

Beginner's
Introduction to Computing at
CARC
with SLURM
(Biodiversity Informatics—
BIOL419/519)

Version 0.1

Goals

- 1) Logging in...
- 2) BASH (entering commands)
- 3) SLURM Scheduler (accessing hardware)

I hope to spend about an hour and 15 min.

Logging into Wheeler



First login to the Linux **workstation** in front of you using the username from the sign in sheet. The initial password is “Welcome2carc”.

Use your CARC username and password.

Matthew will help you get logged in if you have trouble.

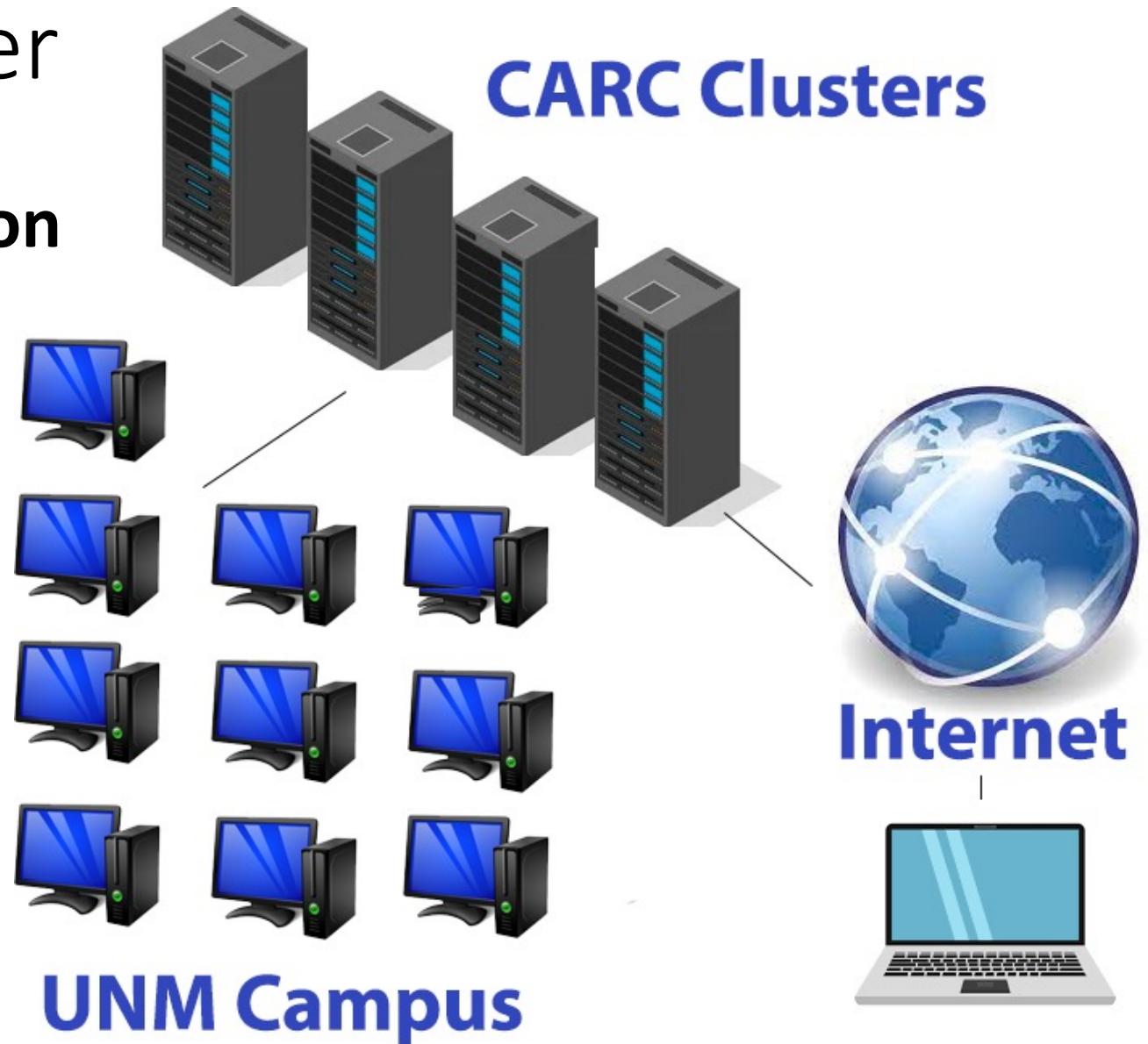
This is an “important step” so don’t let me move on until you have logged in

Logging into Wheeler

First login to the **workstation** in front of you.

You will always login to CARC cluster remotely.

These clusters don't even have monitors.



Logging into Wheeler



```
ssh vanilla@wheeler.alliance.unm.edu
```

Should prompt you for a password...

Don't let me move on until you are able to login.

Logging into Wheeler

```
ast login: Tue Jun 14 14:47:24 2022 from fricke.co.uk
-----
Welcome to Wheeler

Be sure to review the "Acceptable Use" guidelines posted on the CARC website.

For assistance using this system email help@carc.unm.edu.

Tutorial videos can be accessed through the CARC website: Go to
http://carc.unm.edu, select the "New Users" menu and then click
"Introduction to Computing at CARC".

Warning: By default home directories are world readable. Use the chmod command
to restrict access.

Don't forget to acknowledge CARC in publications, dissertations, theses and
presentations that use CARC computational resources:

"We would like to thank the UNM Center for Advanced Research Computing,
supported in part by the National Science Foundation, for providing the
research computing resources used in this work."

Please send citations to publications@carc.unm.edu.
-----
tarting SSH Key Agent...
gent pid 19486
fricke@wheeler:~ $
```

Set your password

```
[vanilla@wheeler beginner]$ passwd
```

Enter “Welcome2carc”

When prompted enter a password you would like to use

Our system will check whether it is too easy to guess.

Please enter the following command



```
cp -r /projects/shared/workshops/beginner/mystuff ~/
```

We will come help you if you have any trouble.

(Later I will go over what this command does)

mfricke@wheeler:~ \$

↑

Username

Understanding the BASH prompt...



Matthew — vanilla@wheeler:~ — ssh wheeler — 47x9

mfricke@wheeler:~ \$



Hostname

Understanding the BASH prompt...



Matthew — vanilla@wheeler:~ — ssh wheeler — 47x9

mfricke@wheeler:~ \$



This is the current working directory.
“~” is short for home directory

Understanding the BASH prompt...



Matthew — vanilla@wheeler:~ — ssh wheeler — 42x13

```
[vanilla@wheeler ~]$ pwd  
/users/vanilla  
[vanilla@wheeler ~]$ █
```

Figuring out where you are in the
filesystem... |



Matthew — vanilla@wheeler:~ — ssh wheeler — 42x13

```
[vanilla@wheeler ~]$ ls  
mystuff  wheeler-scratch  
[vanilla@wheeler ~]$
```

Figuring out where you are in the
filesystem...

 Matthew — vanilla@wheeler:~ — ssh wheeler — 49x13

```
[vanilla@wheeler ~]$ ls mystuff/
myfile1 myfile2
[vanilla@wheeler ~]$ █
```

Figuring out where you going...

```
[vanilla@wheeler ~]$ ls ./mystuff/  
myfile1 myfile2  
[vanilla@wheeler ~]$ ls ~/mystuff/  
myfile1 myfile2  
[vanilla@wheeler ~]$
```

Figuring out where you going...

```
[vanilla@wheeler ~]$ ls -l
total 4
drwxr-xr-x 2 vanilla users 4096 Jun 14 22:05 mystuff
lrwxrwxrwx 1 vanilla users    24 Jun 14 21:20 wheeler-scratch ->
/wheeler/scratch/vanilla
[vanilla@wheeler ~]$
```

Figuring out where you going...

```
[vanilla@wheeler ~]$ ls -l mystuff/
total 473704
-rw-r--r-- 1 vanilla users 483165473 Jun 14 23:20 myfile1
-rw-r--r-- 1 vanilla users          0 Jun 14 22:05 myfile2
[vanilla@wheeler ~]$
```

Figuring out where you going...

```
[vanilla@wheeler ~]$ ls -lh mystuff/
total 463M
-rw-r--r-- 1 vanilla users 461M Jun 14 23:20 myfile1
-rw-r--r-- 1 vanilla users     0 Jun 14 22:05 myfile2
[vanilla@wheeler ~]$
```

Figuring out where you going...

```
[vanilla@wheeler ~]$ quota -S
Disk quotas for user vanilla (uid 659):
  Filesystem    space   quota   limit   grace   files   quota   limit   grace
chama:/home/homes
                  488M    100G    200G
[vanilla@wheeler ~]$
```

Figuring out where you going...

```
[vanilla@wheeler ~]$ cd mystuff/  
[vanilla@wheeler ~/mystuff]$
```

Use the tab key to autocomplete

Going somewhere new...

- Now you know how to find your way around filesystems using bash
- Let's see how to modify the filesystem.
 - In bash to move a file we use the `mv` command.
 - To copy a file it is `cp`.
 - To copy files from CARC to a personal computer use `scp` or `rsync`.

```
[vanilla@wheeler beginner]$ pwd  
/projects/shared/workshops/beginner  
[vanilla@wheeler beginner]$ cd ~  
[vanilla@wheeler ~]$ pwd  
/users/vanilla  
[vanilla@wheeler ~]$
```

First return to your home
directory...

```
[vanilla@wheeler ~]$ cd mystuff  
[vanilla@wheeler ~/mystuff]$ mv myfile1 myfile0  
[vanilla@wheeler ~/mystuff]$ ls  
myfile0 myfile2 myfile3  
[vanilla@wheeler ~/mystuff]
```

Modifying the filesystem...
moving a file.

```
[vanilla@wheeler ~/mystuff]$ cp myfile0 myfile1  
[vanilla@wheeler ~/mystuff]$
```



Source Destination

```
[vanilla@wheeler ~/mystuff]$ ls  
myfile0 myfile1 myfile2 myfile3  
[vanilla@wheeler ~/mystuff]$
```

Modifying the filesystem...
copying a file.

```
[vanilla@wheeler ~]$ cp -r mystuff mystuff2
```

```
[vanilla@wheeler ~]$
```



Source



Destination

```
[vanilla@wheeler ~]$ ls
```

```
mystuff mystuff2 wheeler-scratch
```

Copying a whole directory tree...

```
Lycaon:~ matthew$ scp vanilla@wheeler.alliance.unm.edu:~/mystuff/myfile3 Desktop/
```



Source

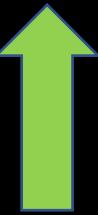


Destination

```
(vanilla@wheeler.alliance.unm.edu) Password:  
myfile3          100%    40      2.0KB/s   00:00
```

Copying data to a personal
computer from CARC...

```
Lycaon:~ matthew$ scp -r vanilla@wheeler.alliance.unm.edu:~/mystuff Desktop/
```



Source



Destination

```
(vanilla@wheeler.alliance.unm.edu) Password:
```

myfile1	100%	1024KB	6.5MB/s	00:00
myfile2	100%	2048KB	382.5KB/s	00:05
myfile3	100%	40	3.2KB/s	00:00
myfile0	100%	1024KB	8.8MB/s	00:00

Copying data to a personal
computer from CARC...

```
Lycaon:~ matthew$ scp -r Desktop/mystuff vanilla@wheeler.alliance.unm.edu:~/
```



Source



Destination

```
(vanilla@wheeler.alliance.unm.edu) Password:
```

myfile1	100%	1024KB	591.5KB/s	00:01
myfile0	100%	1024KB	2.0MB/s	00:00
myfile2	100%	2048KB	2.1MB/s	00:00
myfile3	100%	40	2.1KB/s	00:00

To copy from a personal
computer to CARC...

ssh vanilla@wheeler.alliance.unm.edu

Log back into wheeler...

```
[vanilla@wheeler ~]$ mkdir newdir
```

```
[vanilla@wheeler ~]$
```

```
[vanilla@wheeler ~]$ ls
```

```
mystuff mystuff2 newdir wheeler-  
scratch
```

Creating a new directory...

Software Access

Lmod
Modules

Conda

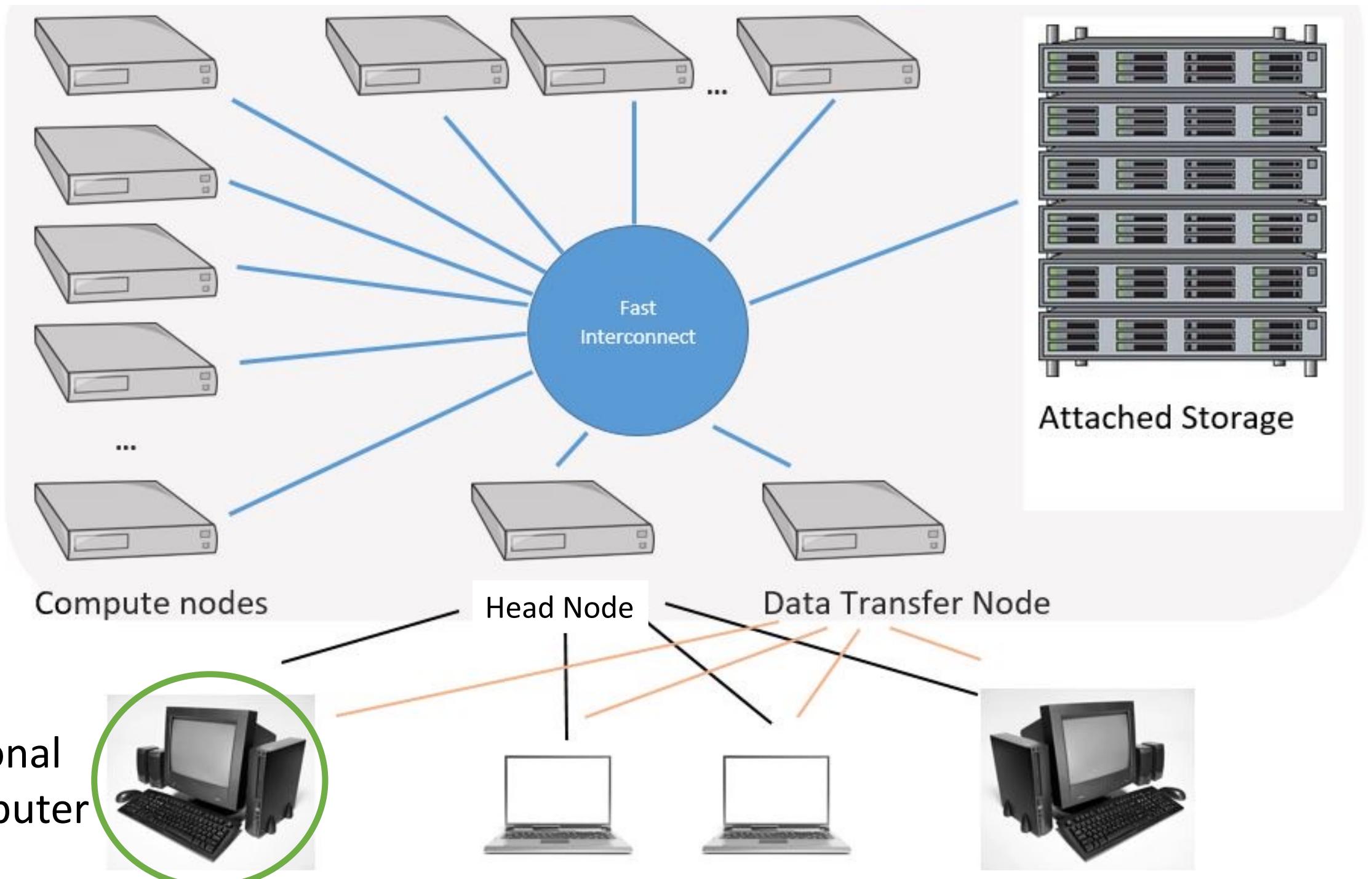
```
[vanilla@wheeler ~]$ module load matlab/R2021a
Lmod has detected the following error: Matlab may only be run on compute
nodes. wheeler is not a compute node. Exiting...
While processing the following module(s):
  Module fullname      Module Filename
  -----      -----
matlab/R2021a      /opt/local/modules/matlab/R2021a.lua
```

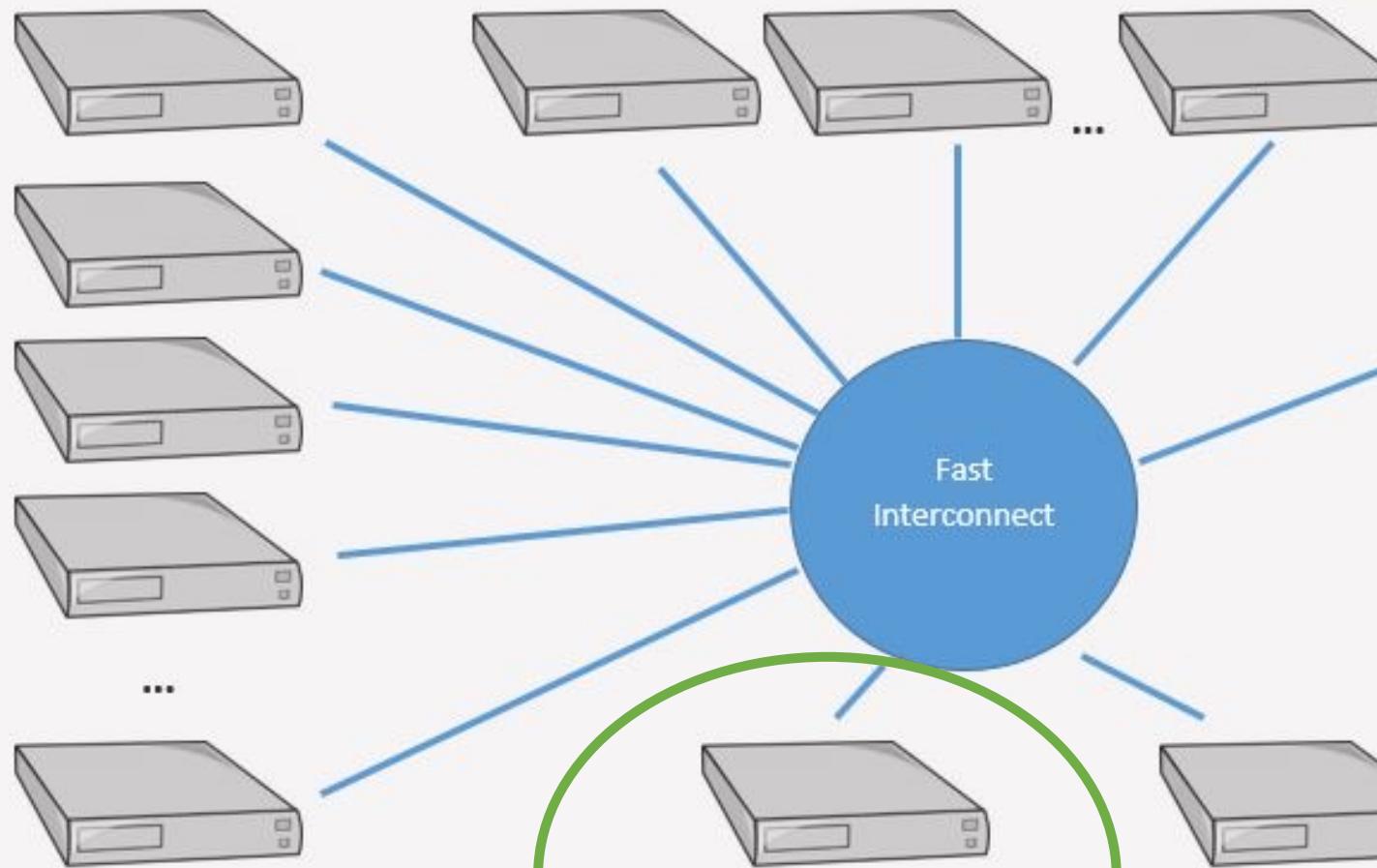
What is a compute node?

Getting access to software...

HPC Cluster







Compute nodes

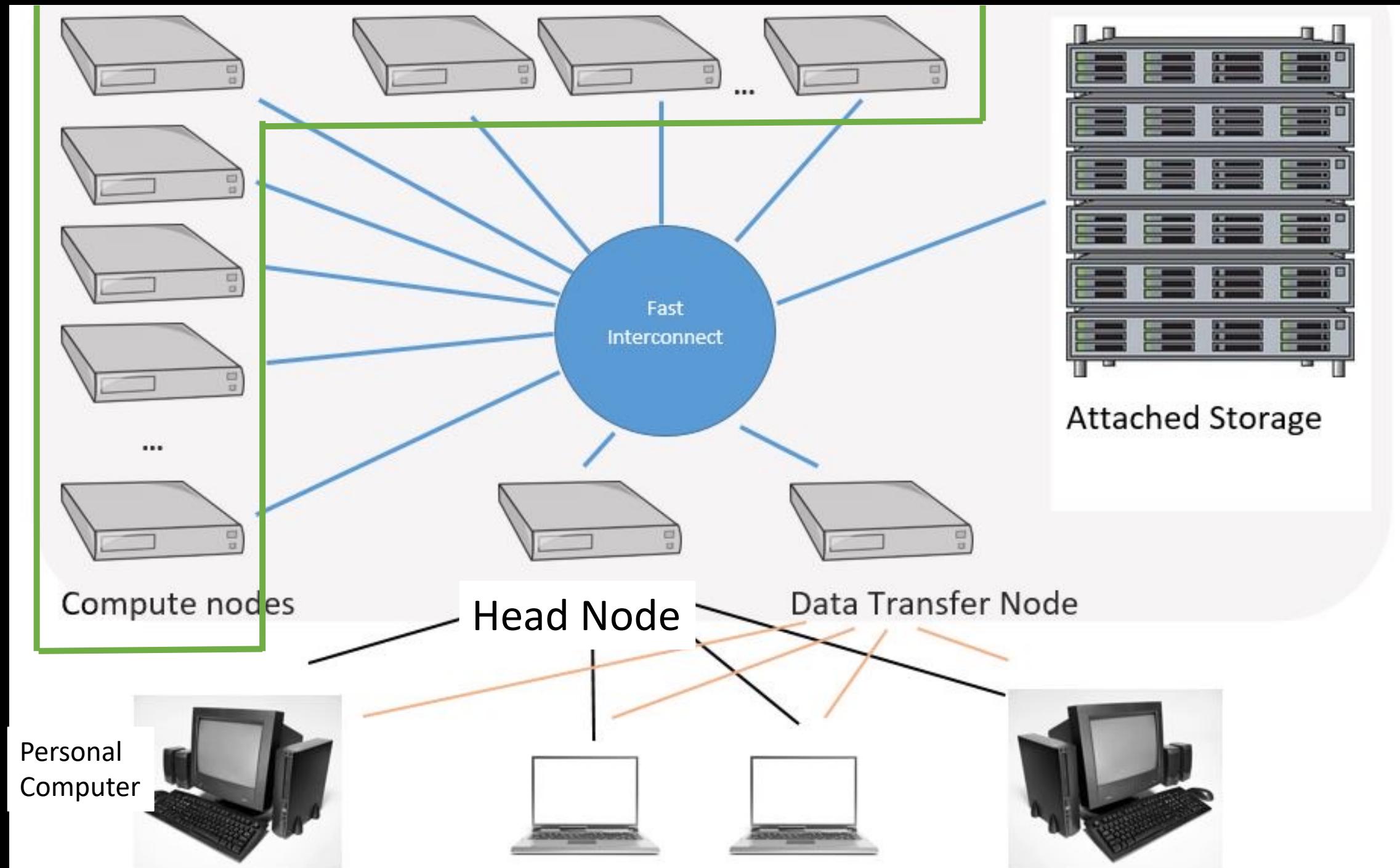
Head Node

Data Transfer Node

Personal Computer



Attached Storage





WARNING !!

Never run computations on the head node

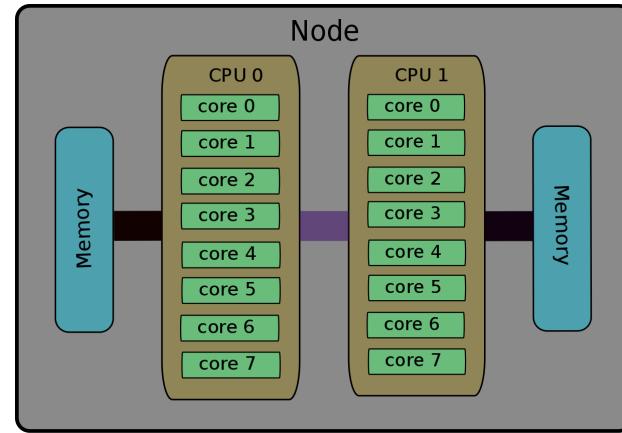
Always use compute nodes

```
[vanilla@wheeler ~]$ qgrok
```

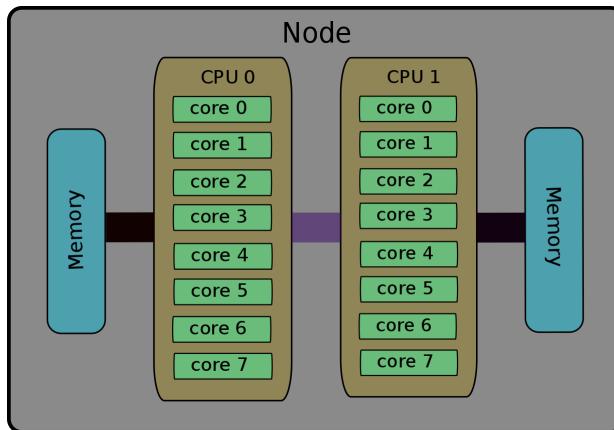
queues	free	busy	offline	jobs	nodes	CPUs
-----	-----	-----	-----	-----	-----	-----
normal	0	299	1	97	300	2400
debug	4	0	0	0	4	32
totals:	4	299	1	97	304	2432

Compute nodes and partitions...

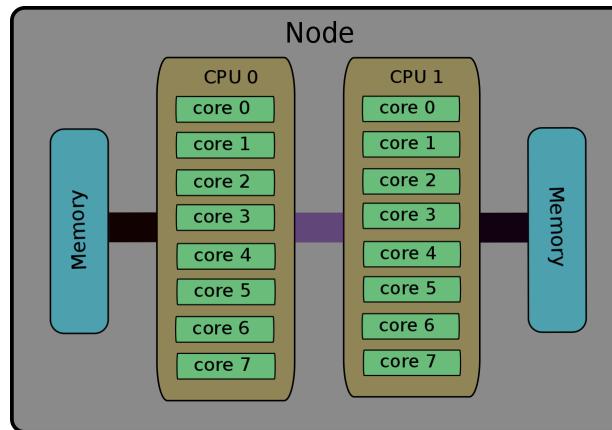
Head Node (wheeler)



Compute Nodes

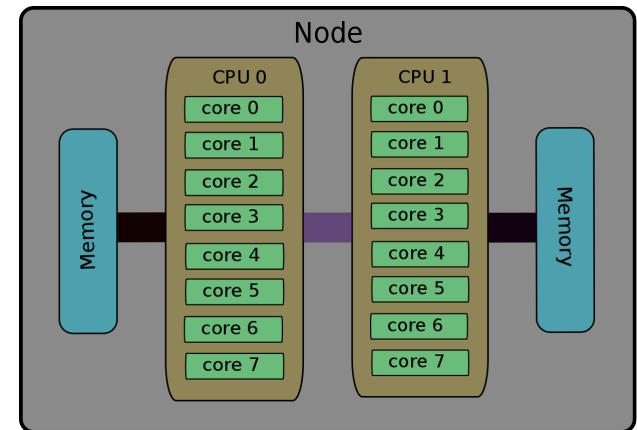


wheeler001



wheeler002

...



wheeler304



Technology, IT etc.

SLURM

means

Simple Linux Utility for Resource Management

ENJOY

Slurm

SODA

IT'S HIGHLY ADDICTIVE!

VOTED #1

SOFT DRINK OF THE 31ST CENTURY!



SELENE MCKENRE

```
[vanilla@wheeler ~]$ Squeue
```

JOBID	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
159914	normal	co-mcpdf	nsharma2	CG	2-00:00:26	1	wheeler257
159915	normal	co-mcpdf	nsharma2	CG	2-00:00:26	1	wheeler257
159916	normal	co-mcpdf	nsharma2	CG	2-00:00:26	1	wheeler257
159917	normal	co-mcpdf	nsharma2	CG	2-00:00:26	1	wheeler257
159918	normal	co-mcpdf	nsharma2	CG	2-00:00:26	1	wheeler257
159919	normal	co-mcpdf	nsharma2	CG	2-00:00:26	1	wheeler257
159912	normal	co-mcpdf	nsharma2	CG	2-00:00:28	1	wheeler257
159913	normal	co-mcpdf	nsharma2	CG	2-00:00:28	1	wheeler257
166800_[21-100%10]	normal	Jannat	jannat	PD	0:00	1	(JobArrayTaskLimit)
167067	normal	WINDENER	rubeldas	PD	0:00	36	
(QOSMaxCpuPerUserLimit)							
167068	normal	WINDENER	rubeldas	PD	0:00	24	

Slurm....

```
[vanilla@wheeler ~]$ srun --partition debug --nodes 2 hostname
srun: Account not specified in script or
~/default_slurm_account, using latest project
wheeler302.alliance.unm.edu
You have not been allocated GPUs. To request GPUs, use the -G
option in your submission script.
wheeler301.alliance.unm.edu
[vanilla@wheeler ~]$ srun --partition debug --nodes 2 hostname
```

The srun command...

```
[vanilla@wheeler ~]$ srun --partition debug --ntasks 8 hostname
srun: Account not specified in script or ~/.default_slurm_account, using
latest project
wheeler302.alliance.unm.edu
wheeler302.alliance.unm.edu
wheeler302.alliance.unm.edu
wheeler302.alliance.unm.edu
wheeler302.alliance.unm.edu
wheeler302.alliance.unm.edu
You have not been allocated GPUs. To request GPUs, use the -G option in your
submission script.
wheeler302.alliance.unm.edu
wheeler302.alliance.unm.edu
```

The srun command...

```
[vanilla@wheeler ~]$ cp -r /projects/shared/workshops/beginner/vecadd ~  
[vanilla@wheeler ~]$
```

Review, what does this command do?

```
[vanilla@wheeler ~]$ cd vecadd/  
[vanilla@wheeler ~/vecadd]$ module load openmpi/4.1.2-q2zi
```

What do these commands do?

```
[vanilla@wheeler ~/vecadd] $ srun --partition debug --ntasks 4 vecaddmpi
```

Now run the program with
“srun”...

```
[vanilla@wheeler ~]$ qgrok
```

queues	free	busy	offline	jobs	nodes	CPUs
normal	0	299	1	97	300	2400
debug	4	0	0	0	4	32
totals:	4	299	1	97	304	2432

srun is good but HPC centers are
busy!

Workflow

Head Node

User 1

Program A

Script A

User 2

Program B

Script B

Compute Node 01

Compute Node 02

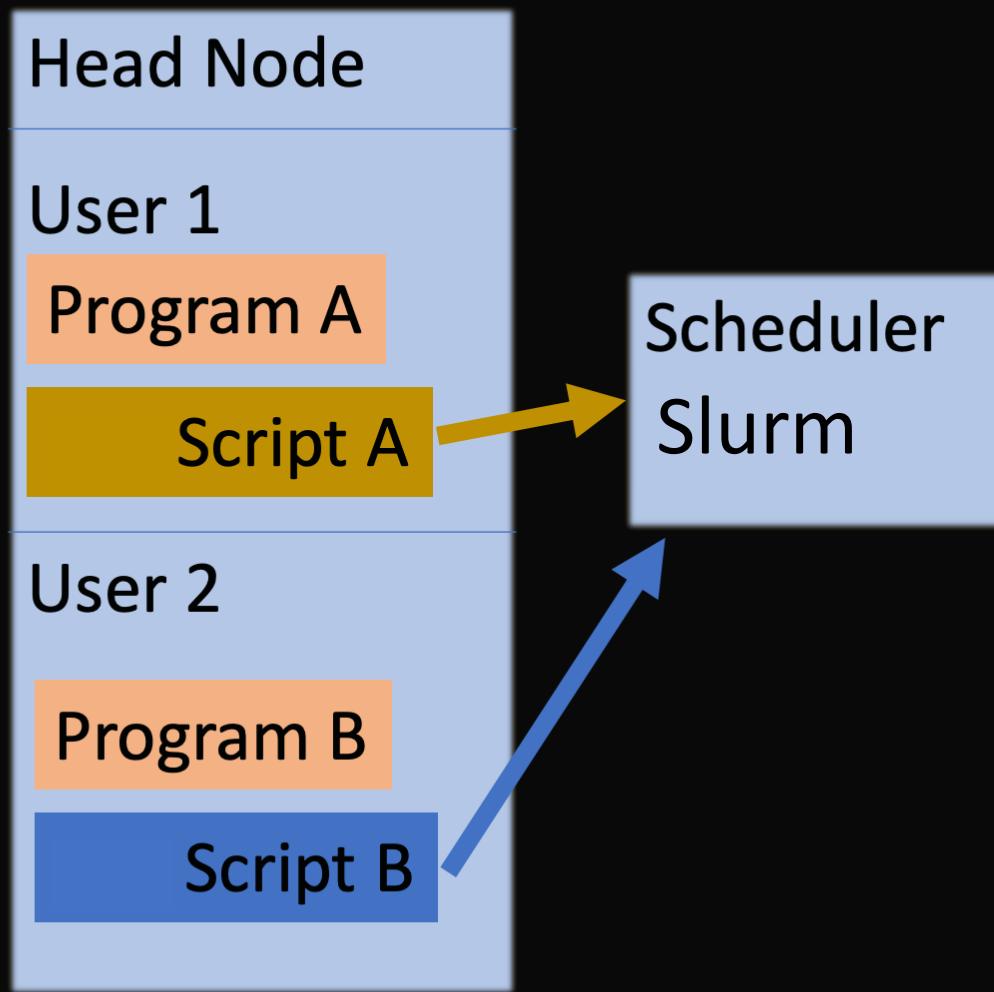
Compute Node 03

Compute Node 04

Compute Node 05

Shared filesystems – All nodes can access the same programs and write output

Workflow



Compute Node 01

Compute Node 02

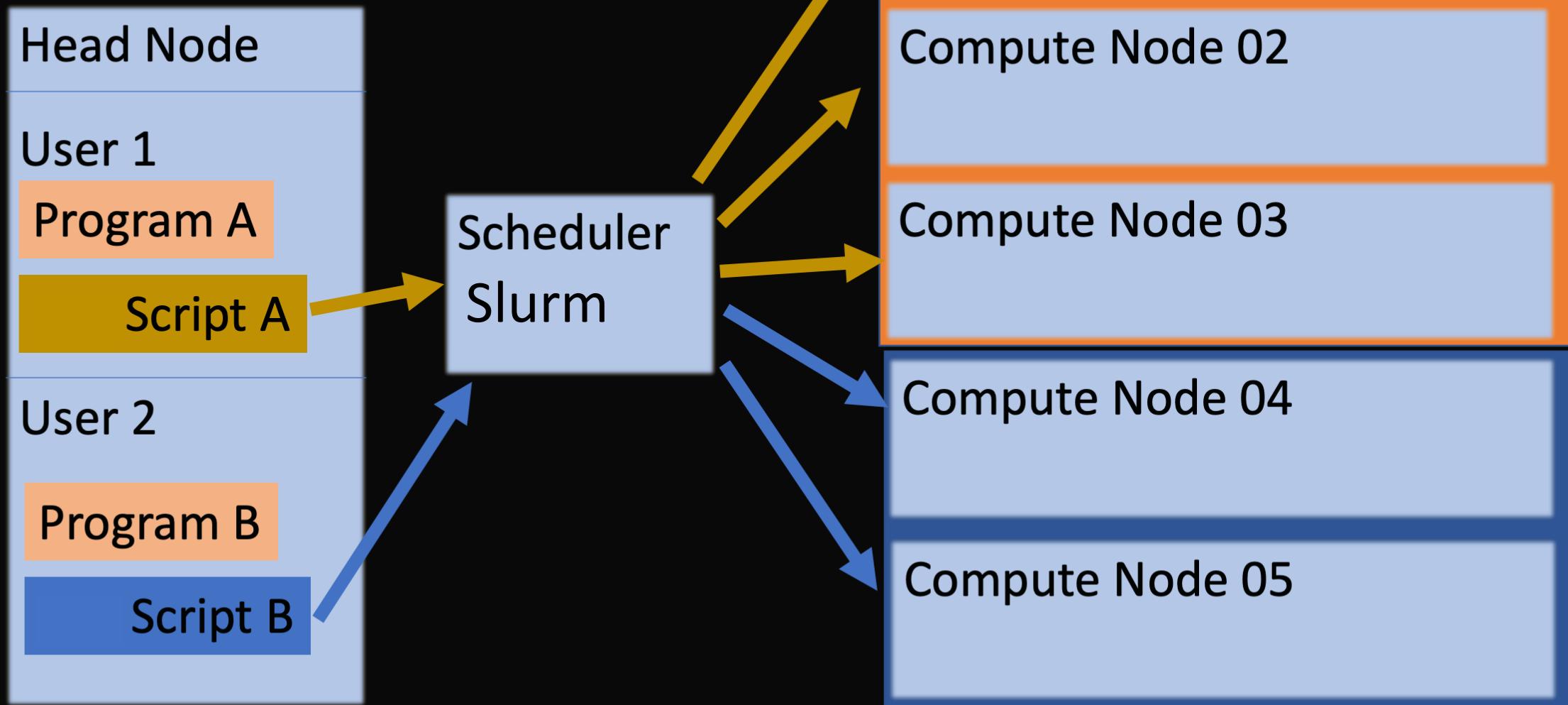
Compute Node 03

Compute Node 04

Compute Node 05

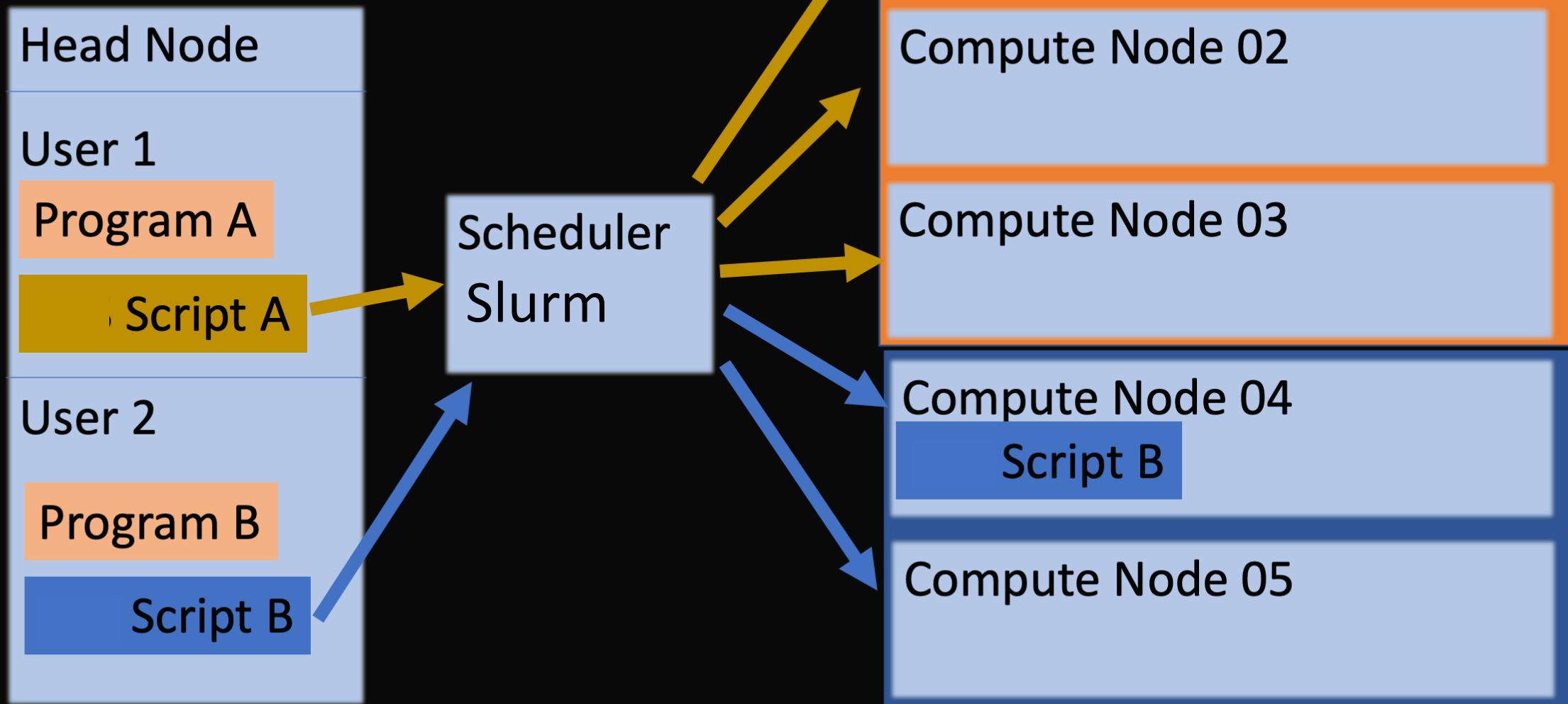
Shared filesystems – All nodes can access the same programs and write output

Workflow



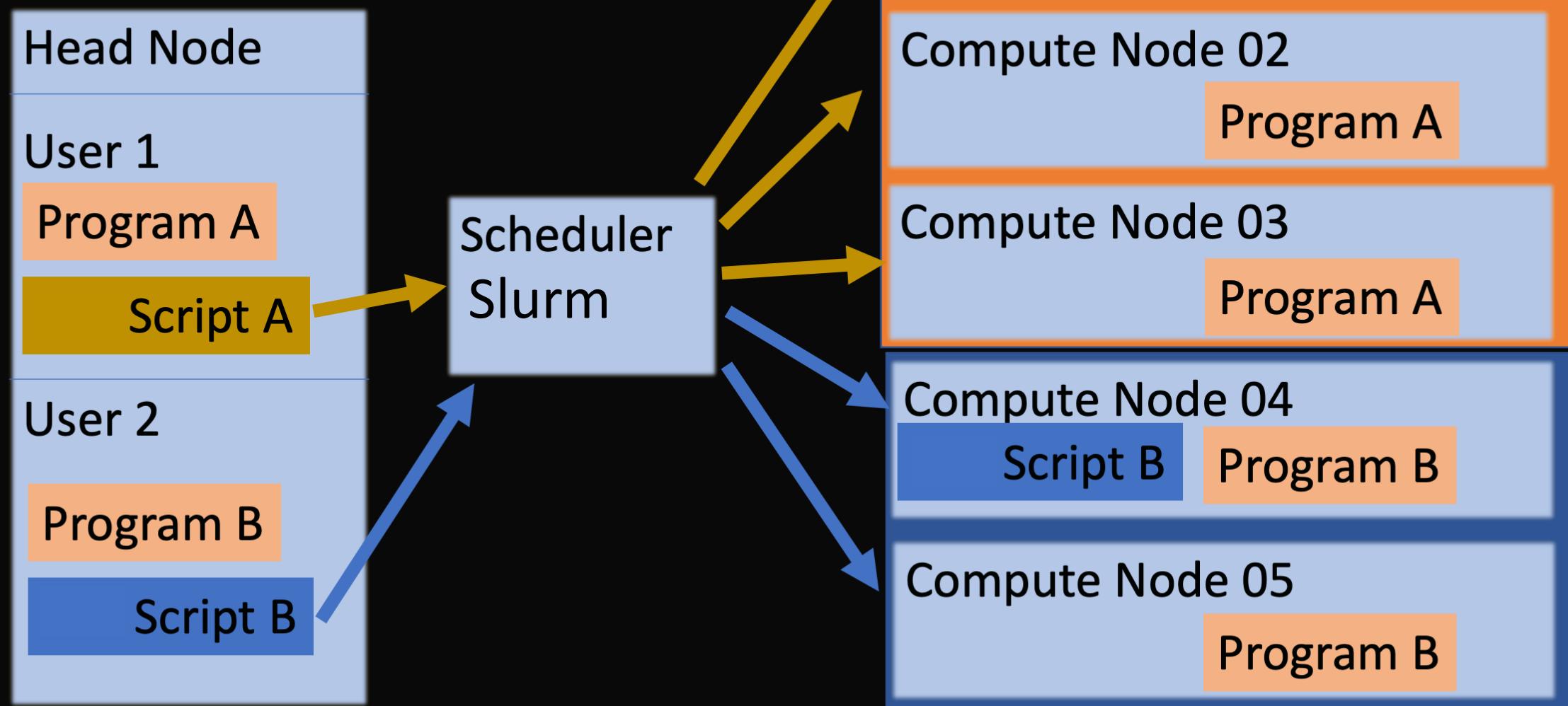
Shared filesystems – All nodes can access the same programs and write output

Workflow



Shared filesystems – All nodes can access the same programs and write output

Workflow



Shared filesystems – All nodes can access the same programs and write output

qgrok

sbatch

squeue -u USERNAME

Scheduler

Running Programs on Compute Nodes

- qgrok
- Intro to the Slurm Scheduler
- The srun command
- sbatch
- sinfo
- squeue
- squeue -u username --start
- <https://www.cism.ucl.ac.be/Services/Formations/slurm/2016/slurm.pdf>
- <https://www.nrel.gov/hpc/assets/pdfs/slurm-advanced-topics.pdf>

The screenshot shows a terminal window with the following details:

- Title Bar:** Matthew — ssh wheeler — 71x19
- Menu Bar:** File Edit Options Buffers Tools Sh-Script Help
- Content:** A Slurm script with syntax highlighting. The code includes Slurm directives (#SBATCH) and a command (sleep).

```
#!/bin/bash
#SBATCH --job-name=demo
#SBATCH --ntasks=4
#SBATCH --time=00:10:00
#SBATCH --mem-per-cpu=4G
#SBATCH --mail-user=yourusername@unm.edu
#SBATCH --mail-type=All

# Enter the commands you want to run below here:
sleep 60
echo Hello from node $HOSTNAME
```

Slurm Script

```
[vanilla@wheeler ~/vecadd]$ cat vecaddmpi.sh
#!/bin/bash
#SBATCH --job-name=vecaddmpi
#SBATCH --ntasks=4
#SBATCH --time=00:10:00
#SBATCH --mem-per-cpu=4G
#SBATCH --mail-user=yourusername@unm.edu
#SBATCH --mail-type=All
#SBATCH --output=vecaddmpi.out

module load openmpi/4.1.2-q2zi
srun --mpi=pmi2 ./vecaddmpi
```

Slurm Script

```
vanilla@wheeler:~/vecadd $ sbatch vecaddmpi.sh
sbatch: Using account 2016199 from ~/.default_slurm_account
Submitted batch job 167571
```

```
vanilla@wheeler:~/vecadd $ squeue --me
              JOBID PARTITION      NAME      USER ST      TIME  NODES
NODELIST(REASON)
      167571    normal  vecaddmp  vanilla  R      0:07      1 Wheeler145
```

Slurm Script

```
vanilla@wheeler:~/vecadd $ tail -f vecaddmpi.out
You have not been allocated GPUs. To request GPUs, use the -G option in your
submission script.
Assigning compute node to rank 1.
ComputeNode: Starting with rank 1.
ComputeNode (1): Waiting for vectors from dataserver with rank 3...
Assigning compute node to rank 2.
ComputeNode: Starting with rank 2.
ComputeNode (2): Waiting for vectors from dataserver with rank 3...
Will try to allocate a vector of size 1 GB.
```

Slurm Script

```
vanilla@wheeler:~/vecadd $ tail -f vecaddmpi.out
You have not been allocated GPUs. To request GPUs, use the -G option in your
submission script.
Assigning compute node to rank 1.
ComputeNode: Starting with rank 1.
ComputeNode (1): Waiting for vectors from dataserver with rank 3...
Assigning compute node to rank 2.
ComputeNode: Starting with rank 2.
ComputeNode (2): Waiting for vectors from dataserver with rank 3...
Will try to allocate a vector of size 1 GB.
```

Slurm Script

Useful Slurm Commands

squeue --me --long	shows information about jobs you submitted
squeue --me --start	shows when slurm expects your job to start
scancel jobid	cancels a job
sacct	shows your job history

```
vanilla@wheeler:~/vecadd $ seff 167573
Job ID: 167573
Cluster: wheeler
User/Group: mfricke/users
State: COMPLETED (exit code 0)
Nodes: 1
Cores per node: 4
CPU Utilized: 00:01:03
CPU Efficiency: 78.75% of 00:01:20 core-walltime
Job Wall-clock time: 00:00:20
Memory Utilized: 39.55 MB (estimated maximum)
Memory Efficiency: 0.24% of 16.00 GB (4.00 GB/core)
```

Slurm Script

CARC Resources

- Tutorial Videos
- Written Tutorials



QuickBytes

Quickbytes are tutorials designed to help CARC users.

- Linux-Intro
- Running jobs
 - Logging in
 - SSH keys and Config file
 - Transferring data
 - PBS/TORQUE
 - Sample PBS script
 - Submitting jobs
 - Check running jobs
 - Managing modules
 - Intro to Slurm
 - Converting PBS to Slurm
 - Intro to Slurm accounting at CARC

A screenshot of a YouTube channel page for 'UNMCARC'. The channel name is 'QuickBytes'. It has 16 videos and 2,870 views, last updated on Jan 5, 2022. A note on the page states: 'Short Tutorials on CARC Systems - DUE TO THE RECENT WHEELER UPGRADE THESE VIDEOS WILL BE REPLACED SOON.' The channel has a logo for 'UNM CENTER FOR ADVANCED RESEARCH COMPUTING'. There is a red 'SUBSCRIBE' button. On the right side, there is a list of six video thumbnails with titles and durations:

- 1 Intro to the UNM Center for Advanced Research Computing (5:53)
- 2 Projects and Accounts (8:47)
- 3 Logging into CARC Systems (12:48)
- 4 Storage Systems (13:11)
- 5 Transferring data (21:56)
- 6 Environment Modules (6:04)

Getting Help

help@carc.unm.edu

Office hours