



Research Computing Club Presents

# Hyak Training Session

February 3, 2021 (3:30pm PST)
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### **Outline**

Where I assume you're at right now:

"I finished the steps to getting access\* to Hyak, but don't really know what to do now. How do I get up and running with the computing I want to do?"

### I. Hyak overview

- A. Hyak architecture
- B. Logging on to Hyak

### **II. Navigating Hyak**

- A. Basic commands
- B. Important locations
- C. Transferring files

#### III. Slurm

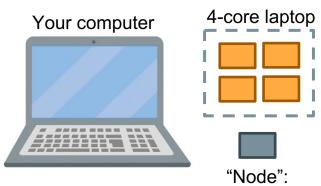
- A. Running a job
- B. Commands
- C. Modules
- D. Interactivity

#### IV. Other resources

- A. Topics outside of this tutorial
- B. Places to get help

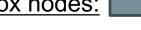
<sup>\*</sup> https://depts.washington.edu/uwrcc/getting-started-2/getting-started/

## Your PC vs. Hyak



Bundle of computing cores

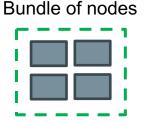
### Mox nodes:



- 28 cores
- 128 GB RAM
- 92 regular nodes stf partition

*parallel* computing

Hyak is a "condominium" supercomputing cluster:



- Research groups own nodes in <u>partitions</u>.
  - There's one partition for all tuition-paying students:
  - Student Technology Fee "stf"
- In addition to our partitions, groups have access to the build and ckpt partitions
- ~10,000 cores in total
  - A typical laptop might have 4-8 cores (CPUs)

One cluster for right now: "mox" (current), soon "klone" (soft-launches this quarter) An old cluster, "ikt", was just retired and is no longer usable

## Accessing Nodes - Hyak "Architecture"

- All nodes share the same filesystem (except /tmp)
- Different "kinds" of nodes have different purposes
  - Don't "clog up" organizational nodes

#### Hyak / Mox

on your screen, but a separate computer





login via ssh command (next slide)



Login Nodes (Shared space)

for navigation, not calculation

- Transfer files to/from Mox
- Submit work
   to other nodes

#### **Build Nodes**

- For compiling <u>new</u> software
- Can access the internet (!)
- Not allowed to use whole node

via Slurm

#### **Computing Nodes**

- High performance, lots of nodes
- Takes batch submission
- Interactive optional
- Actual work is done here

## Logging on to Hyak



<u>Terminal</u> – "command line" Easily accessible on Mac/Linux

```
● ● ♠ home — -bash — 43×7

Last login: Mon Oct 26 13:03:34 on ttys004
(base) Jesses-MacBook-Pro:~ home$
```

"Secure Shell" ssh command Enables connection to remote machine

```
[(base) Jesses-MacBook-Pro:~ home$ ssh -X prelj@mox.hyak.uw.edu]
Password: ₪
```

ssh <uwnetid>@mox.hyak.uw.edu



Two-factor authentication required (Through UW-IT)

#### You're in!

This login node is meant for interacting with the job scheduler and transferring data to and from Hyak. Please work by requesting an interactive session on (or submitting batch jobs to) compute nodes.

Visit the Hyak user wiki for more details: http://wiki.hyak.uw.edu/Hyak+mox+Overview

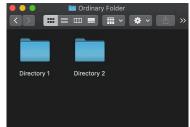
Questions? E-mail help@uw.edu with "hyak" in the subject.

Run "scontrol show res" to see any reservations in place that will prevent your jobs from running with a "(ReqNodeNotAvail,\*" error.

(base) [prelj@mox1 ~]\$

- Notice you are defaulted to the login node
- Jobs are not run here

"Graphical user interface" (GUI)



Navigate via command line

### What if I'm on Windows?

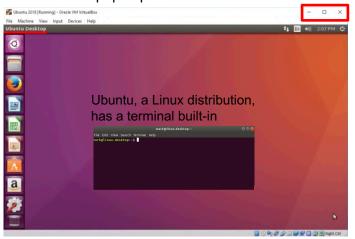
You'll need a terminal somehow, and Windows does not provide a good one by default



My preferred route: "Virtual Machine" (VM)
Sets up a mini environment that emulates a different operating system
Lets your Windows machine have some non-Windows capabilities (like terminal)

"Oracle" is one example of a VM

New window pops up within Windows to interface with Ubuntu



Other options for Windows:

- PuTTY (Terminal emulator)
- CygWin (Runtime environment)
- GitBash
- Windows Subsytem for Linux
- WinSCP (just for transfering files)
- cmder
- xshell
- ... and probably more!

How you get a terminal does not matter, they are all effectively the same

#### More help:

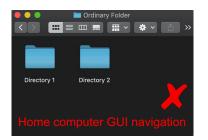
http://wiki.cac.washington.edu/display/hyakusers/Logging+In



## I'm in

... Now what?

## **Exploring Hyak**



#### **Essential First Actions:**

- mkdir
  - "Make directory"
  - Create a place to put your files
- vim, emacs, nano (etc.)
  - Command line text editors
  - These can be a pain, but are important!

Each research group has a folder in gscratch

#### Hyak file systems through command line



Where in the computer am I? pwd - "Print working (current) directory"

[(base) [prelj@mox1 ~]\$ pwd /usr/lusers/prelj

My home directory (see next slide)

What folders and files are here?

1s - "List" files in current directory (folder)

[(base) [prelj@mox1 ~]\$ ls | d g\_perf intel opt

Let's go to where everybody stores files cd - "Change directory"

[(base) [prelj@mox1 ~]\$ cd /gscratch (base) [prelj@mox1 gscratch]\$

## Important locations on Hyak (get there with cd)

- /gscratch/stf
  - Main work location for stf users
  - Any files untouched for >30 days will be auto-deleted!!
- // /usr/lusers/<username>
  - Home directory "~", you are put here by default
  - Only 10 GB of storage per user
  - /tmp
    - Node local storage (separate from shared filesystem)
- /sw
  - All software installs
- /sw/contrib
  - User installed software
- /sw/modules-1.775/modulefiles/contrib
  - User added modulefiles



Where pre-installed programs (and their supporting files) are housed

You will seldom need to go here, as programs can be accessed more easily (in a way we will soon see)

## Basic shell (bash) commands: Try them out!

### File system manipulation:

- ls "List" files in current directory (folder)
  - cd
  - "Change directory"
  - pwd "Print working (current) directory"
- mkdir
  - "Make directory"
- ΜV
  - Move (rename) file or directory
- - Ср "Copy" files and/or directories (-r)
- rm
  - "Remove" files and/or directories (-r)

### File editing and compression:

- nano
  - Edit files
  - Other editors: vim, emacs, etc.
  - tar
  - Compress for a "tape archive"
  - zip (and unzip)
    - Compress via zip algorithm
      - Windows friendly

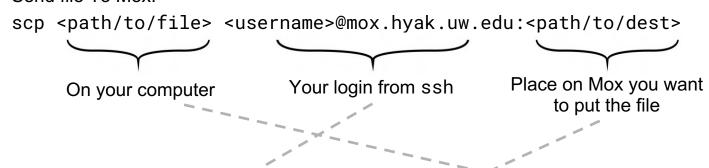
### Many, many more

- - chmod man
    - find curl
  - top grep
  - sed

## Transferring files

### scp - Secure Copy

Send file To Mox:



o Get file From Mox:
 scp <username>@mox.hyak.uw.edu:<path/to/file> <path/to/dest>

Flag –r needed to copy whole folder at once An alternative copier for synchronizing directories is scopy

#### Lolo:

- Magnetic tape archive (lolo archive)
- For long term storage only store compressed large files!
- STF location: /archive/hyak/stf
- Transfer files the same as between local and Hyak

### Running Your First Job

Real computing jobs are passed to Slurm

- Ensures fair share between users
- Run interactive or batch jobs
- Allows for running on the ckpt queue
  - (more on this later)

Some information is needed during job setup:

<u>Partition</u>: whose CPUs/GPUs are we using? (we'll use stf)

Allocation: which bank account pays for these? (also stf)

Locations: where to write/read files to/from

Resources: how many CPUs/GPUs are needed, and for how long?

Modules: which programs should be loaded to use?



https://slurm.schedmd.com/

"Job Scheduler"

Manages multi-node jobs and communication protocols

Packaged into a "Slurm script"

## Anatomy of a slurm script (written in "bash")

In a text file called "submit.slurm" #!/bin/bash #SBATCH --job-name=test\_python ## Partition and Allocation module load contrib/anaconda/anaconda4.4.0 — ## Scripts to be executed here python test\_run.py -

Any line that begins with ## is a comment and is not read Each line that begins with #SLURM specifies info for slurm The #SLURM options can be provided in any order

- Name is optional
- Use stf nodes from the stf budget
- Request (1) node
- Time Hours : Minutes : Seconds
- A single node has 28 cores and 128 GB memory
- This dummy job is not parallel, so only (1) core
- Directory "." is current location to read/write files (the same place submit.slurm is saved)
- Load in a pre-installed python package
- The real run command

To execute this job,

sbatch submit.slurm

### Then We Wait

- sbatch <script>
  - Submits a script for non-interactive use
  - Used this to submit a job on previous slide

Want to check the status?

- squeue
  - Flag –u <uwnetid> for only your jobs
  - Specify –p or –A for whole queue

What it looks like to check queue:

```
[(base) [prelj@mox1 move]$ squeue -p stf
             JOBID PARTITION
                                  NAME
                                           USER ST
                                                                NODES NODELIST(REASON)
            417044
                          stf test_pyt
                                          prelj CG
                                                         0:02
                                                                    1 n2282
            416180
                                                         0:00
                                                                    1 (Dependency)
                                Other peoples'
                                                                    1 (Dependency)
            416186
                                                          0:00
                                job names and
                                                                   10 n[2143,2151,2166,2168,2171-2172,
            413137
                                                 R 1-04:27:53
                          stf
                                                                    6 n[2140,2165,2275,2277,2292,2298]
            415317
                                                     15:51:35
                                                                    6 n[2266,2269-2270,2285,2290,2308]
            414068
                          stf
                                                     22:51:51
                                   censored)
            413181
                                                 R 1-04:04:16
                                                                    6 n[2139,2144,2146,2279,2284,2312]
```

Something wrong? / Taking too long?

- scancel <jobid>
  - Cancels an unfinished job
  - Can only cancel your own

JOBID is used to refer to specific jobs NODELIST has ID #s for individual nodes being used ST column is status

R – Running (currently active)

PD – Pending (in queue)

CG – Completing (in process of termination)

Always check your output!

### Slurm: Commands

- sbatch <script>
  - Submits a script for non-interactive use
- squeue
  - Get status of jobs in batch queue
- scancel <jobid>
  - Cancels an unfinished job

I use these most often

- srun
  - Submits job for interactive use or initiate job steps inside batch script
  - (More on interactive jobs in a minute)
- sinfo
  - Get state of partitions and nodes (is the system operational)
- sacct
  - Gets accounting information about active and completed jobs

### Slurm docs and man <slurm-command> are very useful!

("man" for manual)

## Running Jobs Interactively (command line, not script)

srun -p stf -A stf --ntasks=8 --mem=10G --time=0:10:00 --pty bash -1

- Partition
- Account
- Number of processes (\*)
- Amount of RAM
- Time
- Command

Before running interactive job command

```
[(base) [prelj@mox1 jesse]$
```

After running interactive job command [(base) [prelj@n2232 jesse]\$

 Interactive nodes are computing nodes. You can submit jobs to other nodes from interactive nodes.

- Much of the same specifications as submit.slurm
- --pty bash -1 signifies interactive
- Now you have command line control while accessing a compute node

Be aware of difference between:

- Number of tasks (processes, MPI)
  - --ntasks (-n)
  - --ntasks-per-node
- Number of cpus per task (threads, OpenMP)
  - --cpus-per-task (-c)

https://slurm.schedmd.com/srun.html
man srun

### Loading software: the modules system

- module avail
  - Show all available modules
- module load <module>
- module unload <module>
  - (Un)load a given module
  - Provide full module name
- module list
  - List loaded modules
- module purge
  - Unload all modules
- module help
  - Print help with commands

#### Running module avail

```
(base) [preli@mox1 jesse]$ module avail
                                                 /sw/modules-1.775/modulefiles
anaconda2 4.3.1
                                                              contrib/multiz/20090121
anaconda2 5.3
                                                              contrib/multiz/20190527
anaconda3 4.3.1
                                                              contrib/mummer/3.23
anaconda3_5.3
                                                              contrib/mummer/4.0.0b2
ansys_18
                                                              contrib/muscle/3.8.31
cmake/3.11.2
                                                             contrib/mysql/8.0.11
cmake_3.8
                                                              contrib/NAMD2019/namd2
contrib/3ddna/170123
                                                             contrib/nauty26r11/nauty26r11
contrib/9.0
                                                              contrib/ncbi-blast/2.7.1
contrib/abagus/2020
                                                             contrib/ncbi-vdb/2.9.0
contrib/abyss/2.0.3
                                                              contrib/nektar
contrib/adapter-removal/2.1.7
                                                             contrib/newton-x
contrib/admixtools/1.0.1
                                                             contrib/newtonX
contrib/admixture/1.3.0
                                                             contrib/ngs/2.9.0
contrib/anaconda-2019.03
                                                             contrib/ngsRelate/1.0
contrib/anaconda/2-5.0.1
                                                             contrib/ngsRelate/2.0
                                                             contrib/nvidia_toolkit/9.0
contrib/anaconda/3-4.4.0
contrib/anaconda/3-5.3.0
                                                             contrib/nvidia toolkit/10.0
contrib/anaconda/anaconda4.4.0
                                                              contrib/NWChem/NWChem
```

... and more

- > 400 modules available on Hyak right now! Useful programs you'd use on your own computer, i.e.
- Python/Anaconda, Gromacs, NAMD, R, Mathematica, Matlab, Gaussian, compilers and more

Parallel computing tools

CUDA, IMPI, etc.

#### Advanced user's note:

The modules system works by keeping track of and modifying environment variables (e.g. PATH, LD\_LIBRARY\_PATH, CPATH, etc.) https://modules.readthedocs.io/en/latest/

### Checkpoint queue – special case

The checkpoint queue allows any user to run on other groups' unused nodes!

- Partition: ckpt
- Account: <group>-ckpt (stf-ckpt)
- Jobs can be interrupted at any time
- Jobs will be interrupted after 4 contiguous hours
- Jobs will be resubmitted after interruption (if under total requested time limit)
- Your code must be checkpointed to take advantage of this
  - Save a binary file containing state of some objects, restart from logs, etc.
  - Your script should also account for any checkpointing that is done

## Topics not covered

- How to install new software
  - Installation and build systems
  - Writing your own modulefiles
  - What software would make good examples?
- How to parallelize your own code
  - Different paradigms for parallelism
  - Data locality and contiguity
  - GPU parallelization
  - Parallel patterns
  - Some programs have parallelization options built-in
- Anything with the cloud (This is the Hyak training session!)
- General architecture of HPC systems
  - Interconnectivity and node locality
  - Physical infrastructure



### Where to get help

- Documentation (man or webpages)
- Hyak wiki: <a href="https://wiki.cac.washington.edu/display/hyakusers/WIKI+for+Hyak+users">https://wiki.cac.washington.edu/display/hyakusers/WIKI+for+Hyak+users</a>
- Slack channel: https://uw-rcc.slack.com/
- Website: https://depts.washington.edu/uwrcc/
- Emails: <a href="mailto:hpcc@uw.edu">hpcc@uw.edu</a> or <a href="mailto:uwrcc@uw.edu">uwrcc@uw.edu</a>
- Office hours: Fridays from 1-3 pm

# Happy computing!

