



Getting Started with Perlmutter

Hands-on tutorial to prepare participants for bootcamp activities

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5 Steps to Get Started on Perlmutter

1. Logging into Perlmutter
2. Navigating the Perlmutter File Systems
3. GitHub for Bootcamp
4. Jupyter Notebooks on Perlmutter
5. Running a Job on Perlmutter

1. Logging into Perlmutter

- NERSC account web portal: iris.nersc.gov
- NERSC JupyterHub: jupyter.nersc.gov

	Login Node	Shared GPU Node	Exclusive CPU Node	Exclusive GPU Node	Configurable Job
Perlmutter	start	start	start	start	start
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.

Most bootcamp activities will require logging into Perlmutter via JupyterHub

2. Navigating the Perlmutter File Systems

- **Bootcamp project:** m4388
 - **Storage spaces:**
 - Home (~ 40 GB)
 - Path: `/global/homes/k/kstreu`
 - Access with: `cd $HOME`
 - Scratch (~ 20 TB)
 - Path: `/pscratch/sd/k/kstreu`
 - Access with: `cd $PSCRATCH`
 - Project or Community File System (CFS) (~ 20 TB)
 - Path: `/global/cfs/cdirs/m4388`
 - Access with: `cd $CFS/m4388`
 - **Let's keep the project space organized!**
 - Be careful working in the project space
 - Do not overwrite files and folders owned by other users
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- **`$PSCRATCH` for individual use**
 - **`$CFS/m4388` for collaborating**

3. GitHub for Bootcamp

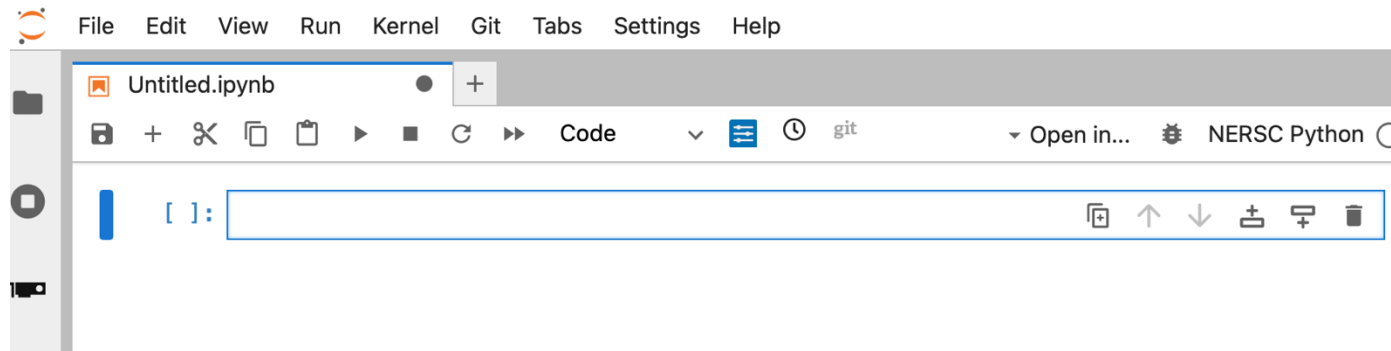
- **GitHub**: a website that stores code online in the form of Git repositories
 - **Git**: a tool that tracks changes to files
 - **Git repository (repo)**: a project folder stored online
 - **Clone**: to make a copy of a repository from GitHub onto Perlmutter, or your computer, etc.)
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- **A GitHub repo is like a shared Google Drive folder**
 - **Cloning the repo is like downloading a working copy of the folder**

How to 'Git' Started

1. **Navigate to the bootcamp repository online:** <https://github.com/Wilber/Intro-HPC-2026>
—Copy the repo code
2. **Open Terminal and navigate to your scratch directory (folder)**
3. **run** `git clone https://github.com/Wilber/Intro-HPC-2026.git`
4. **Go into the cloned repo (project directory) and access files**
—Open and edit Jupyter notebooks
—Run and edit code
5. **Update your cloned repo as necessary with** `git pull`
 - **GitHub is where the shared project lives**
 - `git clone` **copies it to your computer**
 - `git pull` **updated your copy if someone else makes changes**

4. What is a Jupyter Notebook?

- **A Jupyter notebook is an interactive document that combines:**
 - Text:** explanations, notes, equations
 - Code:** typically Python
 - Output:** numbers, tables, plots, images
 - Exploration:** change something → run it → see what happens



- **Google Colab is a Jupyter-style notebook and the basic ideas are the same**
 - Check it out if you're curious:
colab.research.google.com/notebooks/intro.ipynb

Anatomy of a Jupyter Notebook

Markdown cell

- Explains what we're doing

Hello, this is a markdown cell

Code cell

- Instructions for Python to execute

```
[1]: #Hello, this is a code cell  
  
print('Hello, this is the output')  
Hello, this is the output
```

Output

- The result produced by a code cell

```
[ ]:
```

Cells run independently, but variables persist between cells

Basic Workflow of a Jupyter Notebook



**Don't just read a Jupyter notebook.
Change things and see what happens.**

What can you do in a Jupyter Notebook?

1. Markdown cell

—Not code. Allows us to use notebooks to explain our thinking as well as run code.

2. Import a library

—Libraries give us tools that Python doesn't provide automatically.

3. Create some data to explore

`df`

4. Explore the data

`df.head()`

`df.describe()`

5. Change something

`head()` to `tail()`

`head()` to `head(3)`

6. Calculate something

`mean()`

7. Create a Visualization

`plt.scatter()`

Jupyter Notebook Survival Guide

- **Run Cells**

- Shift + Enter

- Runs the current cell and moves to the next one

- Ctrl/Cmd + Enter

- Runs the current cell and stays there

- **Move quickly**

- Esc → A

- Add a cell above

- Esc → B

- Add a cell below

- Esc → M

- Change cell to Markdown

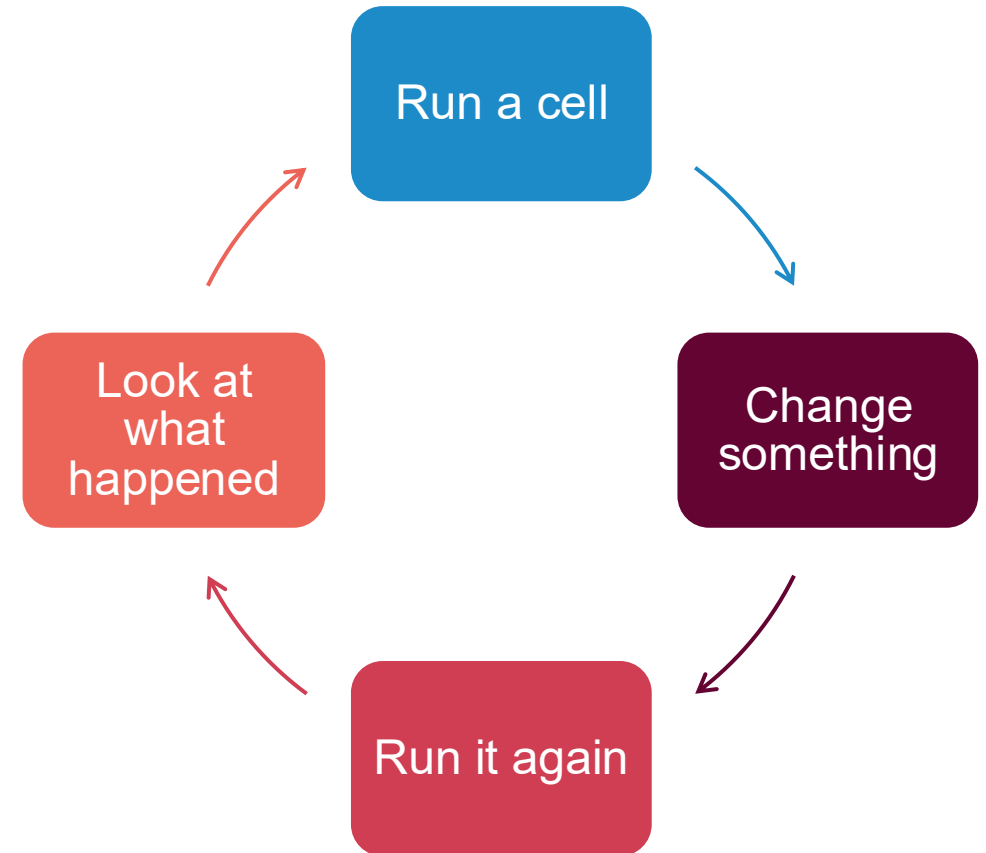
- Esc → Y

- Change cell to Code

- **Explore**

- Place cursor after a function and press Shift + Tab

- See information about the function



Have fun using Jupyter to experiment!

5. Running a Job on Perlmutter

- **Command for running a job in terminal:**

`sbatch filename.sh`

- **Let's try it with `01_hello_res.sh`**

—You can also use `01_hello.sh` when there is no reservation available.

What is going on when you run a job on Perlmutter?

1. Write and submit

—Package your code and inputs into a **job script** and submit it to the scheduler.

2. Queue

—The scheduler (Slurm) waits until the requested resources are available.

3. Allocate

—Perlmutter assigns you **compute nodes / GPUs / CPUs / memory / time**.

4. Run

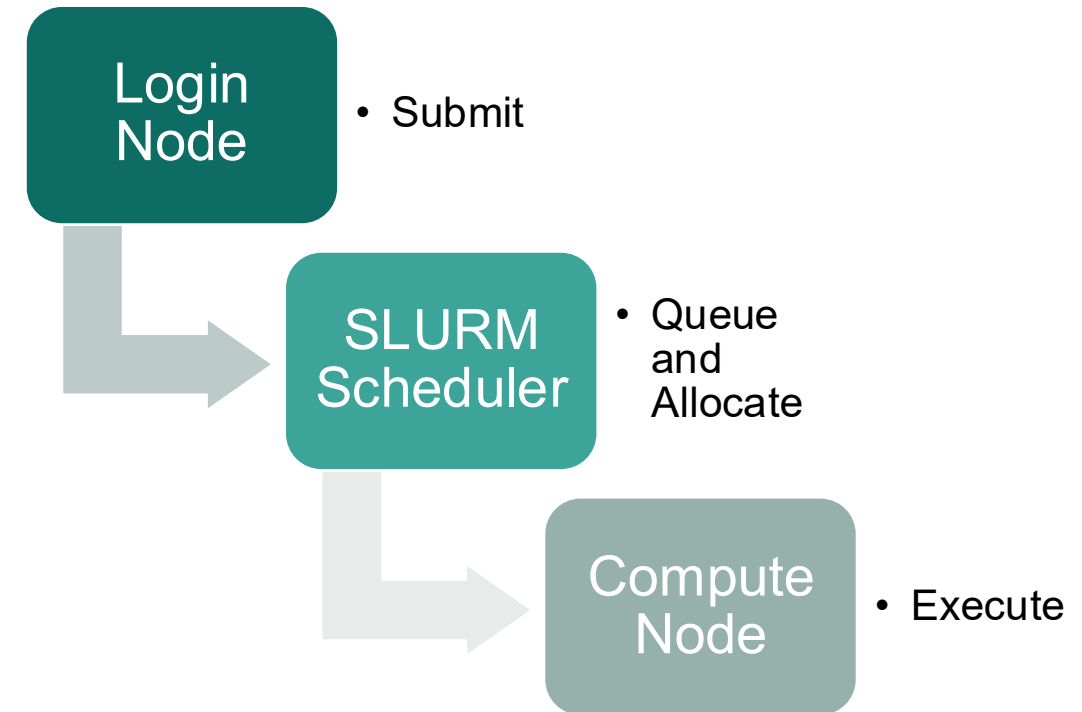
—Your program executes in parallel across the allocated hardware.

5. Communicate

—Processes exchange data over the supercomputer's **high-speed network** and access shared storage.

6. Finish and store

—Results, logs, and output files are written back to **parallel storage**; resources are released.



Resources

- NERSC/Perlmutter
 - docs.nersc.gov/beginner-guide
 - docs.nersc.gov/getting-started
- Jupyter
 - docs.nersc.gov/services/jupyter
 - docs.jupyter.org/en/latest/
- GitHub
 - docs.github.com/en/get-started/using-github/hello-world

