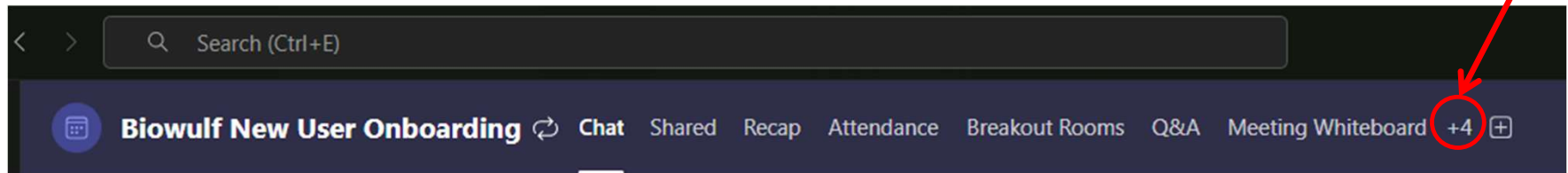


Welcome to Biowulf

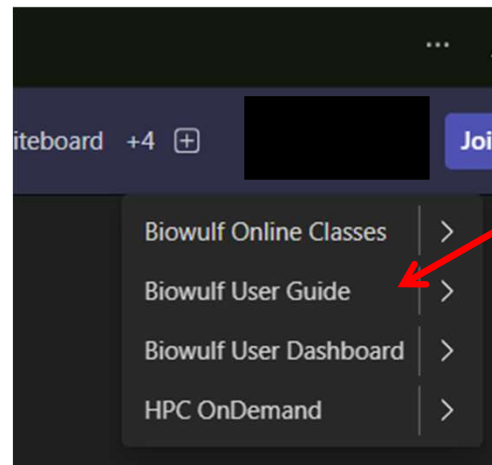
High performance computing @ NIH

Some links!

Click here!



List of Links



Accelerate biomedical research at the NIH by providing convenient access to large scale **computational resources** and **scientific software** (and the **know-how** to use them).

Biowulf staff - staff@hpc.nih.gov

NIH HPC Core Facility Staff



Steve Bailey



Tim Miller



David Hoover, Ph.D.



Helen Ashdown



Simon Carlson-
Thies

Picture
unavailable

Afif Elghraoui



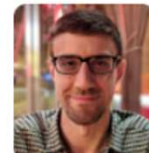
Ali Erfani



Andrew Fant, Ph.D.



Beide (Peter) Fu,
Ph.D.



Jonathan Goodson,
Ph.D.



Patsy Jones

Picture
unavailable

Charles Lehr



Jean Mao, Ph.D.



Nitish Narula

Picture
unavailable

David O'Brien

Picture
unavailable

Ifeanyi Okoye



Antonio Ulloa, Ph.D.



Renbin Yang, Ph.D.



Qi Yu, Ph.D.

Computational resources: The Biowulf system

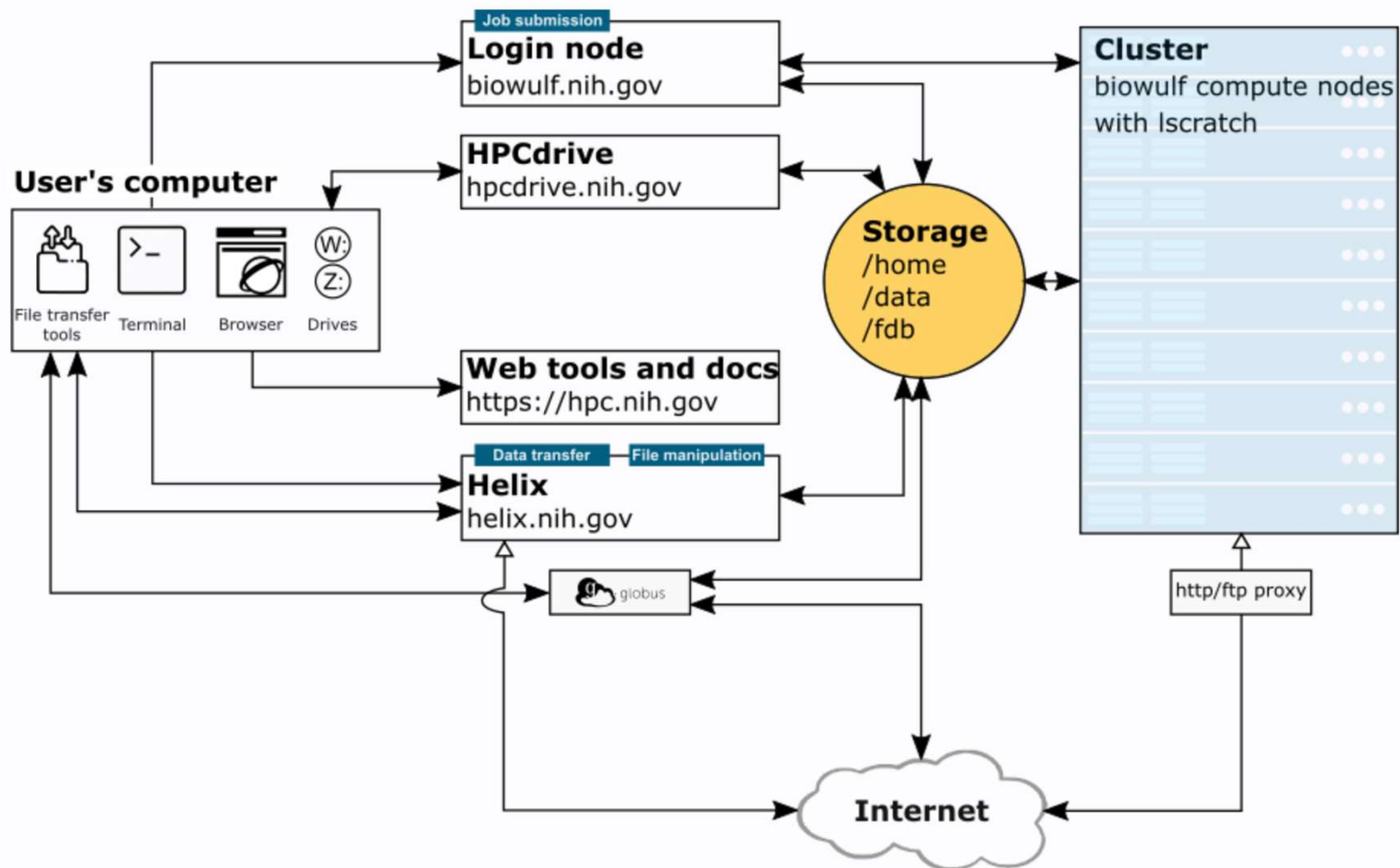
What is Biowulf?



Where is
Biowulf?



Architecture

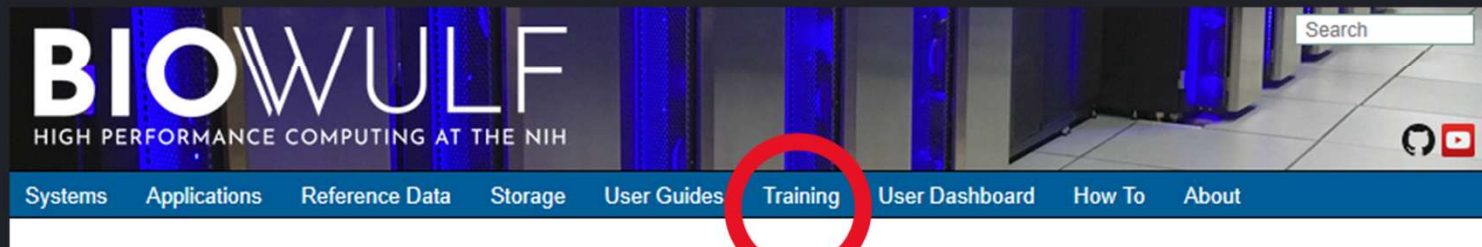


Software

Applications

- multiple versions for ~1000 applications available
- Multiple versions of python with ~500 packages each
- Multiple versions of R with about 1600 packages each
- singularity for containerization
- jupyter, rstudio (desktop, community edition),
rstudio-server
- <https://hpc.nih.gov/apps/>

Know how - training and outreach



Training

- Online, self-paced classes (intro to biowulf, bash)
- Videos: https://hpc.nih.gov/training/intro_biowulf/
- Live action classes/recorded (e.g. Deep learning by example, R, matlab, snakemake)
- Documentation (<https://hpc.nih.gov>) and tutorials (e.g. https://hpc.nih.gov/training/gatk_tutorial)
- BTEP Intro to Biowulf at: <https://bioinformatics.ccr.cancer.gov/btep/courses/introduction-to-unix-on-biowulf-january-2024>

Outreach

- Monthly Virtual consult via teams
 - Link on Training page- no need to register!
- Meeting with individual groups or 1:1
 - Presentation to group or lab on campus
- Cranky email from staff if/when you break something

Some things to keep in mind...

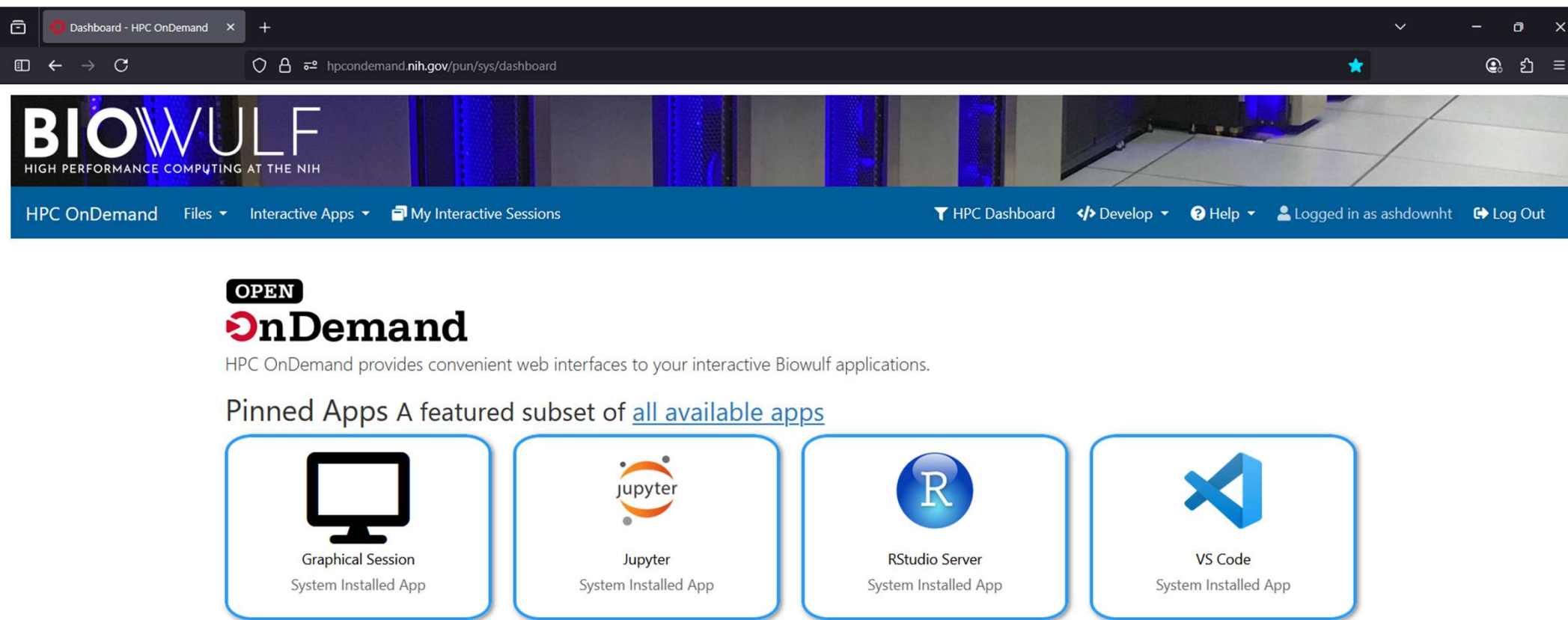
- Please do not use `sudo`, `apt-get`, `dnf`, or `yum`
 - Biowulf user's do not have root access – they will not work
- Be mindful of copy and pasting things directly from the internet
 - *Especially when using chatbots*

Live Demo: Getting started on Biowulf

- With Open OnDemand
 - Allows for users to work on the Biowulf cluster via web browser
 - <https://hpcondemand.nih.gov>

Open On Demand

<https://hpcondemand.nih.gov/>



The screenshot shows a web browser window with the address bar displaying `hpcondemand.nih.gov/pun/sys/dashboard`. The page header features the **BIOWULF** logo with the tagline "HIGH PERFORMANCE COMPUTING AT THE NIH". Below the header is a navigation bar with links for "HPC OnDemand", "Files", "Interactive Apps", and "My Interactive Sessions". On the right side of the navigation bar, there are links for "HPC Dashboard", "Develop", "Help", and a user status indicator "Logged in as ashdownht" with a "Log Out" button.

The main content area displays the **OPEN OnDemand** logo. Below the logo, a text line states: "HPC OnDemand provides convenient web interfaces to your interactive Biowulf applications." This is followed by the heading "Pinned Apps A featured subset of [all available apps](#)".


Four application tiles are shown, each with an icon, the application name, and the status "System Installed App":

- Graphical Session**: Represented by a monitor icon.
- Jupyter**: Represented by the Jupyter logo.
- RStudio Server**: Represented by the R logo.
- VS Code**: Represented by the Visual Studio Code logo.

Interactive Apps

Desktops

Graphical Session

 SPersist Desktop

GUIs

 IGV

 MATLAB


 Maestro

Servers


 GFA Server

 Jupyter

 OmicCircosShiny

 RStudio Server

 VS Code

 iDEP

Shell

 sinteractive

Graphical Session

This app will launch an interactive desktop on a compute node. The session will have access to 4 CPUs (shared) and 8GB of memory and may last up to seven days. This session and the resources it uses is separate from and in addition to your two interactive job limit.

This job is suitable for both data transfer/management and running heavy compute tasks within the limit of the 4C/8GB resources. You may submit additional interactive or batch jobs from within this session.

☐ I would like to receive an email when the session starts

Launch

***Choose from any of these options** for the [data root directory](#).

Interactive Apps


Desktops

 Graphical Session

 SPersist Desktop


GUIs

 IGV

 MATLAB


 Maestro

Servers


 GFA Server

 Jupyter

 OmicCircosShiny

 RStudio Server

 VS Code

 iDEP

Shell

 sinteractive

Graphical Session (21343)

Queued

Created at: 2025-09-09 15:08:02 EDT

Time Requested: 168 hours

Session ID: 05a2101b-63b3-43bd-8ff4-d4631f74c9ea

 Cancel


Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested.

This means your session is in the queue and loading

Interactive Apps

Desktops

 Graphical Session

 SPersist Desktop

GUIs

 IGV

 MATLAB


 Maestro

Servers


 GFA Server

 Jupyter

 OmicCircosShiny

 RStudio Server

 VS Code

 iDEP

Shell

 sinteractive

Graphical Session (21343)

1 node | 4 cores | Running

Host: cn2061

 Cancel

Created at: 2025-09-09 15:08:02 EDT

Time Remaining: 167 hours and 55 minutes

Session ID: 05a2101b-63b3-43bd-8ff4-d4631f74c9ea

noVNC Connection

Native Instructions

Compression



0 (low) to 9 (high)

Image Quality

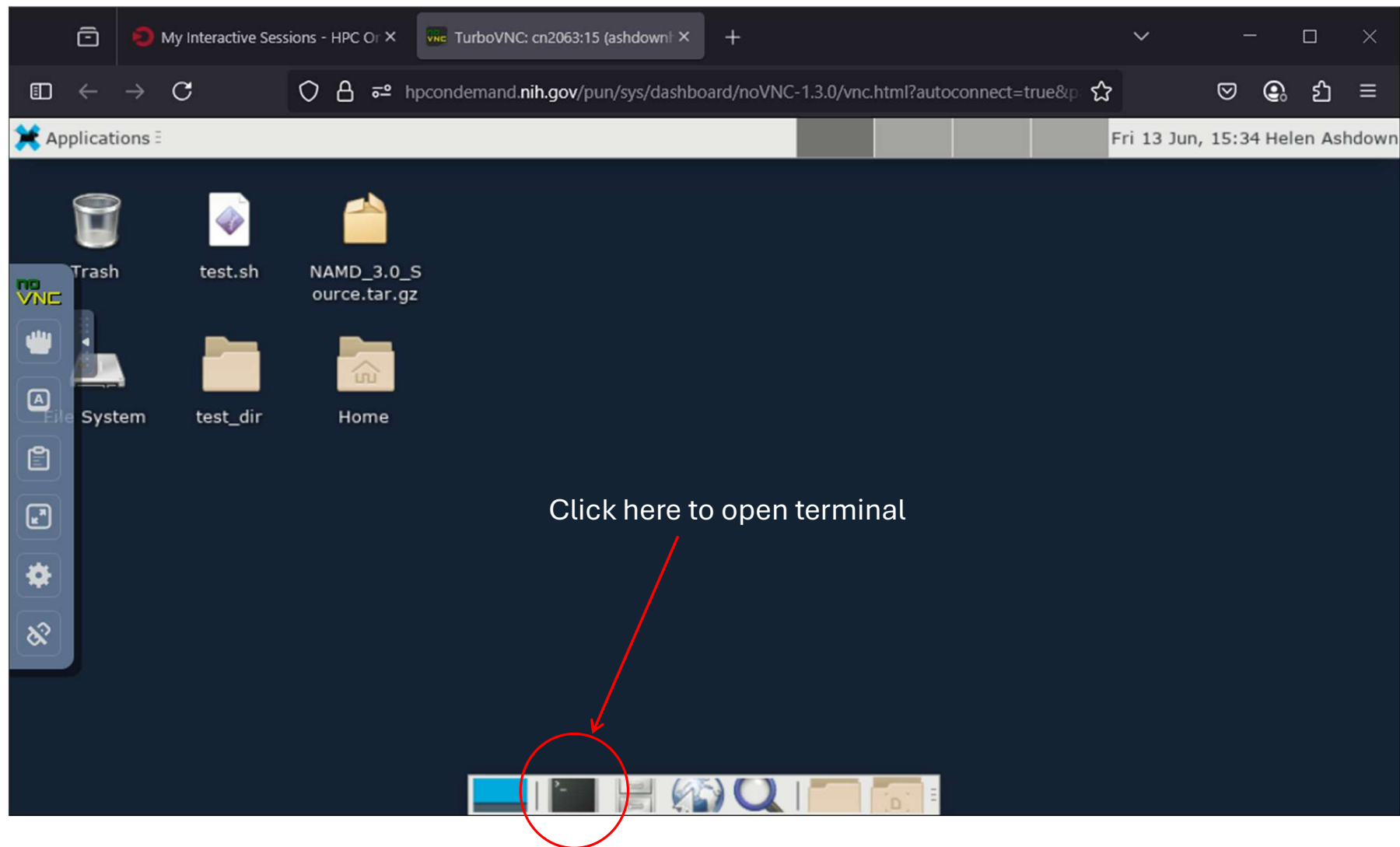


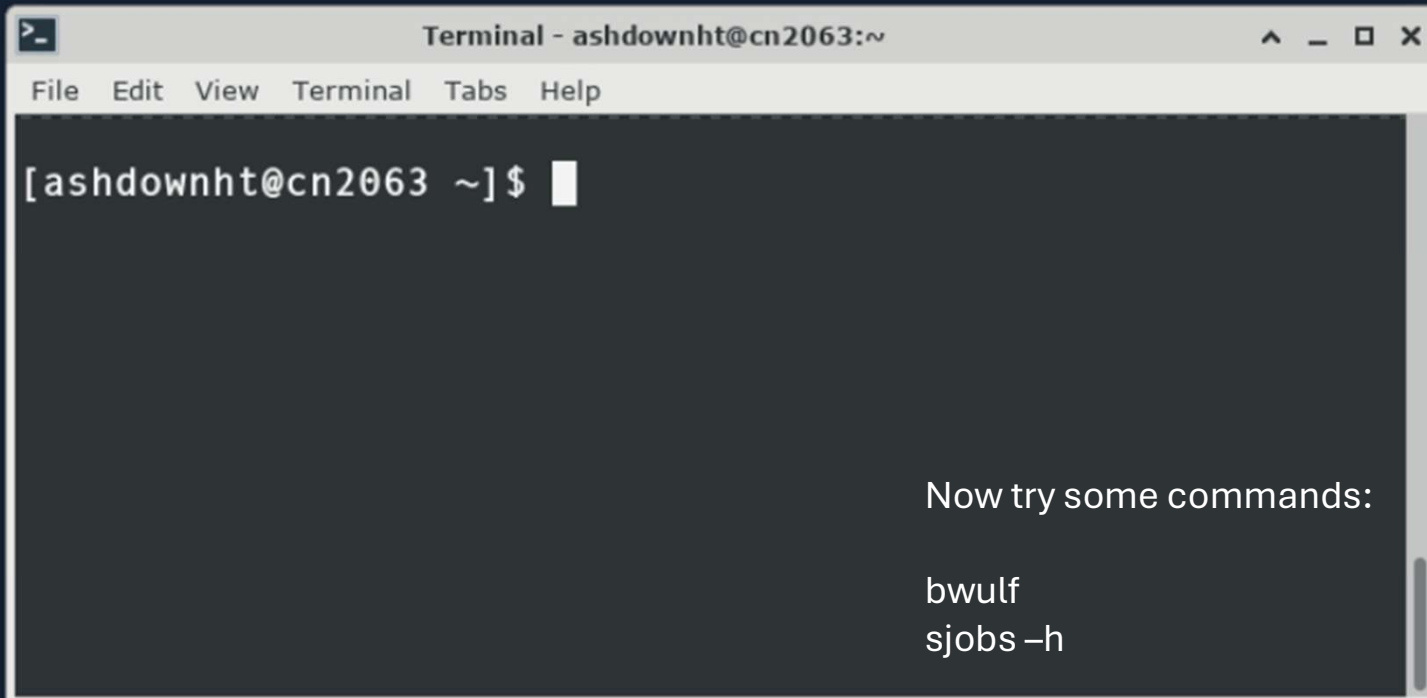
0 (low) to 9 (high)

Launch Graphical Session

now it's ready to run!

View Only (Share-able Link)





Transfer files to Biowulf

- Large data volumes: **globus**
- Medium/large: **scp/rsync/sftp** (use helix; graphical clients available)
- For convenient small transfers **mount hpcdrive**
- Transfer directly from biowulf to/from NIH Box/OneDrive: **rclone** or **globus**
- Transfer to/from cloud storage: **globus**

Questions?

- Email us!
- Staff@hpc.nih.gov

Thank you!