

Illinois Campus Cluster: Basics of Access and Usage

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**National Center for
Supercomputing Applications**

UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGN

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Outline

Block A

- What is the Campus Cluster?
- What is it designed for?
- How to request an allocation

- How to access ICC
- How to navigate the file system
- How to run jobs
- How to transfer files to/from ICC

Block B

- Q&A session



What is the Campus Cluster?

- It is a shared supercomputer available to University of Illinois researchers.
- Any individual, research team, or campus unit can invest in compute nodes.
- It is managed by NCSA whose staff have decades of experience; you don't have to manage your own system.
- Investors can purchase hardware that meets their specific needs (high memory, GPUs)



ICC Resources: Hardware

The hardware on the Campus Cluster is varied and it changes over time as new hardware is added and older hardware is retired. The system currently contains a mix of nodes with different Intel, AMD, and Nvidia hardware.

- Intel processors in the Xeon family
- AMD processors in the Genoa, Rome, and Milan families
- Nvidia A10, A30, A100, H100 and H200 GPUs

<https://campuscluster.illinois.edu/access/buy-compute/> contains information about what investors can purchase to add to the Campus Cluster



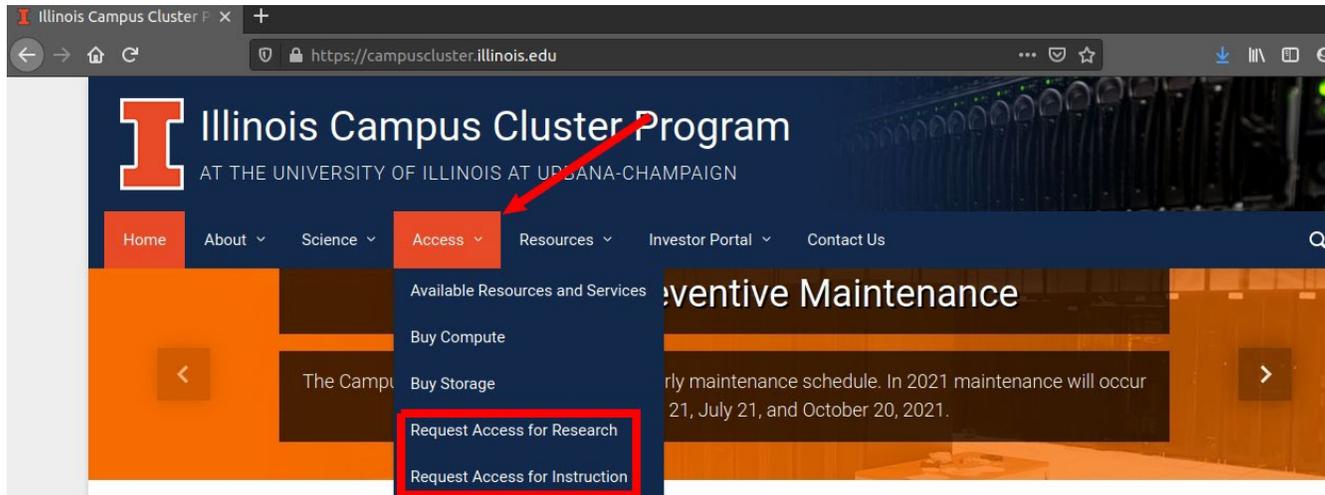
Requesting an account

If you don't have an account yet, you can request it. Check to see if your department is an investor already!

<https://campuscluster.illinois.edu/>

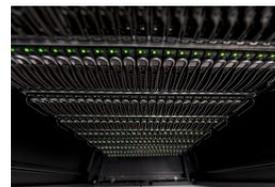
List of Investors:

<https://campuscluster.illinois.edu/about/investors/>



- **Access for Research** is likely to be your option

1. You will be redirected to **Shibboleth**
2. Authenticate with your NetID and password
3. Fill out the form
 - Info about you
 - Info about Professor/Advisor
 - Name, NetID and queue



Illinois Computes Allocations

Another way to get access to the system is through Illinois Computes. It is a program offering computing and data storage resources, technical expertise and support services to researchers from domains across the University of Illinois System who also may have a broad range of needs, whether they be simple or more complex.

To apply for an allocation through Illinois Computes:

- <https://computes.illinois.edu/submitrequest/>
 - create an NCSA identify (if do not already have one)
 - complete the [XRAS form for Illinois Computes](#)
 - if you get stuck, email illinois-computes@illinois.edu



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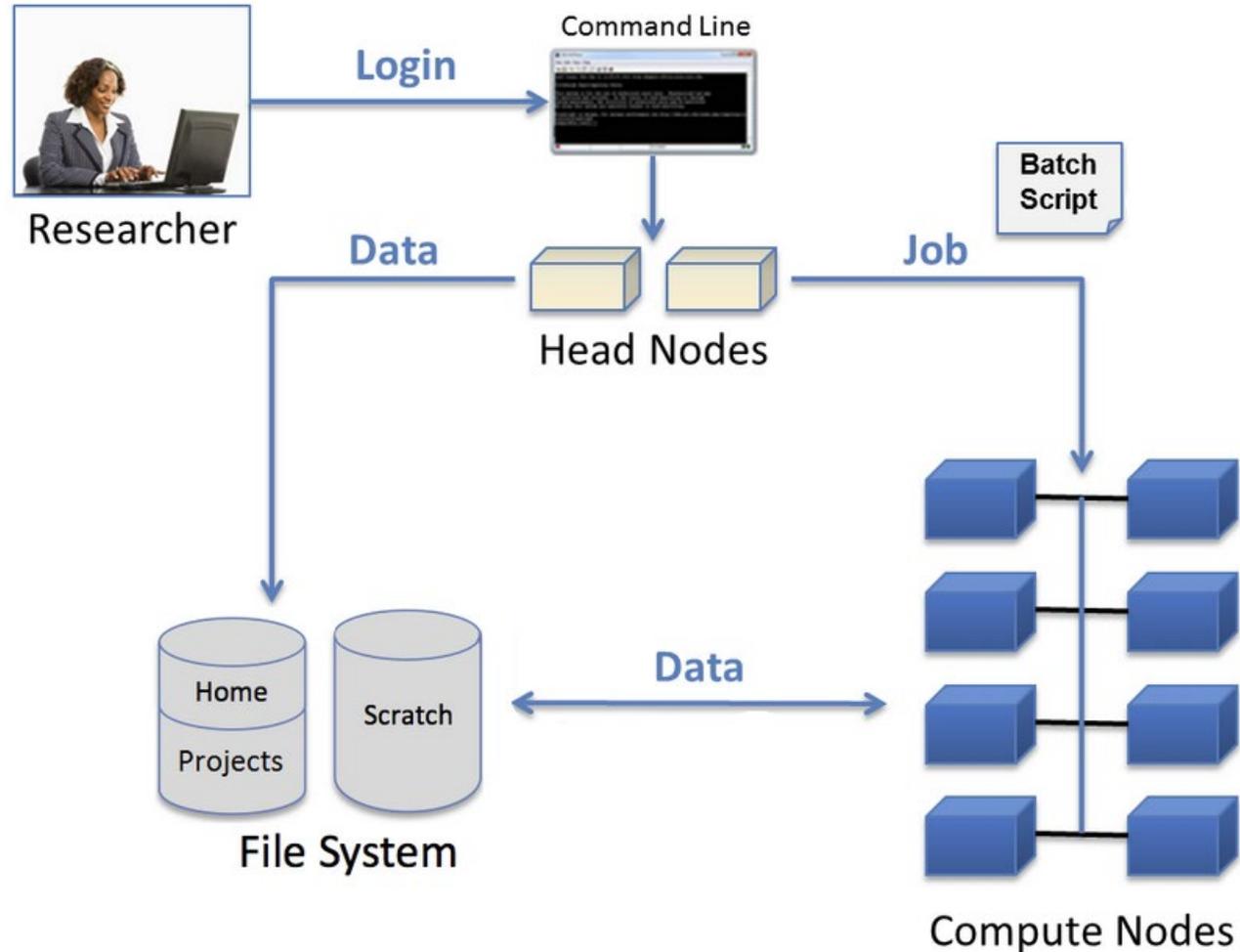
- How to access the ICC
- How to navigate the file system
- How to run jobs
- How to transfer files to/from ICC

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ICC Access and Usage Overview



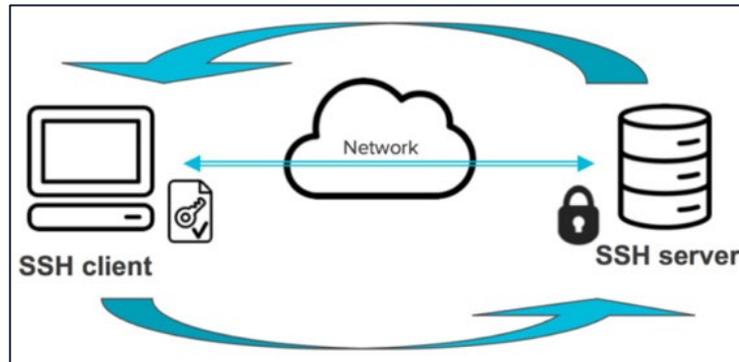
We will discuss each one of these components with 6 hands-on exercises:

1. Accessing via SSH
2. The file system
3. Copying and moving file
4. Compiling code
5. Using modules
6. Job scripts
7. Keeping track of your jobs
8. Transferring files



SSH – Secure Shell Protocol

- SSH Provides a secure channel over an unsecured network by using client-server architecture.



- SSH access is often done via a *command line interface (CLI)*. Operating systems (Mac, Windows, and Linux) have a default *Terminal* installed that you can use as a CLI to SSH into Delta.

Exercise 1: Access the ICC via Terminal

1. Open your Terminal

Mac OS

“Terminal” in
Spotlight Search
(Command+Space)

Windows OS

Start ->
Windows System ->
Command Prompt

Linux OS

Ctrl+Alt+T

2. Connect to Delta via your Terminal:

```
ssh username@cc-login.campuscluster.illinois.edu
```

3. After entering the SSH command, you will be prompted to your **UIUC identity password**.

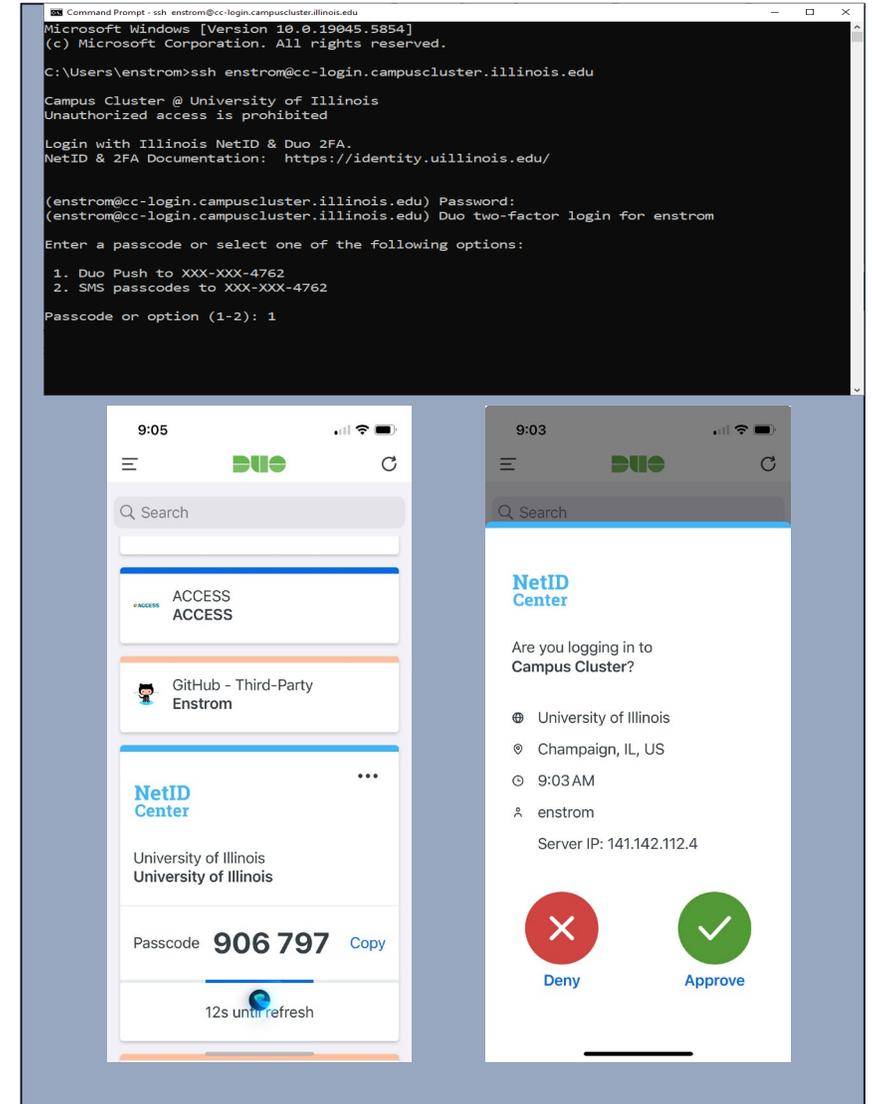


UIUC Duo Authentication

Illinois Duo MFA is required after logging in.
Authenticate with **ONE** of the following:

- **Passcode:** Enter the passcode generated in the Duo app on your phone into your terminal (without spaces).
- **Push:** Type **1** in the terminal and hit **enter**. Within a few seconds, you will receive a push notification to your phone to validate your login attempt, which you can then approve with one click.

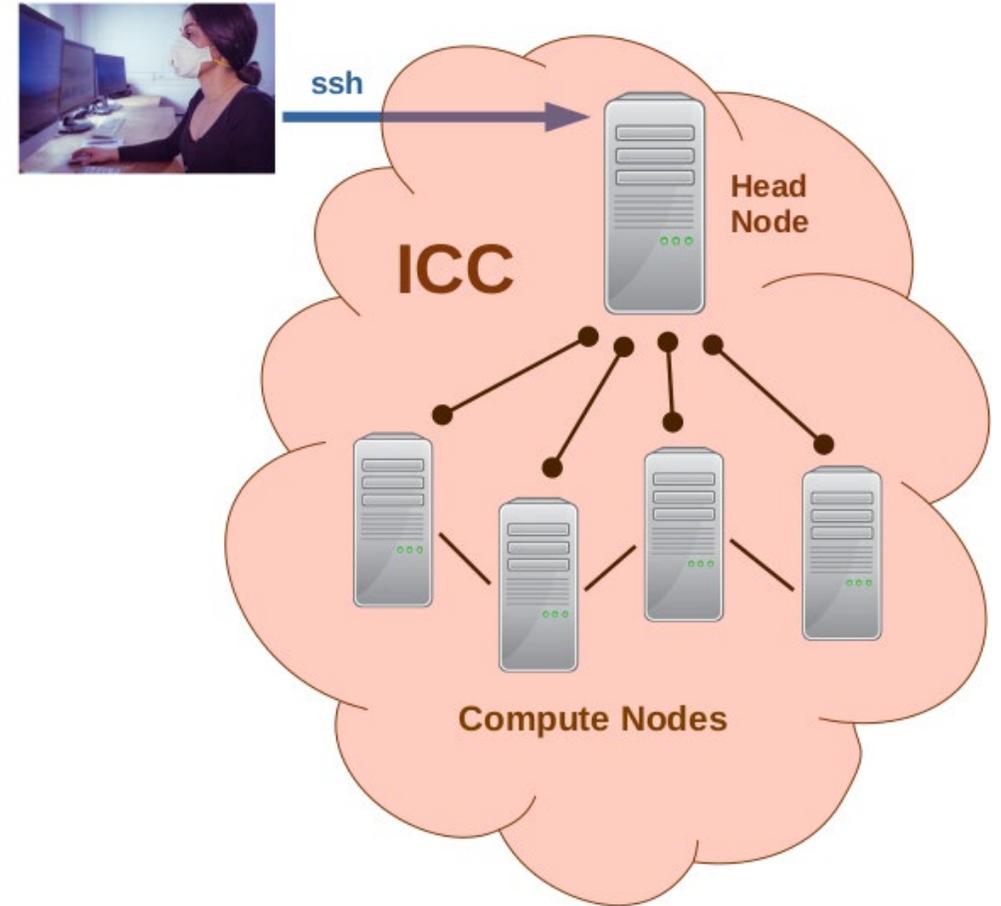
Your **UIUC Duo** account is separate from your **NCSA Duo** account.



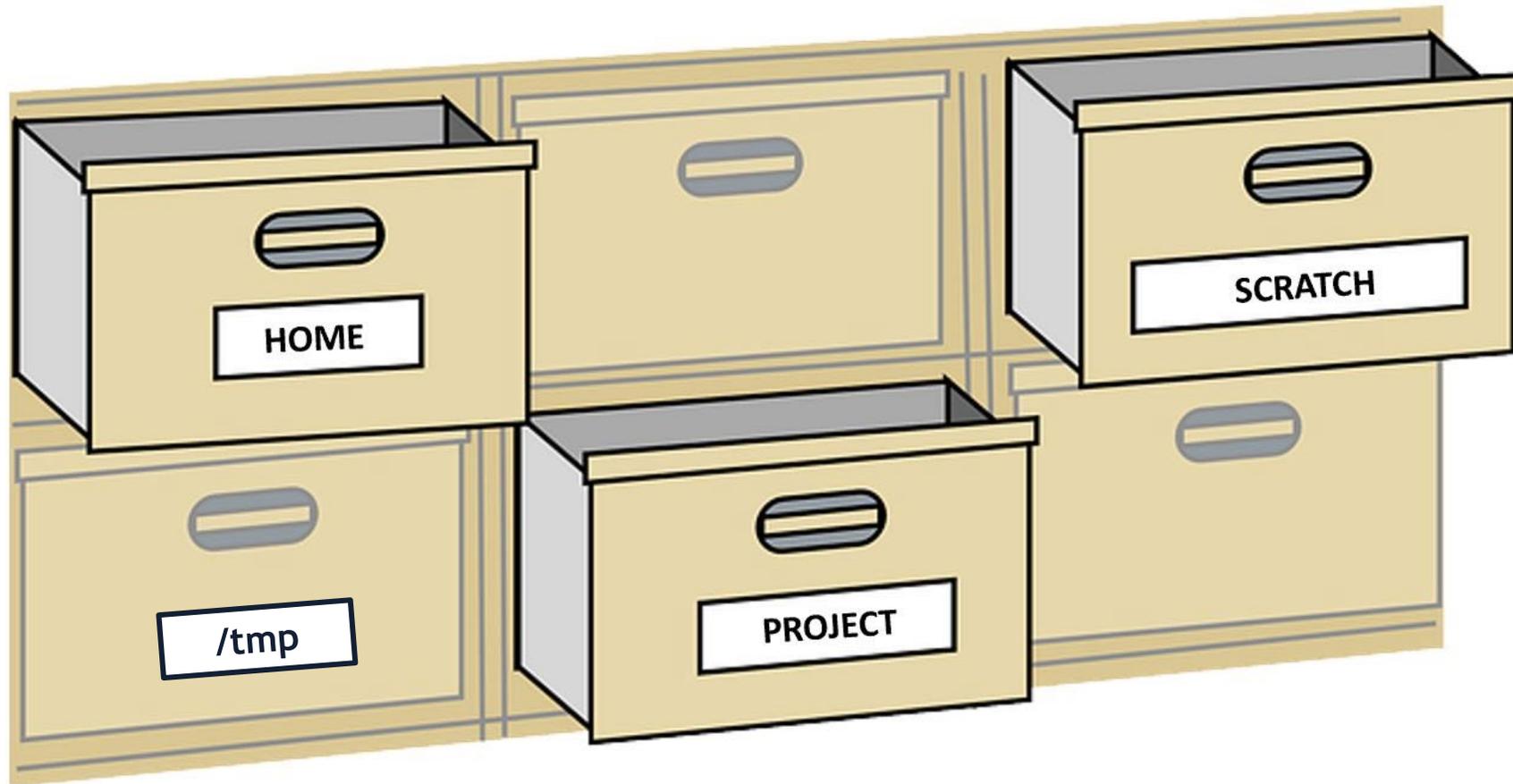
Where are you After Connecting?

- You start on one of the **login (head) nodes**, which is shared by many users.
- Your terminal window is now essentially a Bash Shell in the Linux cluster environment.
- Use **login nodes** for tasks such as:
 - file editing
 - code compilation
 - job submission and tracking
- **! DO NOT** run applications on the **login nodes** (short, test runs are okay).
 - Run applications on the **compute nodes**.

You (local machine)



The File System



Exercise 2: Navigating the file system

a) Use **pwd** to verify your current folder/area

b) Use **ls** to see what files/folders you have there

c) Use **cd** to change current directory to **scratch**. Repeat a, b.

```
cd <target_directory>
```

d) Use **quota** to verify your usage in each area

Symbol	Target
.	Current directory
..	Parent directory
~	Home directory
-	Previously accessed directory



Home Directory

- Directory name: `/u/<username>`
- Default space upon login
- 100GB quota
- Store files you want to keep long-term such as source code, scripts, data input files, and software
- Not for job input/output due to its smaller quota
- Not purged, daily snapshots kept for 30 days



Project Directory

- Directory name: `/projects/Illinois/$college/$department/$pi_netid`
- Quota Investment-based for # of Bytes; 1.5 million inodes/TB
- `/projects` is hosted on NCSA's center-wide (Taiga) file system
- Area for shared data for a project, common data sets, software, results, and so on
- Not purged



Scratch Directory

- Directory name: `/scratch/$your_netid`
- Quota: 10TB/User; No inode quota
- A temporary space for job output
- Larger temporary files – like intermediary files in a pipeline that you don't need to keep
- Daily purge of files older than 30 days



Local Scratch

- Directory name: `/scratch.local`
- Unique to each node and job – not a shared file system
- No quotas in place, the size varies across nodes of different investments
- Locally attached disk for fast small file input/output
- Purged after each job



Quotas

Use the **quota** command to view your system use and use by your project(s). This example output is for a person, with the username “<NetID>”.

• Quota usage for user <NetID>:

```
• -----  
• | Directory Path | Block | Soft | Hard | Files | Soft | Hard |  
• | | Used | Quota | Limit | Used | Quota | Limit |  
• -----  
• | /u/<NetID> | 16G | 100G | 103G | 97000 | 750000 | 760000 |  
• -----  
• | /projects/nsf/delta/bbka | 1.43T | 1.953T | 2.002T | 1834896 | 3000000 | 3300000 |  
• | /projects/nsf/delta/bccu | 266G | 500G | 550G | 1081283 | 1500000 | 1700000 |  
• | /projects/industry/mg | 6.412P | 6.543P | 6.543P | 910700911 | 10050000000 | 10050000000 |  
• | /projects/illinois/ovcri/nca/shared | 37.57T | 62T | 62T | 17767766 | 93000000 | 93000000 |  
• -----  
• | /scratch/<NetID> | 512B | 10T | 10T | 1 | none | none |  
• | /scratch_new/<NetID> | 4k | 10T | 10T | 1 | none | none |  
• -----
```



Exercise 3: Copying and moving files

a) Use `mkdir` to create a new folder in your home area named *HeLLoWoRld*

```
mkdir <new_folder_name>
```

b) Use `cp` to copy the *HeLLoWoRld.cpp* file located at */sw/cc.users/training/2025.06.03/* to your home folder

```
cp <original_file_location> <copy_location>
```

c) Use `mv` to move this file to the folder you created in a)

```
mv <current_file_location> <target_file_location>
```

d) Use `cp` to copy the file that you just moved from *HeLLoWoRld* to home

e) Verify that copies are indeed in both folders using `ls`

f) Remove the copy in your home folder using `rm`

```
rm <file_location>
```

Tip: after each item, use `ls` to check if it worked!



Editing Files

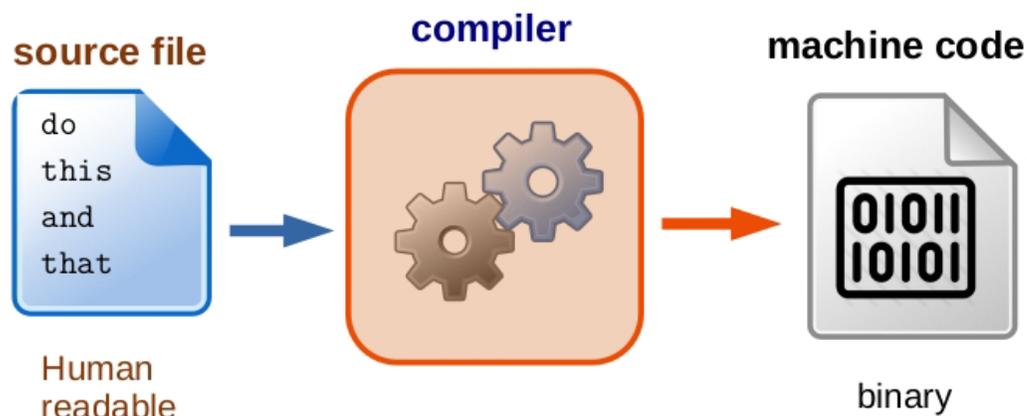
- Two common Linux file editors are **vi** and **nano**.
 - **nano** is a text editor that is friendly for inexperienced Linux users.
 - **vi** (and its improved version, **vim**) is very powerful but harder to use.
- **nano**:
 - The general syntax to open a file in **nano** is: `nano <filename>`
 - If the file exists, it will open. Otherwise, a new file with that name is created.
 - Press control(**Ctrl**)+**X** to exit (you will be prompted to save).
 - Press control(**Ctrl**)+**O** to save without exiting.



Compiling code

GNU compilers are by default available when you log in the **Head Nodes**

- **gcc**: compiles C code
- **g++**: compiles C++ code
- **gfortran**: compiles Fortran code



General compiling syntax is

```
compiler <source_code_file> -o <binary_file>
```

Language	GNU compiler command
C	<code>gcc MyProg.c -o MyProg.exe</code>
C++	<code>g++ MyProg.cpp -o MyProg.exe</code>
Fortran	<code>gfortran MyProg.f -o MyProg.exe</code>



Other compilers are available in ICC, but if you want to use them, you need to **load** them – *we will cover that too!*



Exercise 4: Compiling code

a) Go to the directory where the file from the previous exercise is located

b) Check the version of the GNU compiler that is available to you in the Head Node

```
gcc --version
```

c) Compile *HelloWorld.cpp* using **g++**

```
g++ HelloWorld.cpp -o HelloWorld.exe
```

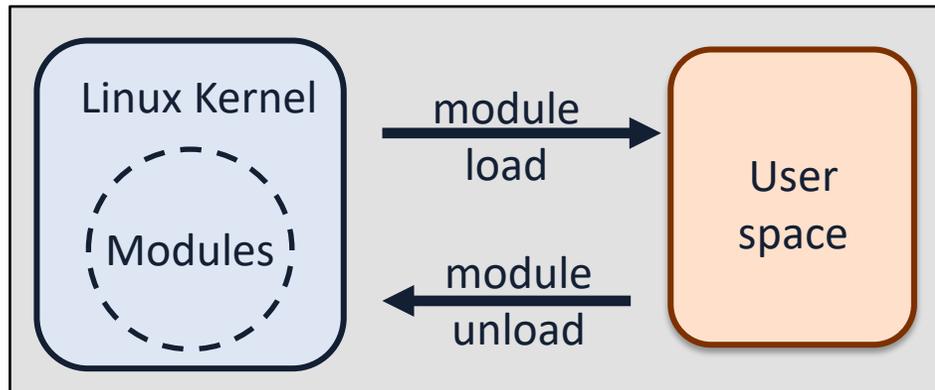
d) Verify that the binary has been generated in your folder



Working with modules

Modules allow you to load and unload components of the operating system as you need them!

The same approach applies to loading a variety of software and libraries.



Command	Description
<code>module list</code>	Lists modules loaded in your session
<code>module avail</code>	Lists all available modules
<code>module help <module_file></code>	Information about <module_file>
<code>module load <module_file></code>	Loads <module_file> to your environment
<code>module unload <module_file></code>	Removes <module_file> from your environment

Demonstration: Working with modules

```
[enstrom@cc-login1 ~]$ module list
```

```
Currently Loaded Modules:
```

```
...
```

```
[enstrom@cc-login1 ~]$ module avail
```

```
...
```

```
[enstrom@cc-login1 ~]$ which icx
```

```
/usr/bin/which: no icx in
```

```
[enstrom@cc-login1 ~]$ module load intel/tbb intel/umf intel/compiler-rt intel/compiler
```

```
[enstrom@cc-login1 ~]$ ls -l a.out
```

```
ls: cannot access 'a.out': No such file or directory
```

```
[enstrom@cc-login1 ~]$ icx HelloWorld.c
```

```
[enstrom@cc-login1 ~]$ ls -l a.out
```

```
-rwx----- 1 enstrom root 17472 May 29 09:47 a.out
```

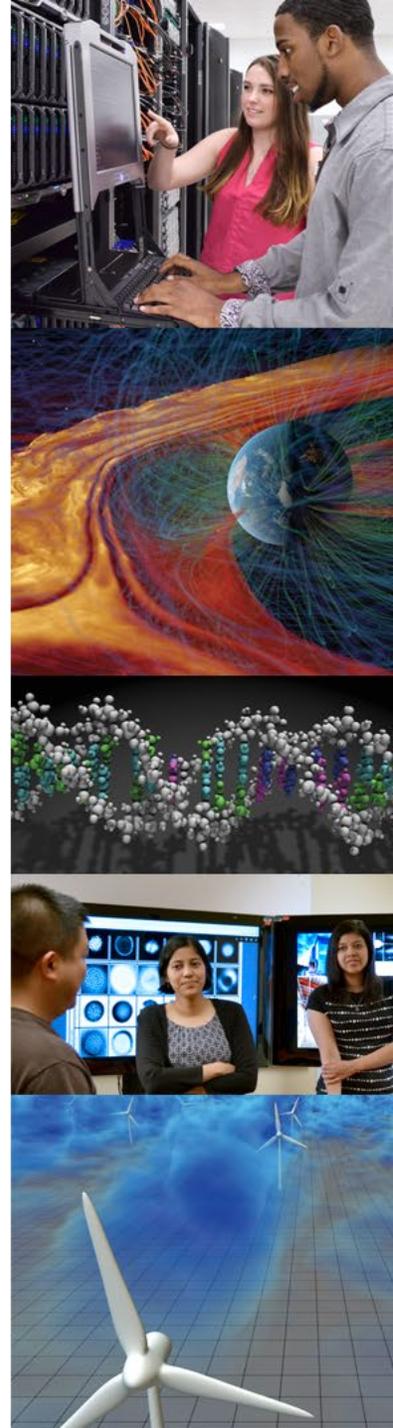


Let's Talk About Jobs

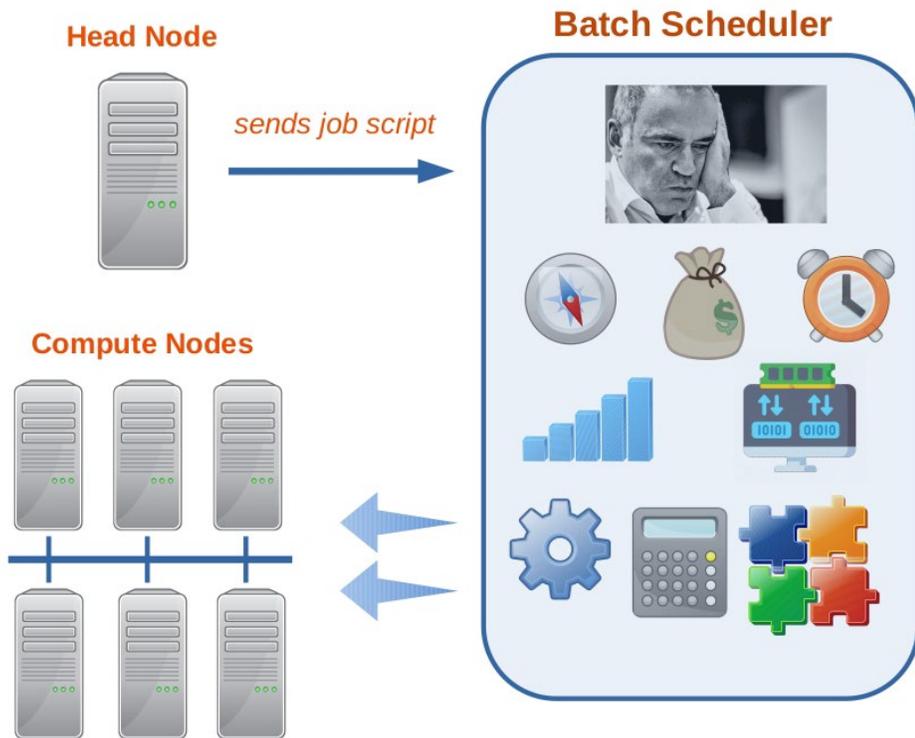
Now that we know how to:

- 💡 Log in to the ICC
- 💡 Navigate the file system
- 💡 Load modules

It's time to use the cluster's power!



Batch schedulers (Slurm)



Batch processing runs jobs that can run without end-user interaction or can be scheduled to run as resources permit.

The **batch scheduler** is a computer application that weighs several factors to determine where, how, and when a certain request is going to run on the compute nodes.

The ICC uses **Slurm** for batch scheduling.



Typical workflow

- User accesses login node
- Launches interactive session to a single node within a queue
 - Example: `srun --nodes=1 --ntasks-per-node=1 --partition=secondary --account=cheller-ic -pty /bin/bash`
- Configure your application to run in this interactive session and exit the session
- Put your application into a batch job script, as covered in the next few slides



Batch job scripts

For Slurm to do its magic, we need to provide it with some information...

Job Script

```
#!/bin/bash
#SBATCH --time=XX:YY:ZZ
#SBATCH --nodes=N
#SBATCH --ntasks-per-node=M
#SBATCH --partition=Where
#SBATCH --account=account_name
#SBATCH --output=OutFile
#SBATCH --error=ErrorFile
#SBATCH --mail-user=Email
#SBATCH --mail-type=When
./HelloWorld.exe
```

We will send bash commands

Required time

Number of nodes

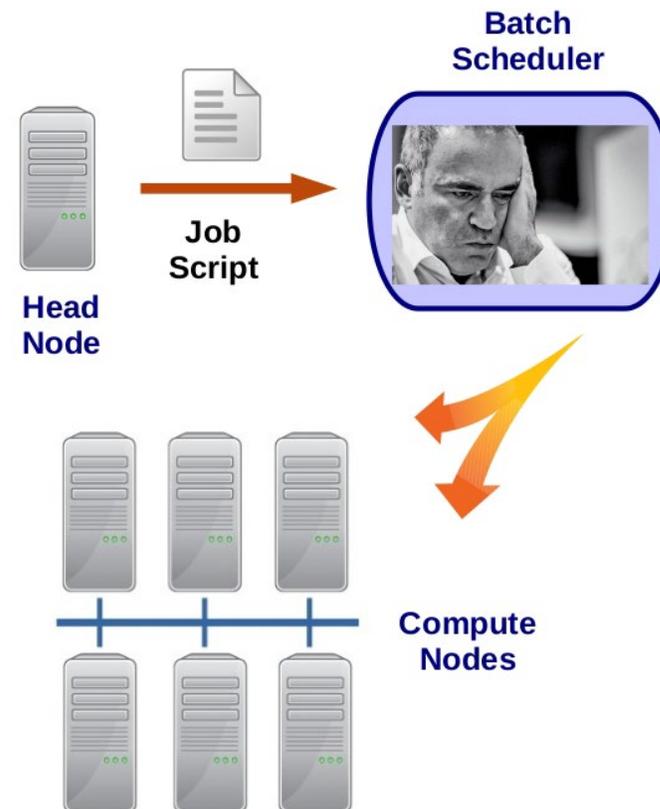
Where to run it

Account to charge

Who to email

When to email

What to run



Partitions and Accounts

- To determine what partitions (or queues) you have access to, you can use the “sinfo -o %P” command.

```
PARTITION  
secondary  
secondary-sg  
IllinoisComputes  
IllinoisComputes-GPU
```

- To see what accounts are available for you to use, you can use the “/sw/cc.users/tools/my.accounts” command.

```
Campus Cluster user enstrom's Account list:  
Account=rfst
```



Exercise 4: Job script for HelloWorld

1. Copy the file **HelloWorld.sbatch** to your HelloWorld folder.

```
cp /sw/cc.users/training/2025.06.03/HelloWorld.sbatch $HOME/HelloWorld/
```

2. Use **cat** to verify the information that is being passed to the scheduler.

```
cd ~/HelloWorld; cat HelloWorld.sbatch
```

3. Submit your job scrip to the batch scheduler using **sbatch**.

```
sbatch HelloWorld.sbatch
```

4. Take note of your JobID.



Exercise 5: Keeping track of your job

Use **queue** commands to monitor the status of your job

1. List the JobIDs tied to your username.

```
queue -u <username>
```

2. Look up the status of your job based on the JobID

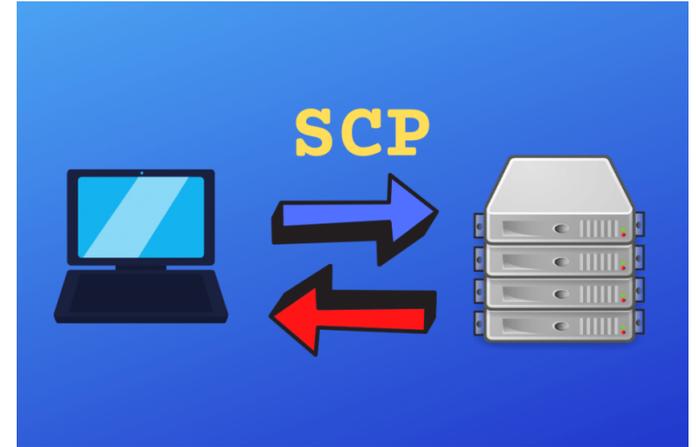
```
queue -j <JobID>
```

Command	Action
queue -a	List status of all jobs in the batch system
queue -u <username>	List status of all your jobs
queue -j <JobID>	Lists information about a job
scancel <JobID>	Kills a job



File transfers using SCP

- Secure Copy Protocol (SCP)
 - Works basically like SSH
 - Safe channel to copy/transfer data to/from your local machine
- Taiga has data transfer nodes (DTN) for file transfers
- Pulling files **from the DTNs** to your machine:
 - `scp <username>@cli-dtn.researchdata.illinois.edu:<path_to_file> <destination>`
- Pushing files **to the DTNs** from your machine
 - `scp <path_to_file> <username>@cli-dtn.researchdata.illinois.edu:<destination>`
- There are many other options available for managing file transfers on the ICC (https://docs.ncsa.illinois.edu/systems/icc/en/latest/user_guide/storage_data.html#)



Exercise 6: Transfer files with SCP

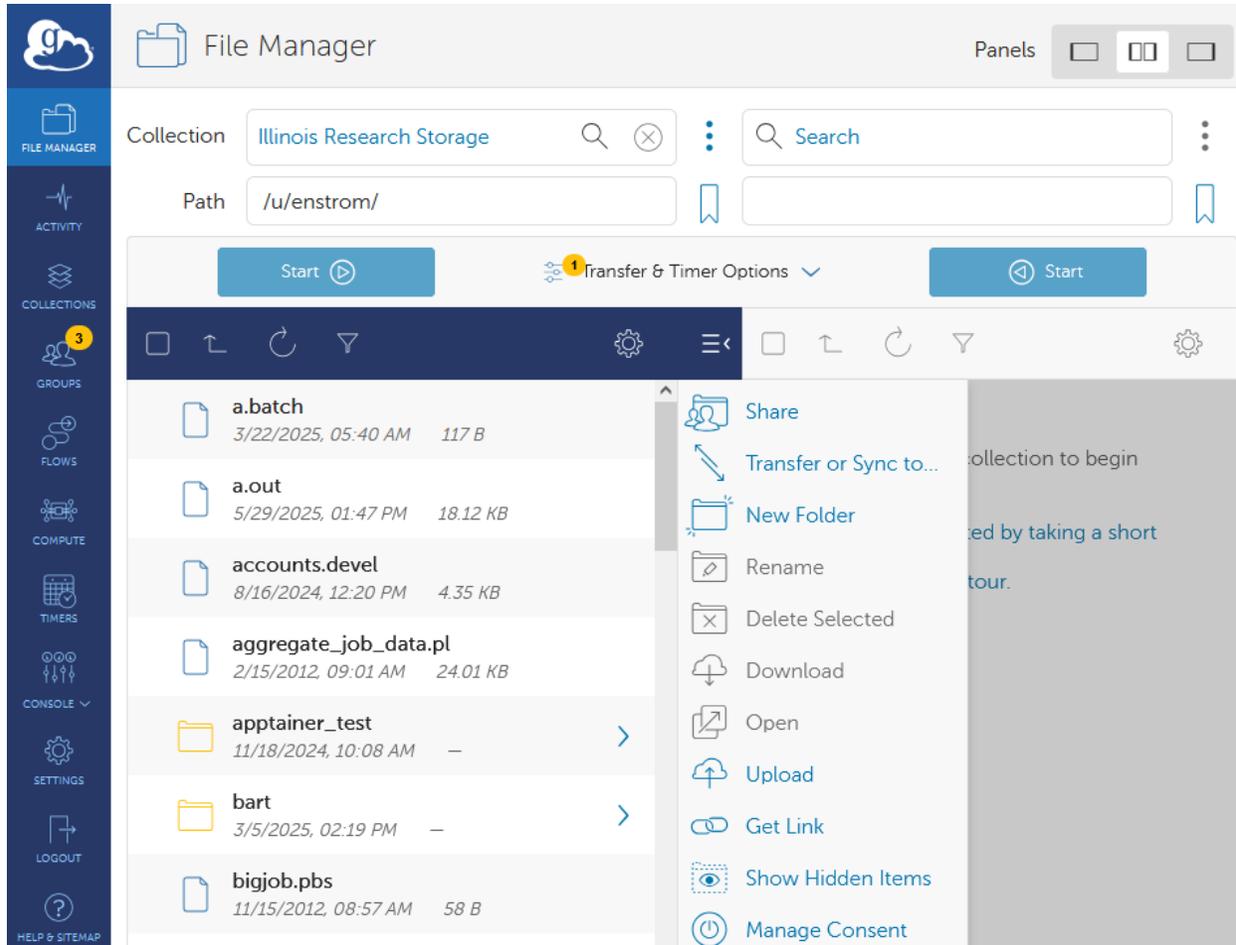
1. Log out of your cluster session using **logout**.
2. Use **scp** to copy the **HelloWorld.out** file to your local machine

```
scp <username>@cli-dtn.researchdata.illinois.edu:~/HelloWorld/HelloWorld.out .
```

3. Look for the file on your machine and try to open it using a text editor.



Large File Transfers with Globus

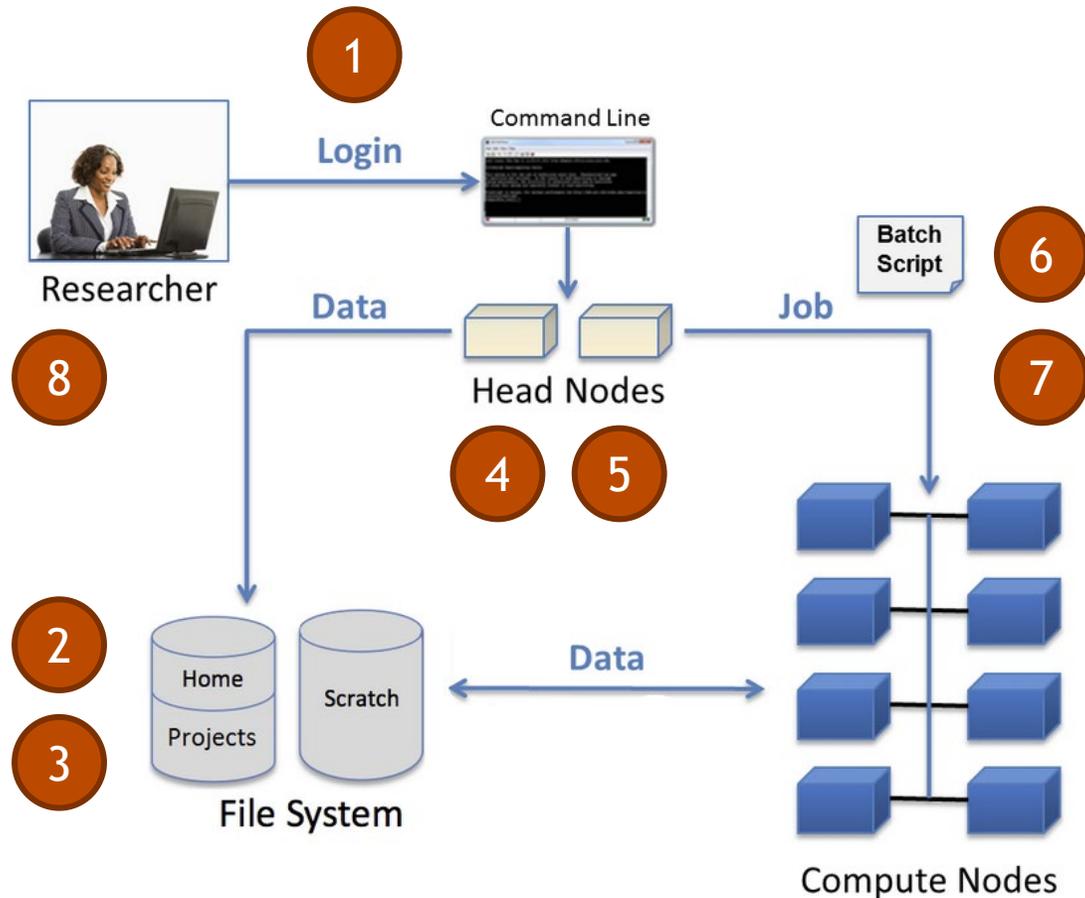


- Globus is recommended for large file transfers.
- Create a Globus account at www.globus.org
- ICC Globus endpoint:
 - “Illinois Research Storage”



Cooling down

We now have a pretty good idea about navigating the Illinois Campus Cluster...



1. Login using SSH client
2. Understand and use the file system
3. Copy and move files around
4. Compile code
5. Load and unload modules
6. Write and submit a job script
7. Keep track of your jobs
8. Transfer files to your local machine



Resources

- **ICCP official *Getting Started***

https://docs.ncsa.illinois.edu/systems/icc/en/latest/getting_started.html

- **ICCP *User Guide***

<https://docs.ncsa.illinois.edu/systems/icc/en/latest/>

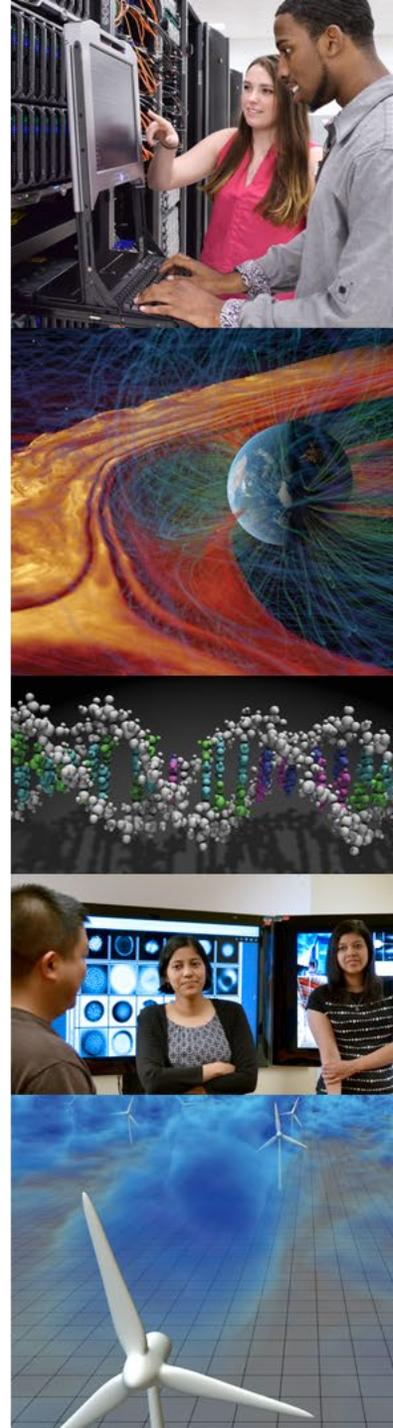
- **Self-paced *Getting Started on ICC – HPC Moodle page***

<https://www.hpc-training.org/xsede/moodle/>



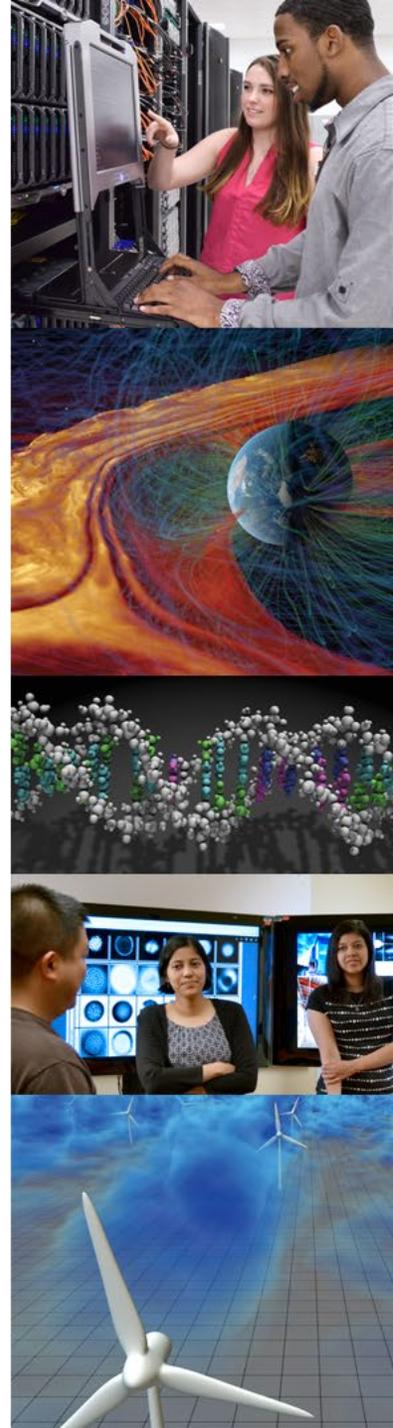
Resources

- Slurm documentation:
 - <https://slurm.schedmd.com/documentation.html>
- Environment modules documentation:
 - <https://modules.readthedocs.io/en/latest>
- Best practices for running jobs, in general:
 - <https://docs.nersc.gov/jobs/best-practices>
- Customizing Your Computer Environment Training:
 - <https://www.hpc-training.org/moodle/course/view.php?id=77>



Getting Help

- Go to the **NCSA Help Portal** (<https://help.ncsa.illinois.edu>)
- When you submit a ticket, include:
 - What you were trying to do
 - How you tried to do it
 - Why you think it isn't working
 - Copy/paste the commands you ran and what output you saw on screen
- You will get emails as your ticket is worked on, please respond to questions that are asked.





Questions?



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Have questions after the workshop?

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