

Intro to Monsoon and Slurm

2026-09-25 presentation with Jason Buechler

These slides:

<https://rcdata.nau.edu/hpcpub/workshops/odintro.pdf>



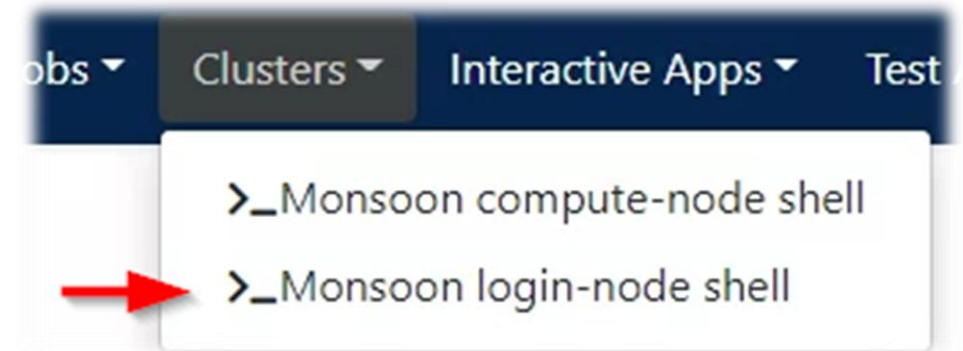
NAU NORTHERN ARIZONA UNIVERSITY

Get logged in!



From a computer:

- Connect to the NAU VPN *if off-campus!*
 - Info: <https://in.nau.edu/its/remote-services>
- Open any web browser
- Login to <http://ondemand.hpc.nau.edu>
 - Standard 'abc123' Louie ID & password
- Optional: try out the command-line
 - Clusters > Monsoon login-node shell



These slides:

<https://rcdata.nau.edu/hpcpub/workshops/odintro.pdf>

- HIT RECORD! 🎥

Introductions



- Introduce yourself
 - Name
 - Department / Group
 - What project(s) do you plan to use monsoon for?
 - Linux or Unix experience
 - Previous HPC experience?

I am Jason Buechler

- Aero, Mech Engineering
fluid-thermodynamics, renewable energy, & grid-engineering
- With Monsoon since 2019
- Linux/supercomputing since 2000

*Don't worry: few researchers
have prior linux/HPC experience!*

Agenda

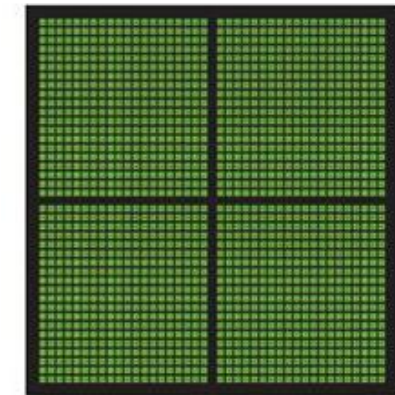
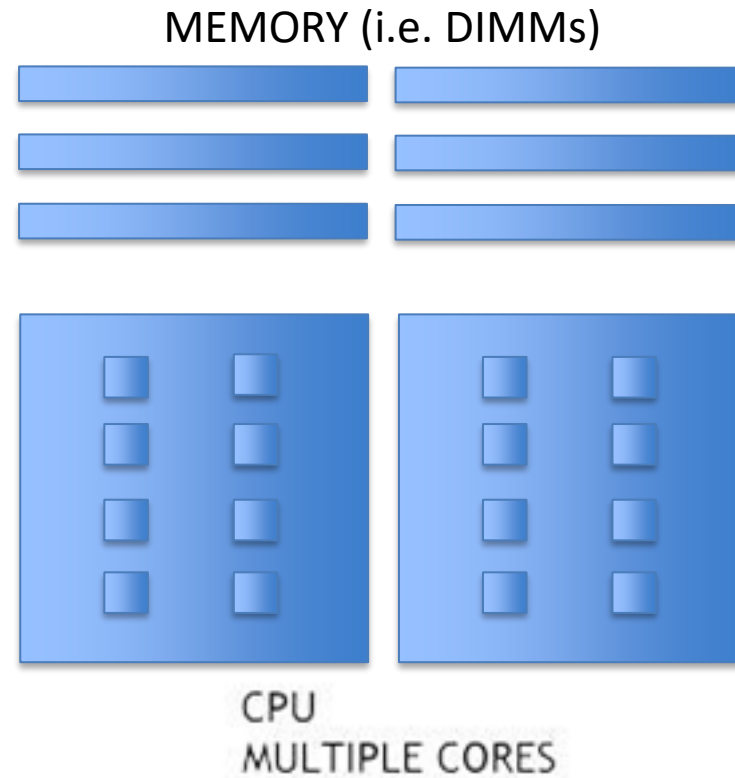


- (High-Performance-Computing) Cluster education
 - *What is a cluster, exactly?*
 - Job-queues, scheduling, and resource management
- Monsoon Cluster orientation
 - *How do I use this cluster?*
 - Resource limits
 - Exercises
 - Question and answer

Cluster (of) resources

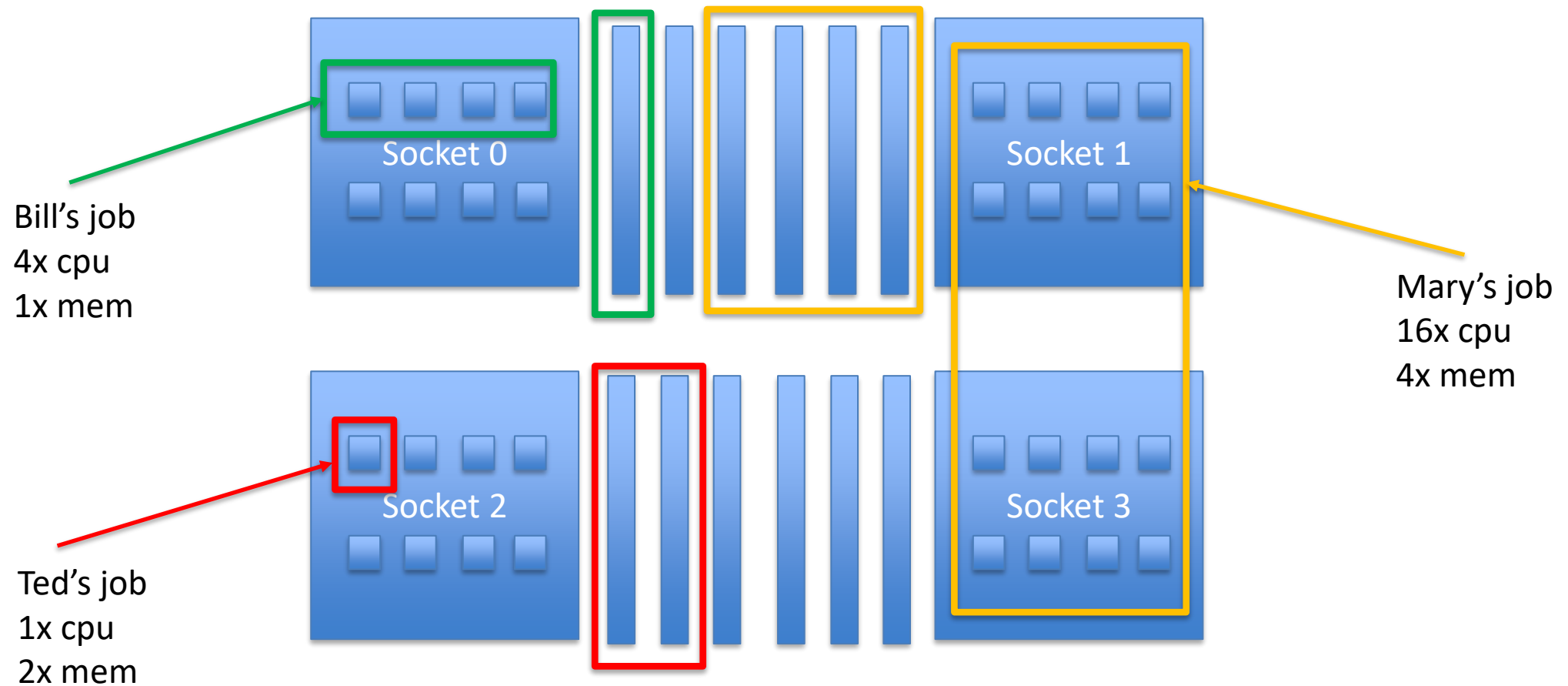


- Node itself
 - Memory
 - CPU's
 - GPU's
- Networking
- Licenses

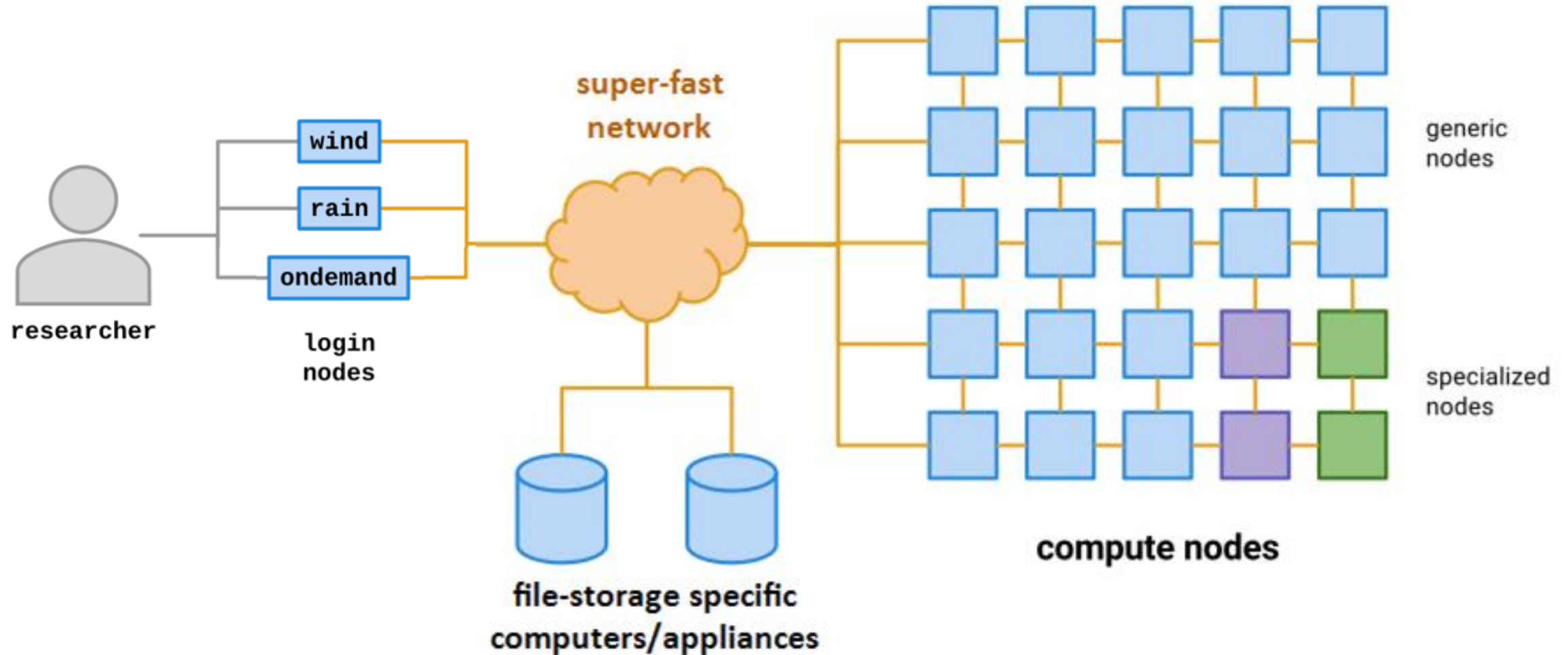


GPU
THOUSANDS OF CORES

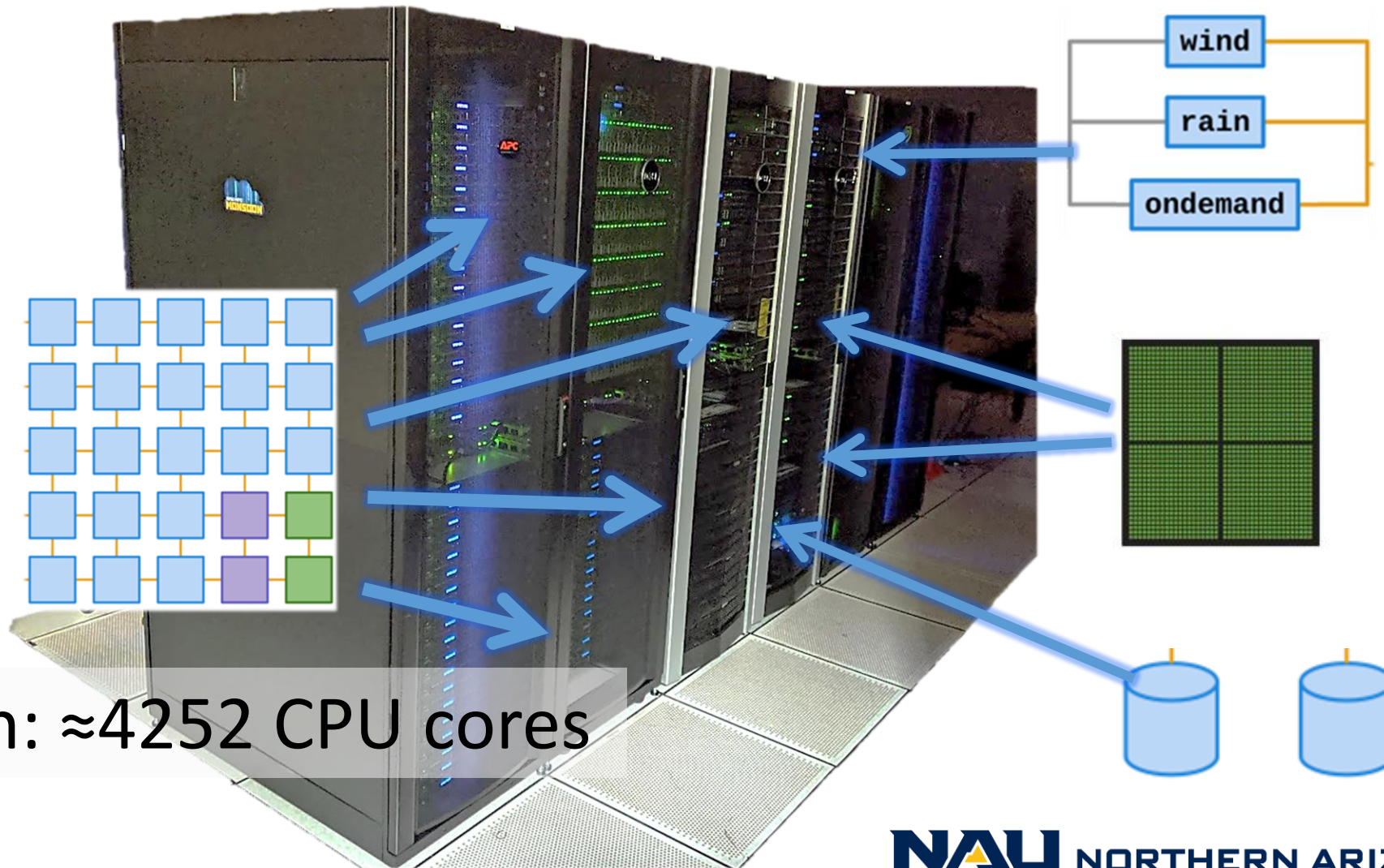
Inside a (single) compute-node



Cluster = Login-nodes + Compute-nodes + More



Monsoon



Monsoon: ≈ 4252 CPU cores

Largest Cluster!



LineShine:
13.8M cores



Small Cluster!



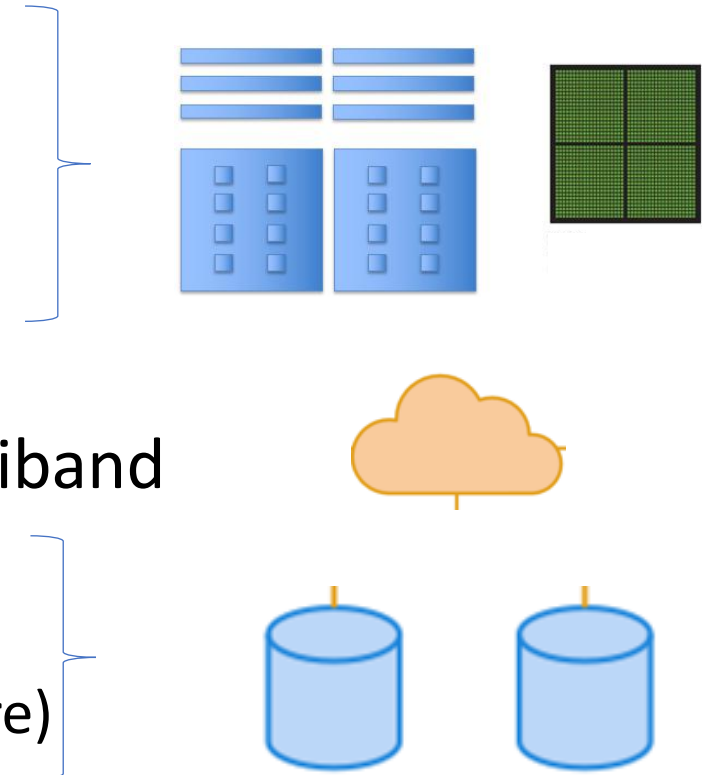
2 cores? 2 jobs!

Monsoon Today

(from <https://in.nau.edu/arc/details>)



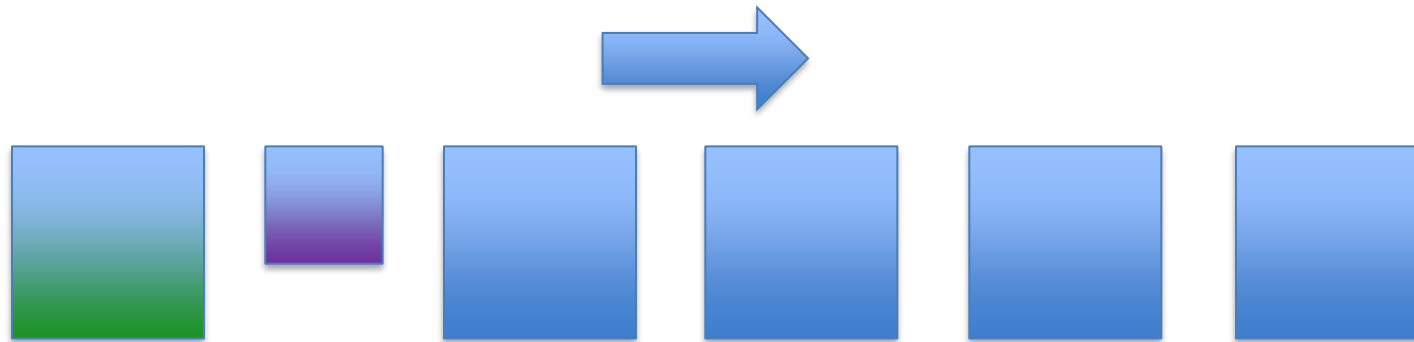
- The Monsoon cluster is a resource available to the NAU research enterprise
- 109 compute-nodes (cn1 ~ cn109)
 - 27TB memory - 128GB/node min, 2TB max
 - 28 GPUs (P100, V100, A100, H200, RTX6000)
 - 4252 cores (Intel + AMD)
- Red Hat Enterprise Linux 10.2
- High speed interconnect: FDR, and HDR Infiniband
- Storage
 - 1PB *scratch* high-speed storage (Lustre)
 - 1.6PB *home,proj* storage (proprietary object-store)



What is a queue?



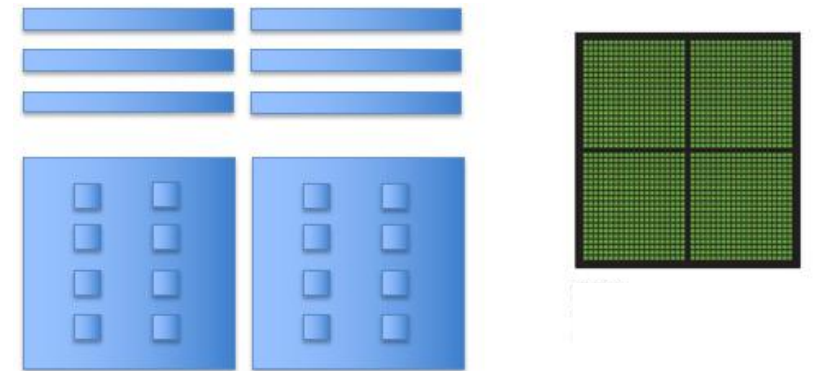
- Normally thought of as a line, FIFO (Line at Starbucks)
- Queues on a cluster can be as basic as a FIFO, or more advanced with dynamic priorities taking into consideration **many factors**
- A ***scheduler*** needs to know what resources are available on the cluster in order to make accurate scheduling decisions



Resource Manager



- Resource availability changes by the second!
- Assignment of work on a cluster is carried out most efficiently with the **scheduler** and **resource manager** working together
- Monitoring resource availability and health
 - Accounting of resources
 - Allocation of resources
 - Execution of resources



Slurm ... yummm



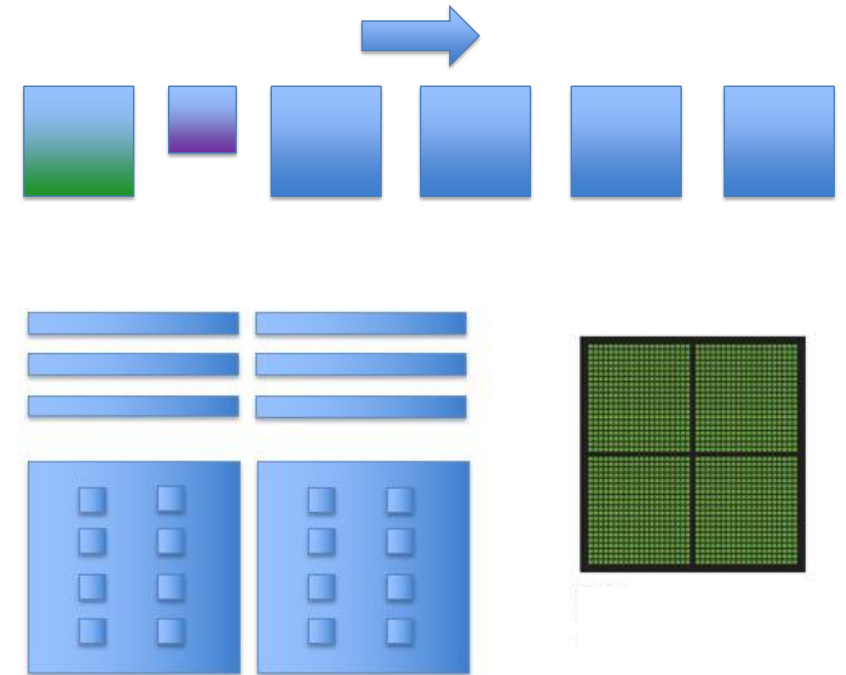
- Slurm (*Simple* Linux Utility for Resource Management)
- Excellent resource manager and scheduler
- Precise control over resource requests
- Developed at LLNL, continued by SchedMD
- Used everywhere from small clusters to the largest clusters:
 - LineShine (#1), 13.8M cores, 2.2 PF/s, 42.2 MW - China
 - El Capitan (#2), 11.3M cores, 1.8 PF/s, 29.7 MW - USA



Our Scheduling Goals



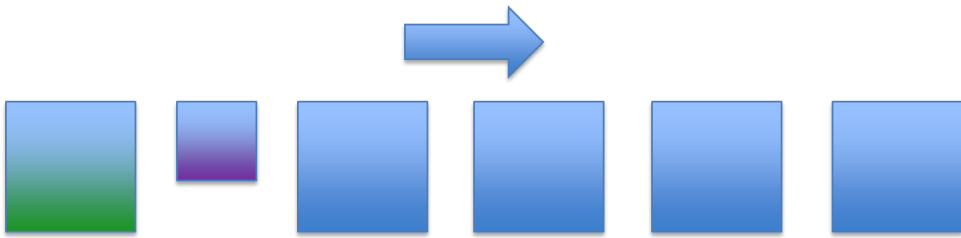
- Optimize quantity of work
- Optimize usage of resources
- Service all users and projects justly
- Make scheduling decisions transparent



Monsoon scheduling



Monsoon utilizes a combination of scheduling methods to optimize cluster productivity and resource usage:



- FIFO
 - Simply first in first out
- Backfill
 - Runs smaller jobs with lower resource requirements while larger jobs wait for higher resource requirements to be available
- Fairshare
 - Prioritizes jobs based on multiple factors such as users' recent resource consumption
- Additional factors
 - Including job-specific and user-specific

Factors attributing to priority

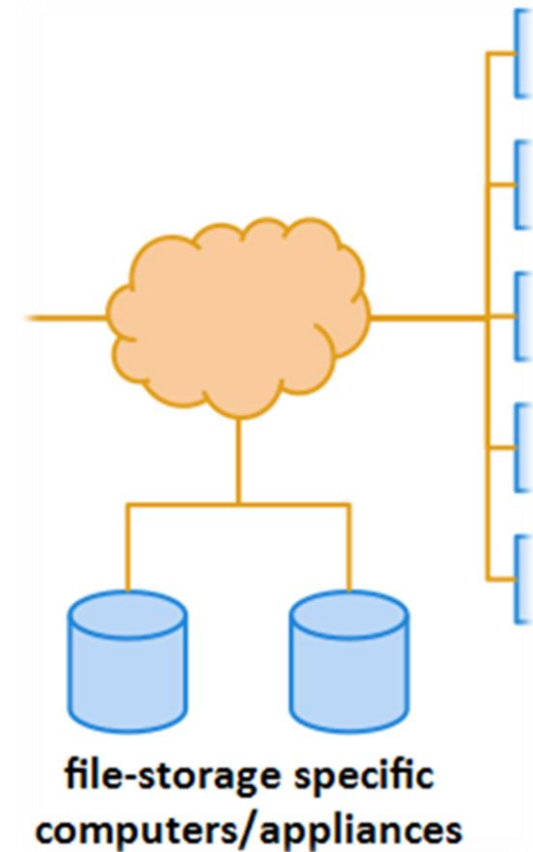


- Fairshare (predominant factor)
 - Priority points determined on users' recent resource usage
 - Decay half life over 12 hours
- Age – how long has the job sat pending
- Job size - the number of nodes/cpus a job is requesting
- QOS (Quality of Service)
 - Some QOS have higher priority than others, for instance: debug

Storage



- /home – 20 GB quota
 - Keep your scripts and executables here
 - Backed up to tape
 - Snapshotted twice a day: /home/.snapshot
 - Please do not write job output (logs, results) here!!
 - Run the command “getquotas” now
- /scratch – 15000 GB quota (also 2M files quota)
 - 1PB total space, 30 day retention
 - Very fast storage, capable of 20GB/sec
 - Checkpoints, logs
 - Keep all temp/intermediate data here
 - Should be your default location to perform input/output

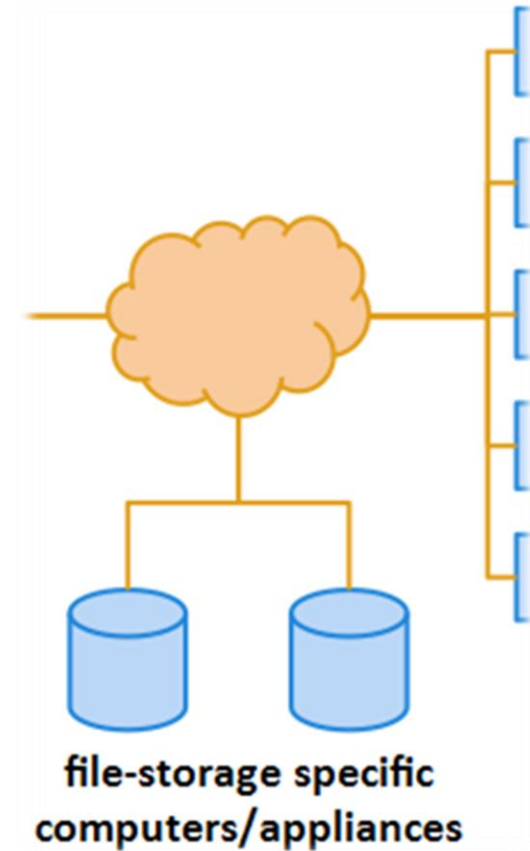


Storage



- /projects – 1.6 PB
 - Long-term storage project shares
 - 5TB is assigned to faculty member for group to share
 - \$48/TB/year above 5TB
 - Snapshots available
 - Option to make datasets available to the web
- /common
 - Cluster support share

NOTE: the only storage area on monsoon backed-up* is your /home area (due to size limitations)



Data Workflow



1. Keep scripts and executables in /home
2. Write logs/temp/intermediate data to /scratch/<uid>
3. Copy data to /projects/<group_project>, for group storage and reference in other projects
4. Cleanup /scratch files

** Remember, /scratch is a scratch filesystem, used for high-speed temporary and intermediate data

Remote storage access



Quick transfers via web
<10 GB, <100 files

Ondemand's file-browser, or Globus*

Very large/numerous files

Globus: <https://in.nau.edu/arc/globus>

General purpose

scp: 100's of GBs, 1000's of files

smb: 10's of GBs, 100's of files

SCP/SMB: <https://in.nau.edu/arc/file-management>

scp protocol / shell-command

- GUI apps: **WinSCP** on windows, **Fetch** for mac
- `scp <files> <nauid>@<dtn>:/scratch/<nauid>/`

smb / samba / "shared drive"

- Windows: `\\shares.hpc.nau.edu\cirrus`
- Mac: `smb://shares.hpc.nau.edu/cirrus`

Data transfer nodes



We have dedicated, specialized login-nodes for transferring data



These hosts' names are

`dtn1.hpc.nau.edu` & `dtn2.hpc.nau.edu`



Use dtn1/dtn2 for moving large datasets around on monsoon, and to/from the internet

Enterprise Groups



- NAU has a resource called Enterprise groups. Enterprise Groups are utilized to manage who has access to specific folders and files on the cluster
- They are available to your group on the cluster if you'd like to manage access to your data
- What groups are you in? Run the command "groups", or "id"
- More info in our FAQs <https://in.nau.edu/arc/faqs>
 - "Creating and Managing an Enterprise Group"

(Software) Modules



- Software environment management handled by the *modules* package management system. This is available through the Command Line Interface (cli)
- `module avail` ...*what modules are available*
- `module load <module name>` ...*load a package module*
- `module list` ...*modules currently loaded*

Modules on Monsoon



What's already available?

module -d avail

- Anaconda Python
- R
- Matlab
- Qiime2
- Many bioinformatics programs

```
ricky@wind:~  
[ricky@wind ~]$ module --default avail  
----- Monsoon Modules (MPI) -----  
amber/22  
cdo/2.1.0  
cp2k/2024.1  
elpa/2021.11.001  
exabayes/1.5.1-v3  
fftw/3.3.10  
hdf5/1.12.2-v2  
lammps/20240829.1-gpu-mc  
madingley/2020-04-01  
mrbayes/3.2.7a-v2  
ncl/6.6.2  
nco/5.3.3  
netcdf-c/4.9.0-v3  
netcdf-cxx4/4.3.1  
netcdf-fortran/4.5.4  
netlib-scalapack/2.2.0  
nwchem/7.0.2  
osu-micro-benchmarks/7  
----- Monsoon Modules (Core) -----  
R/4.5.1  
alsa-lib/1.2.3.2  
amd-blis/3.0  
amd-libflame/3.0  
anaconda2/2019.10  
googletest/1.12.1-yjsk  
gperf/3.1  
grass/7.8.2  
gsl/2.6  
guppy-cpu/5.0.11c  
ninja/1.11.1-7zaz  
node/v22.18.0  
numactl/2.0.14  
oc2/2.0  
ollama/0.9.5
```

Requesting Software



- You can install quite a bit of R, and anaconda/python software yourself!
- For R
 - `module load R`
 - `R`
 - `install.package(c(package))`
- For python/anaconda/miniforge3
 - `module load anaconda3`
 - `conda create -n myenv`
 - `conda activate myenv`
 - `conda install package`
- You are also welcome to compile your own programs
- If you'd like our help installing a piece of software, please have your research sponsor request it

More info:

<https://in.nau.edu/arc/installing-software-packages>

MPI



Quick PSA for advanced users

- Message Passing Interface for parallel computing
- Open MPI set as default MPI
- Example MPI job script:
 - `/common/contrib/examples/job_scripts/mpijob.sh`

Interacting with Slurm



1. What resources are needed?
 - 2 **cpus**, 12GB **memory**, for 2 **hours**?
 - You can (must!) start with an educated guess
2. What software environment is needed?
3. What steps are required? (*must prog1 run before prog2?*)
4. Can your work, or project be broken into pieces?
 - Smaller pieces can make the workload more agile
 - Is each step dependent on the last?
 - Is your software multithreaded, uses OpenMP or MPI?

Job Scripts and sbatch



- Except for limited testing and debugging, all jobs on the cluster should be run via a shell script which is typically denoted by the extension .sh on the filename
- sbatch shell scripts are composed of **three sections**:
 1. Slurm job parameters (“#SBATCH ...”)
 2. Software environment/module loading (“module load ...”)
 3. srun job-steps/cmd-statements for actual work (“srun <command>”)

Example Job script



- `#!/bin/bash`
 - `#SBATCH --job-name=test`
 - `#SBATCH --time=20:00` # shorter jobs usually start sooner
 - `#SBATCH --chdir=/scratch/NAUID` # default location of files
 - `#SBATCH --output=/scratch/NAUID/output.txt` # the job's output/errors go here
-
- *# replace this module with software-*
 - *# modules required by your jobscript*
 - `module load anaconda3/2025.06` # loads a specific anaconda-python
-
- *# example job commands: each srun command is*
 - *# a job step, so this job will have 2 steps*
 - `srun sleep 300`
 - `srun python -V`

Example Job script (in Ondemand)

A screenshot of a web browser window showing a code editor for a job script. The browser address bar shows "ondemand.hpc.nau.edu". The file path in the editor is "/home/jtb49/ondemand/data/sys/myjobs/projects/default/15/main_job.sh". A red arrow points to a "Save" button. The code is a bash script with various SBATCH directives and application commands. Blue arrows point from a callout box to specific parts of the script: one to the SBATCH directives, one to the module load command, and one to the application commands.

```
1 #!/bin/bash
2 #SBATCH --job-name=exercise1           # the name of your job
3 #SBATCH --output=/scratch/abc123/output1.txt # this is the file your output and errors go to
4 #SBATCH --time=20:00                   # 20 min, shorter time, quicker start, max run time
5 #SBATCH --chdir=/scratch/abc123       # your work directory ("pwd")
6 #SBATCH --mem=2000                     # 2000MB = 2GB of memory
7 #SBATCH --mail-type=FAIL
8
9 # load a module, for example
10 module load anaconda3
11
12 # Run your application: precede the application command with 'srun'
13 # A couple example applications...
14 srun date
15 srun python --version
16 srun sleep 30
17 srun pwd
18 srun date
19
20
```

1. Job parameters (for slurm)
2. Software environment setup
3. Job commands

Job Parameters



You want	Switches needed
More than one cpu for the job	--cpus-per-task=2 (or: -c 2)
To specify an ordering of your jobs	--dependency=afterok:job_id (or: -d job_id)
Split up the output, and errors	--output=result.txt --error=error.txt
To run your job at a particular time/day	--begin=16:00 --begin=2026-02-14T12:34:00
Add MPI tasks/ranks to your job	--ntasks=2, or -n 2
To control job failure options	--norequeue --requeue
To receive status email	--mail-type=ALL

More info:

<https://slurm.schedmd.com/sbatch.html>

Constraints and Resources



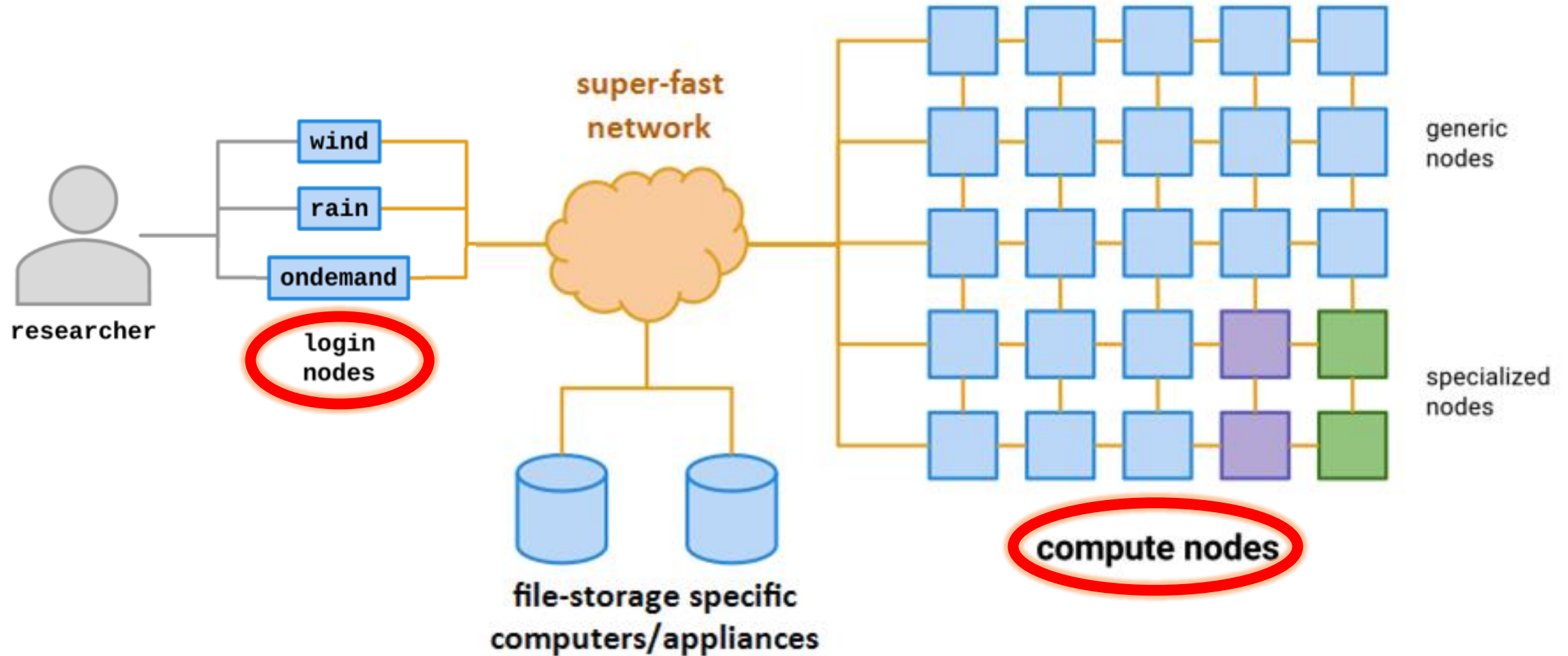
You want	Switches needed
To choose a specific node feature (e.g. avx2)	--constraint=avx2
To use a generic resources (e.g. a gpu)	--gpus=a100 , -G 1
To reserve a whole node for yourself	--exclusive
To chose a partition	--partition

More info:

<https://slurm.schedmd.com/sbatch.html>

<https://in.nau.edu/arc/gpus/>

Cluster Review



Login node vs Compute node



- When you log into “monsoon” interactively or via Ondemand you are “placed” on a (shared!) login node.
- The login node is a shared system used solely for:
 - Developing scripts
 - Transferring small data
 - Submitting work to the scheduler
 - Analyzing results
 - Debug work* less than 30 minutes in length
- The compute nodes are what make the cluster powerful!

Interacting with Monsoon



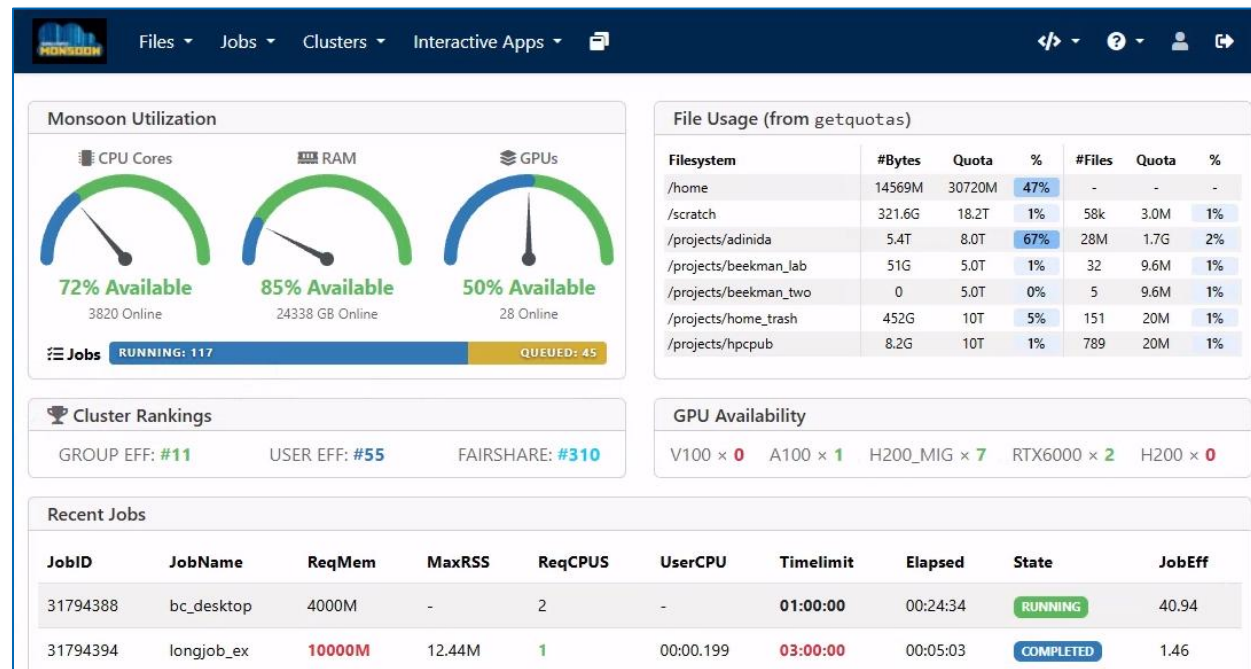
Three Methods (**must be on NAU network or NAUVPN**):

- Connect to OpenOnDemand web interface at: <https://ondemand.hpc.nau.edu>
- Via SSH protocol in a command-line shell
 - Enter “**ssh <nau-id>@<login-node>**”
 - ...within **Powershell** (Windows), or **Terminal** (Mac, Win, Linux)
 - ...using Monsoon’s login nodes:
 - monsoon.hpc.nau.edu (for research)
 - wind.hpc.nau.edu
 - ondemand.hpc.nau.edu
 - rain.hpc.nau.edu (for class work)
- Remote storage access_{__}* (files only -- no command interface)

Ondemand



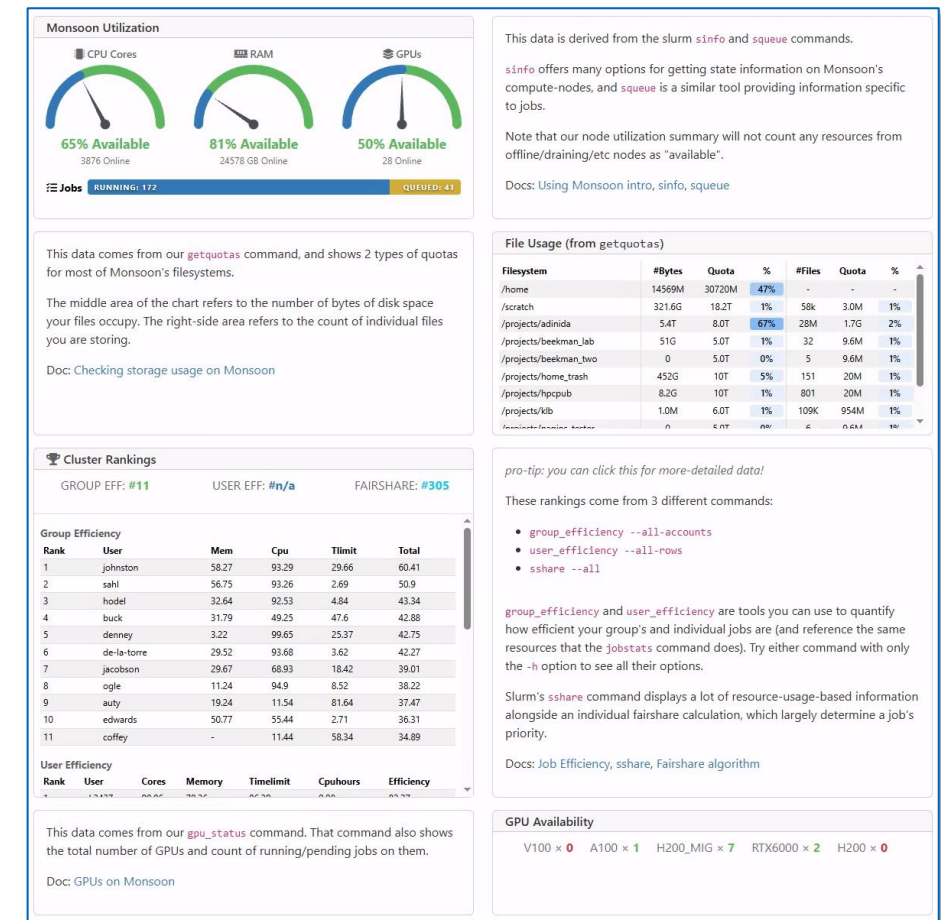
- Open Ondemand (OOD) is an interactive Graphical User Interface (gui) to the Cluster. You access it from your web browser at <https://ondemand.hpc.nau.edu>



OnDemand's Dashboard



- Metrics on Monsoon and your account
 - Available cluster resources & job activity
 - Personal filesystem usage & quotas
 - Recent job activity ([jobstats](#))
 - Job efficiency & fairshare rankings
- Most info straight from CLI commands
- The extra-info version is linked at the very bottom of the main dashboard!



Ondemand's File Explorer



- The file explorer is used to explore, and transfer the files in your home, **scratch**, or other areas on the cluster.

The screenshot shows the Ondemand File Explorer web interface. At the top, there's a navigation bar with tabs for Files, Jobs, Clusters, and Interactive Apps. Below this is a toolbar with buttons for 'Open in Terminal', 'Refresh', 'New File', 'New Directory', 'Upload', 'Download', 'Copy/Move', and 'Delete'. The main area shows the current directory as '/ home / jtb49 /'. A sidebar on the left lists 'Home Directory', '/scratch/jtb49', and '/projects'. A filter box is set to 'cluster', showing 9 of 192 rows. The file list contains four PDF files related to a cluster workshop.

Type	Name	Size	Modified at
PDF	cluster_workshop_OOD_CLI_250917.pdf	2.93 MB	9/18/2025 7:52:56 PM
PDF	cluster_workshop_OOD_CLI_250917.pptx	9.02 MB	9/18/2025 7:52:58 PM
PDF	cluster_workshop_OOD_CLI_250917_withHidden.pdf	2.97 MB	9/18/2025 7:52:55 PM
PDF	cluster_workshop_OOD_CLI_250918.pdf	2.97 MB	9/18/2025 8:02:06 PM

OnDemand Job Composer



- The Job Composer *can be* used to create and run jobs.

The screenshot shows the OnDemand Job Composer interface. At the top, there's a navigation bar with "Open OnDemand / Job Composer", "Jobs", "Templates", and a "Help" icon. Below this, the "Jobs" section is active. It features a "+ New Job" button and a "Create Template" button. A toolbar contains "Edit Files", "Job Options", "Open Terminal", "Submit", "Stop", and "Delete" buttons. A "Show 25 entries" dropdown and a "Search:" input are present. The main table lists jobs with columns for "Created", "Name", "ID", "Cluster", and "Status". The first job, "2samplertest", is highlighted in blue and marked as "Completed". The second job, "(default) Simple Sequential Job", is marked as "Not Submitted". The third job, "Job from Template", and the fourth job, "job_array.sh", are both marked as "Completed". At the bottom, it says "Showing 1 to 4 of 4 entries" with "Previous", "1", and "Next" navigation links. On the right, the "Job Details" panel shows the "Job Name" as "2samplertest", "Submit to:" as "Monsoon Cluster", "Account:" as "Not specified", "Script location:" as "/home/wew/ondemand/data/sys/myjobs/projects/default/8", and "Script name:" as "study1.sh".

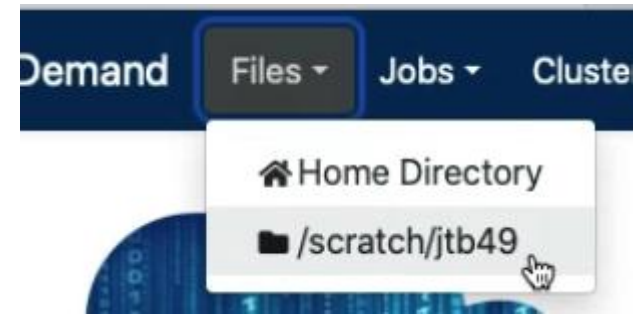
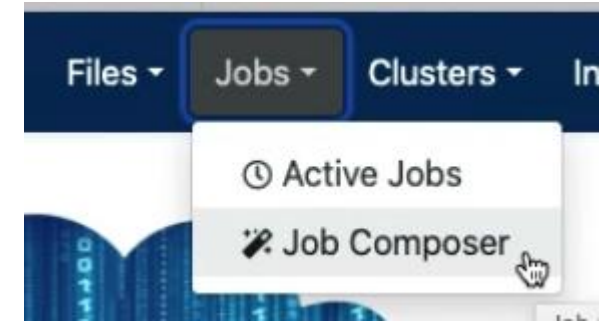
Created	Name	ID	Cluster	Status
December 21, 2018 11:12am	2samplertest	15728774	Monsoon Cluster	Completed
December 4, 2018 11:20am	(default) Simple Sequential Job		Monsoon Cluster	Not Submitted
November 16, 2018 11:05am	Job from Template	15505031	Monsoon Cluster	Completed
November 15, 2018 12:47pm	job_array.sh	15326951	Monsoon Cluster	Completed

Exercise 1



Create a simple job and run it on the compute nodes

- From Ondemand, click the **Jobs > Job Composer** menu
- Click on **New Job** and select **From Default Template**
- From the *bottom of the right-column*, click the blue **Open Editor** button
- Change all “**NAUID**” to be **your** nau user-ID, e.g.: **abc123**!
- Set your job-name to: “**simple**”
- Set your output location to `/scratch/<NAUID>/exercise1.txt`
- Make your jobscript load the module named “**workshop**”
- Make sure it runs the “**date**” command (i.e. “**srun date**”)
- Finally, have it run the “**exercise1**” command, as well
- Save (in this tab), and then submit your job via the composer (previous tab)
- Use the File Explorer to examine your output (**Files > /scratch/NAUID**)
- Make a note of the secret code written to `exercise1.txt`



[Exercise 1 \(CLI\)](#)

Exercise 2



- Create a new job using **New Job > From Template**
- Select the 'Long Job' template, optionally rename it, and click **Create New Job**
- From the Jobs list, select the new draft job, and click **Open Editor** as before
- Change all "NAUID" to be your nau user-ID, again
- Make your jobscript load the module named "`workshop`"
- Make your jobscript run the "`exercise2`" command
 - i.e. "`srun exercise2`"
- Make your job sleep for 5 minutes
 - i.e. "`srun sleep 300`" (Sleep is a command that does nothing for N seconds)
- Save your jobscript, and submit this job
- Monitor your job by selecting **Jobs > Active Jobs** from your Dashboard
- When it has completed, examine the output in long.txt
- Make a note of the secret code from long.txt

[Exercise 2 \(CLI\)](#)

Command-line access



Once you have the basics down using Ondemand, then the power of the cluster is exposed through the command-line interface (CLI)

- We will be utilizing a CLI built-in to Ondemand
- Feel free to **tryout the commands** we discuss
- Reminder: The Monsoon CLI is most commonly accessed via an “ssh client” (ex: Putty on Windows, or via the ssh command in your OS’s PowerShell or Terminal app)
- Now open a **login-node shell** (from the “Clusters” menu) and follow along!



The Ondemand CLI



You may access the Ondemand's CLI from the dashboard by selecting **Clusters > Monsoon login-node shell**

Note: Linux does NOT give interactive feedback when you enter passwords!* But it will evaluate your password attempt upon hitting enter!

```
ricky@wind:~  
Last login: Tue Sep 16 09:31:24 MST 2025 on pts/24  
#####  
#  
# Welcome to Monsoon - login node: [wind]  
#  
# Information:  
# - Monsoon now running Enterprise Linux 8  
# - /scratch : files auto DELETED after 30 days  
#  
# Issues or questions: ask-arc@nau.edu  
#  
# Next Maintenance:  
# - Winter break  
#  
#####  
[ricky@wind ~ ]$
```

Cluster info



- `sinfo`
 - view state information about SLURM nodes and partitions.
- `sinfo -N -l`
 - view state and specs on all individual nodes
- `sinfo -R`
 - List reasons for downed nodes and partitions

```
[ricky@wind ~]$ sinfo
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
core*      up    14-00:00:0    4    drain cn[35,40,52-53]
core*      up    14-00:00:0   79     mix cn[1,4-19,28-30,38-39]
core*      up    14-00:00:0   10   alloc cn[20-26,36-37,107]
core*      up    14-00:00:0    3    idle cn[3,32-33]
core*      up    14-00:00:0    4    down cn[31,42,51,65]
gpu        up    14-00:00:0    1     mix cn1
gpu        up    14-00:00:0    3    idle cn[3,32-33]
gpu        up    14-00:00:0    1    down cn31
```

More info:

<https://slurm.schedmd.com/sinfo.html>

Interactive / Debug Work



- Run your compiles and testing on the cluster nodes by:

- `srun gcc hello.c -o a.out`
- `srun --qos=debug -c12 make -j12`
- `srun Rscript analysis.r`
- `srun python analysis.py`
- Try this now:
 - `srun hostname`
 - `hostname`

```
[ricky@wind ~]$ srun -c 4 --mem=9000 hostname
cn37
[ricky@wind ~]$ jobstats
JobID           JobName      ReqMem      MaxRSS      ReqCPUS
=====
22695207         hostname    8.79G       4.25M        4
=====

Memory       : 00.05%
CPU           : 01.18%
Time Limit   : 00.01%
=====
Efficiency Score: 0.41
=====
```

More info:

<https://slurm.schedmd.com/srun.html>

Long Interactive work



- **salloc**
 - Obtain a SLURM job allocation that you can work interactively with for an extended amount of time
 - This is useful for testing/debugging for an extended amount of time
 - For when you need more than a single srun but aren't ready for sbatch

```
[ricky@wind ~ ]$ salloc -c 8 --time=2-00:00:00
salloc: Granted job allocation 33442
[ricky@wind ~ ]$ srun python analysis.py
[ricky@wind ~ ]$ exit
salloc: Relinquishing job allocation 33442
```

```
[ricky@wind ~ ]$ salloc -N 2
salloc: Granted job allocation 33443
[ricky@wind ~ ]$ srun hostname
cn3
cn2
[ricky@wind ~ ]$ exit
salloc: Relinquishing job allocation 33443
```

More info:

<https://slurm.schedmd.com/salloc.html>

Submitting non-interactive jobs



The sbatch command is used to submit batch jobs to the slurm workload manager. Jobs submitted with sbatch are placed in a queue where they wait for resources to become available.

```
[ricky@wind ~]$ sbatch jobscript.sh
```

Submitted batch job 6880341

- slurm returns a job id for your job that you can use to monitor or modify constraints

More info:

<https://slurm.schedmd.com/sbatch.html>

Monitoring your job



- **jobstats**
 - Your main tool
 - Show usage stats for slurm jobs
 - combines features of scontrol and sacct tools
- **jobstats -h**
 - Usage instructions
- **jobstats -r**
 - Also show **running jobs**
- **jobstats -j <jobid>**
- **queue**
 - View information about jobs located in the SLURM scheduling queue.
- **queue --start**
- **queue -u <nauid>**
- **queue -o "%j %u ..."**
- **queue -p partitionname**
- **queue -S sortfield**
- **queue -t <state> (PD or R)**

More info:

<https://slurm.schedmd.com/queue.html>

Monitoring your job



- `sstat`
 - Display various statistics and information of a running job
 - Only works with jobs where analysis is executed with “`srun`”
- `sstat -j <jobid>`
- `sstat -o "AveCPU,AveRSS"`
- `sprio`
 - View the factors that comprise jobs’ scheduling priority
 - Shows only pending by default
- `sprio -l`
- `sprio -o "%j %u ..."`
- `sprio -w`

More info:

<https://slurm.schedmd.com/sstat.html>

<https://slurm.schedmd.com/sprio.html>

Controlling your job



- `scancel`
 - Used to signal jobs or job steps that are under the control of Slurm.
- `scancel <jobid>`
- `scancel -n <jobname>`
- `scancel -u <nauid>`
- `scancel -t pending (only yours)`

More info:

<https://slurm.schedmd.com/scancel.html>

Controlling your job



- `scontrol`
 - Used to view and modify Slurm configuration and state
 - Can change job constraints while it's in the pending state, but once the job starts, it can no longer be modified
- `scontrol show job 6880341`
 - When scheduled to start
 - Path to jobscript
 - Requested resources
 - Target node
- `scontrol update jobid=6880341 timelimit=4:00:00`

More info:

<https://slurm.schedmd.com/scontrol.html>

Job Accounting



- `sacct`
 - displays accounting data for of your jobs and job steps in the SLURM job accounting log or SLURM database
- `sacct -j <jobid> -o "jobid,elapsed,maxrss"`
- `sacct -N <nodelist>`
- `sacct -u <nauid>`
- Try our `sacct` wrapper "**jobstats**"
 - `jobstats -r`
 - `jobstats -j <jobid>`

More info:

<https://slurm.schedmd.com/sacct.html>

Job Accounting



- `sshare`
 - Tool for listing the shares of associations to a cluster.
- `sshare -l` : view and compare your groups cpu minutes usage
- `sshare -a` : view all users fairshare
- `sshare -a -A <account>` : view all members in your account (group)
- `group_efficiency <account>`

More info:

<https://slurm.schedmd.com/sshare.html>

Limits on the account (group)



- Limits are in place to prevent intentional or unintentional misuse of resources to ensure quick and fair turn around times on jobs for everyone.
- Groups are limited to a total number of *resource-minutes* in use at one time: 5M CPU-minutes, 64K GPU-minutes*
- This resource limit mechanism is referred to as: “TRESRunMins”.
- This limiting mechanism has nothing to do with priority!

Helpful Linux Commands



List Files	ls With “-l” option (“ls -l”) will show more information
Change Directory	cd <directory path> (e.g.: “cd /scratch/NAUID/”) cd by itself will return you to your home directory
Show/print current working directory	pwd
Copy Files	cp <source> <destination> use a period (“.”) as the destination to copy to your current directory
Move or rename a file	mv <source> <destination>
Delete a file	rm <filename>
Create a directory	mkdir <directory name>
View contents of a file	more <filename> less <filename> cat <filename>
Edit a file	nano <filename> (save=ctrl-o & exit=ctrl-x)
Exit your terminal session (log off)	exit

Exercise 3 via CLI



Get to know monsoon and Slurm, on your own. Start by opening a shell to Monsoon.

- How many nodes make up monsoon?
 - Hint: use “sinfo”
- How many nodes are in the gpu partition?
- How many jobs are currently in the running state ?
 - Hint: use “squeue -t R”
- How many jobs are currently in the pending state? Why?
 - Hint: use “squeue -t PD”

Exercise 4 via CLI



- Copy this job script to your scratch area:
 - `/common/contrib/examples/job_scripts/lazyjob.sh`
- Edit that copy: change any “NAUID” to be your id
- **Save the job script**
- Submit the job (`sbatch lazyjob.sh`), it will take 65 sec to complete
- Use `sstat` and `squeue` to monitor the job
 - `sstat -j <jobid>`, and `squeue -u <nauid>`
- Review the resources that the job used
 - `jobstats -r`
- We are looking for “MaxRSS”: *MaxRSS is the max amount of memory used*
- Edit the job scripts memory request (“`--mem`”): reduce the number of MB of memory being requested, eg: `--mem=600`; and resubmit
- Use `jobstats` to review the resources that the optimized job utilized, once again
- Ok, memory looks good, but notice that the `usercpu` is the same as the elapsed time
$$Usercpu = num\ utilized\ cpus * elapsed\ time$$
- This is because the application we were running only used 1 of the 4 cpus that we requested
- Edit the lazy job script: comment out first `srun` command, uncomment the second `srun` command; and resubmit
- Rerun `jobstats -r`, notice now `usercpu` is multiple times the elapsed time, in this case (4). Because we were allocated 4 cpus, and **used** 4 cpus.
- Now address the egregious time estimate!
- Make a note of the secret code from `lazy.txt`!

Archived Job scripts



Every job script that is submitted to slurm on monsoon is archived for three reasons:

1. Convenience – if you forget what script was used for what job, you can find out!
2. Support assistance – we can find the job script that was used in your job to help troubleshoot with you.
3. Security / stability – in case of any security or stability issues, we can connect issues and outages to associated jobs

Retrieval of a job script



- Archived job scripts, and their environment are stored here:
 - /common/jobscript_archive/<NAUID>/<year>/<month>
 - <job id>.sh – job script
 - <job id>.env – job script’s environment
 - Only the individual researcher and our support group can access their job scripts
- Example:
 - User abc123, accessing job id 2600 from March, 2021
 - `cat /common/jobscript_archive/abc123/2021/03/2600*.sh`
 - `cp /common/jobscript_archive/abc123/2021/03/2600*.sh ~/`
- Use “showscript” to make it easy!!!!

Showscript Demo



```
[ricky@wind ~ ]$ jobstats
JobID           JobName      ReqMem    MaxRSS    ReqCPUS    UserCPU      Timelimit    Elapsed     State      JobEff
=====
22696318        simple      1.95G     17.0M     1          00:00.372    00:20:00     00:00:03    COMPLETED  0.55
22696443        long        9.77G     17.6M     1          00:00.374    03:00:00     00:05:02    COMPLETED  1.49
=====

Memory       : 00.29%
CPU          : 100.00%
Time Limit   : 02.54%
=====
Efficiency Score: 34.28
=====

[ricky@wind ~ ]$ showscript 22696318
/common/jobscript_archive/ricky/2025/09/22696318.sh
=====
#!/bin/bash
#SBATCH --job-name=simple           # the name of your job
#SBATCH --output=/scratch/ricky/exercise1.txt # this is the file your output and errors go to
#SBATCH --chdir=/scratch/ricky      # your work directory
#SBATCH --time=20:00                # (max time) 20 min (shorter time=quicker start)
#SBATCH --mem=2000                  # (total mem) 2GB of memory
#SBATCH --mail-type=FAIL            # email notification if it fails

module load workshop
srun date
srun exercise1
=====
Job Efficiency - OVERALL: 33.7%, CPU: 100.00%, Mem: 00.85%, TIME: 00.25%
```

Checking your disk usage



- You can use the “**getquotas**” command to examine how much space you are using in the various monsoon storage areas

```
$ getquotas
Filesystem      #Bytes  Quota  %    |  #Files  Quota  %
/home           23592M  30000M  78%  |  -        -      -
/scratch        70.5G   36.4T   0%   |  31K      2.9M   1%
```

Changing Your Default Account



- All researchers have a default slurm account to track usage
 - **See it now** by: “`sacctmgr show user name=<NAUID>`”
 - Some researchers belong to multiple slurm accounts
 - Example to override the default:
-
- `#SBATCH --account=inf503-fall24`
 - `#SBATCH --account=prof_lastname`

Confirming Your Account



- This is a required step for your account to be fully enabled!
- After completing the exercises: one, two, and four, you will have three, 32 character alpha-numeric codes
- With the codes in hand, confirm your monsoon account with the commands:
 - module load workshop
 - confirm_user
- More information here:
 - <https://in.nau.edu/arc/obtaining-an-account/>

Optimizing Your Cluster Use



- To get the most out of the cluster for yourself and your team, it is important to optimize the settings for your jobs.
- Optimization includes memory requested, time for the job to run, number of cpus

Slurm Arrays!



2. Job script is submitted

```
analysis
--array=1-8
```



3. Job is launched with eight instances running in parallel



`$SLURM_ARRAY_JOB_ID` (%A): the (parent) job-ID
`$SLURM_ARRAY_TASK_ID` (%a): the ID of (child) job array member n

Slurm Arrays Exercise



From your scratch directory: (`cd /scratch/NAUID`)

- `tar xvf /common/contrib/examples/bigdata_example.tar`
- `cd bigdata`
- edit the file `job_array.sh` so that it works with your nau id, replacing all `NAUID` with your own
- Submit the script `sbatch job_array.sh`
- Run `squeue` and notice you have 5 jobs running, how did that happen!

Keep these tips in mind



- Know the software you are running, is it multi-threaded?
- Request resources accurately
- Supply an accurate time limit for your job
- Don't be lazy, it will affect you and your group negatively

Common Questions



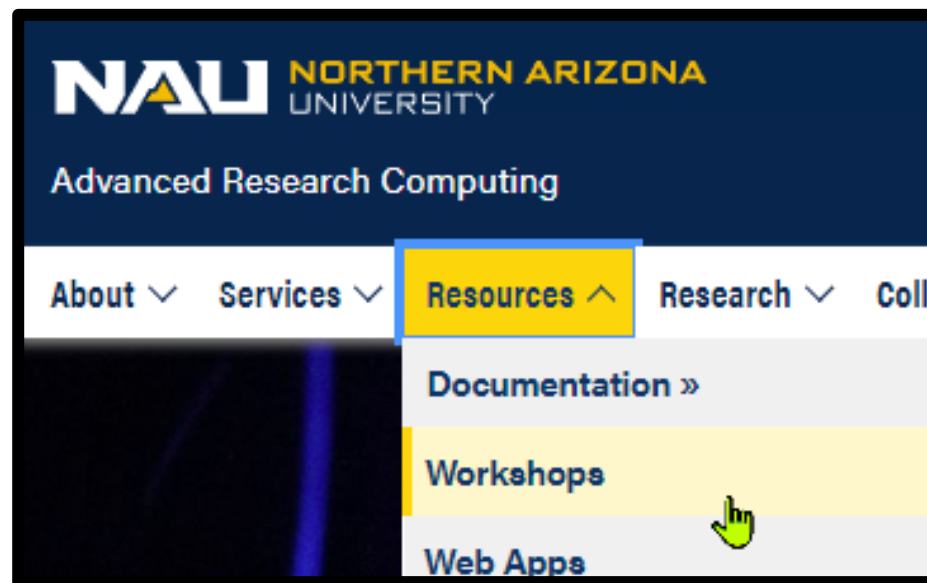
- Should I use OnDemand or the command line?
 - Power users will tend to use command line
 - However, the terminal in ondemand is worth using all the time
- Can I use/How should I use AI tools on Monsoon?
 - Guidelines: <https://in.nau.edu/arc/ai-tool-guidelines>
 - Data classification: <https://in.nau.edu/its/data-classification>

Workshops, Office-, and Coffee-hours!



Schedule

Date	Time	Location
Wednesday 09/04/2024	2:00 PM - 4:00 PM	B54 ITS Room of Requirement (Room 106) AND Online via Zoom
Tuesday 10/01/2024	2:00 PM - 4:00 PM	B54 ITS Room of Requirement (Room 106) AND Online via Zoom



Helpful Tip: [Linux on the command-line](#) is a great beginner friendly resource for those who are just starting with Monsoon!

Workshop Dates

Workshop	Date	Time	Location
Intro to Monsoon	Thursday, September 5, 2024	2:00 PM - 4:00 PM	ITS (Building 54), Room 106
Intro to Monsoon (In Depth)	Thursday, September 26, 2024	2:00 PM - 4:00 PM	ITS (Building 54), Room 106
Linux in HPC	Thursday, October 3, 2024	2:00 PM - 4:00 PM	ITS (Building 54), Room 106

Question and Answer



- More info here:
<http://in.nau.edu/arc>
ask-arc@nau.edu
- Job efficiency
 - <http://metrics.hpc.nau.edu>
- FREE – Linux command line book:
 - <http://linuxcommand.org/tlcl.php>
 - Info here: <https://in.nau.edu/arc/external-resources/linux-resources/>
- And on the nauhpc listserv
 - nauhpc@lists.nau.edu

Exercise 1 (CLI)



Create a simple job and run it on the compute nodes

- `cp /common/contrib/examples/job_scripts/exercise1.sh ~/`
- `nano exercise1.sh` (or another editor)
- Change all “**NAUID**” to be ***your*** nau user-ID, e.g.: **abc123**!
- Set the name of your job (`--job-name`) to “simple”
- Set your `--output` path to be `/scratch/<NAUID>/exercise1.txt`
- Make your jobscript load the module named “workshop”
- Make your jobscript run the “**date**” command (i.e. “`srun date`”)
- Finally, have it run the “**exercise1**” command, as well
- Save the file (for nano: ctrl-x, and y(es))
- Submit the batch script to slurm: `sbatch exercise1.sh`
- Make a note of the secret code written to `exercise1.txt`

[Next Slide: Exercise 2 \(CLI\)](#)

Exercise 2 (CLI)



- `cp /common/contrib/examples/job_scripts/exercise2.sh ~/`
- `nano exercise2.sh` (or another editor)
- Change all “**NAUID**” to be ***your*** nau user-ID, e.g.: **abc123**!
- Set your `--output` path to be `/scratch/<NAUID>/long.txt`
- Make your jobscript load the module named “workshop”
- Make, have it run the “`exercise2`” command (i.e. “`srun exercise2`”)
- Finally, make your job sleep for 5 minutes
 - i.e. “`srun sleep 300`” (Sleep is a command that does nothing for N seconds)
- Save the file (for nano: ctrl-x, and y(es))
- Submit the batch script to slurm: `sbatch exercise2.sh`
- When it has completed, examine the output in `long.txt`
- Make a note of the secret code from `long.txt`

[Next Slide: Command Line Access](#)