Intro to Monsoon and Slurm

2025-9-18 presentation with Jason Buechler

These slides:

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

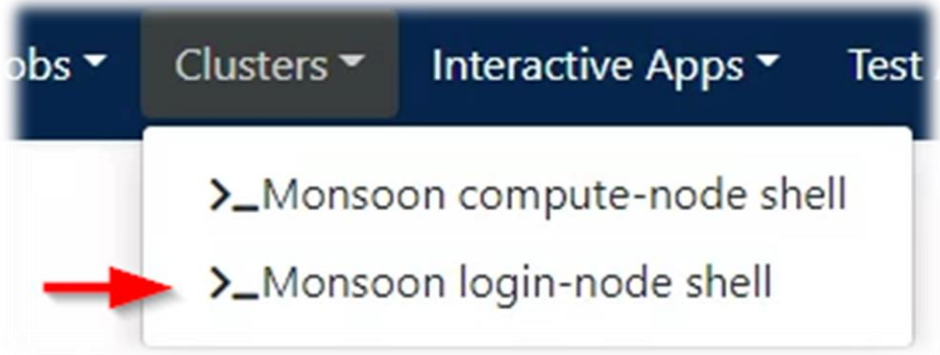
NAU ARC MONSOON

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
- Click on Clusters tab
- Select 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?

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

I am Jason Buechler

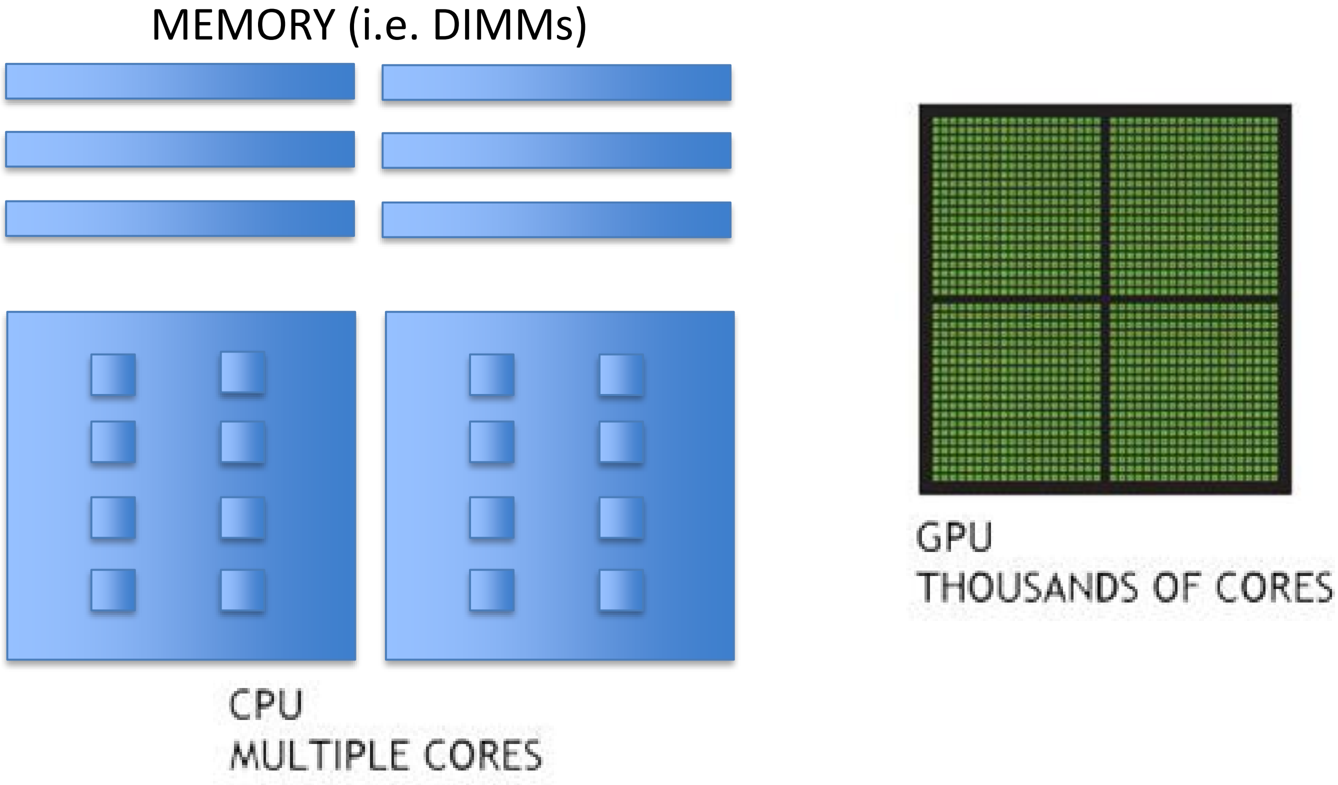
- Aero, Mech Engineering
  fluid-thermodynamics, renewable energy, & grid-engineering
- With Monsoon since 2019
- Linux/supercomputing since 2000

Agenda

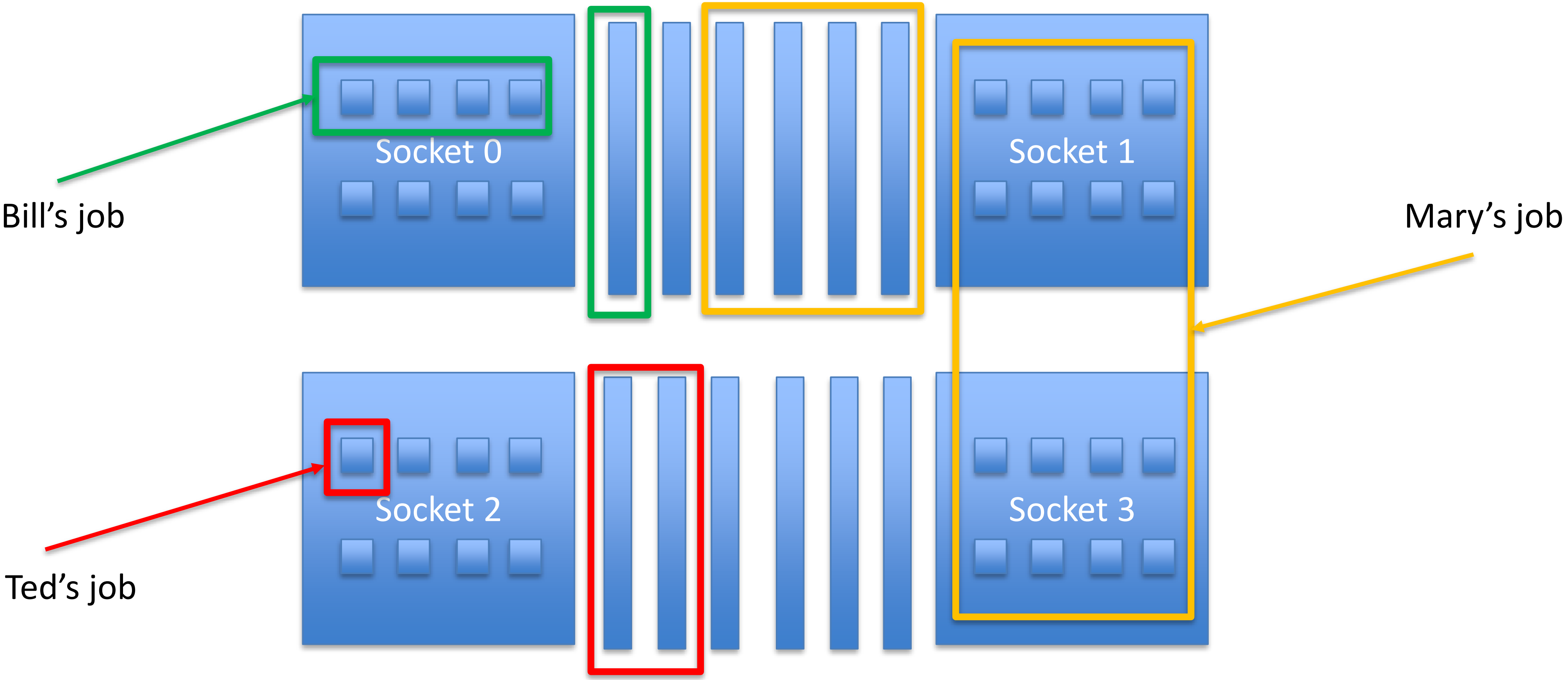
- (High-Performance) Cluster education
  – What is a cluster, exactly?
  – Job-queues, scheduling, and resource management
- Monsoon Cluster orientation
  – How do I use this cluster?
  – Group resource limits
  – Exercises
  – Question and answer

Cluster (of) resources

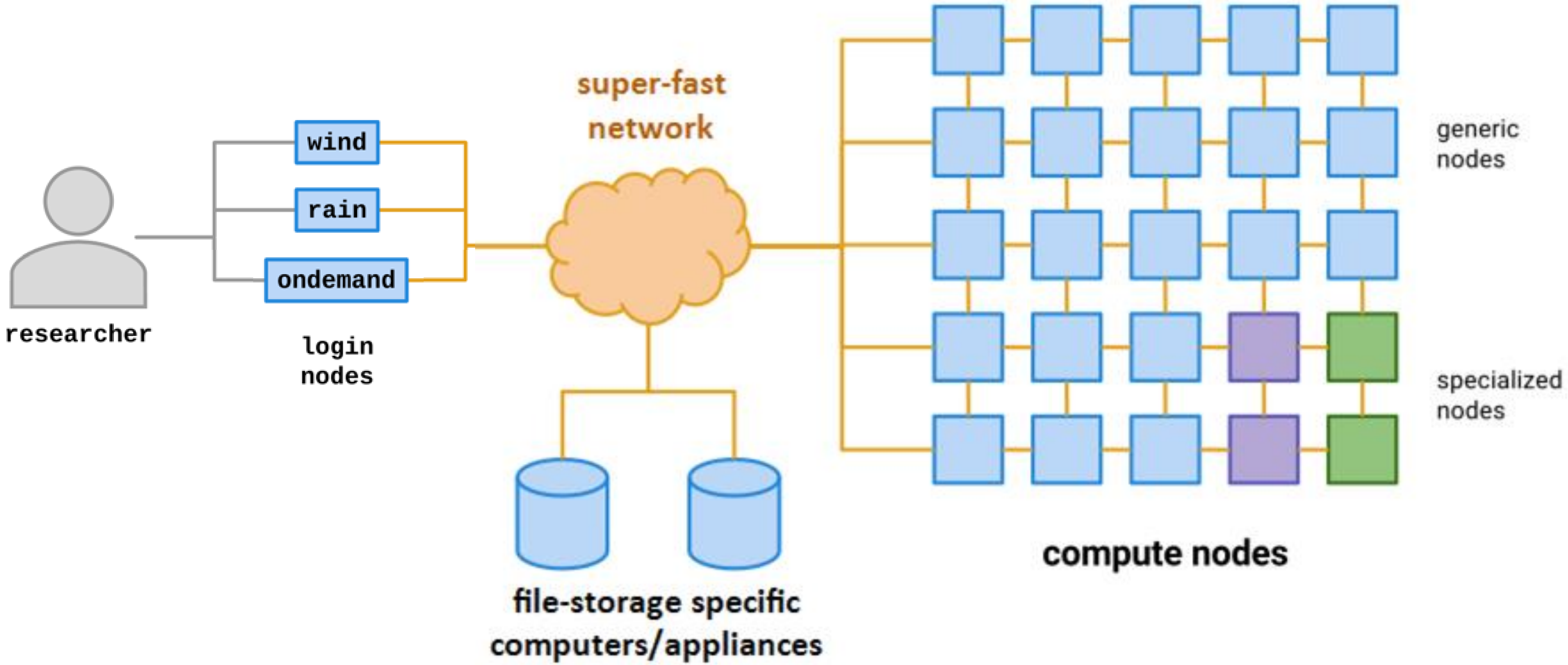
- Node itself
  - Memory
  - CPU’s
  - GPU’s
- Networking
- Licenses



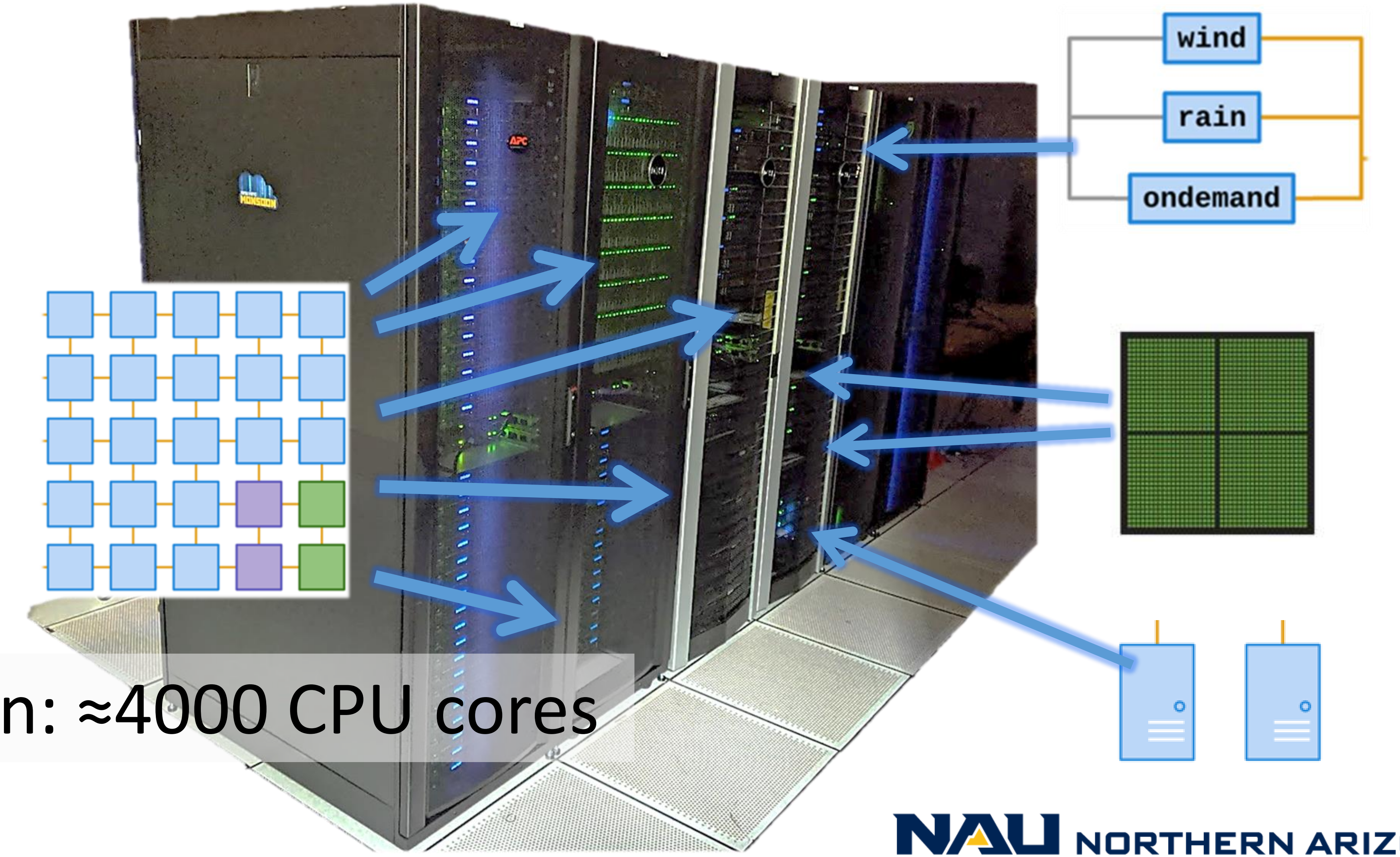
Inside a (single) compute-node



Cluster = Login-nodes + Compute-nodes + More



Monsoon



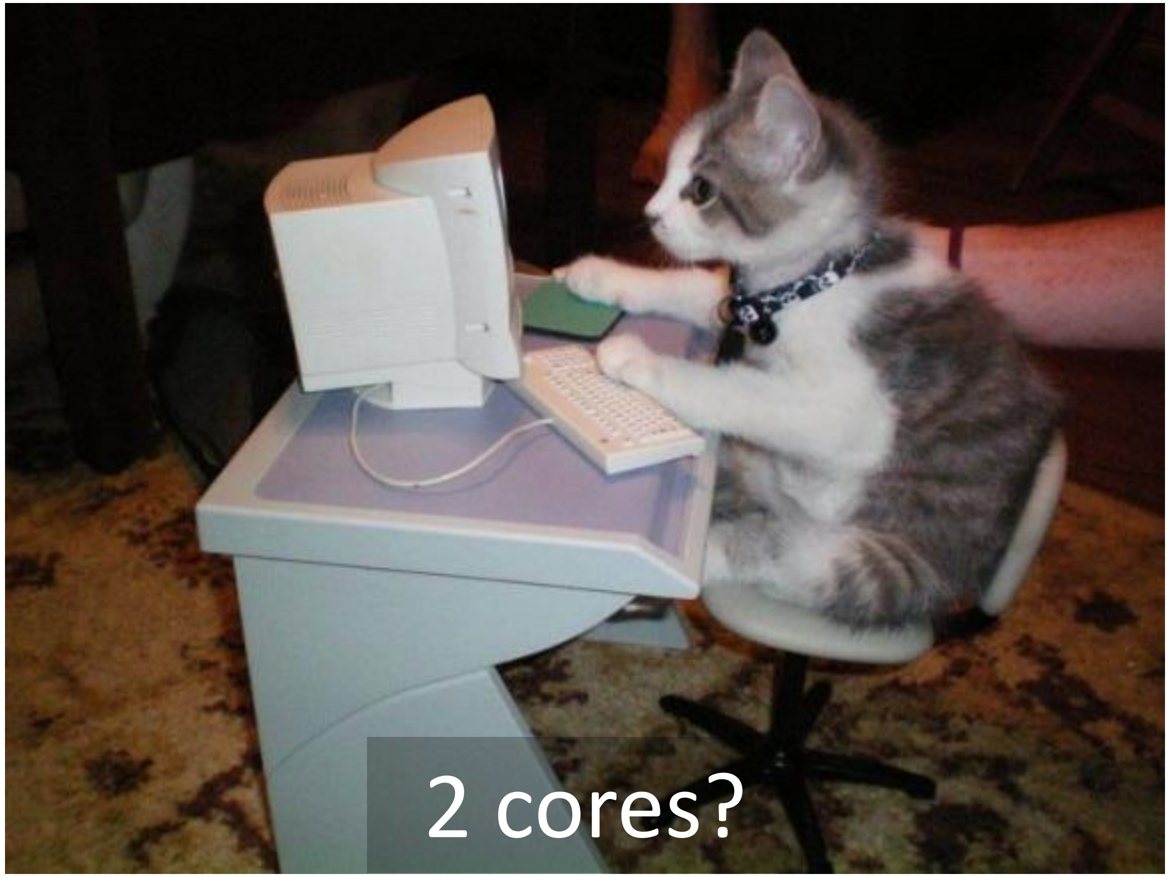
Monsoon: ≈4000 CPU cores

Largest Cluster!

Lawrence Livermore National Laboratory
U.S. DEPARTMENT OF ENERGY
NNSA
Hewlett Packard Enterprise
AMD
Red Hat
EL CAPITAN
ADVANCED SIMULATION & COMPUTING
HPE Cray
Mike Carter Photography

El Capitan: 11.0M cores

Small Cluster!

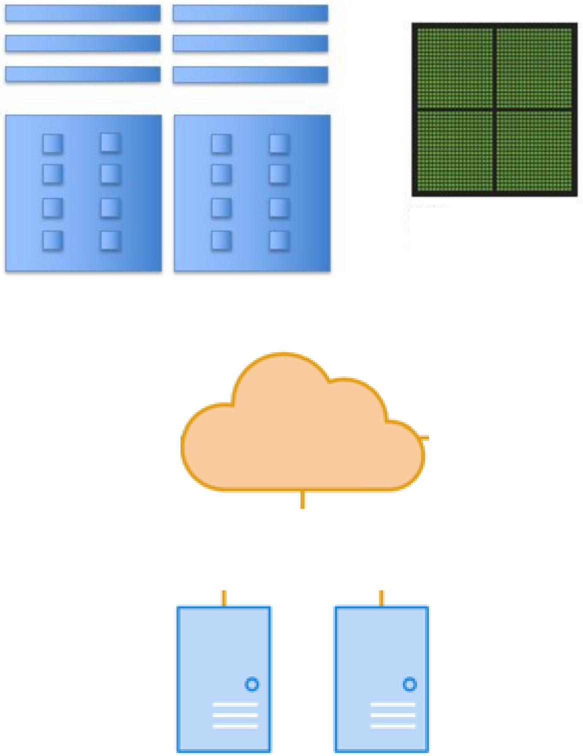


2 cores?

Monsoon Today

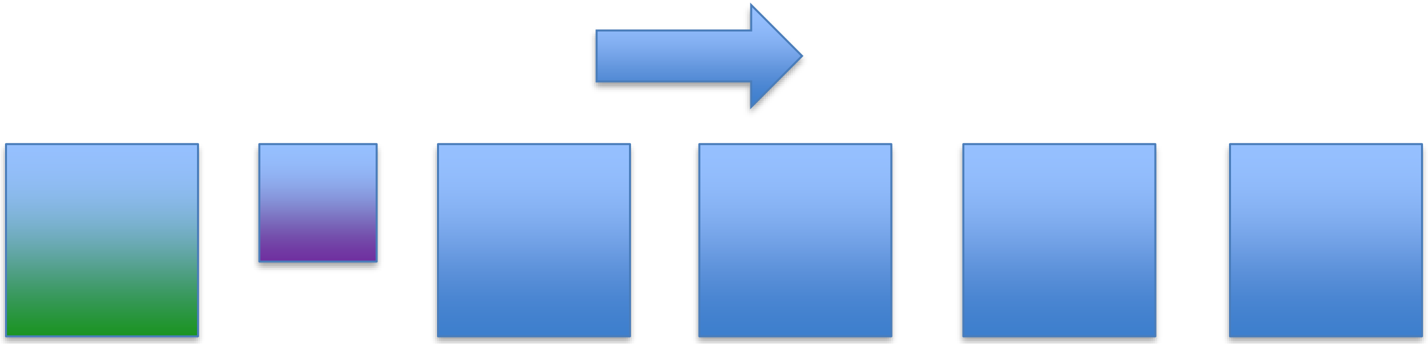
(from https://in.nau.edu/arc/details)

- The Monsoon cluster is a resource available to the NAU research enterprise
- 107 compute-nodes (cn1 ~ cn108)
  - 26TB memory - 128GB/node min, 2TB max
  - 27 GPUs, NVIDIA Tesla K80, P100, V100, A100
  - 4048 cores (Intel + AMD)
- Red Hat Enterprise Linux 8.10
- High speed interconnect: FDR, and HDR Infiniband
- Storage
  - 1PB *scratch* high-speed storage (Lustre)
  - 1.6PB *long-term* storage (proprietary object-store)



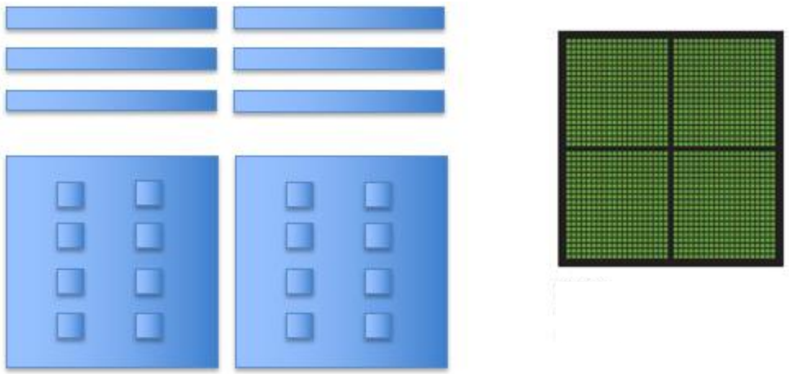
What is a queue?

- Normally thought of as a line, FIFO (Line at Starbucks)
- Queues on a cluster can be as basic as a FIFO, or far 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

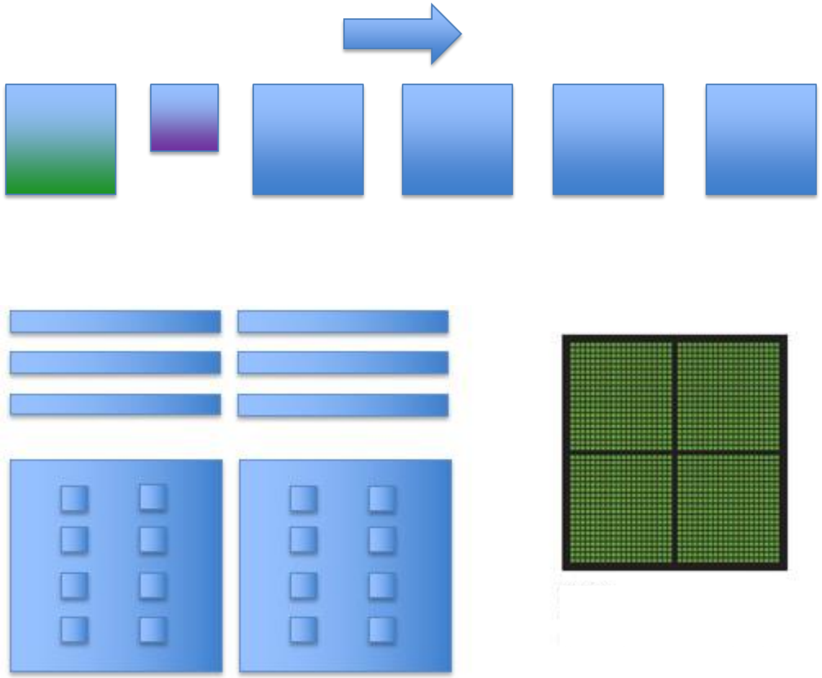


Slurm … yummm

- 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:
  - El Capitan (#1), 11.0M cores, 1742 PF, 29.6 MW - USA
  - Frontier (#2), 9.1M cores, 1353 PF, 24.6 MW - USA

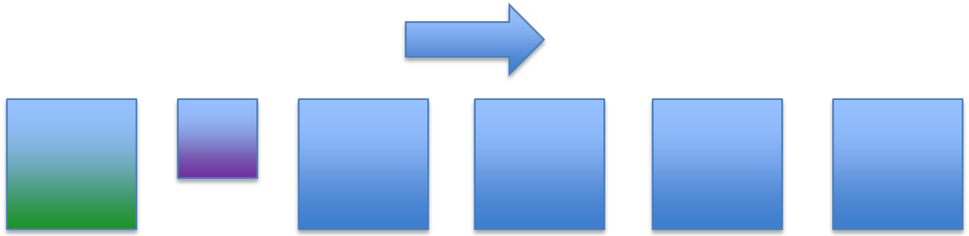
Our Scheduling Goals

- 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:



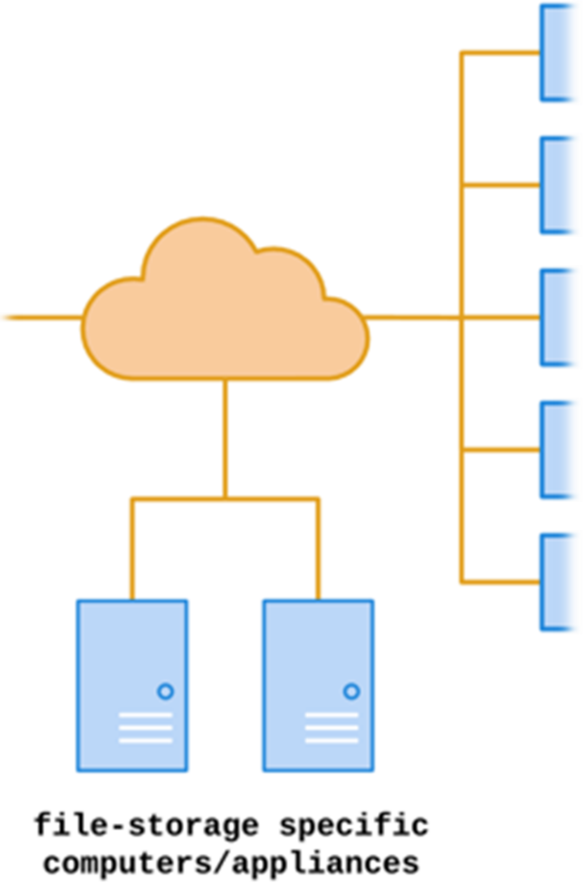
- FIFO
  - Simply first in first out
- Backfill
  - Runs smaller jobs with lower resource requirements while larger jobs wait for higher resource requirements to be available
- Fairshare
  - Prioritizes jobs based on multiple factors such as users’ recent resource consumption
- Additional factors
  -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

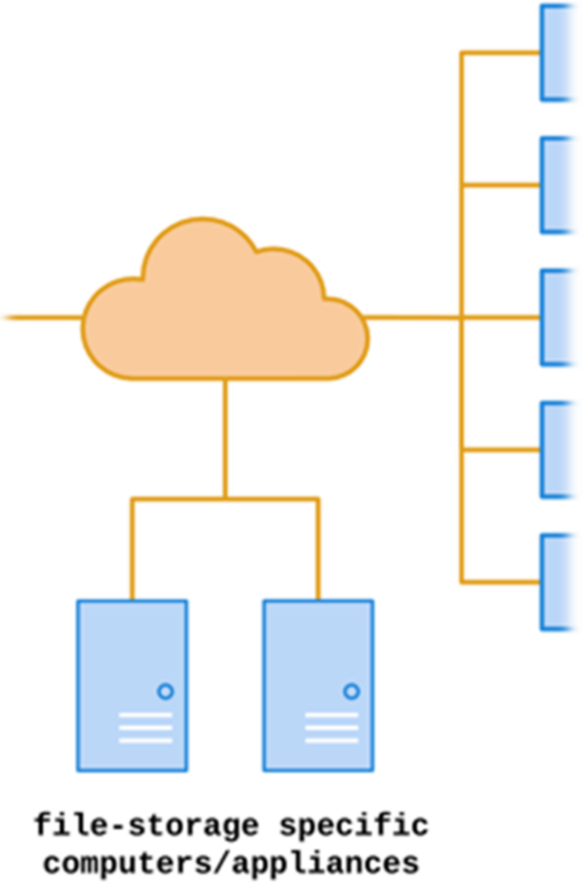
- /home – 20 GB quota
  - Keep your scripts and executables here
  - Backed up to tape
  - Snapshotted twice a day: /home/.snapshot
  - Please do not write job output (logs, results) here!!
  - Run the command “getquotas” now
- /scratch – 15 TB quota (also 2M files quota)
  - 1PB total space, 30 day 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 (or on Ondemand)
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 you on the cluster if you'd like to manage access to your data
- https://my-old.nau.edu
  - "Open directory services"
  - "Enterprise groups"
  - Take a look at our FAQ :: https://nau.edu/high-performance-computing/faqs/
  - If they are not working for you, contact ITS Solution Center
- What groups are you in? Run the command "groups", or "id"

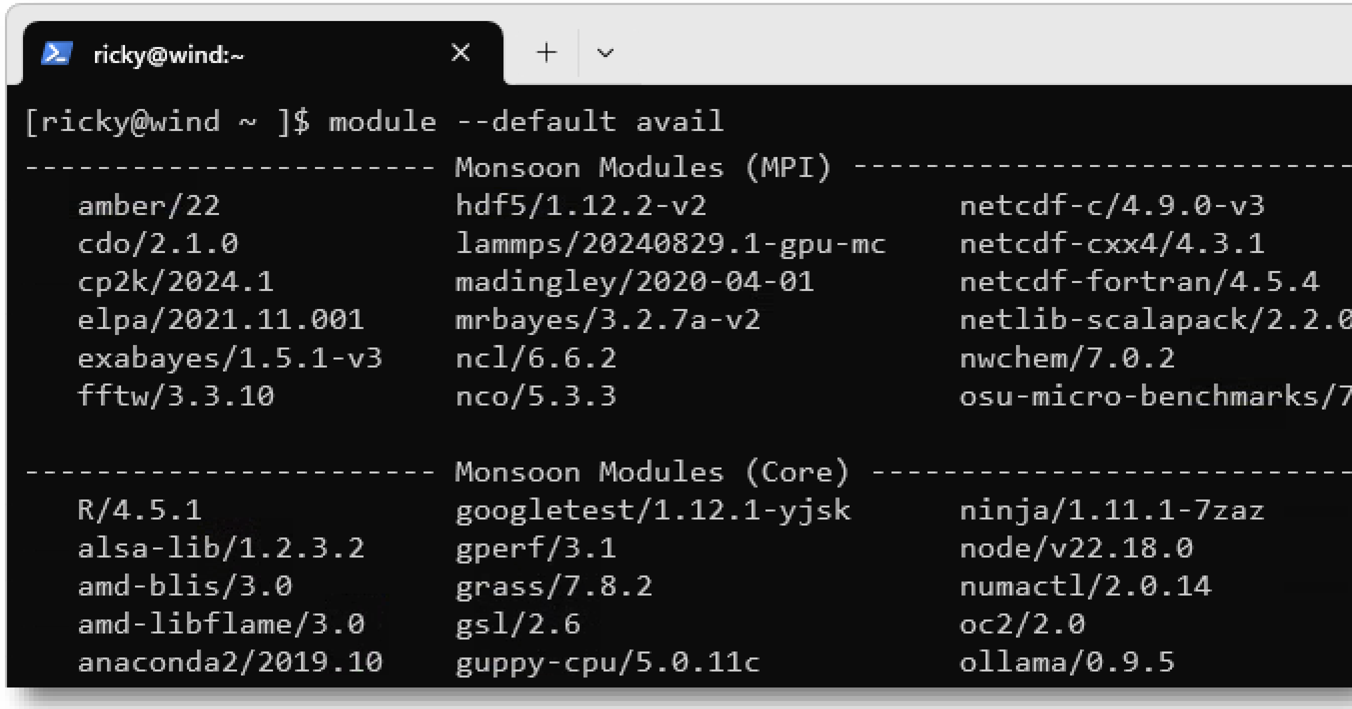
Modules

- 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 list` *…modules currently loaded*
- `module load <module name>` *…load a package module*

Software

- Anaconda Python
- R
- Matlab
- SAS
- Qiime2
- Lots of bioinformatics programs
- Request additional software to be installed!



```
[ricky@wind ~ ]$ module --default avail
----------------------- Monsoon Modules (MPI) ----------------------------
   amber/22             hdf5/1.12.2-v2               netcdf-c/4.9.0-v3
   cdo/2.1.0            lammps/20240829.1-gpu-mc     netcdf-cxx4/4.3.1
   cp2k/2024.1          madingley/2020-04-01         netcdf-fortran/4.5.4
   elpa/2021.11.001     mrbayes/3.2.7a-v2            netlib-scalapack/2.2.0
   exabayes/1.5.1-v3    ncl/6.6.2                    nwchem/7.0.2
   fftw/3.3.10          nco/5.3.3                    osu-micro-benchmarks/7

----------------------- Monsoon Modules (Core) ---------------------------
   R/4.5.1              googletest/1.12.1-yjsk       ninja/1.11.1-7zaz
   alsa-lib/1.2.3.2     gperf/3.1                    node/v22.18.0
   amd-blis/3.0         grass/7.8.2                  numactl/2.0.14
   amd-libflame/3.0     gsl/2.6                      oc2/2.0
   anaconda2/2019.10    guppy-cpu/5.0.11c            ollama/0.9.5
```

Requesting Software

- You can install quite a bit of R, and python software yourself!
- For R
  - `module load R`
  - `R`
  - `install.package(c(package))`
- For python
  - `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

- What resources are needed?
  - 2 **cpus**, 12GB **memory**, for 2 **hours**?
- What steps are required?
  - Run prog1, then prog2 … etc
  - Are the steps dependent on one another?
- Can your work, or project be broken into pieces?
  - Smaller pieces can make the workload more agile.
- How long should your job run for? (i.e.: *educated guess*)
- 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. module loading (“`module load` …”)
3. srun job steps/statements for the actual work (“`srun <command>`”)

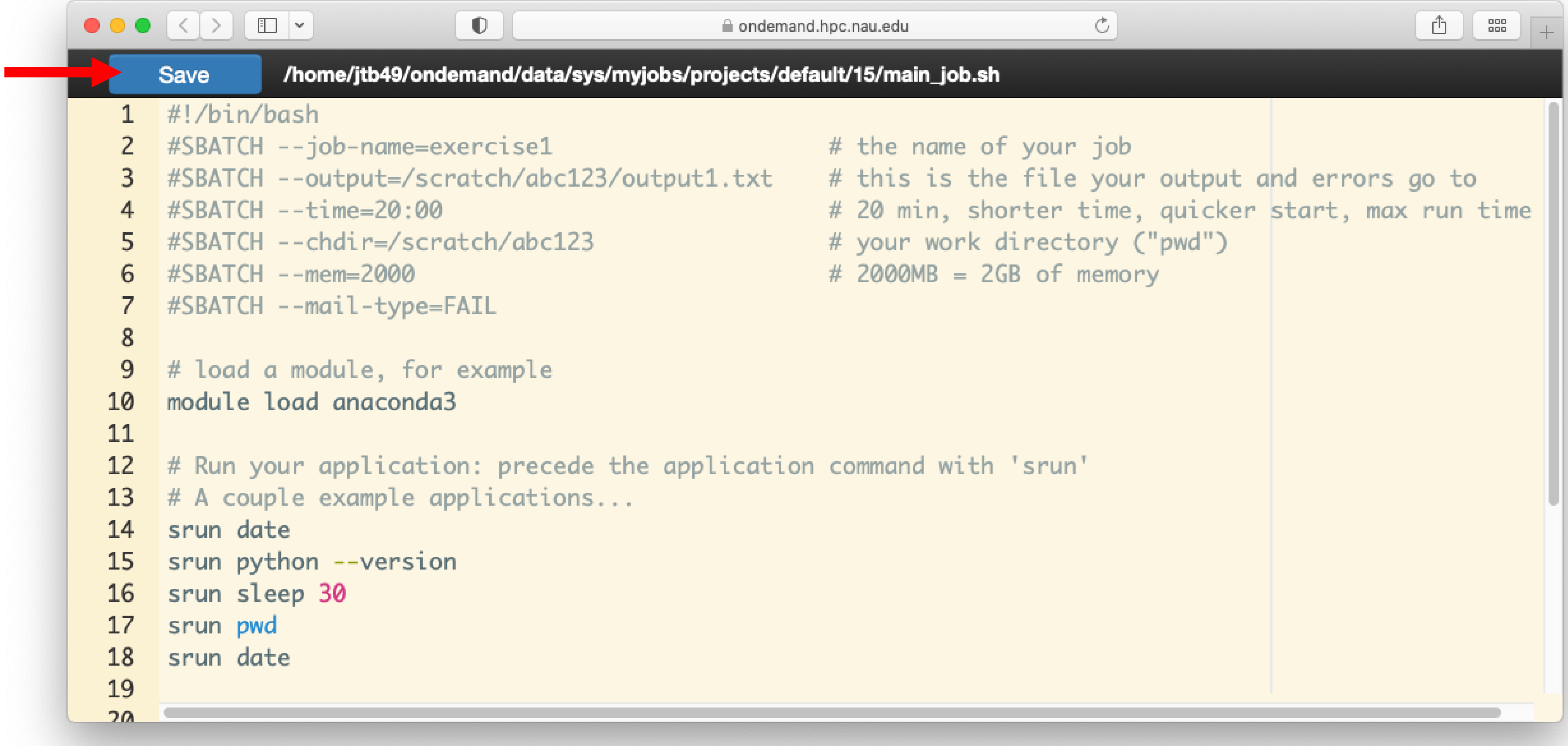
Example Job script

```
#!/bin/bash
#SBATCH --job-name=test
#SBATCH --output=/scratch/NAUID/output.txt     #  the job's output/errors go here
#SBATCH --time=20:00                           #  shorter time = sooner start
#SBATCH --chdir=/scratch/NAUID                 #  default location slurm searches

# 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)



/home/jtb49/ondemand/data/sys/myjobs/projects/default/15/main_job.sh

```
#!/bin/bash
#SBATCH --job-name=exercise1                    # the name of your job
#SBATCH --output=/scratch/abc123/output1.txt    # this is the file your output and errors go to
#SBATCH --time=20:00                            # 20 min, shorter time, quicker start, max run time
#SBATCH --chdir=/scratch/abc123                 # your work directory ("pwd")
#SBATCH --mem=2000                              # 2000MB = 2GB of memory
#SBATCH --mail-type=FAIL

# load a module, for example
module load anaconda3

# Run your application: precede the application command with 'srun'
# A couple example applications...
srun date
srun python --version
srun sleep 30
srun pwd
srun date

```

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=now+1hour --begin=2010-01-20T12:34:00
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

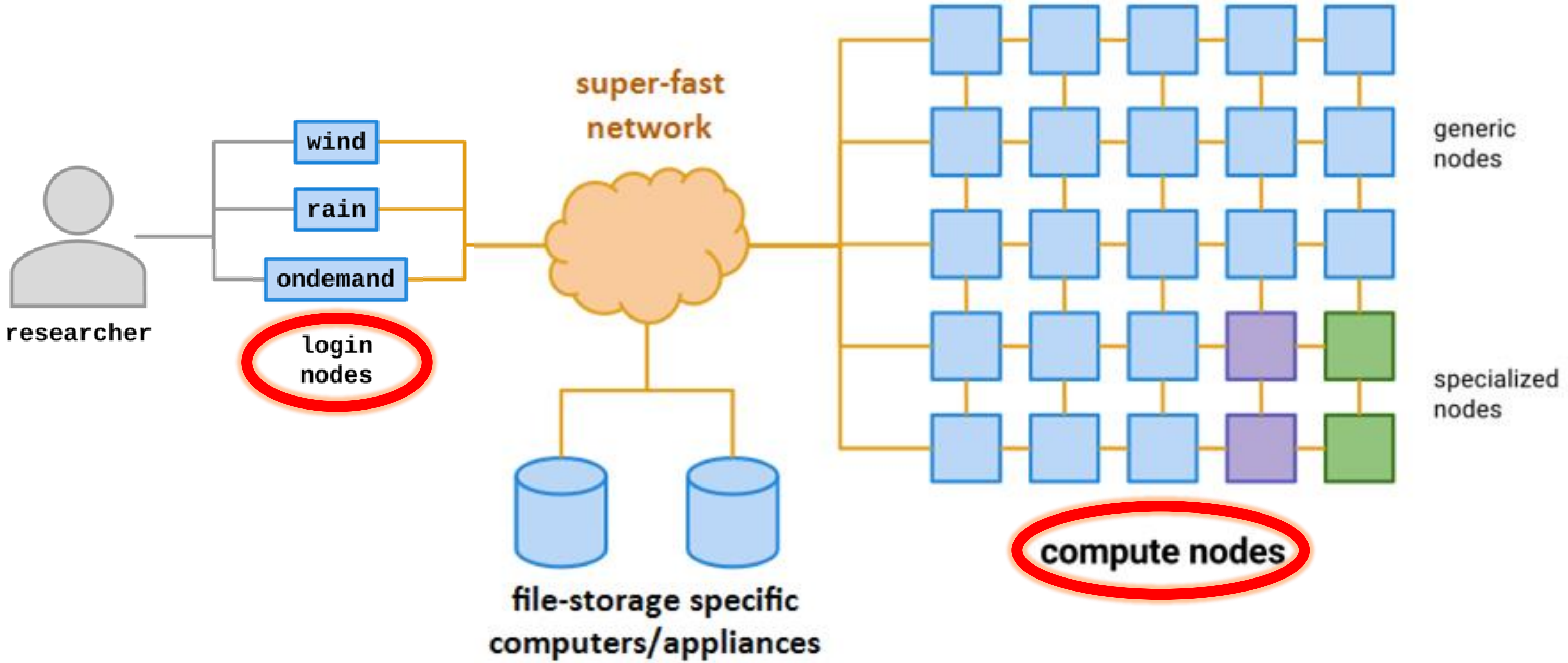
Contraints and Resources

You want	Switches needed
To choose a specific node feature (e.g. avx2)	--constraint=avx2
To use a generic resources (e.g. a gpu)	--gres=gpu:tesla:1, -G1
To reserve a whole node for yourself	--exclusive
To chose a partition	--partition

More info:

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

Cluster Review



Login node vs Compute node

- When you log into “monsoon” interactively or via Ondemand you are “placed” on a 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!

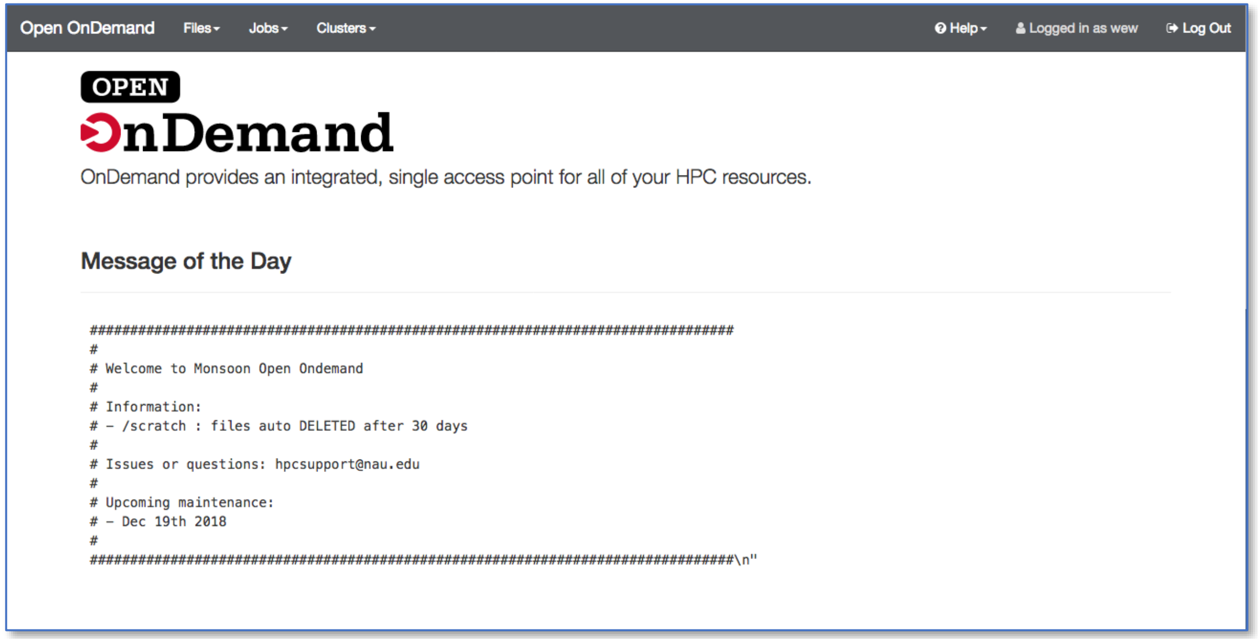
Interacting with Monsoon

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 shellll
  - 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 linux tools/commands)

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



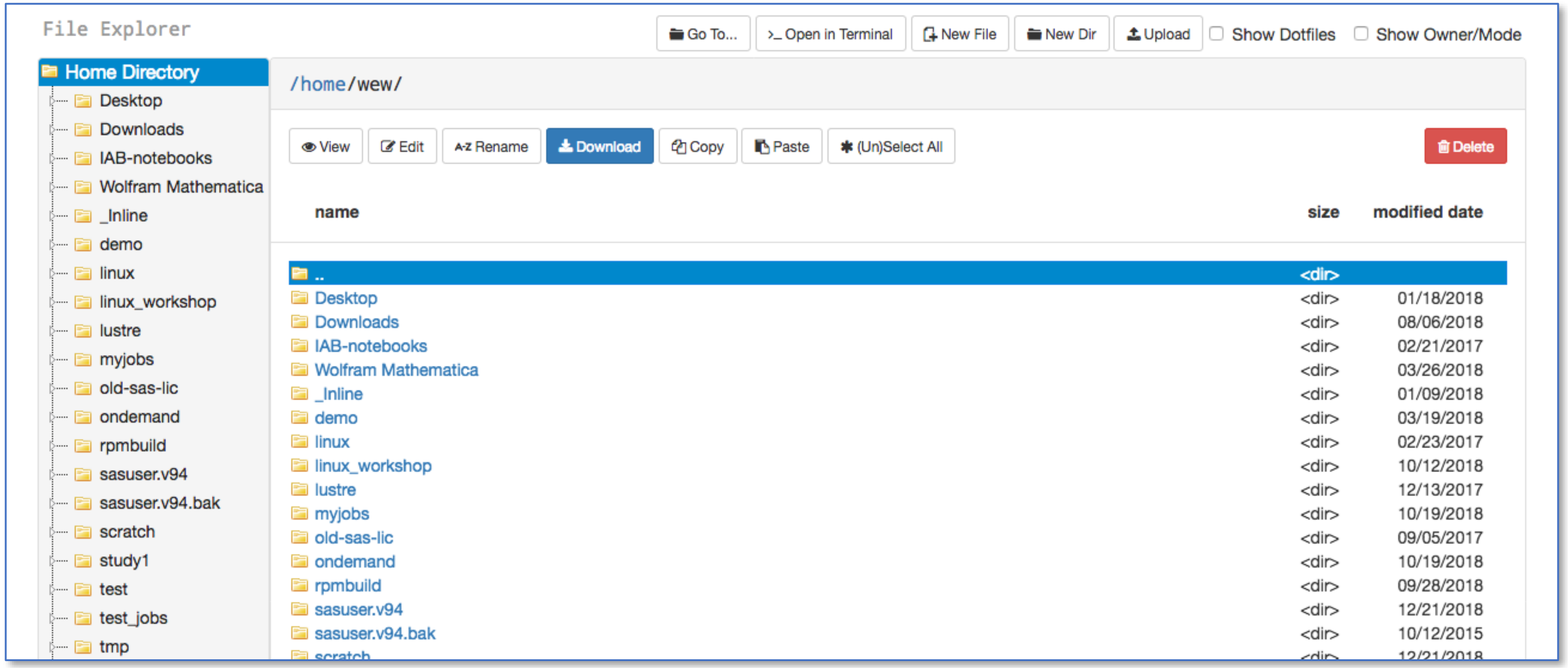
OnDemand provides an integrated, single access point for all of your HPC resources.

Message of the Day

```
################################################################################
#
# Welcome to Monsoon Open Ondemand
#
# Information:
# - /scratch : files auto DELETED after 30 days
#
# Issues or questions: hpcsupport@nau.edu
#
# Upcoming maintenance:
# - Dec 19th 2018
#
################################################################################\n"
```

Ondemand File Explorer

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



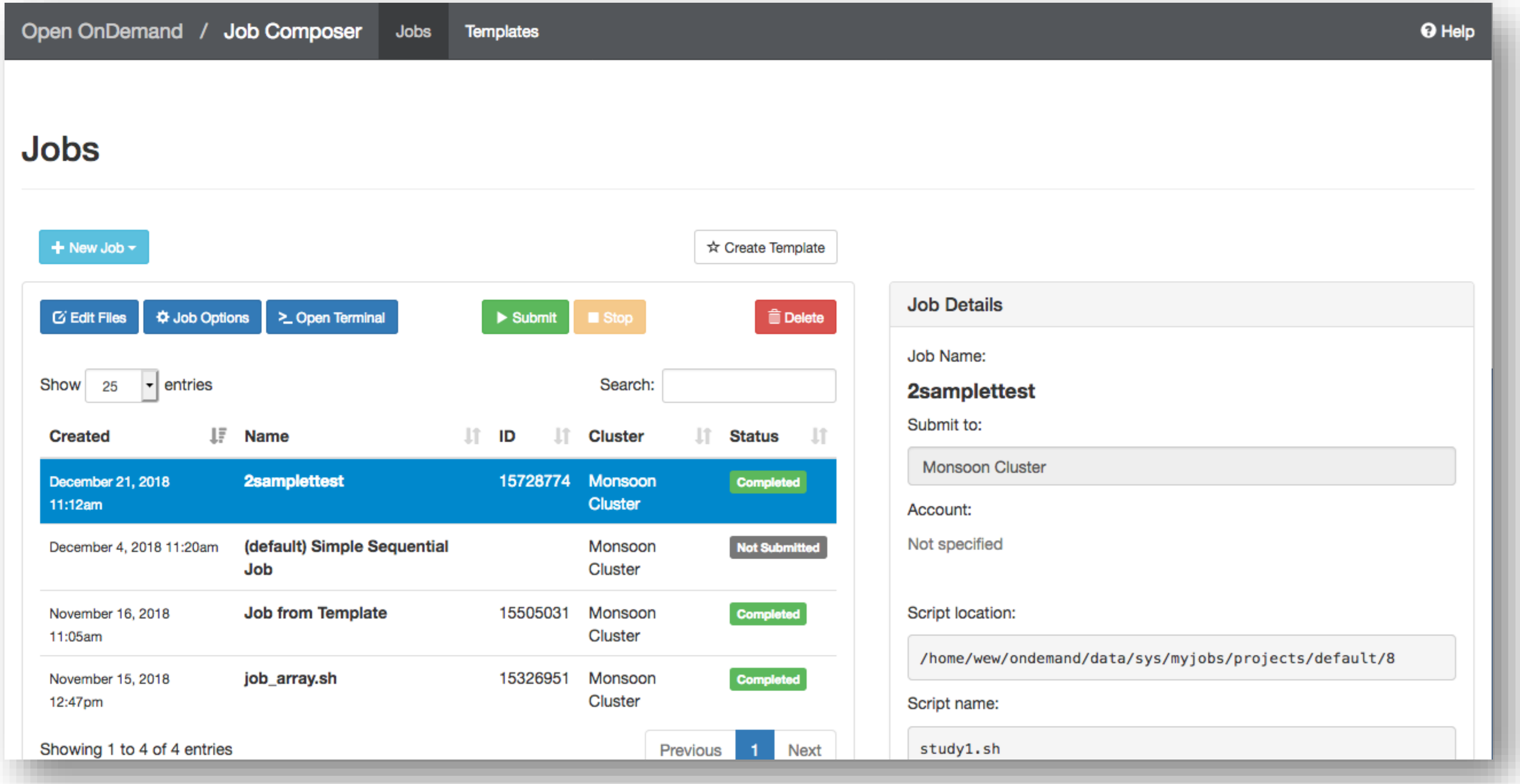
Home Directory
- Desktop
- Downloads
- IAB-notebooks
- Wolfram Mathematica
- _Inline
- demo
- linux
- linux_workshop
- lustre
- myjobs
- old-sas-lic
- ondemand
- rpmbuild
- sasuser.v94
- sasuser.v94.bak
- scratch
- study1
- test
- test_jobs
- tmp

/home/wew/

name	size	modified date
..	<dir>	
Desktop	<dir>	01/18/2018
Downloads	<dir>	08/06/2018
IAB-notebooks	<dir>	02/21/2017
Wolfram Mathematica	<dir>	03/26/2018
_Inline	<dir>	01/09/2018
demo	<dir>	03/19/2018
linux	<dir>	02/23/2017
linux_workshop	<dir>	10/12/2018
lustre	<dir>	12/13/2017
myjobs	<dir>	10/19/2018
old-sas-lic	<dir>	09/05/2017
ondemand	<dir>	10/19/2018
rpmbuild	<dir>	09/28/2018
sasuser.v94	<dir>	12/21/2018
sasuser.v94.bak	<dir>	10/12/2015
scratch	<dir>	12/21/2018

Ondemand Job Composer

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



Jobs

Created	Name	ID	Cluster	Status
December 21, 2018 11:12am	2samplettest	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

Showing 1 to 4 of 4 entries

Job Details

Job Name:

2samplettest

Submit to:

Monsoon Cluster

Account:

Not specified

Script location:

`/home/wew/ondemand/data/sys/myjobs/projects/default/8`

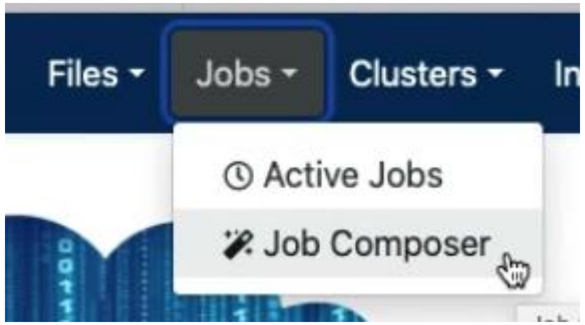
Script name:

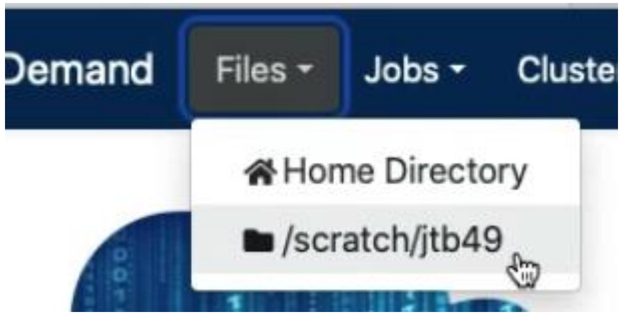
`study1.sh`

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 your jobscript run 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

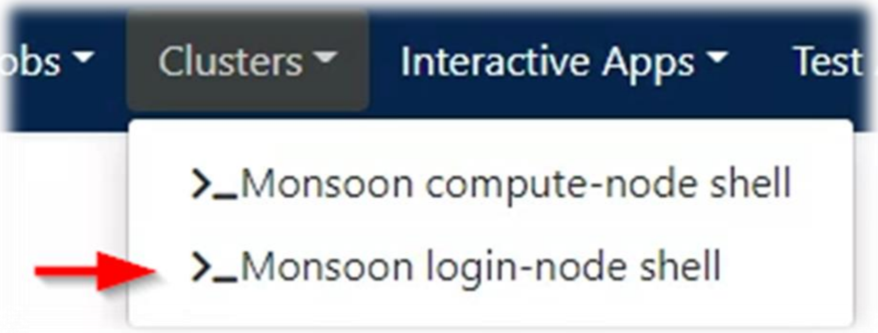
- Create a new job using **New Job > From Template**
- Select the ‘Long Job’ template, optionally rename it, and click **Create New Job**
- From the Jobs list, select the new draft job, and click **Open Editor** as before
- Change all “NAUID” to be your nau user-ID, again
- Make your jobscript load the 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)

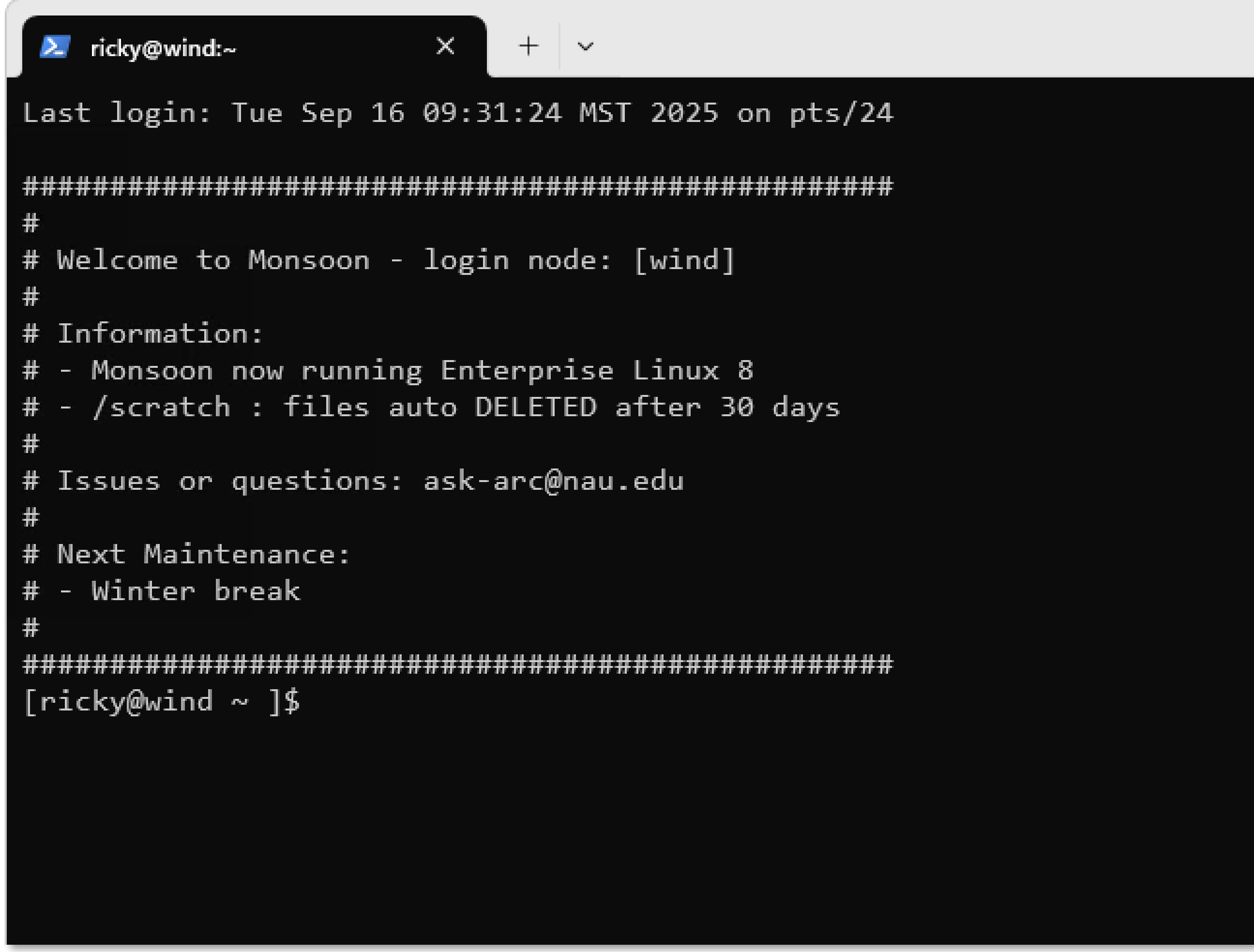
- We will be utilizing a CLI built-in to Ondemand
- Feel free to tryout the commands we discuss
- Tip: The Monsoon CLI may also be accessed outside of Ondemand using any other "ssh client" (ex: Putty on Windows, or via the ssh command in your PowerShell or Terminal app)
- Now open a **login-node shell** (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!

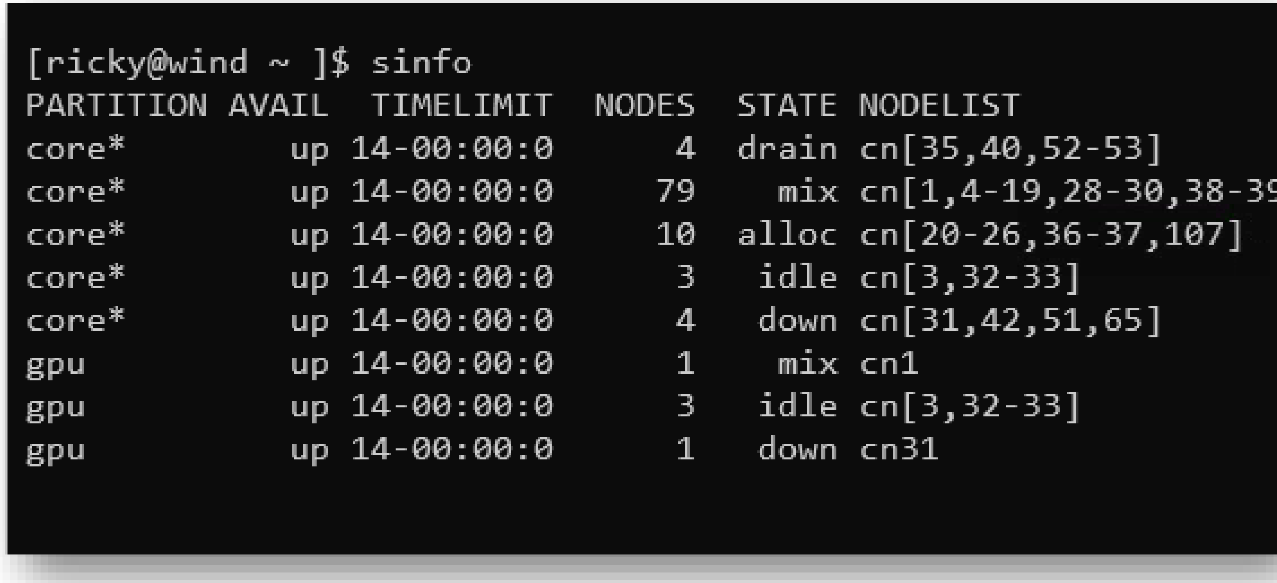


```
Last login: Tue Sep 16 09:31:24 MST 2025 on pts/24

##################################################
#
# 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



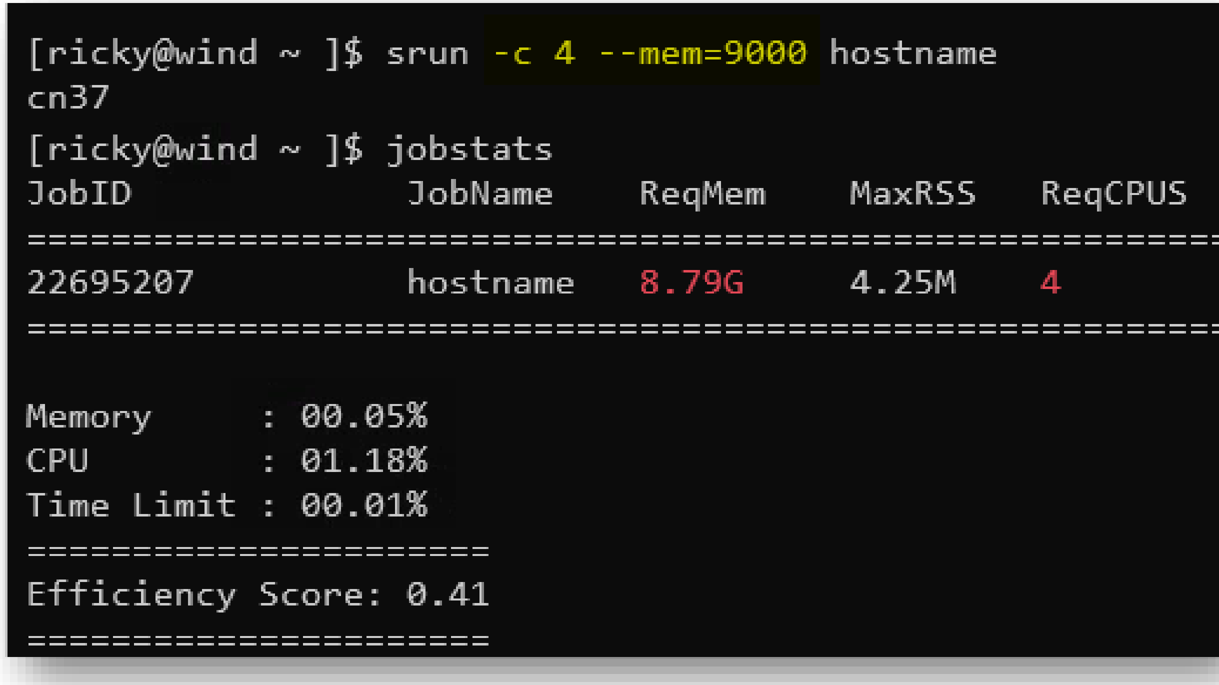
```
[ricky@wind ~ ]$ sinfo
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
core*        up 14-00:00:0      4  drain cn[35,40,52-53]
core*        up 14-00:00:0     79    mix cn[1,4-19,28-30,38-39
core*        up 14-00:00:0     10  alloc cn[20-26,36-37,107]
core*        up 14-00:00:0      3   idle cn[3,32-33]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

- squeue
  - View information about jobs located in the SLURM scheduling queue.
- squeue --start
- squeue -u <nauid>
- squeue -o "%j %u ..."
- squeue -p partitionname
- squeue -S sortfield
- squeue -t <state> (PD or R)

More info:

https://slurm.schedmd.com/squeue.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

Account hierarchy

- Your user account belongs to a parent faculty account (group)
- Your user account shares resources that are provided for your group
- Example:
  - account1
    - user1
    - user2
- View the account structure you belong to with: “sshare -a –A <account>”
- Example:
  - sshare -a -A account1

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!

TRESRunMins Limit

- What the heck is that!?
- A number which limits the total number of remaining resource minutes which your ***running*** jobs can occupy.
- Enables flexible resource limiting
- Staggers jobs
- Increases cluster utilization
- Leads to more accurate resource requests

- Sumofjobs(resource * timelimit remaining)

Examples

- 14400 = 10 jobs, 1 cpu, 1 day in length
- 144000 = 10 jobs, 10 cpu, 1 day in length
- 720000 = 10 jobs, 10 cpu, 5 days in length
- 720000 = 1000 jobs, 1 cpu, ½ day in length
- 1105920 = 1 job, 1024 cpus, 18 hrs in length

Questions?

- Check your groups resource min usage:
  - sshare -l

TRES run minutes (demo)

- Say, groupA's total cpu minute limit is: 5000
- Example, groupA submits three jobs
  - Job1:
    - 1 core
    - 1 day timelimit (1440 minutes)
    - 1 GB memory
  - Job2:
    - 2 core
    - 1 days (1440 minutes)
    - 16 GB memory
    - 2880 minutes total !
  - Job 3:
    - 1 core
    - 1 day (1440 minutes)
    - 1GB memory

TRES run minutes

– Assuming there are available monsoon resources

– How many jobs start?

– How many cpu minutes are in use?

– When is job 3 ELIGIBLE to start?

TRES run minutes

- Assuming there are available monsoon resources
- How many jobs start?
  - 2
- How many cpu minutes are in use?
  - 1440+2880 = 4320
- When is job 3 ELIGIBLE to start?
  - After ~6 hours (6*60 = 360), and 2 jobs (360*2) = 720 minutes

  - We have only 5000-4320 = 680 minutes available initially
  - After ~ 1/4 day goes by (360 minutes) * 2 (two jobs) = 720 minutes
  - 680 + 720 = 1400
  - After another 40 minutes we'll have 1440 at which point job starts

Helpful Linux Commands

List Files	ls options -l – to show more information
Change Directory	cd <directory path> cd by itself will return you to your home directory
Show/print current working directory	pwd
Copy Files	cp <source> <destination> use a period for the destination to copy a file 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>
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

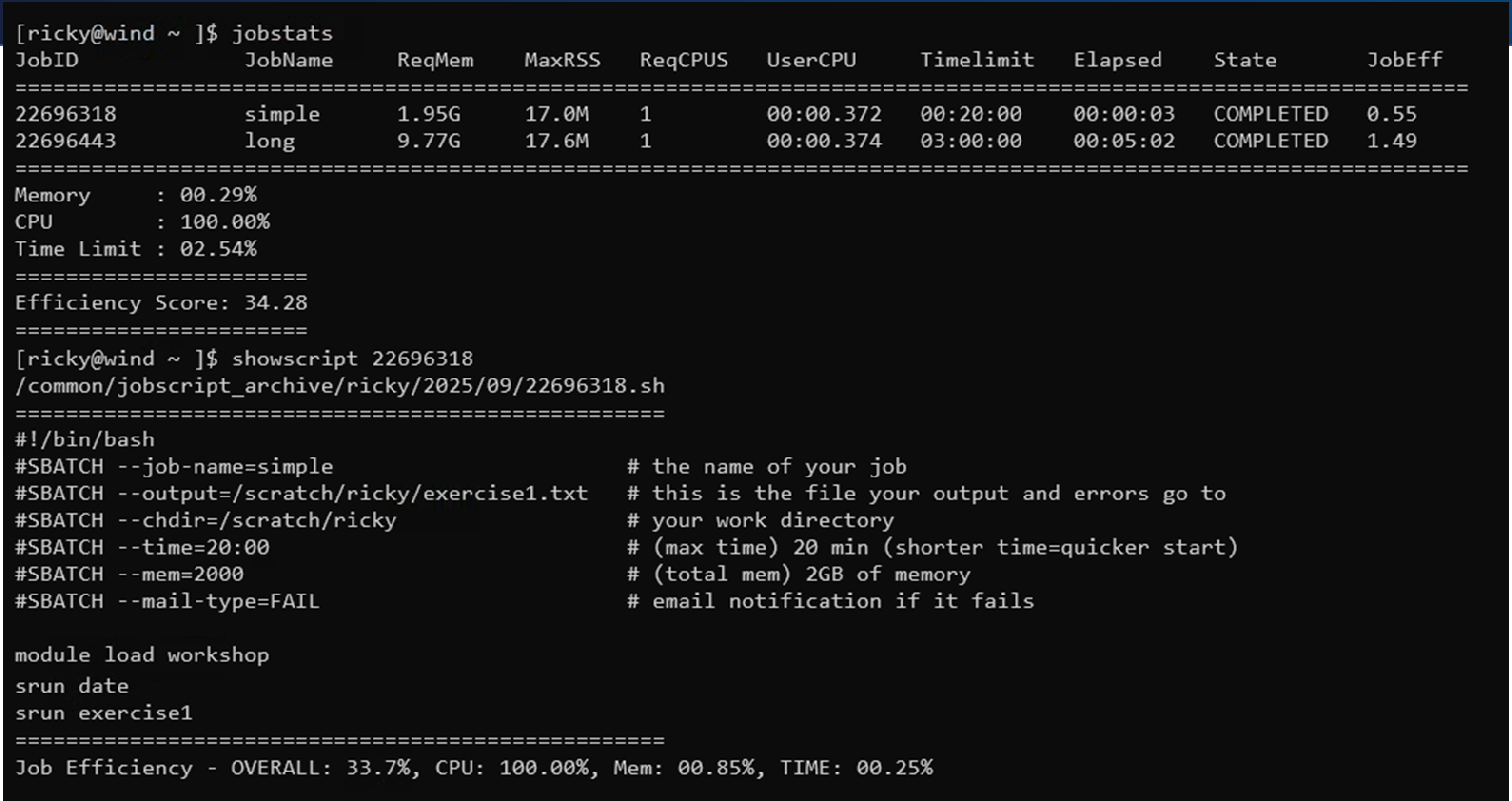
Retrieval of a job script

- 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

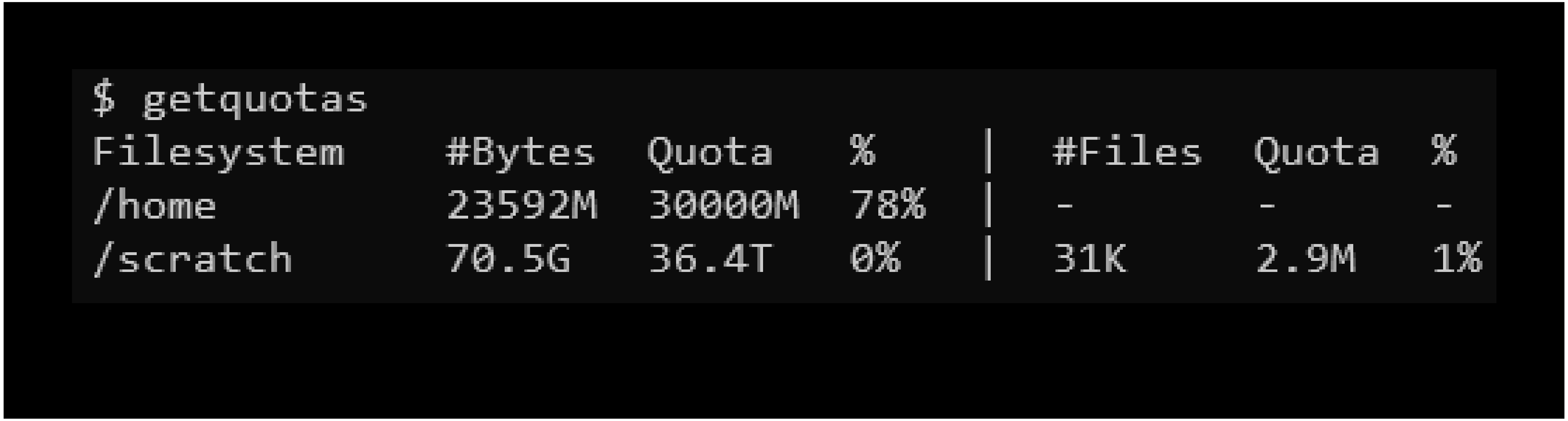


```
[ricky@wind ~ ]$ jobstats
JobID            JobName     ReqMem    MaxRSS    ReqCPUS   UserCPU      Timelimit    Elapsed      State        JobEff
==================================================================================================================
22696318         simple      1.95G     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

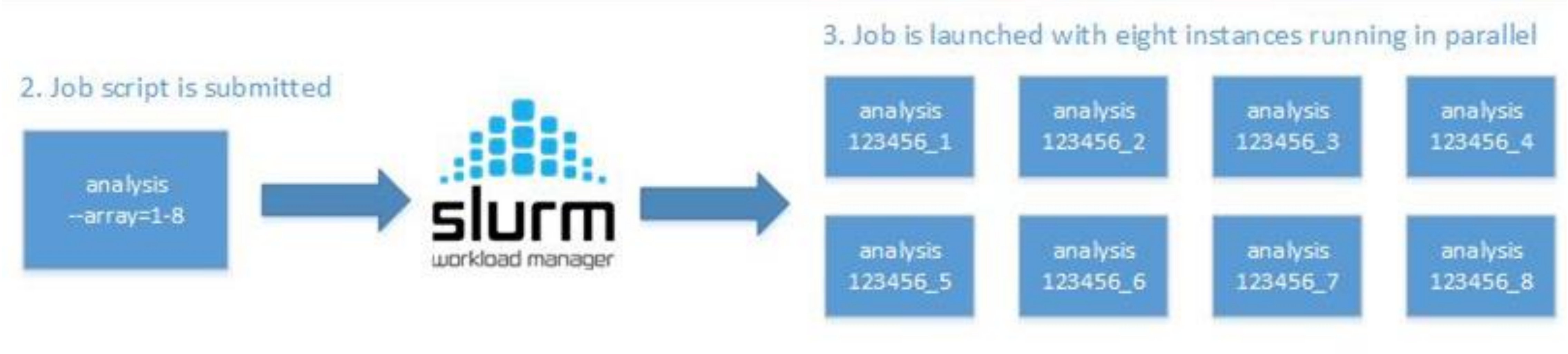
Confirming Your Account

- 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!



$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!

MPI Example

- Refer to the MPI example here:
  - /common/contrib/examples/job_scripts/mpijob.sh
- Edit it, for your work areas, then experiment:
  - Change number of tasks, nodes … etc
- Also can run the example like this:
  - srun --qos=debug –n4 /common/contrib/examples/mpi/hellompi

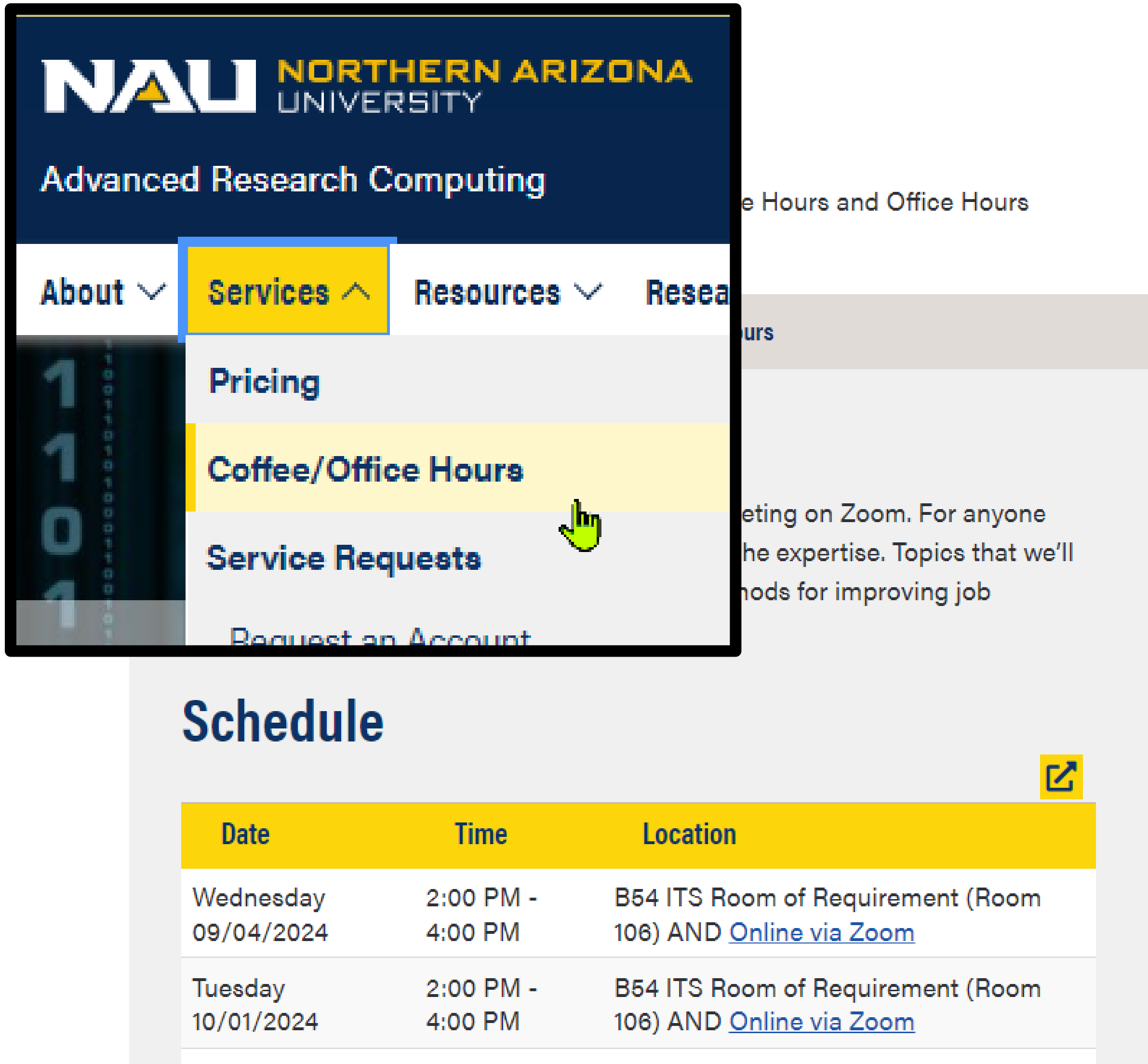
Keep these tips in mind

- 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

Workshops, Office-, and Coffee-hours!



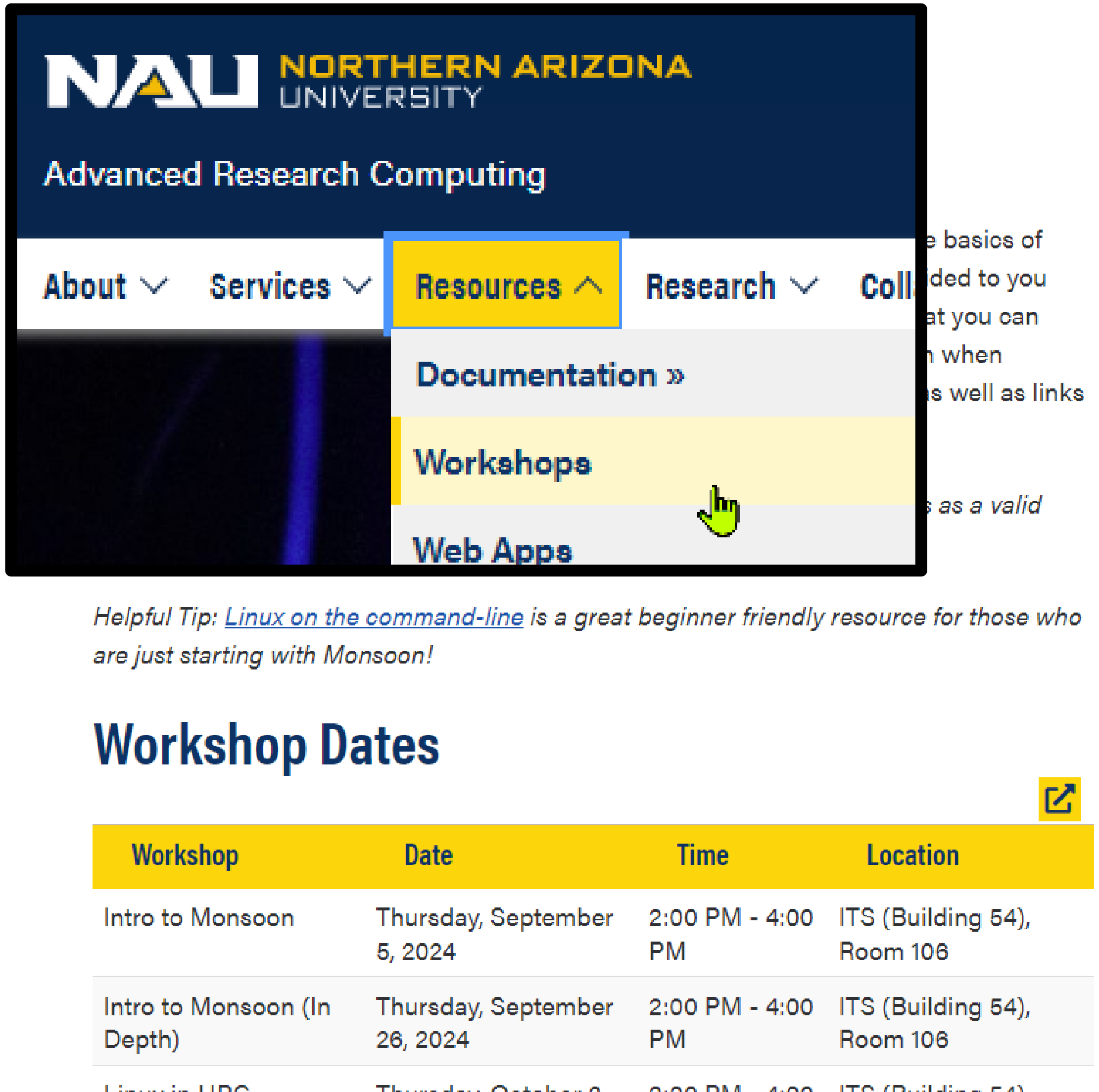
e Hours and Office Hours

urs

eting on Zoom. For anyone he expertise. Topics that we'll hods for improving job

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



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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	2:00 PM - 4:00	ITS (Building 54),

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