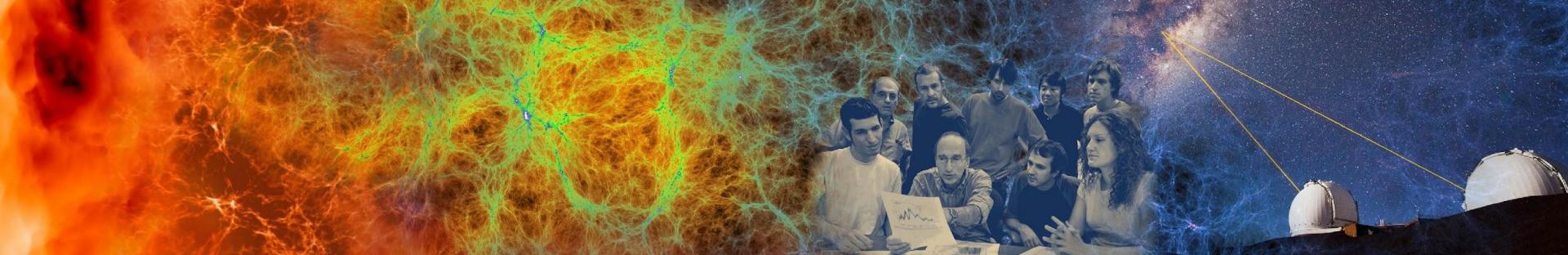
```
#!/bin/bash
#SBATCH -q debug
#SBATCH -N 2
#SBATCH -t 10:00
#SBATCH -C haswell
#SBATCH -L SCRATCH
#SBATCH -J myjob
srun -n 64 ./helloWorld
```

To run via batch queue

```
% sbatch my_batch_script.sh
```

To run via interactive batch

```
% salloc -N 2 -q interactive -C gpu -t 10:00
<wait_for_session_prompt. Land on a compute node>
% srun -n 64 ./helloWorld
```



Accessing NERSC and submitting your first Job



BERKELEY LAB



Office of
Science

Access to Perlmutter and Use Julia Module

- NERSC users have been added to trn019 project
- Non-users were sent the instruction to get a training account
 - Account valid through July 29
- Login to Perlmutter: ssh username@perlmutter.nersc.gov
- Julia modules:
 - % module load julia
- Running Jobs examples:
 - <https://docs.nersc.gov/jobs/>

Accessing Compute Nodes

- To use 1 GPU only (sample flags for sbatch or salloc):
 - `-A trn019 -C gpu -N 1 -c 32 -G 1 -t 30:00 -q shared`
- To use multiple nodes (sample flags for sbatch or salloc):
 - `-A trn019 -C gpu -N 2 -t 30:00 -q regular`
(or `-q interactive` for salloc)
- Or for faster queue access:
 - `-q premium` At most 5 jobs in the queue (incl running)
 - `-q debug` At most 5 8-node 30min jobs

Make Sure to Clone The Tutorial Repo

github.com/JuliaParallel/julia-hpc-tutorial-icpp25



Pro tip: \$HOME is not the best file system for running jobs at scale. For large-scale jobs, add

```
export JULIA_DEPOT_PATH=$SCRATCH/depot
```

to your scripts for optimal performance (remember to do this in the config script, **and** the job script) ... or use a container!



Make Sure to Clone The Tutorial Repo

github.com/JuliaParallel/julia-hpc-tutorial-icpp25

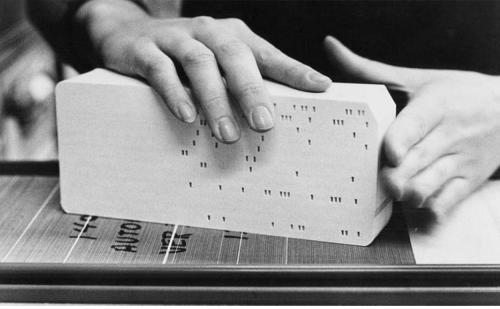
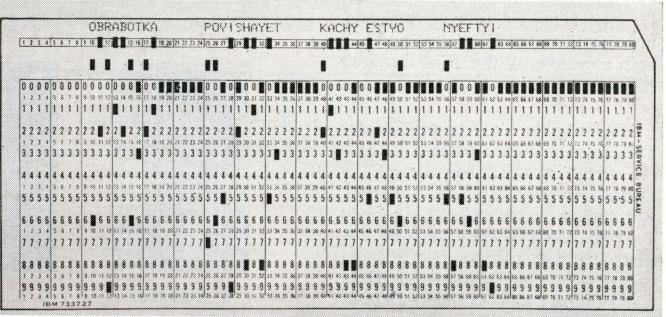


Pro tip: \$HOME is not the best file system for running jobs at

Automatically generate assets / configs by running:

```
$ git clone git@github.com:JuliaParallel/julia-hpc-tutorial-icpp25.git  
$ cd julia-hpc-tutorial-icpp25/  
$ make nersc
```

HPC User Interface



Terminal Shell Edit View Window Help

namehtd4 -- ssh namehtd4@perlmutter-pt.nersc.gov -t 16x4

Lawrence Berkeley National Laboratory operates this computer system under contract with the United States Department of Energy. This system is the property of the United States Government and is for authorized use only. Users (authorized or unauthenticated) have no explicit or implicit expectation of privacy.

Any or all uses of this system and all files on this system may be monitored, recorded, copied, audited, inspected, and disclosed to authorized site, Department of Energy, and law enforcement personnel, as well as authorized officials of other agencies, both domestic and foreign, for administrative, operational, and security purposes, including recording, copying, auditing, inspection, and disclosure at the discretion of authorized site or Department of Energy personnel.

Unauthorized or improper use of this system may result in administrative disciplinary action and civil and criminal penalties. By continuing to use this system, you acknowledge your awareness of and consent to these terms and conditions of use. LOG OFF IMMEDIATELY if you do not agree to the conditions stated in this warning.

Login connection to host x3116e870@n0:

```
(namehtd4@perlmutter-pt.nersc.gov) Password + OTP:  
Last login: Thu May 9 19:01:12 2024 From en-05-6f-r2-fe-dd.dhcp.lbnl.us  
#  
  
Welcome to perlmutter!  
#  
For all planned outages, see: https://my.nersc.gov/live-status/motd/  
For past outages, see: https://my.nersc.gov/outage-log-cs.php  
namehtd4@perlmutter:login23=>
```

perlmutter

nersc

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Instances Instances

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Spot Requests

Savings Plans

Reserved Instances

Dedicated Hosts

Scheduled Instances

Capacity Reservations

Images

AMIs AMIs

AMI Catalog

Elastic Block Store

Volumes Volumes

Snapshots Snapshots

Feedback Looking for language assistance? Find it in the new Unified Settings

Resources

EC2 Global view C ⓘ

Instances (running) 0 Dedicated Hosts 0 Elastic IPs 0

Instances 0 Key pairs 0 Load balancers 0

Placement groups 0 Security groups 1 Snapshots 0

Easily size, configure, and deploy Microsoft SQL Server Always On availability groups on AWS using the AWS Launch Wizard for SQL Server. Learn more

Launch instance

Service health

Region US East (N. Virginia)

Status This service is operating normally

Zones

Save Up to 45% on ML Inference

Get Up to 40% Better Price Perf

File Edit View Run Kernel Tabs Settings Help

Launcher README.md Lorenz.ipynb Terminal 1 Console 1 Data.ipynb Python 3 (pykern)

https://docs.jupyter.org/en/latest/_images/jupyterlab.png

notebooks /

Name Last Modified

- Default VPC a day ago
- vpc-0c7141015084ae08 a day ago
- Cpp.ipynb a day ago
- Data.ipynb a day ago
- Fasta.ipynb a day ago
- julia.ipynb a day ago
- Lorenz.ip... a day ago
- Lorenz.py a day ago
- R.ipynb a day ago

Explore AWS

Save Up to 45% on ML Inference

Get Up to 40% Better Price Perf

The Lorenz Differential Equations

Before we start, we import some preliminary libraries. We will also import (below) the accompanying `lorenz.py` file, which contains the actual solver and plotting routine.

```
[1]: %matplotlib inline
from ipywidgets import interactive, fixed
```

We explore the Lorenz system of differential equations:

```
[2]: x = dy - x
y = rho * z - y
z = x * y - beta * z
```

Output View

lorenz.py

```
[3]: sigma = 10.00
beta = 2.67
rho = 28.00
```

```
[4]: from matplotlib import pyplot as plt
2 from mpl_toolkits.mplot3d import Axes3D
3 import numpy as np
4 from scipy import integrate
5
6 def solve_lorenz(sigma=10.0, beta=8.0, rho=28.0):
7     """Plot a solution to the Lorenz differential equations."""
8
9     max_time = 4.0
10    N = 30
11
12    fig = plt.figure()
13    ax = fig.add_axes([0, 0, 1, 1], projection='3d')
14    ax.axis('off')
```



Logging into Jupyter

- Go to <https://jupyter.nersc.gov>
- Sign in using your training account credentials
- Select your preferred jupyter instance:

	Login Node	Shared GPU Node	Exclusive CPU Node	Exclusive GPU Node	Configurable Job
Alvarez	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	
Muller	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
Perlmutter	<button>stop</button> <button>server</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
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 defaults.	Use your own 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.	Multi-node analytics jobs, jobs in reservations, custom project charging, and more.	



Logging into Jupyter

- Go to <https://jupyter.nersc.gov>
- Sign in using your training account credentials
- Select your preferred jupyter instance:

	Login Node	Shared GPU Node	Exclusive CPU Node	Exclusive GPU Node	Configurable Job
Alvarez	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	
Muller	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
Perlmutter	<button>stop</button> <button>server</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
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 defaults.	Use your own 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 most a quarter of a GPU host and host memory.			

For now, let's use the “Shared GPU Node” – or the “Login Node”

Logging into Jupyter

- Go to <https://jupyter.nersc.gov>
- Sign in using your training account credentials
- Select your preferred jupyter instance:

	Login Node	Shared GPU Node	Exclusive CPU Node	Exclusive GPU Node	Configurable Job
Alvarez	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	
Muller	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
Perlmutter	<button>stop</button> <button>server</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>

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 defaults. Use your own node within a job allocation using defaults. Use multiple compute nodes with specialized settings.

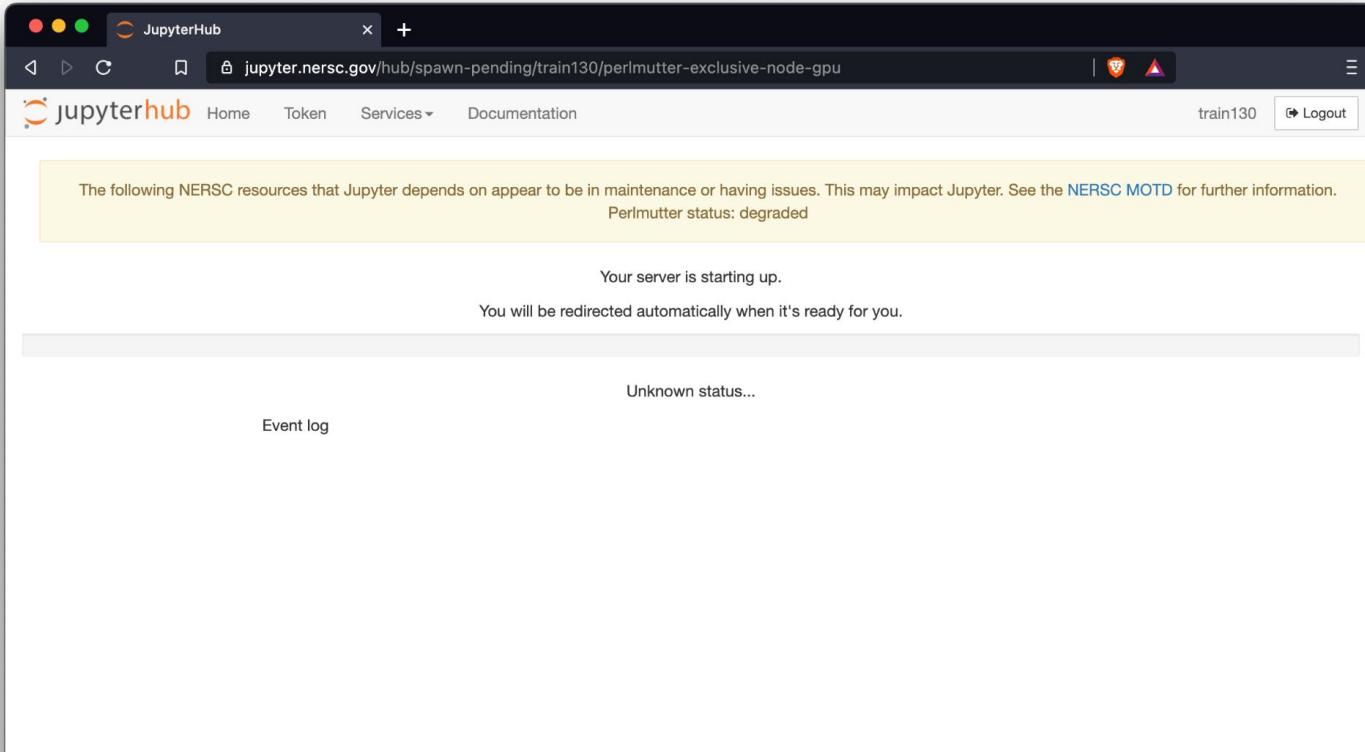
Later we'll be using the “Exclusive GPU Node” or reservations (using the “Configurable Job”)

Analytics, machine learning that is compute intensive but can be done on a single node. Multi-node analytics jobs, jobs in reservations, custom project charging, and more.



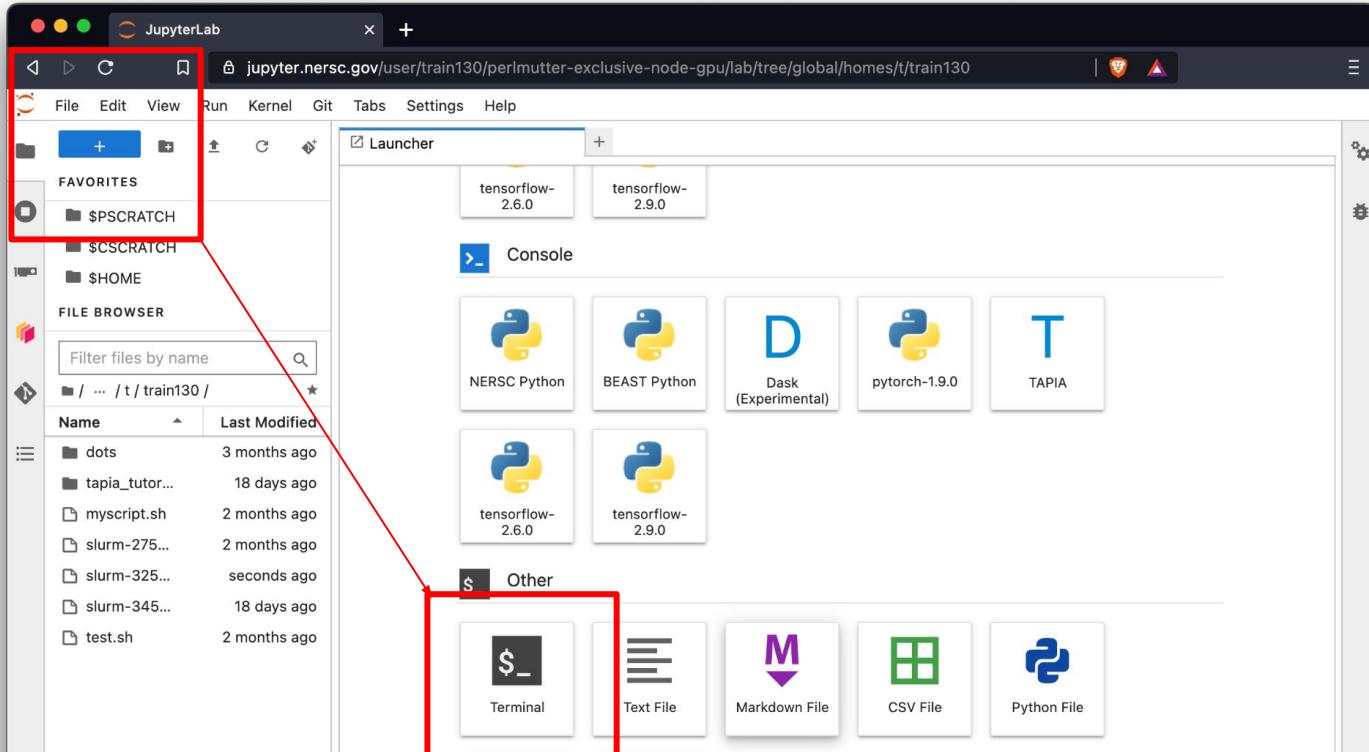
Getting a Terminal in Jupyter

- Jupyter should take a minute to start:



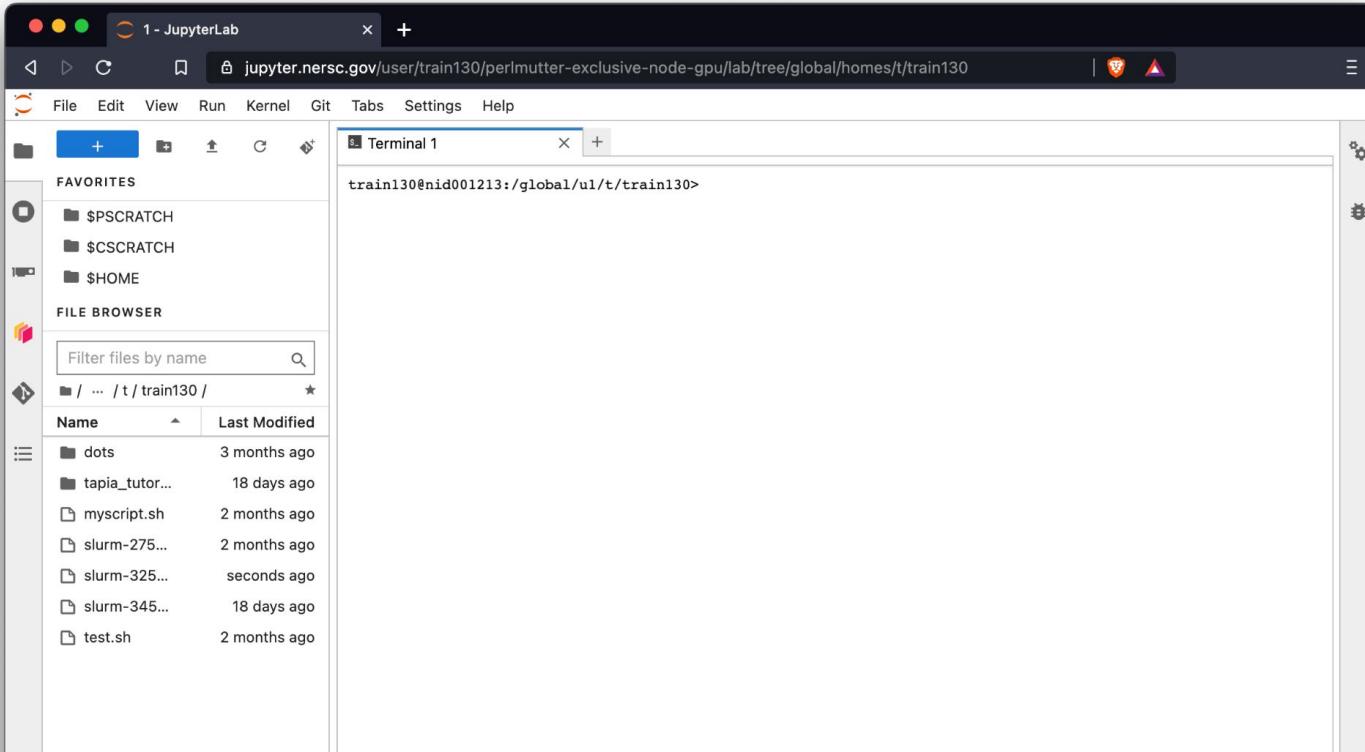
Getting a Terminal in Jupyter

- (If you don't see a terminal), select “+” followed by “Terminal”



Setup

- Once started you should see a terminal



Pro Tip: Projects handle dependencies

- Run: `import Pkg; Pkg.activate("path/to/the/repo");
Pkg.instantiate()` to insure all dependencies are installed:

The screenshot shows a JupyterLab interface with a Julia notebook titled "Untitled61.ipynb". The code cell contains the following Julia code:

```
[1]: import Pkg  
[2]: Pkg.instantiate()
```

The output of the second cell is a list of installed packages and their versions:

Installed	Package	Version
Installed	Scratch	v1.2.1
Installed	GPUArraysCore	v0.1.6
Installed	Crayons	v4.1.1
Installed	MPICH_jll	v4.2.3+0
Installed	ColorTypes	v0.11.5
Installed	Adapt	v4.1.1
Installed	demumble_jll	v1.3.0+0
Installed	TableTraits	v1.0.1
Installed	PrettyTables	v2.4.0
Installed	Hwloc_jll	v2.11.2+0
Installed	CUDA_Driver_jll	v0.10.3+0
Installed	SentinelArrays	v1.4.6
Installed	GPUCompiler	v0.27.8
Installed	DataAPI	v1.16.0
Installed	Tables	v1.12.0
Installed	LLVMLoopInfo	v1.0.0
Installed	PkgVersion	v0.3.3
Installed	MPI	v0.20.22
Installed	OpenMPI_jll	v5.0.5+0
Installed	MicrosoftMPI_jll	v10.1.4+2
Installed	InlineStrings	v1.4.2
Installed	PooledArrays	v1.4.3
Installed	FixedPointNumbers	v0.8.5
Installed	StaticArrays	v1.9.8
Installed	TimerOutputs	v0.5.25

Pro Tip: Sanity Check

- The `versioninfo()` function can be used to check if any backends are configured correctly. Eg. for `MPI.jl` and `CUDA.jl`:

```
[3]: import MPI
```

```
[4]: MPI.versioninfo()
```

```
MPIPreferences:  
  binary: system  
  abi: MPICH  
  libmpi: libmpi_gnu_123.so  
  mpieexec: srun
```

```
Package versions  
  MPI.jl: 0.20.22  
  MPIPreferences.jl: 0.1.11
```

```
Library information:  
  libmpi: libmpi_gnu_123.so  
  libmpi dlpath: /opt/cray/pe/lib64/libmpi_gnu_123.so
```

```
MPI version: 3.1.0
```

```
Library version:
```

```
  MPI VERSION : CRAY MPICH version 8.1.28.29 (ANL base 3.4a2)  
  MPI BUILD INFO : Wed Nov 15 20:57 2023 (git hash 1cde46f)
```

```
[5]: import CUDA
```

```
[6]: CUDA.versioninfo()
```

```
CUDA runtime 12.2, local installation  
CUDA driver 12.2  
NVIDIA driver 535.183.6
```

```
CUDA libraries:
```

- CUBLAS: 12.2.1
- CURAND: 10.3.3
- CUFFT: 11.0.8
- CUSOLVER: 11.5.0
- CUSPARSE: 12.1.1
- CUPTI: 2023.2.0 (API 20.0.0)
- NVML: 12.0.0+535.183.6

```
Julia packages:
```

- CUDA: 5.5.2
- CUDA_Driver_jll: 0.10.3+0
- CUDA_Runtime_jll: 0.15.3+0
- CUDA_Runtime_Discovery: 0.3.5

```
Toolchain:
```

- Julia: 1.10.4
- LLVM: 15.0.7

```
Preferences:
```

Using Reservations in Tutorials

- Go to <https://jupyter.nersc.gov> and select:
“Configurable GPU” in the “Perlmutter” row

	Login Node	Shared GPU Node	Exclusive CPU Node	Exclusive GPU Node	Configurable Job
Alvarez	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	
Muller	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
Perlmutter	<button>stop</button> <button>server</button>	<button>start</button>	<button>start</button>	<button>start</button>	<button>start</button>
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 defaults.	Use your own 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.		Multi-node analytics jobs, jobs in reservations, custom project charging, and more.



Jupyter Options:

Leave defaults, except:

Account:

trn019

Reservation
(leave blank)

Time

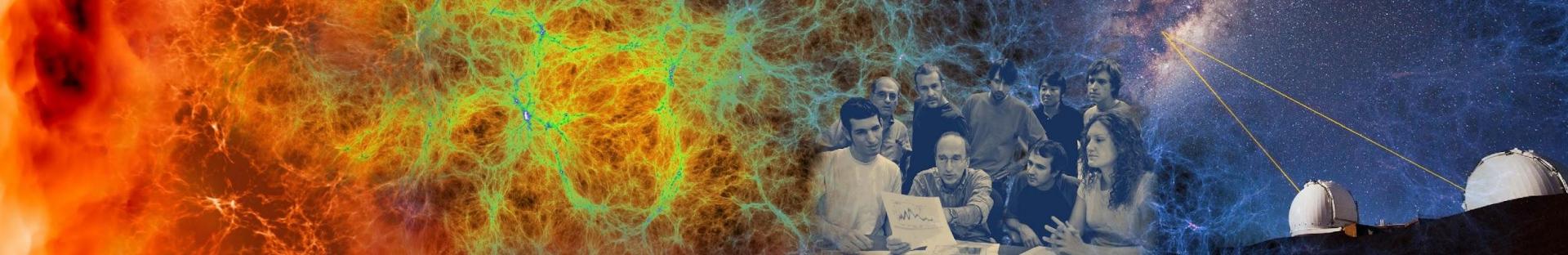
180

The screenshot shows a web browser window titled "JupyterHub" with the URL "jupyter.nersc.gov/hub/spawn/train130/perlmutter-configurable-gpu". The page displays a message about NERSC resources being in maintenance or having issues, specifically mentioning "Perlmutter status: degraded". Below this, the title "Server Options" is centered. The form contains the following fields:

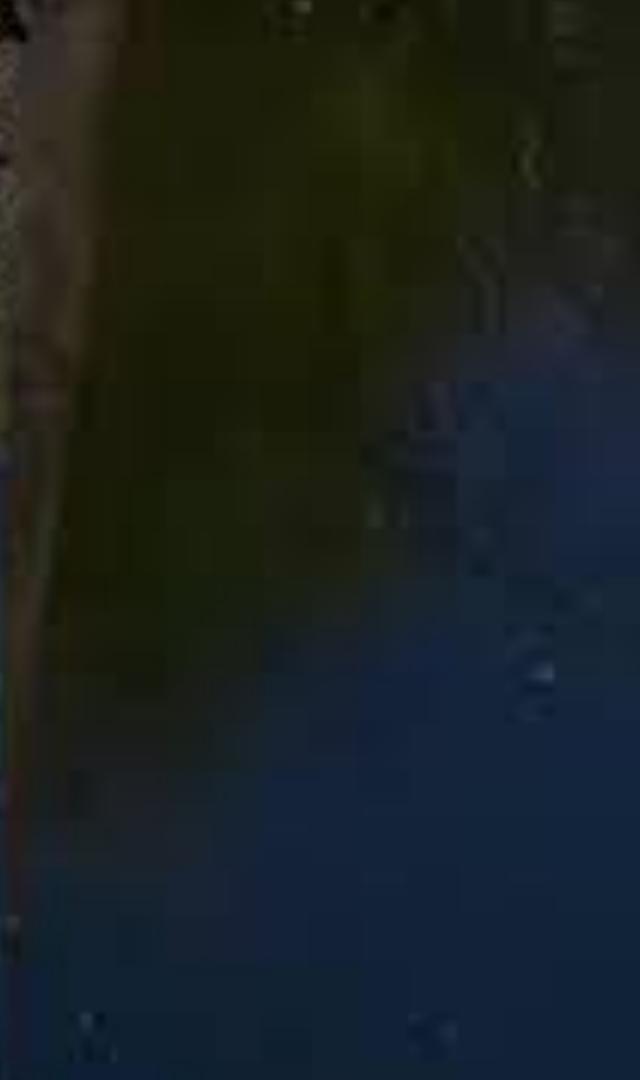
- Account ("_.g" suffix will be added as needed): ntrain8
- Constraint: gpu
- QOS: jupyter
- cpus-per-task (node has 128 cpus): 128
- gpus-per-task (node has 4 GPUs): 4
- nodes (maximum of 4 for jupyter QOS): 1
- ntasks-per-node: 1
- Reservation: siam_intro_gnn
- time (time limit in minutes): 120

A large orange "Start" button is located at the bottom of the form.





Building HPC Julia Workflows



Building a HPC Workflow in Julia

WF node

High-speed network

Compute 1

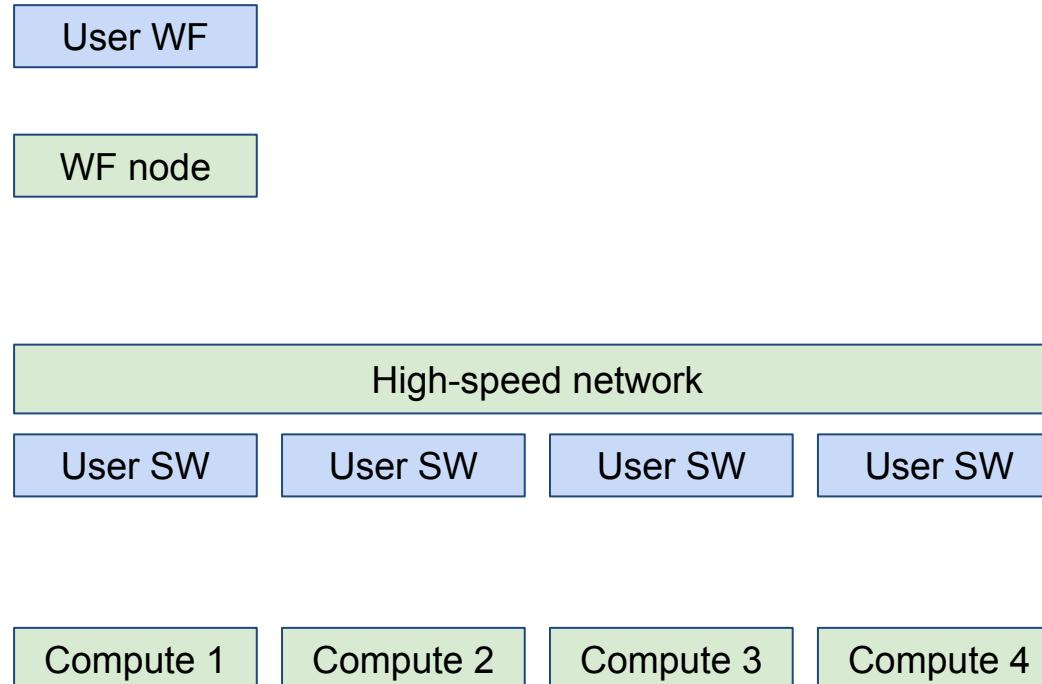
Compute 2

Compute 3

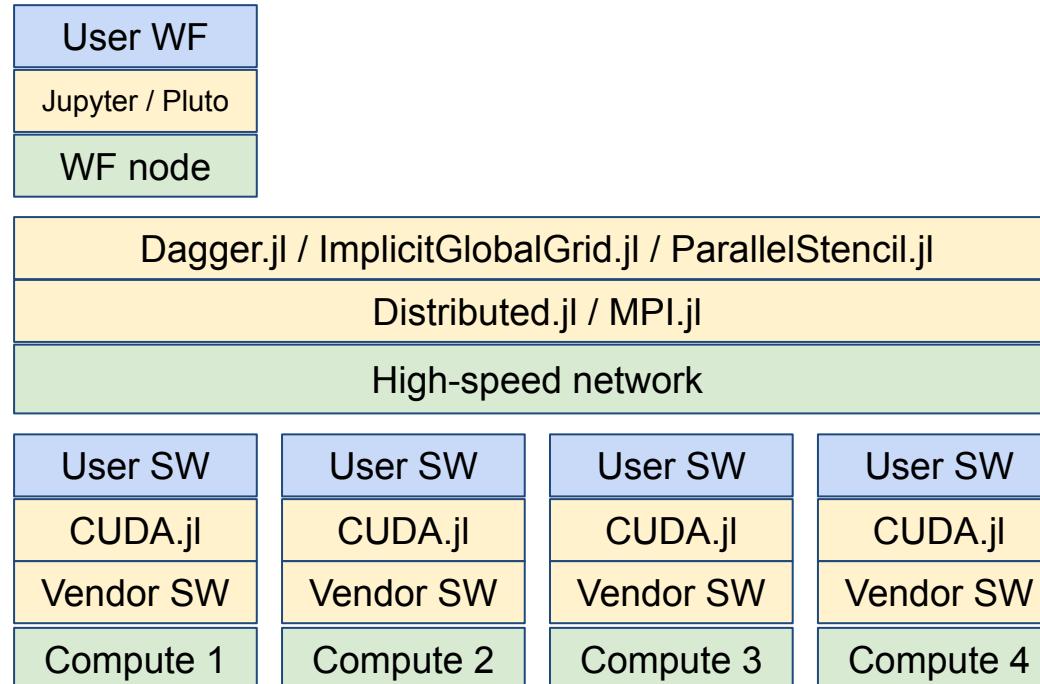
Compute 4



Building a HPC Workflow in Julia



Building a HPC Workflow in Julia



Building a HPC Workflow in Julia

