

Welcome to Biowulf

High performance computing @ NIH

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).

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Computational resources: The Biowulf system

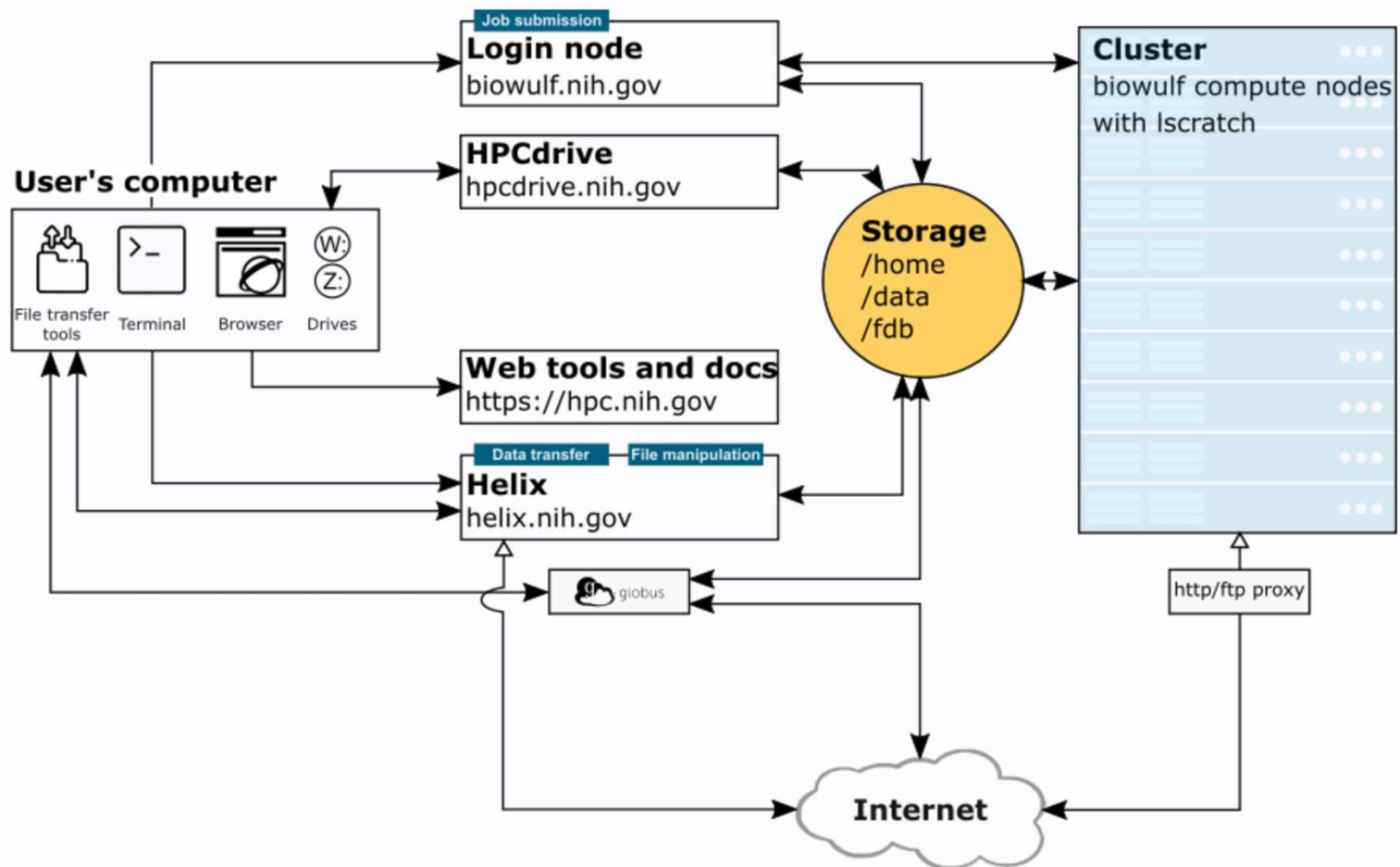
What is Biowulf?



Where is
Biowulf?



Architecture

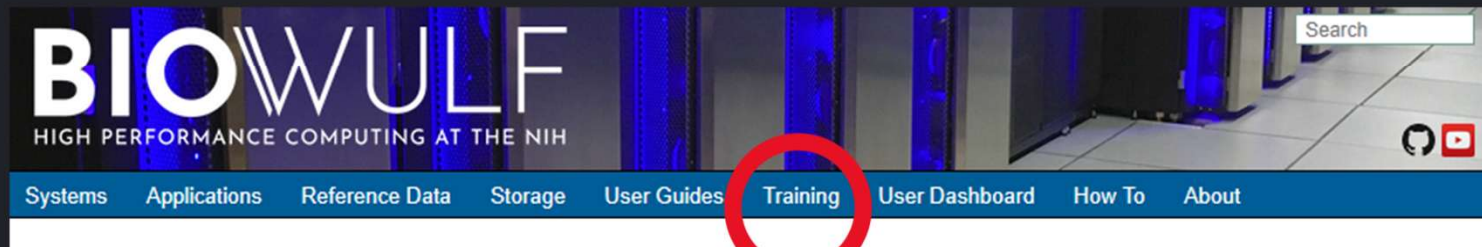


Software

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>



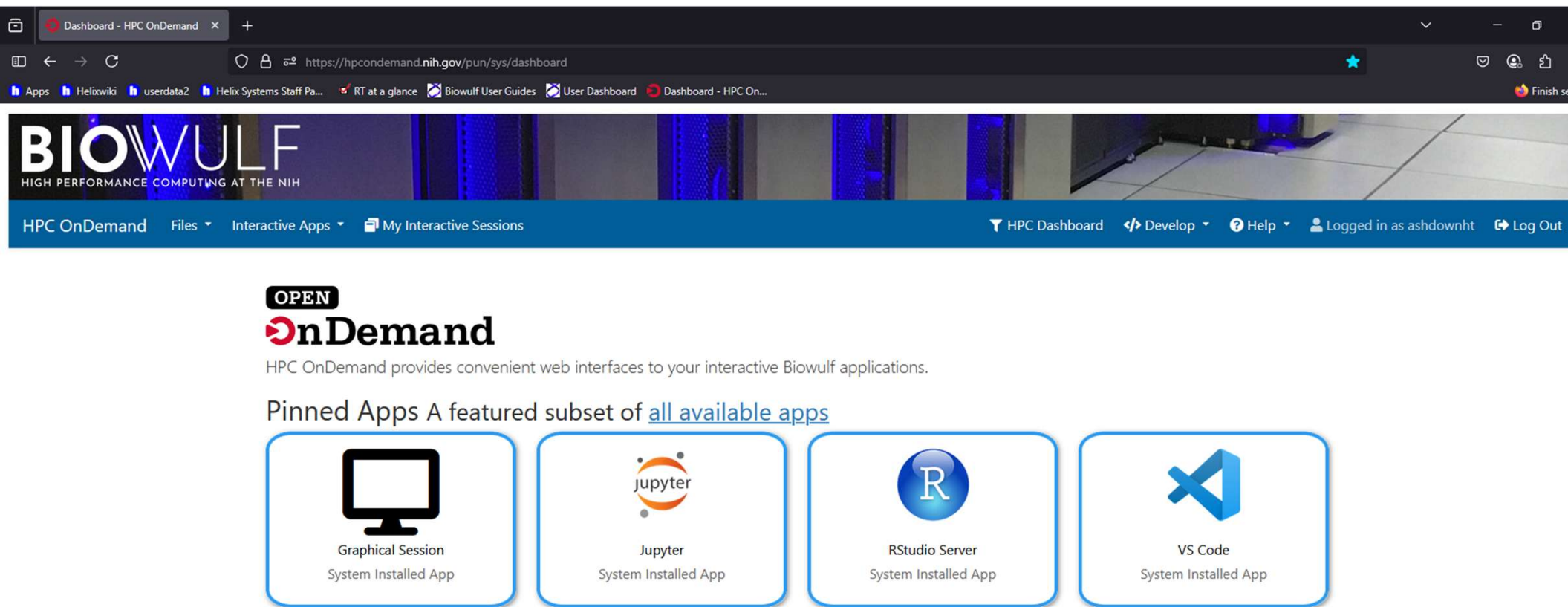
Outreach

- Monthly *Zoom-in* consult
- Meeting with individual groups or 1:1
- 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*

Open On Demand







The screenshot shows a web browser window with the URL <https://hpcondemand.nih.gov/pun/sys/dashboard>. The browser's address bar and tabs are visible at the top. Below the browser window is a banner for **BIOWULF** with the tagline "HIGH PERFORMANCE COMPUTING AT THE NIH". A navigation bar below the banner contains links for "HPC OnDemand", "Files", "Interactive Apps", "My Interactive Sessions", "HPC Dashboard", "Develop", "Help", and a user login status "Logged in as ashdownht" with a "Log Out" button.

OPEN
OnDemand

HPC OnDemand provides convenient web interfaces to your interactive Biowulf applications.

Pinned Apps A featured subset of [all available apps](#)

Icon	App Name	Status
	Graphical Session	System Installed App
	Jupyter	System Installed App
	RStudio Server	System Installed App
	VS Code	System Installed App

Interactive Apps

Desktops

 Graphical Session

GUIs

 IGV


 MATLAB

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 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

* The Graphical Session session data for this session can be accessed under the [data root directory](#).

Session was successfully created.



[Home](#) / [My Interactive Sessions](#)


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Shell

 sinteractive

Graphical Session (54570166)

Queued

Created at: 2025-04-21 11:59:35 EDT

 Cancel

Time Requested: 168 hours

Session ID: 2e9b308a-509f-4657-bba1-4b9284bcf541

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

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!