HIGH PERFORMANCE RESEARCH COMPUTING

HPRC Training

Introduction to HPRC Computing Resources

September 15, 2023

High Performance
Research Computing
DIVISION OF RESEARCH

Outline

- **Introduction**
  - Setup
  - Usage Policies
  - HPRC Cluster Overview
- **Getting Started**
  - Accessing HPRC Clusters
  - HPRC Portal
- **Software Infrastructure**
  - Module System
  - Python Virtual Environments
- **Cluster Computing with Slurm**
- **Need Help?**

Introduction

Setup For This Course

To access the resources:

- HPRC Account: https://hprc.tamu.edu/user_services/#accounts
- TFA set up: https://it.tamu.edu/duo/

To do the exercises:

- Basic Linux/Unix skills
  - Slides from our LINUX short course are at: hprc.tamu.edu/training/intro_linux.html
  - Watch the relevant Introduction and Primer videos on our YouTube Channel: https://www.youtube.com/texasamhprc

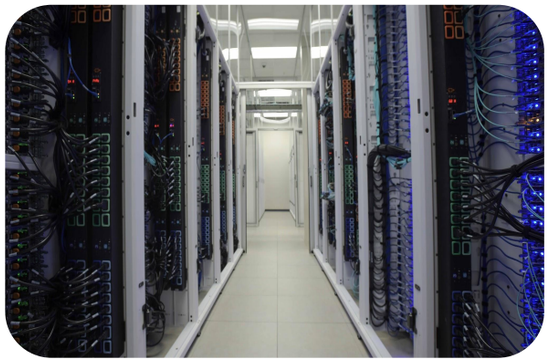
Answers to frequently asked questions can be found on our KB: https://hprc.tamu.edu/kb/FAQ/Accounts/

HPRC Clusters

- We operate four clusters
- Today we'll just cover the two "traditional" clusters:
  - Terra
  - Grace
- We have a separate course for the "composable" clusters:
  - FASTER
  - ACES

Terra

FASTER



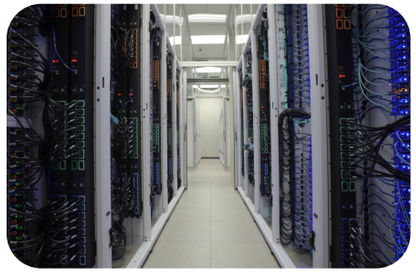
Grace

ACES

hprc.tamu.edu/resources

HPRC Clusters: Terra and Grace

Terra

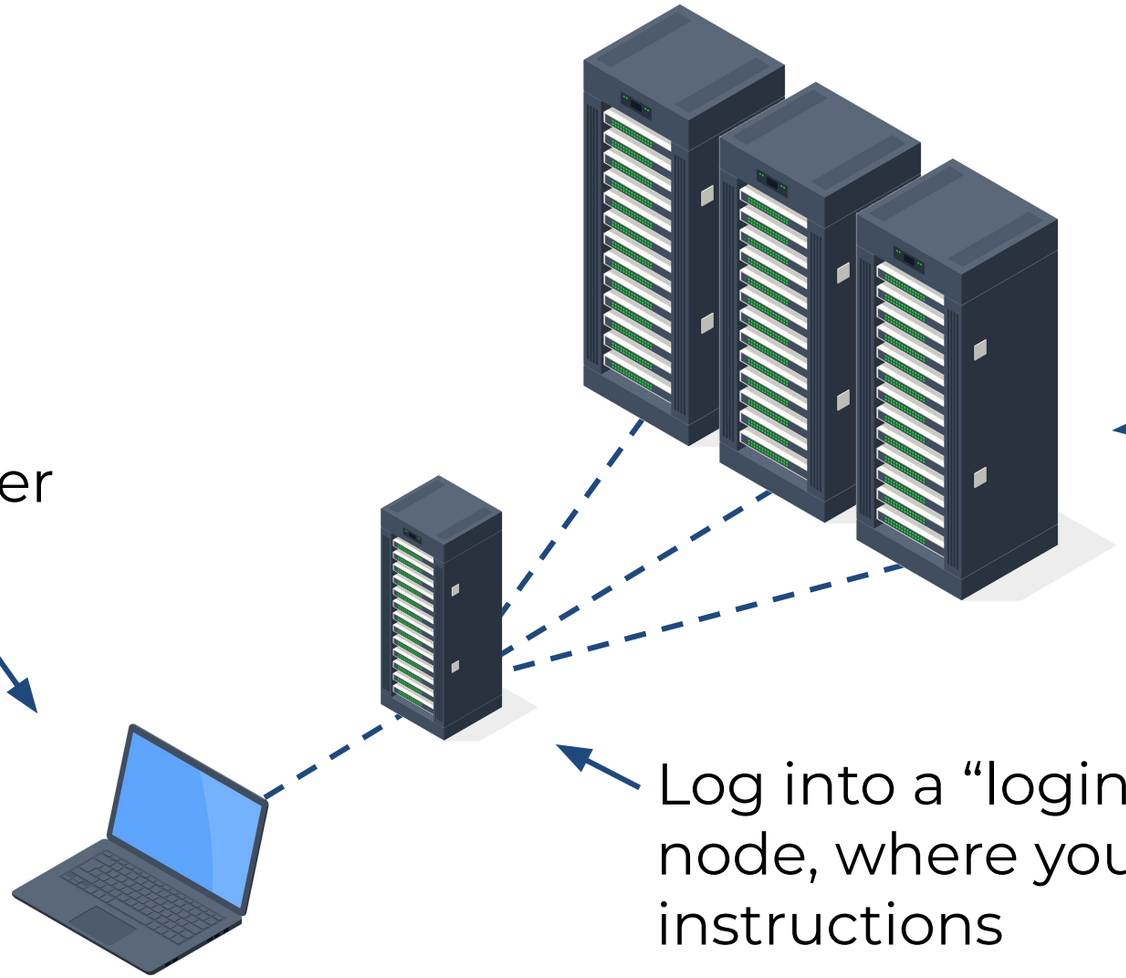


Grace

	Terra	Grace
Total Nodes (Cores)	320 (9,632)	925 (44,656)
General Nodes	28 cores 64GB	48 cores 384GB
Features	GPUs	GPUs - multiprecision Big Memory Nodes
Job Scheduler	Slurm	Slurm
Online Since	2017	2021

hprc.tamu.edu/resources

Computing on HPRC Clusters



You interact with your own computer

Make login node send instructions to “compute nodes” to do the heavy-lifting

Log into a “login” node, where you write instructions

(This image is not to-scale: we have way more machines than this!)

Clusters Are For You!

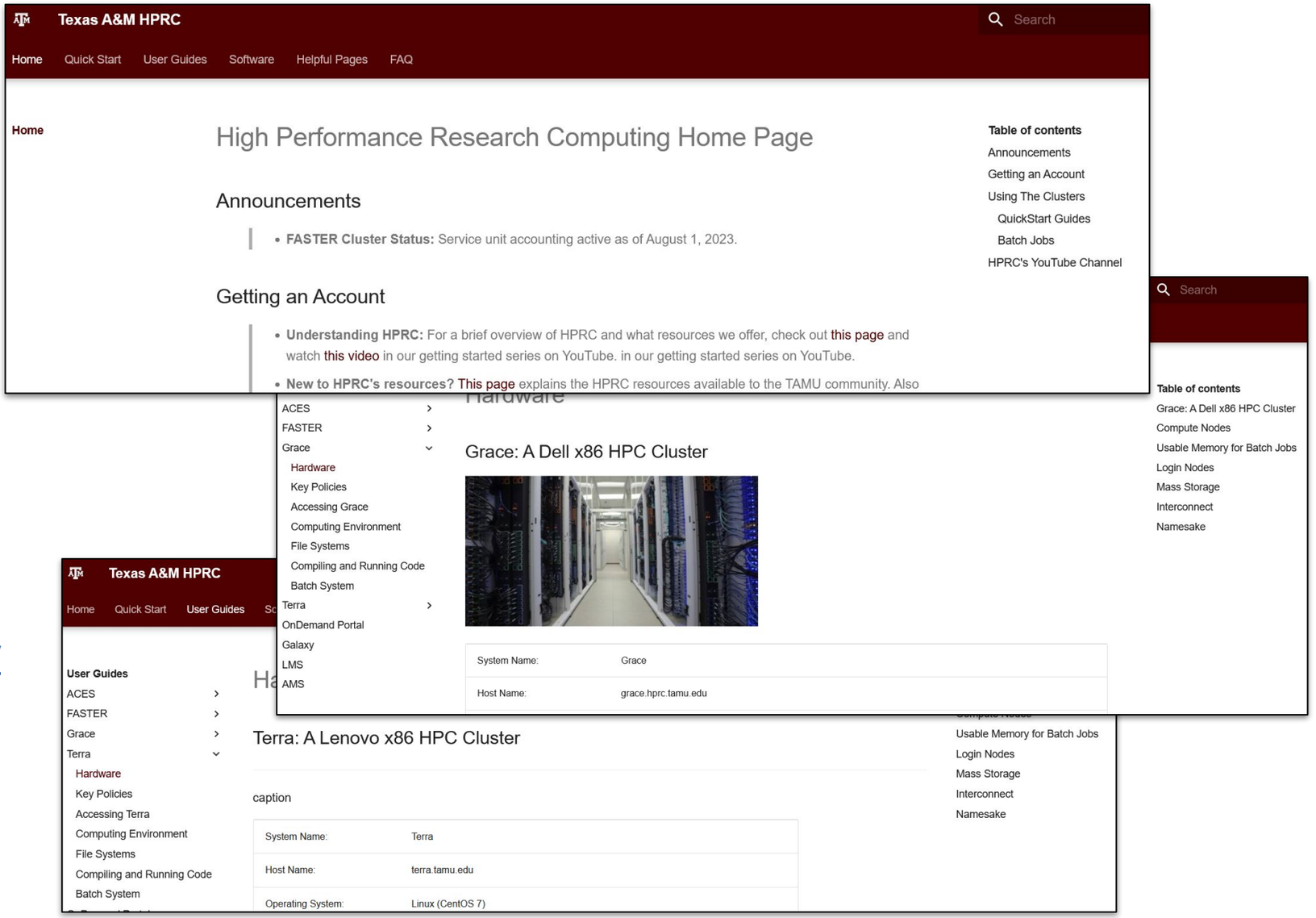
What kinds of problems are solved by cluster computing?

- Problems that are too big to fit in a laptop or workstation, due to limitation on memory, core count, or node count
- Problems that scale well with more CPU cores or memory
- Single-threaded problems with many permutations
- Problems that require large high speed storage and/or interconnect

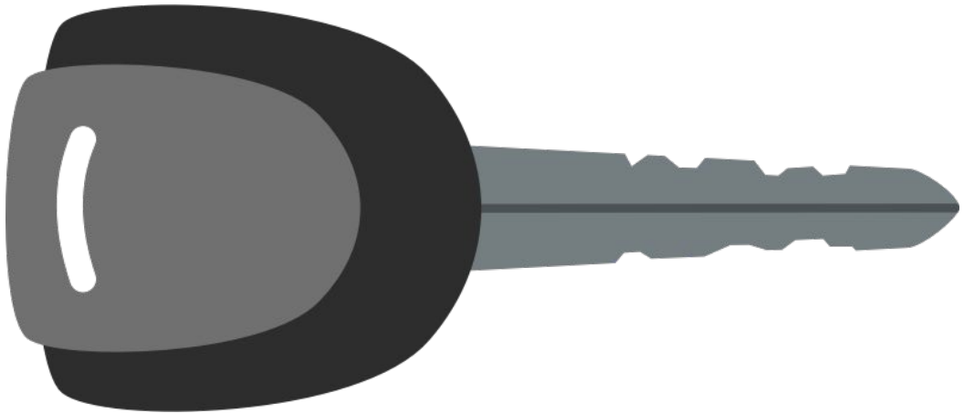
HPRC Knowledge Base

See our Knowledge Base for announcements, more hardware details, and more about the subjects we cover today.

https://hprc.tamu.edu/kb/
https://hprc.tamu.edu/kb/User-Guides/Grace/
https://hprc.tamu.edu/kb/User-Guides/Terra/



Getting Started



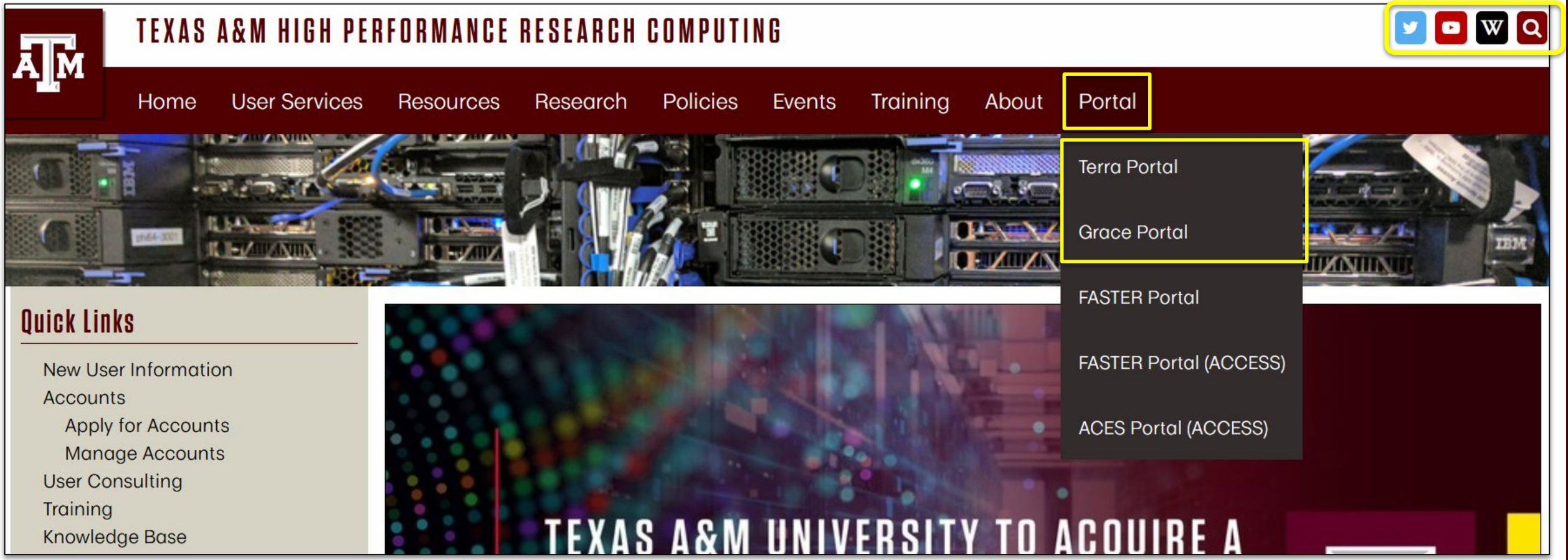
Usage Policies
(Be a good compute citizen)

- It is illegal to share computer passwords and accounts by state law and university regulation
- It is prohibited to use HPRC clusters in any manner that violates the United States export control laws and regulations, EAR & ITAR
- Abide by the expressed or implied restrictions in using commercial software

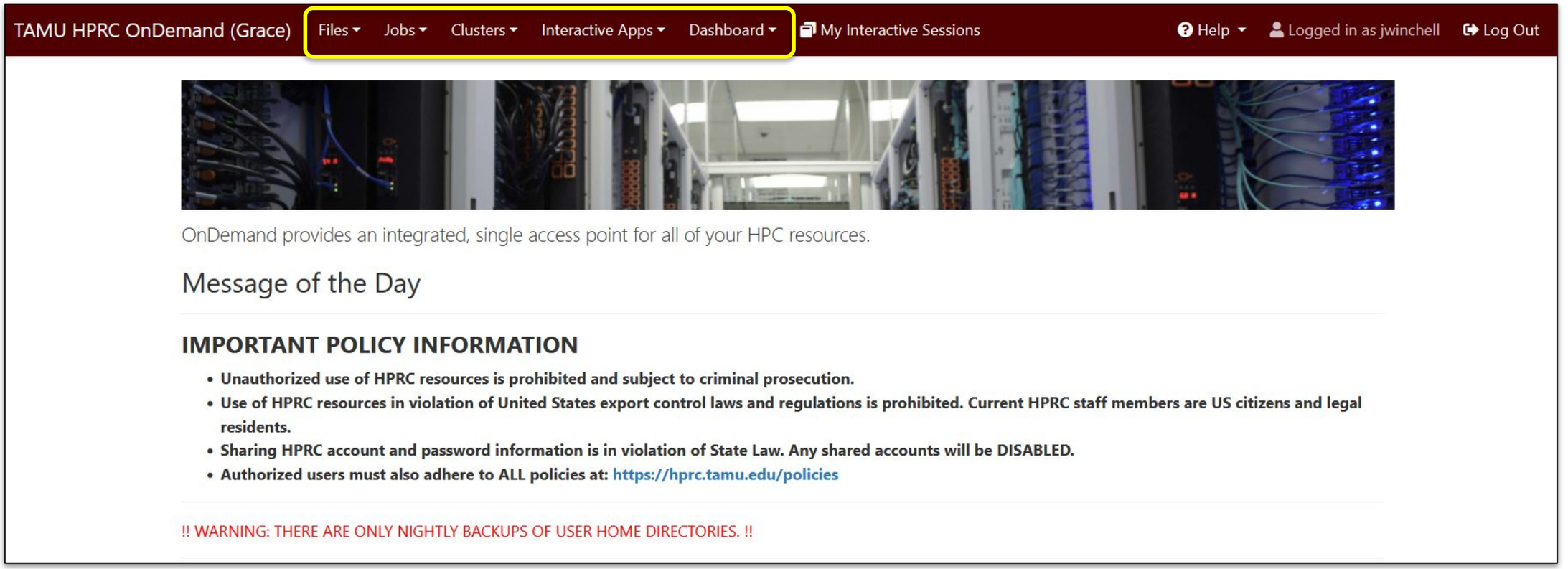
hprc.tamu.edu/policies

Accessing the HPRC Portal

- (First, if you're off-campus, connect to TAMU VPN: u.tamu.edu/VPnetwork)
- HPRC webpage: hprc.tamu.edu: Portal dropdown menu



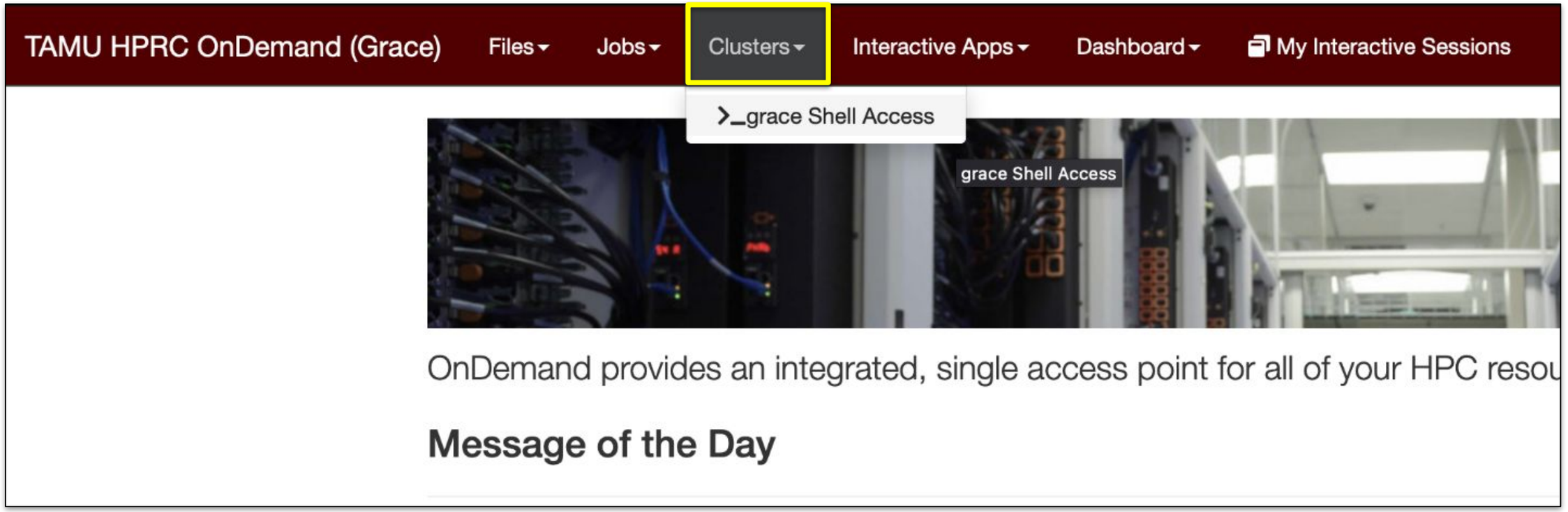
HPRC Portal Overview



Files: copy and edit files on the cluster's filesystems
Jobs: submit and monitor cluster jobs
Clusters: open a shell terminal (command line) on a login node
Interactive Apps: start graphical software on a compute node and connect to it
Dashboard: view file quotas and computing account allocations

Accessing Clusters via the HPRC Portal

- In Portal: “Clusters” dropdown ➜ “Shell Access”



(Works with most web browsers)

Accessing Clusters via SSH

- SSH (Secure SHell) allows users to establish a connection between their local machine and the TAMU HPRC clusters.
- SSH Programs:

Operating System	Windows	MacOS	Linux
Programs	MobaXTerm* PuTTY SSH Windows Subsystem for Linux (WSL) Windows Command Prompt	Terminal*	Terminal*
* Recommended			

- If off-campus, connect with VPN first: u.tamu.edu/VPnetwork
- If on-campus or connected to VPN, log in with:

```
ssh [NetID]@grace.hprc.tamu.edu
```

```
ssh [NetID]@terra.tamu.edu
```

Green box/highlights = text typed into a shell

Logging In to Clusters

```
Host: grace.hprc.tamu.edu
********************************************************************************
This computer system and the data herein are available only for authorized
purposes by authorized users. Use for any other purpose is prohibited and may
result in disciplinary actions or criminal prosecution against the user. Usage
may be subject to security testing and monitoring. There is no expectation of
privacy on this system except as otherwise provided by applicable privacy laws.
Refer to University SAP 29.01.03.M0.02 Acceptable Use for more information.
********************************************************************************

Password: (Type password, not no characters will show up)
Duo two-factor login for [NetID]

Enter a passcode or select one of the following options:

 1. Duo Push to XXX-XXX-1234
 2. Phone call to XXX-XXX-1234
 3. SMS passcodes to XXX-XXX-1234 (next code starts with: 9)

Passcode or option (1-3): 1
Success. Logging you in…
…….
[NetID@grace5 ~]$
```

Once connected via Portal or SSH, sign in with TFA

Hands-on Exercise

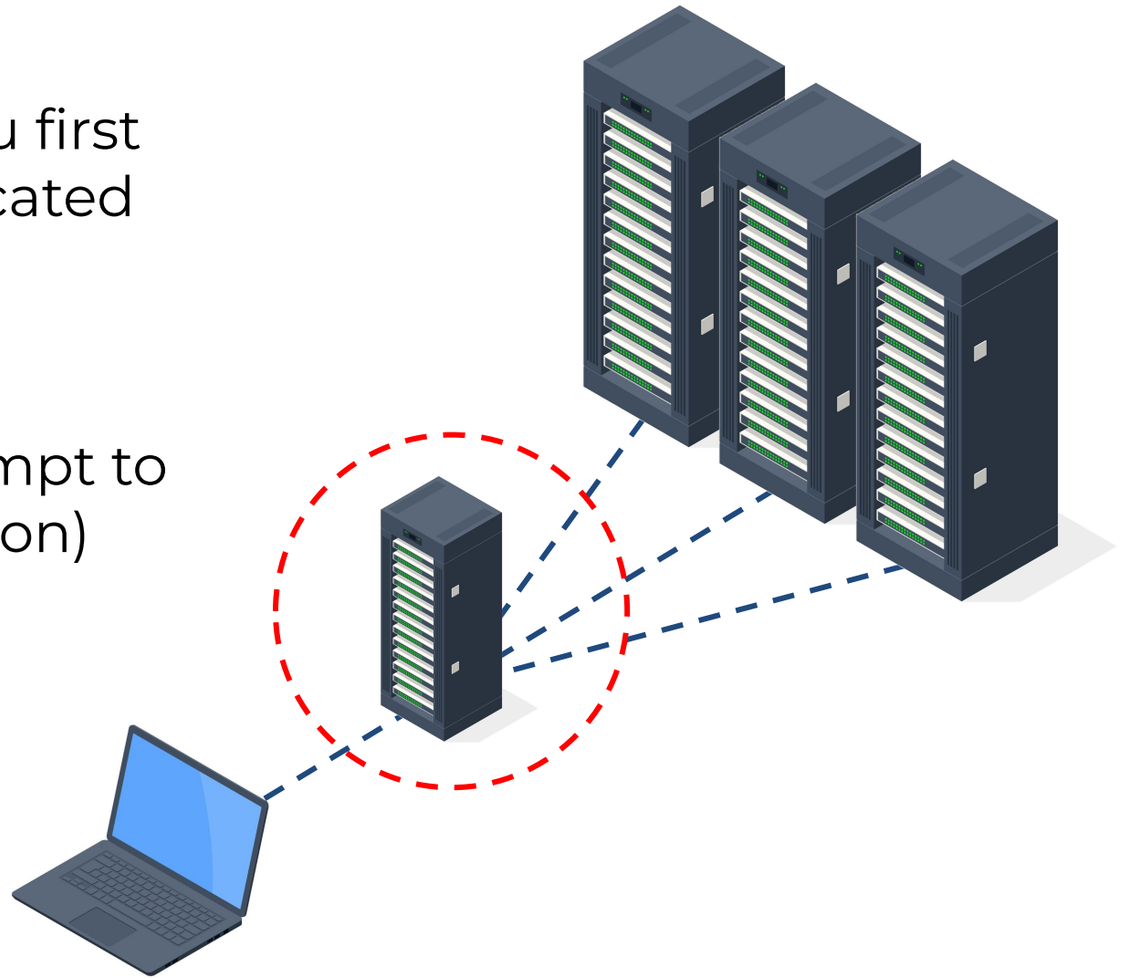
1. Log in to the HPRC portal: hprc.tamu.edu
2. Open a terminal on Grace in the portal:
   Clusters ➜ _Grace Shell Access
3. Use your NetID password and your two-factor Authentication method

Logged-In

Remember, when you first log in, you're on dedicated *login nodes*.

- Grace has 5
- Terra has 3

(check your shell prompt to see which one you're on)



These are not for running big processes!
There are rules:

- No processes longer than 1hr
- Sessions idle for 1hr will be killed
- Don't use more than 8 cores
- Don't use `sudo`

File Systems and User Directories

Directory	Environment Variable	Space Limit	File Limit	Intended Use
/home/$USER	$HOME	10 GB	10,000	Small to modest amounts of processing. Backed-up.
/scratch/user/$USER	$SCRATCH	1 TB	250,000	Temporary storage of large files for on-going computations. Not intended to be a long-term storage area; NOT backed up.

`$SCRATCH` is shared between FASTER (TAMU/ACCESS) and Grace (TAMU) clusters.

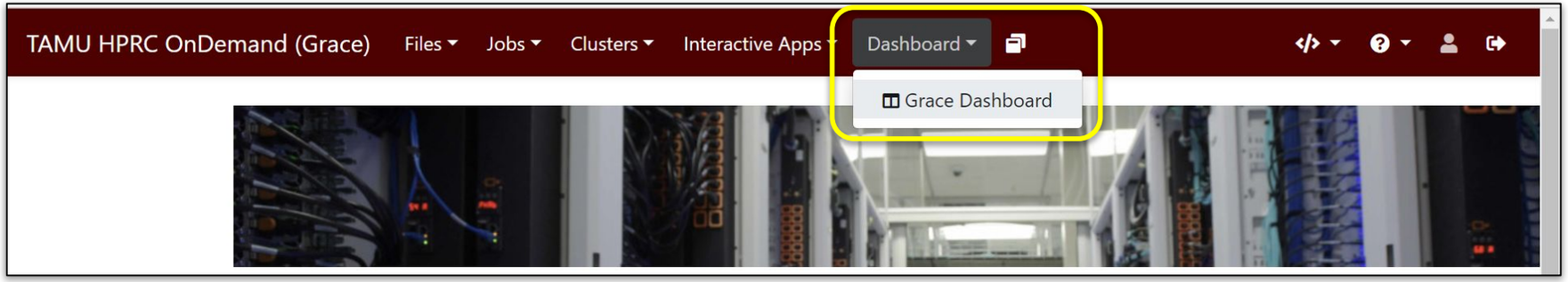
View file usage and quota limits on the command line with: **`showquota`**

Do **NOT** share your home or scratch directories.
Request a group directory for sharing files.

https://hprc.tamu.edu/kb/User-Guides/Grace/Filesystems_and_Files/
https://hprc.tamu.edu/kb/User-Guides/Terra/Filesystems_and_Files/

HPRC Portal Quota Increase Request

Portal Homepage → Grace Dashboard

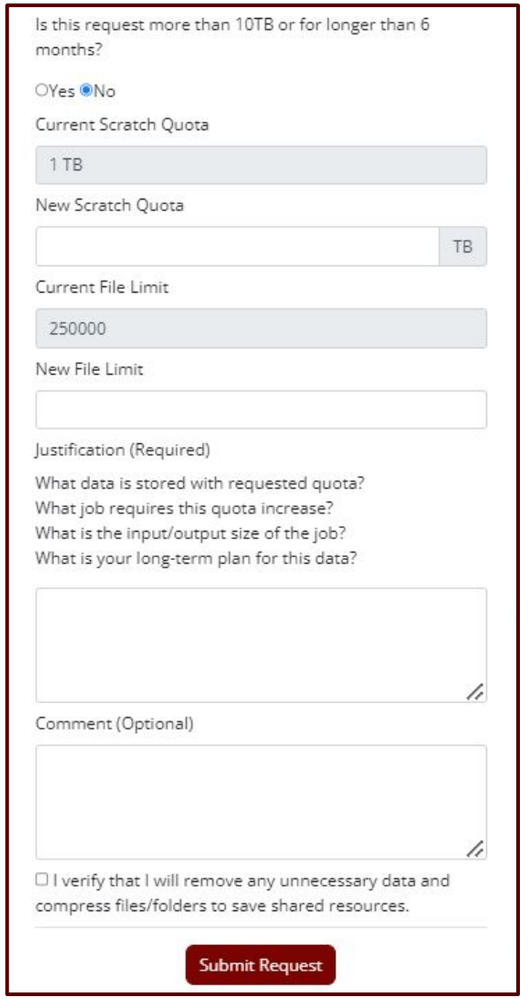


Request quota increases directly from the dashboard with a guided form

Disk Quotas

Disk	Disk Usage	Limit	File Usage	Limit
/home	160 KB (0.00 %)	10 GB	35 (0.35 %)	10000
/scratch	837.84 MB (0.08 %)	1 TB	11795 (4.72 %)	250000

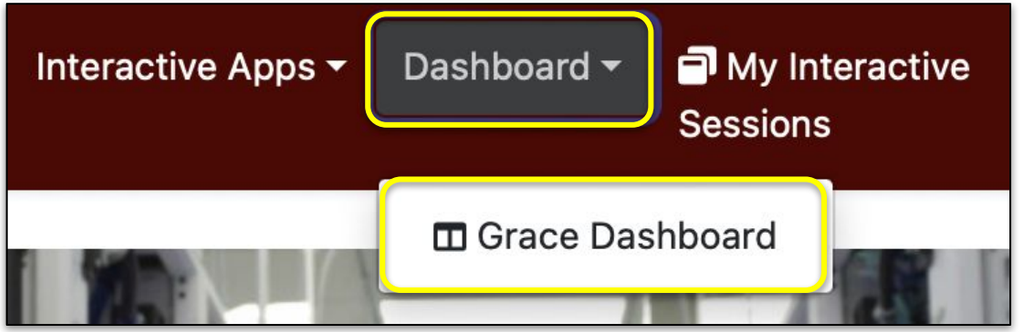
Request Quota Increase



Hands-on Exercise

Check your file Quota:

1. In the Portal:
   Dashboard ➜ Grace Dashboard

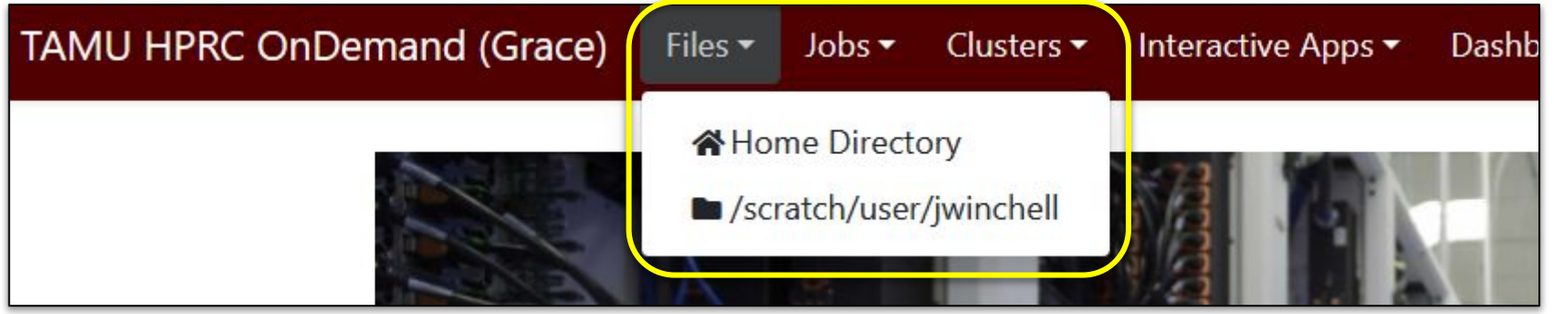


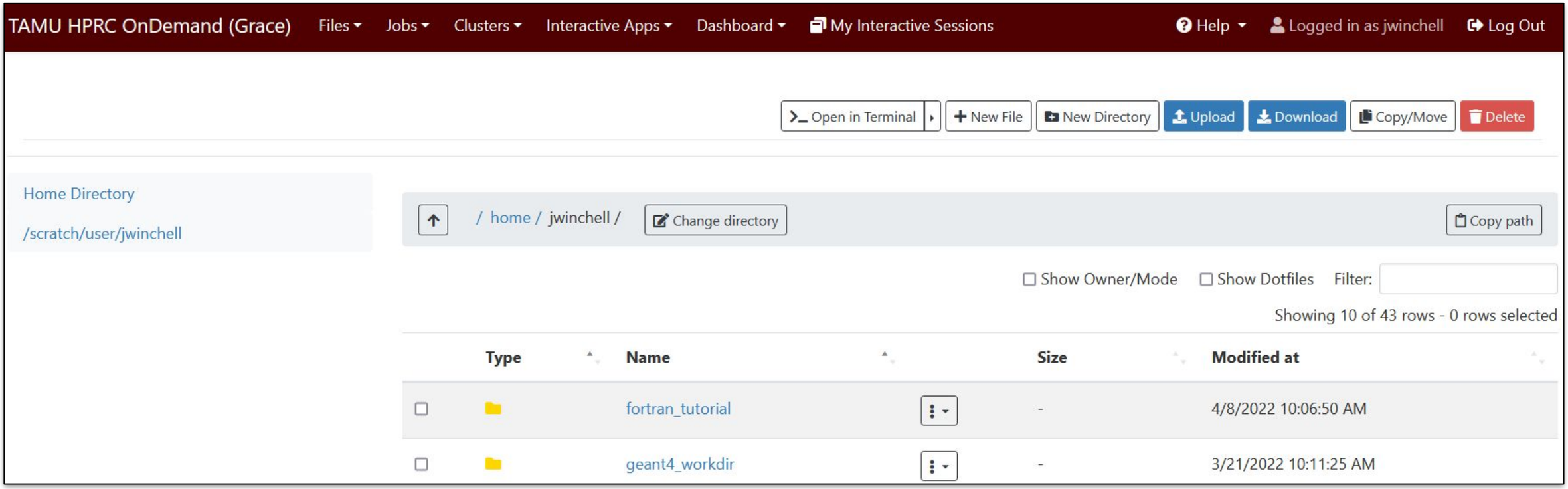
2. In the shell:
   (use `showquota`)

3. Locate your `/scratch` disk usage stats

Portal File Browser

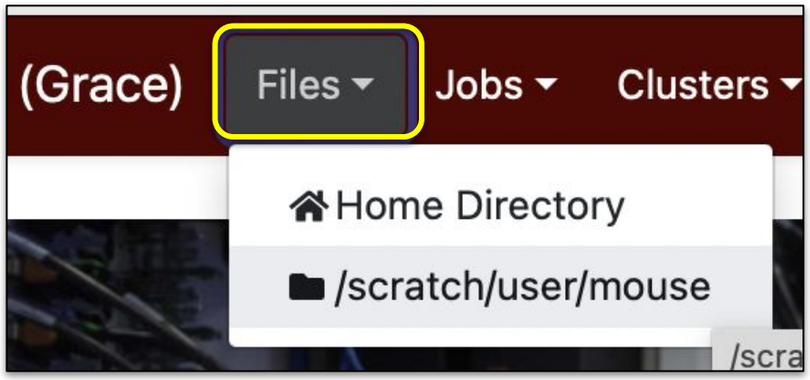
The Portal includes a file browser in which you can do many of the things a terminal would do… or just launch a terminal.



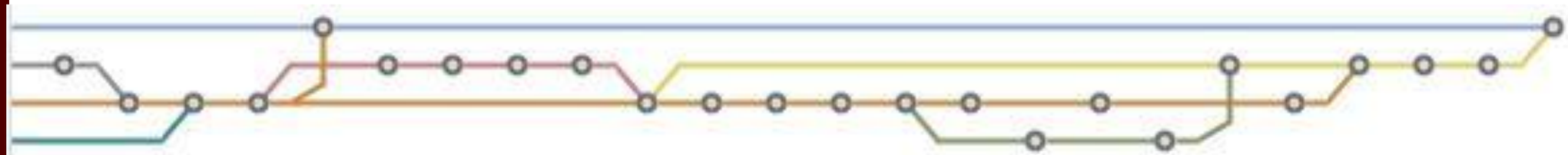


Hands-on Exercise

1. Enter your Scratch directory from the Portal:
   Files ➜ `/scratch/user/<NetID>`
2. Create or upload a file
3. Move the file to your home directory



Software Infrastructure



Software

- HPRC provides both pre-installed software and installation assistance
- See the Software pages for instructions and examples:
  - https://hprc.tamu.edu/kb/Software/
  - hprc.tamu.edu/software/
- License-restricted software
  - Check on command line with `license_status` (example later)
  - Contact help@hprc.tamu.edu
- Contact us for software installation help/request
  - User can install software in their home/scratch directories
  - Do NOT run the "`sudo`" command when installing software

Computing Environment

- `PATH`: the location on disk where an executable or library may be found.
- Paths are saved as environment variables, so you can choose which libraries and executables will be used by modifying the variables.
- There is a lot of software, many versions, and many paths to manage.

……. How do you manage all these software versions?

https://hprc.tamu.edu/kb/Software/useful-tools/Modules/

Modules

Managing software versions using `lmod`

- Each version of a software, application, library, etc. is available as a module.
  - Module names have the format:

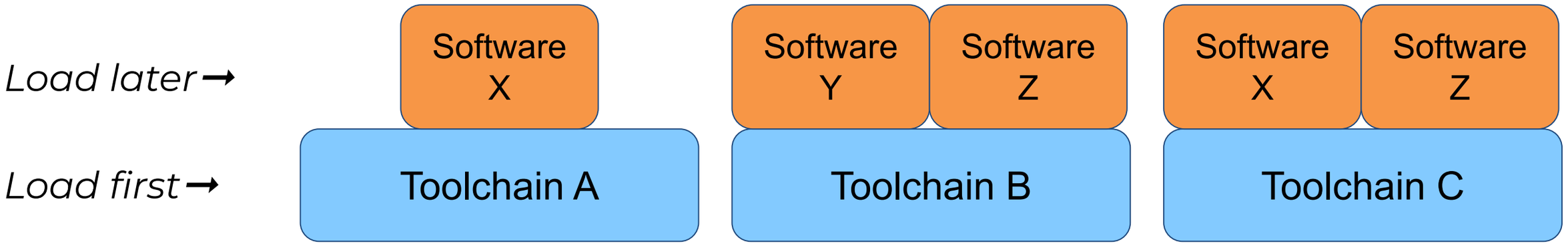
```
software-name/version[-dependency-version (optional)]
TensorFlow/2.5.0-Python-3.7.4
```

(Note: module names on Terra will have additional information that won't be included on the newer clusters)

- Loading a module adds its location on disk to your `Path` environment variable.
  - Its dependencies will also be loaded automatically.

Modules

- Modules are organized *hierarchically*
- The base modules that must be loaded before anything else are called “Toolchains”:
  - The same software may be available from multiple toolchains
  - Don’t mix up software from different toolchains!
- Loading the toolchain makes other modules available



Modules: Toolchain Details

- Toolchains are combinations of compilers, MPI libraries, and highly optimized math libraries.
- Toolchain components are primarily either Intel or Open Source.

Example toolchains for C++ development:

Components	Open Source	Intel Source	Mixed Source
Compiler only	`GCCcore`	`iccifort`	-
Compiler + MPI	`gompi`	`iimpi`	`iompi`
Compiler + MPI + MKL, BLAS, FFTW, LAPACK	`foss`	`intel`	`iomkl`
Compiler + all of the above + CUDA Compiler	`fosscuda`	`intelcuda`	`iomklc`

Example usage:

```
module load foss/2022a
```

https://hprc.tamu.edu/kb/Software/useful-tools/Toolchains/

Module Usage Basics

`module avail`

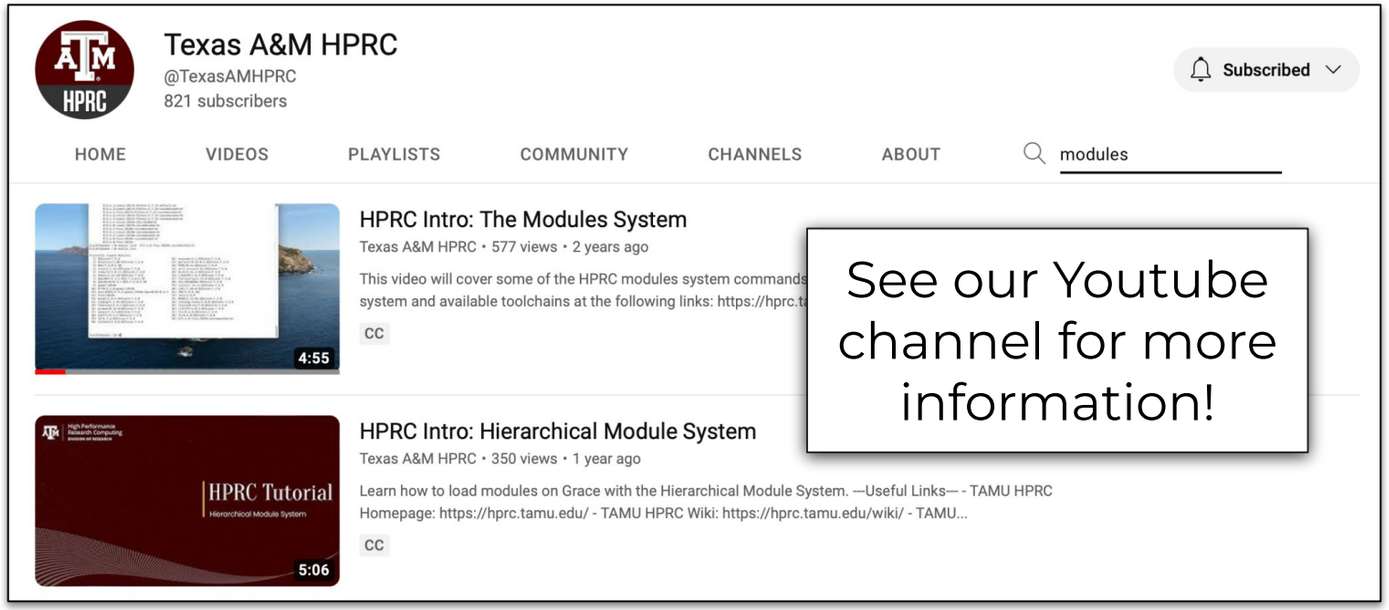
- Lists all available modules (may be slow).
- Navigation:
  -spacebar, arrows, or `j` and `k`
  -quit with `q`
- Case-sensitive search: `/`
- Use **`mla`** instead to save results to a file as well

`module load <module>`

- add <module> paths to the current environment variables

`module spider <word>`

- Case-sensitive search for modules with “word” in name.
- Provide an exact name to see dependencies.



See our Youtube channel for more information!

Module Commands Reference

- Commonly-used module commands
- Note that on HPRC clusters we've created some shorthands for you to use

Command	HPRC Shorthand	Description
`module avail`	`mla` *(saves a searchable file as well)*	See what modules can be loaded now
`module spider`		Search for modules and find dependencies
`module list`	`ml`	See what modules have been loaded already
`module load foo bar`	`ml foo bar`	Load specified module
`module unload foo bar` `module load baz goo`	`ml -foo -bar baz goo`	Load and unload specified modules
`module purge`	`ml purge`	Unload all modules

Module Usage Example

```
mla snakemake
```

Search for the software “snakemake”; saves a file of available modules

```
snakemake/5.2.4-Python-3.6.6
snakemake/5.7.1-Python-3.7.2
snakemake/5.7.1-Python-3.7.4
snakemake/5.26.1-Python-3.8.2
snakemake/6.1.0
snakemake/6.10.0
```

Choose a specific version and use it to search for its dependencies

```
module spider snakemake/6.10.0
```

```
----------------------------------------------------------------------------------------------------
  snakemake: snakemake/6.10.0
----------------------------------------------------------------------------------------------------
    Description:
      The Snakemake workflow management system is a tool to create reproducible and scalable data analyses.

    You will need to load all module(s) on any one of the lines below before the "snakemake/6.10.0" module is
available to load.

      GCC/11.2.0  OpenMPI/4.1.1
```

```
module load GCC/11.2.0  OpenMPI/4.1.1 snakemake/6.10.0
```

Load the base dependency module(s) first then the full module name

Hands-on Exercise: Module Loading

1. `mla blast+` -see which versions of BLAST+ are available
2. `ml BLAST+/2.13.0` -error; you can't do that yet
3. `module spider BLAST+/2.13.0` -learn how to load this module
4. `ml _____ BLAST+/2.13.0` -fill in the blank (with the correct toolchains) to load this module
5. `ml list` -list all loaded modules
6. `ml GCC/10.2.0` -change version of a loaded Toolchain module (GCC); notice the message about reloaded modules
7. `ml list` -list all loaded modules
8. `ml purge` -remove all loaded modules

Module Usage Practices

- Software installed as modules are available to all users
  - (except for restricted modules)
- It's a good habit to unload unused modules before loading new modules: `module purge`
- It is recommended to load a specific software version instead of the defaults: `ml GCC/12.2.0` instead of `ml GCC`
- Avoid loading modules in your $HOME/.bashrc
- Avoid mixing toolchains when loading multiple modules at the same time. This usually leads to one of them not working.

https://hprc.tamu.edu/kb/Software/useful-tools/Modules/

Python and Virtual Environments

Python is a language which supports many external libraries in the form of extensions. (called Python Packages).

Some commonly used packages:

- SciPy & NumPy
- Jupyter notebook
- Scikit-learn

Once you've loaded the appropriate Python module, you can install these additional packages yourself using the *Virtual Environment* feature. Instructions are on our KB:

https://hprc.tamu.edu/kb/Software/Python/#create-a-virtual-environment

Hands-on Exercise: Python Software Install

1.
```
cd $SCRATCH
mkdir python_envs
cd python_envs
```
-Move to $SCRATCH
Make a place for virtualenvs

2.
```
module purge
module load GCC/10.2.0 Python/3.8.6
```
-Set up Python module

3.
```
virtualenv my_example_venv
source my_example_venv/bin/activate
```
-Create and activate virtual environment

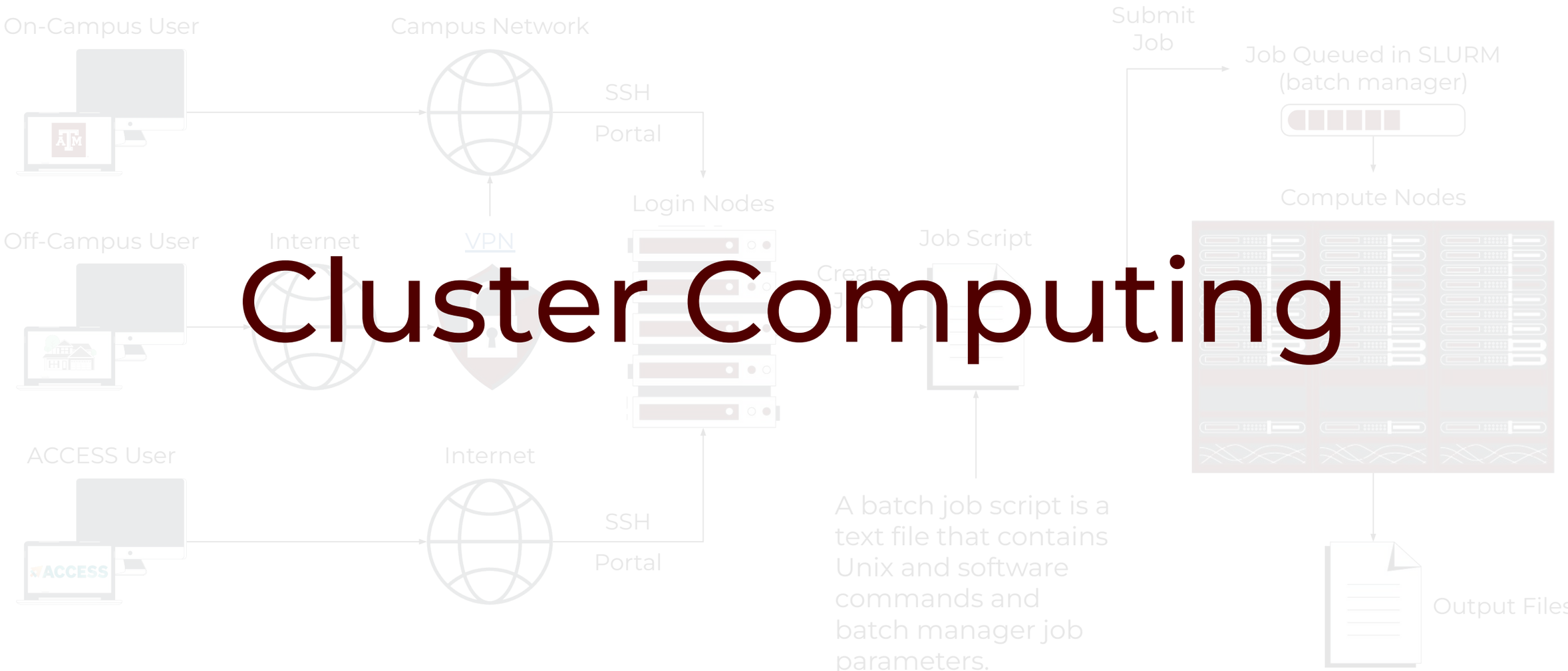
4.
```
python -c "import pytime"
```
-Check if python-time is installed (it's not)

5.
```
pip install python-time
```
-Install python-time

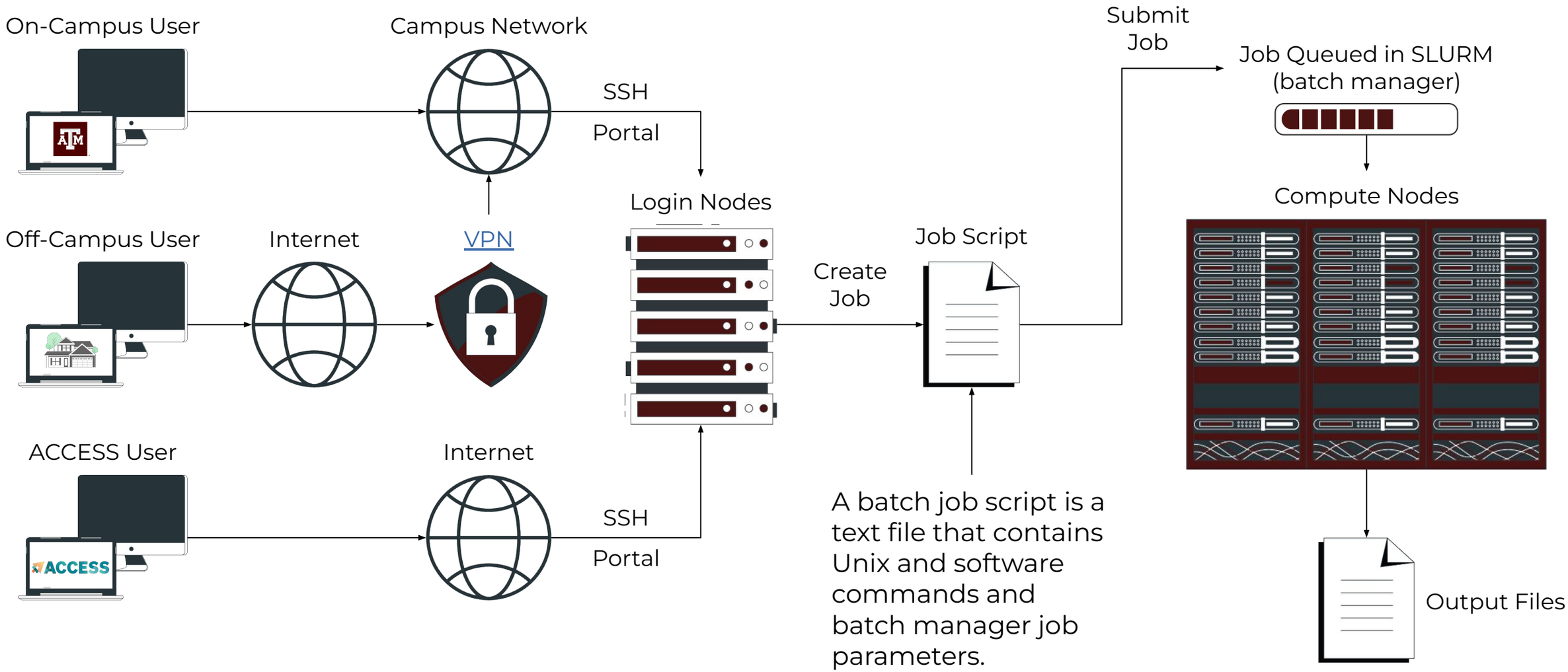
6.
```
python -c "import pytime; print(pytime)"
```
-Where is python-time installed?

7.
```
deactivate
```
-Close virtual environment

Cluster Computing



Batch Computing on HPRC Clusters: Overview



Consumable Computing Resources

Computing resources are shared!

You won't be able to use an infinite amount!

- Resources external to jobs:
  - Service Unit (SU)
  - Software license/token
- Resources specified in a job file:
  - Processor cores
  - Memory
  - Wall time
  - GPU

Software Licenses

To check the availability of licensed software on the clusters, use the command **`license_status`**.

- List software the tool knows about:

```
license_status -l
```

- Help for this command:

```
license_status -h
```

- Find available license for "ansys":

```
license_status -s ansys
```

```
License status for ANSYS:
-------------------------------------------------------------
|License Name                |  # Issued|  # In Use|# Available|
-------------------------------------------------------------
|aa_mcad                     |        50|         0|         50|
|aa_r                        |        50|        32|         18|
|aim_mp1                     |        50|         0|         50|
|   ......                                                    |
-------------------------------------------------------------
```

Exact availability varies by license policy.
Contact us if you have questions.

https://hprc.tamu.edu/kb/Software/useful-tools/License_Checker/

Service Units

- Service Units (SUs) are part of our account management system (AMS).
- With a default allocation, you start with 5000 SUs
- SUs are charged as your jobs spend time on the compute nodes (we'll see how later).
  (Work on login nodes is not charged, but you can't do big computing there!)
- You can check your SU balance on both:
  - The command line
  - The HPRC Portal

https://hprc.tamu.edu/kb/User-Guides/AMS/Service_Unit/
https://hprc.tamu.edu/kb/User-Guides/AMS/UI/

Check your (SU) Balance: Command Line

- List the SU Balance of your Account(s) with:

```
myproject
```

```
 ================================================================================
               List of YourNetID's Project Accounts
--------------------------------------------------------------------------------
|   Account    |    FY    | Default | Allocation |Used & Pending SUs|   Balance  |    PI    |
--------------------------------------------------------------------------------
|1228000223136|  2023    |       N|    10000.00|              0.00|    10000.00|Doe, John |
--------------------------------------------------------------------------------
|1428000243716|  2023    |       Y|     5000.00|            -71.06|     4928.94|Doe, Jane |
--------------------------------------------------------------------------------
|1258000247058|  2023    |       N|     5000.00|             -0.91|     4999.09|Doe, Jane |
--------------------------------------------------------------------------------
```

- Run **`myproject -d <Account#>`** to change default project account

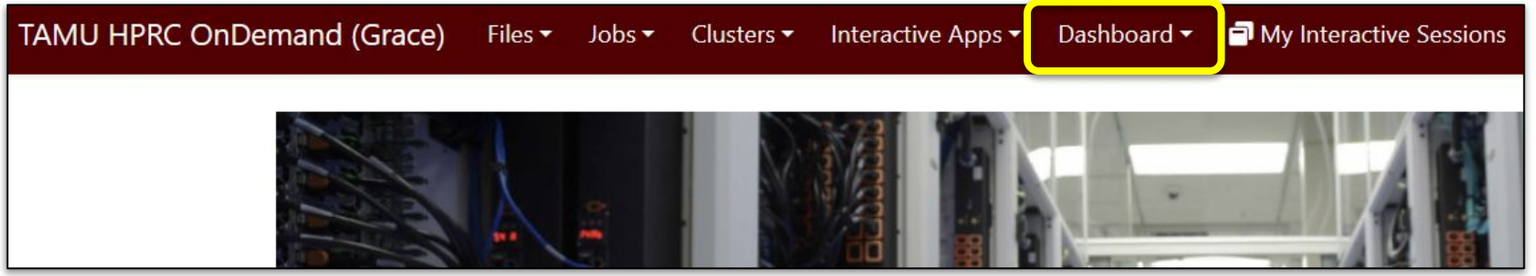
  (replace <Account#> with your number!)

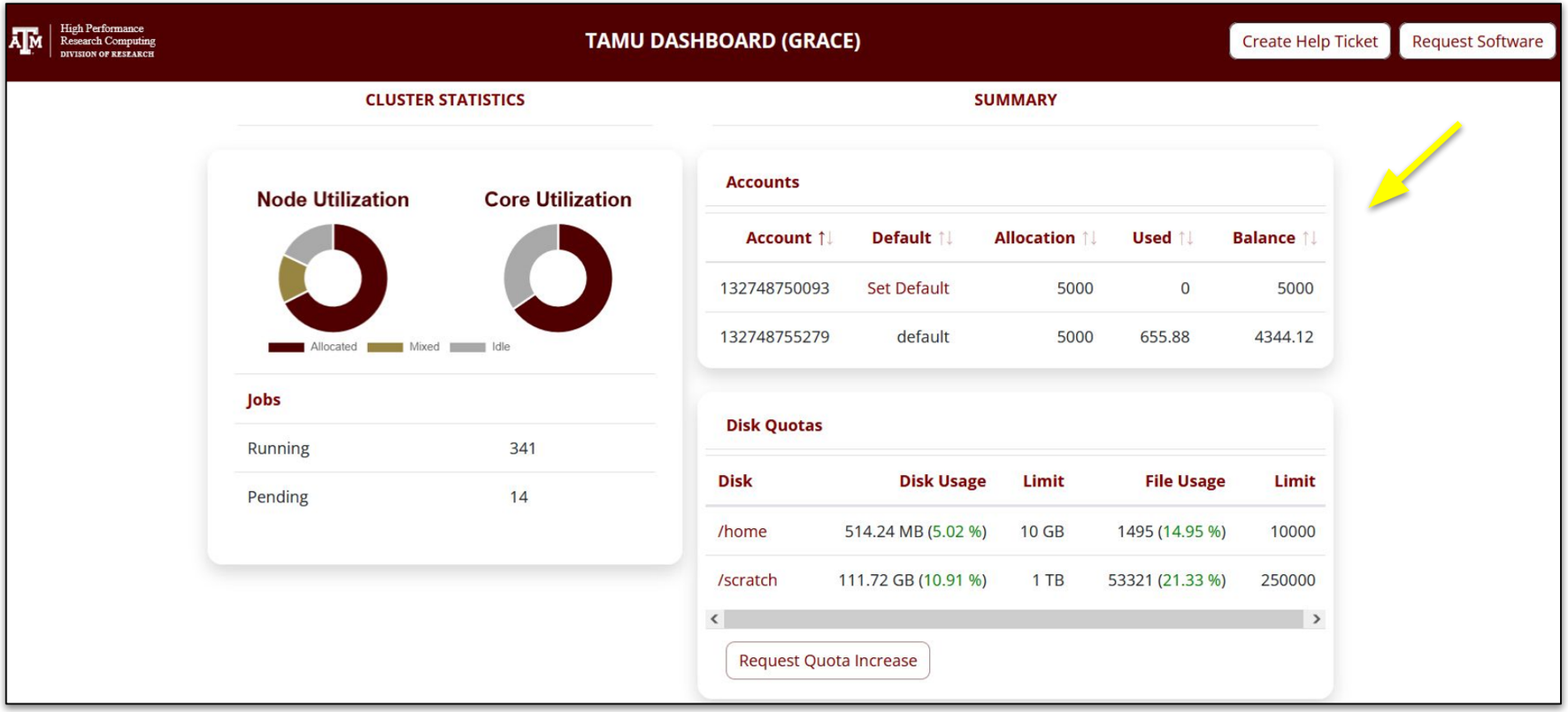
- Run **`myproject -h`** to see more options

Check your (SU) Balance: Portal

SUs can also be checked in the Dashboard

(The same place we checked file quotas previously)

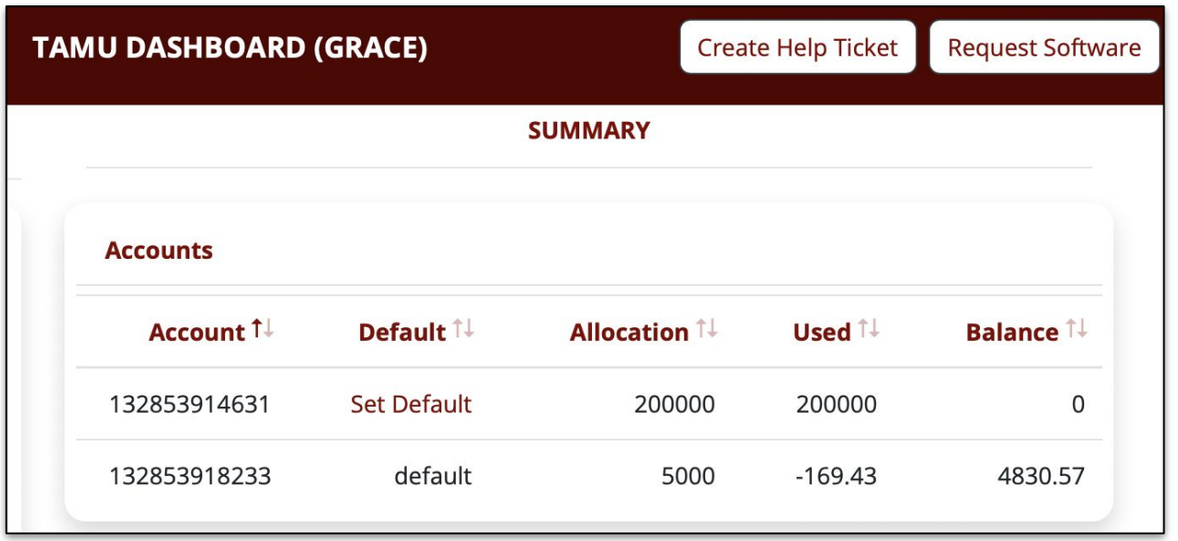




Hands-on Exercise

1. Check your SUs in both the command line and the Portal
2. Check that you have a default account set

```
myproject
```

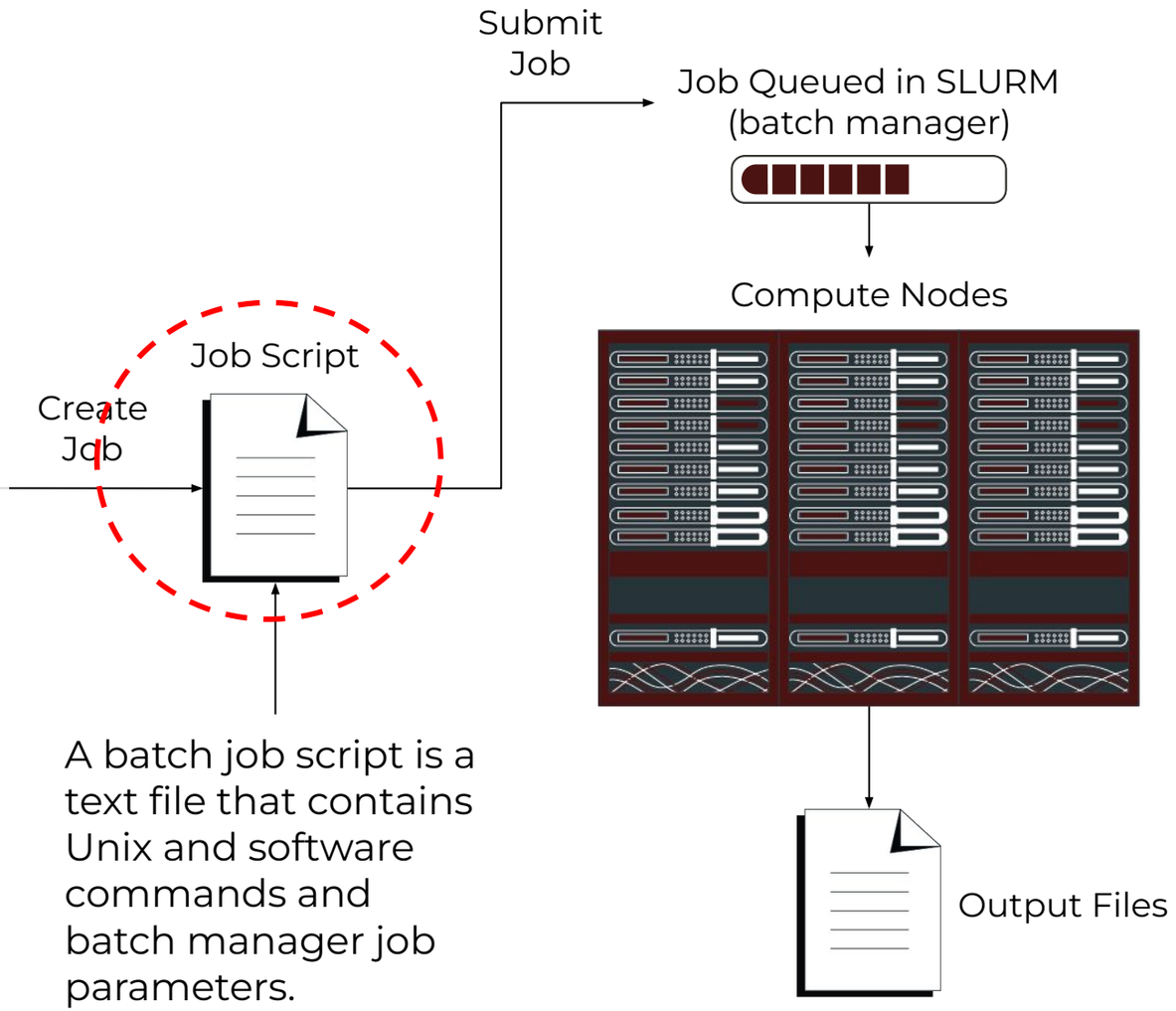


We'll return to SUs once we've talked about SLURM and the resources your jobs use up.

Slurm Job Scripts

The number of SUs you get charged depends on the resources your job uses

Your job script is where you request the resources you need and provide the instructions you want executed



Sample Job Script Structure

```
#!/bin/bash

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=hello_world
#SBATCH --time=00:15:00
#SBATCH --ntasks=2
#SBATCH --ntasks-per-node=2
#SBATCH --nodes=1
#SBATCH --mem=3G
#SBATCH --output=hello_world_log.%j

# load required module(s)
module purge
module load GCCcore/11.3.0
module load Python/3.10.4
python hello_world.py

# Job Environment variables
echo $SLURM_JOBID
echo $SLURM_SUBMIT_DIR
echo $TMPDIR
echo $SCRATCH
```

This is a single-line comment and not run as part of the script.

These parameters describe your job to the job scheduler.
The lines starting with #SBATCH are NOT comments!
See the Knowledge Base for more info.

Whatever commands or scripts you want to run.
Here, we set up the modules we need for our environment, run a python program, and print out some environment variables.

Submit a Job and Check Job Status

Submit job

```
sbatch example01.job
```

```
Submitted batch job 6853258
(from job_submit) your job is charged as below
              Project Account: 122792016265
              Account Balance: 1687.066160
              Requested SUs:   3
```

Check status

```
squeue -u $USER
```

```
JOBID    NAME      USER      PARTITION  NODES  CPUS  STATE    TIME         TIME_LEFT  START_TIME          REASON     NODELIST
6853258  jobname   someuser   xlong       2     96   RUNNING  3-07:36:50   16:23:10   2023-01-23T17:27:3   None      c[180,202]
6853257  jobname   someuser   xlong       2     96   RUNNING  3-07:36:56   16:23:04   2023-01-23T17:27:2   None      c[523-524]
```

Hands-on Exercise

Submit a simple job file:

1. Navigate to `/scratch/training/Intro-to-Grace`, either on the command line or in the Portal's file browser
2. Copy the files `hello_world.slrm` and `hello_world.py` to your home directory
3. Return to your home directory yourself
4. Submit the job file with: `sbatch hello_world.slrm`
5. Check the job's status with: `squeue -u $USER`
6. Check the output file (will be named like `hello_world_log.#`)

Job Environment Variables

Each job has access to several self-referential variables:

- **`$SLURM_JOBID`** = job id
- **`$SLURM_SUBMIT_DIR`** = directory where job was submitted from
- **`$TMPDIR`** = /work/job.$SLURM_JOBID

You can also still use non-Slurm variables like:

- **`$SCRATCH`** = /scratch/user/NetID

https://hprc.tamu.edu/kb/Helpful-Pages/Batch-Translation/#environment-variables

Important Batch Job Parameters

Slurm	Comment
`#SBATCH --time=HH:MM:SS`	Specifies the time limit for the job. Must specify seconds SS on ACES
`#SBATCH --ntasks=NNN`	Total number of tasks (cores) for the job.
`#SBATCH --ntasks-per-node=XX`	Specifies the maximum number of tasks (cores) to allocate per node

`#SBATCH --mem=xxxxM`
`or`
`#SBATCH --mem=xG`
 	
`(memory per NODE)`
	Sets the maximum amount of memory (MB) per node.
	G for GB is supported on ACES

`#SBATCH --nodes=x`	Specifies the number of nodes to use

https://hprc.tamu.edu/kb/Helpful-Pages/Batch-Translation/#job-specifications

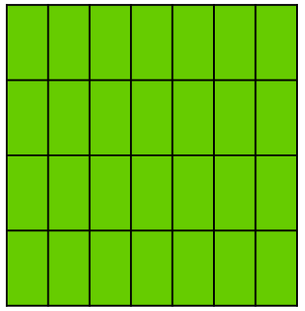
(Job Template)

```
#!/bin/bash
##ENVIRONMENT SETTINGS; CHANGE WITH CAUTION
#SBATCH --export=NONE          #Do not propagate environment
#SBATCH --get-user-env=L       #Replicate login environment

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=JobExample1      #Set the job name to "JobExample1"
#SBATCH --time=01:30:00             #Set the wall clock limit to 1hr and 30min
#SBATCH --ntasks=1                  #Request 1 task
#SBATCH --ntasks-per-node=1         #Request 1 task/core per node
#SBATCH --mem=2560M                 #Request 2560MB (2.5GB) per node
#SBATCH --output=Example1Out.%j     #Send stdout/err to "Example1Out.[jobID]"

#First Executable Line
```

https://hprc.tamu.edu/kb/Quick-Start/Grace/#running-your-program-preparing-a-job-file

Mapping Jobs to Cores per Node on Terra

A.

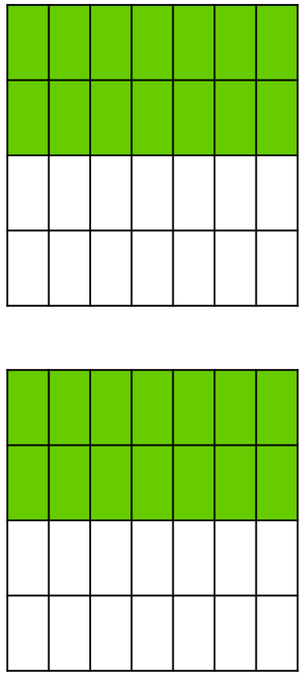


28 cores on
1 compute node

#SBATCH --ntasks 28
#SBATCH --tasks-per-node=28

Preferred Mapping
(if applicable)

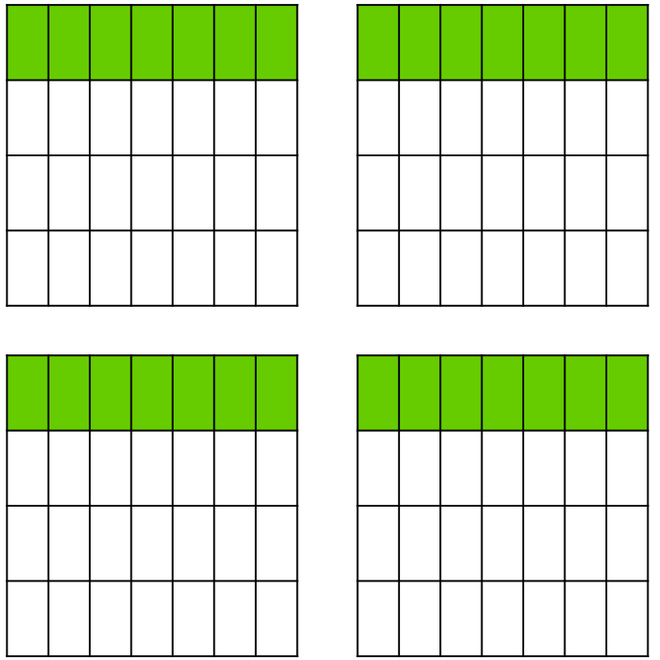
B.



28 cores on
2 compute nodes

#SBATCH --ntasks 28
#SBATCH --tasks-per-node=14

C.

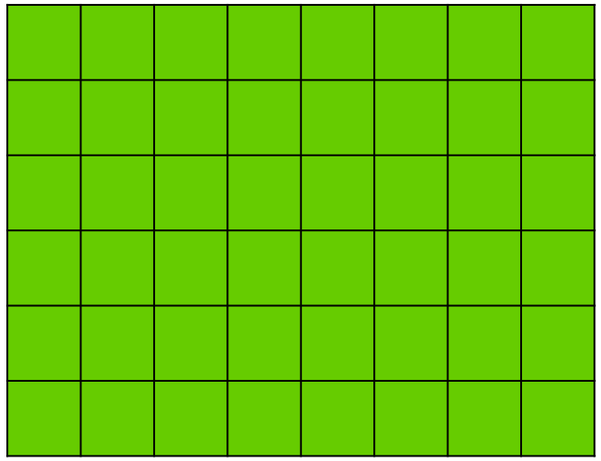


28 cores on
4 compute nodes

#SBATCH --ntasks 28
#SBATCH --tasks-per-node=7

Mapping Jobs to Cores per Node on Grace

A.

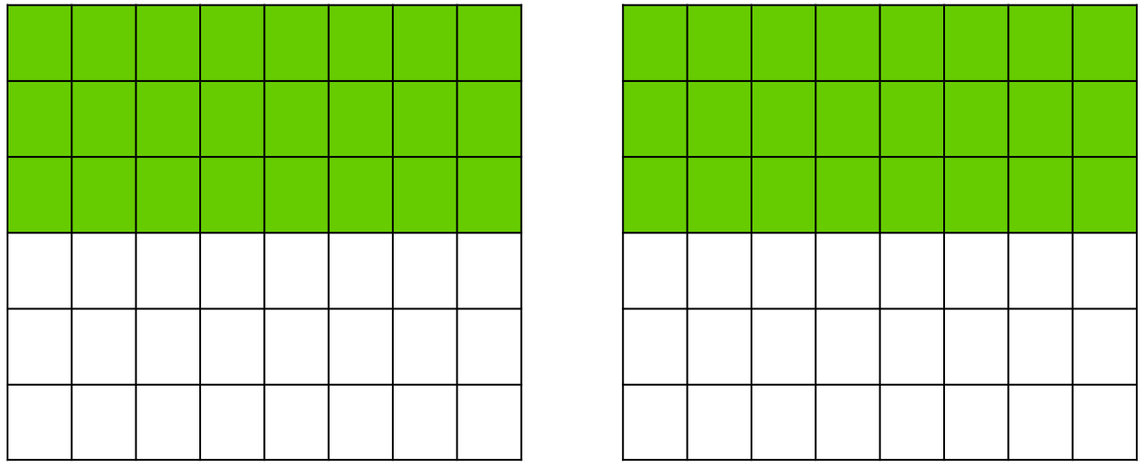


48 cores on
1 compute node

#SBATCH --ntasks=48
#SBATCH --tasks-per-node=48

Preferred Mapping
(if applicable)

B.



48 cores on
2 compute nodes

#SBATCH --ntasks=48
#SBATCH --tasks-per-node=24

Slurm Pop Quiz

```
#SBATCH --job-name=stacks_S2
#SBATCH --ntasks=80
#SBATCH --ntasks-per-node=20
#SBATCH --mem=40G
#SBATCH --time=48:00:00
#SBATCH --output stdout.%J
#SBATCH --error stderr.%J
```

How many nodes is this job requesting?

A. 1600
B. 80
C. 20
D. 4

Job Memory Requests on Terra

- Specify memory request based on memory per node:

  #SBATCH --mem=xxxxM # memory per node in MB

  or

  #SBATCH --mem=xG # memory per node in GB
- On 64GB nodes, usable memory is at most 56 GB. The per-process memory limit should not exceed 2000 MB for a 28-core job.
- On 128GB nodes, usable memory is at most 112 GB. The per-process memory limit should not exceed 4000 MB for a 28-core job.

Job Memory Requests on Grace

- Specify memory request based on memory per node:

  #SBATCH --mem=xxxxM # memory per node in MB

  or

  #SBATCH --mem=xG # memory per node in GB

- On 384GB nodes, usable memory is at most 360 GB.
  The per-process memory limit should not exceed ~7500 MB for a 48-core job.

- On 3TB nodes, usable memory is at most 2900 GB.
  The per-process memory limit should not exceed 37120 MB for a 48-core job.

Slurm: Examples of SUs charged based on Job Cores, Time and Memory Requested

An SU is equivalent to one core hour *or* a proportional amount of memory on the node for one hour.
On **Grace**: a typical node has 48 cores and 360 GB usable for jobs. (7.5 GB per core)

Number of Cores	GB of memory per core	Total Memory (GB)	Hours	SUs charged
1	7.5	7.5	1	1
24	1	24	1	24
1	360	360	1	48
48	7.5	360	1	48

https://hprc.tamu.edu/kb/User-Guides/AMS/Service_Unit/

Slurm: SU Charges for GPU jobs

GPUs will use more SUs per hour than CPUs

Effective GPU	SU charge per one hour (wall_time)
A100	72
RTX 6000	48
T4	24

Job Submission and Tracking

Slurm commands	Description
`sbatch jobfile1`	Submit jobfile1 to batch system
`squeue [-u user_name] [-j job_id]`	List jobs
`scancel job_id`	Kill a job
`sacct -X -j job_id`	Show information for a job (can be when job is running or recently finished)
`sacct -X -S YYYY-HH-MM`	Show information for all of your jobs since YYYY-HH-MM
`pestat -u $USER`	Show resource usage for a running job
`seff job_id`	Check CPU/memory efficiency for a job

https://hprc.tamu.edu/kb/Helpful-Pages/Batch-Translation/#job-specifications

Batch Queues

- Job submissions are auto-assigned to batch *queues* (also called *partitions*) based on the resources requested:
  - number of cores/nodes and walltime limit
  - specific resources requested
- Some jobs can be directly submitted to a queue:
  - E.g. if gpu nodes are needed, use the gpu partition/queue:

  #SBATCH --partition=gpu
- Batch queue policies are used to manage the workload and may be adjusted periodically.

https://hprc.tamu.edu/kb/User-Guides/Common/BatchProcessing/#batch-queues

sinfo : Current Queues on Grace

Check the status of the partitions with **`sinfo`**

```
username@login1:~$ sinfo
PARTITION       AVAIL TIMELIMIT    JOB SIZE     NODES(A/I/O/T)      CPUS(A/I/O/T)
short*          up    2:00:00      1-32         711/0/89/800        33689/439/4272/38400
medium          up    1-00:00:00   1-128        711/0/89/800        33689/439/4272/38400
long            up    7-00:00:00   1-64         711/0/89/800        33689/439/4272/38400
xlong           up    21-00:00:00  1-32         711/0/89/800        33689/439/4272/38400
vnc             up    12:00:00     1-32         100/5/12/117        985/4055/576/5616
gpu             up    4-00:00:00   1-32         100/5/12/117        985/4055/576/5616
bigmem          up    2-00:00:00   1-4          7/0/1/8             560/0/80/640
staff           up    infinite     1-infinite   817/14/101/932      34689/5199/4848/4473
special         up    7-00:00:00   1-infinite   811/5/101/917       34674/4494/4848/4401
gpu-a40         up    4-00:00:00   1-15         6/9/0/15            15/705/0/720
```

For the NODES and CPUS columns:

- A = Active (in use by running jobs)
- I = Idle (available for jobs)
- O = Offline (unavailable for jobs)
- T = Total

pestat : Processor Status

- **pestat** allows you to check the status of the nodes on ACES
- -p allows you to show a specific partition
- Example:

```
pestat -p gpu -G
```

```
GPU GRES (Generic Resource) is printed after each jobid
Print only nodes in partition gpu
Hostname        Partition     Node Num_CPU  CPUload  Memsize  Freemem  GRES/node   Joblist
                            State Use/Tot  (15min)     (MB)     (MB)
ac036                 gpu   alloc  72    96    2.95    500000   492233* gpu:h100:2  <jobid>
ac037                 gpu   idle   0     96    0.00    500000   479355  gpu:h100:2
ac038                 gpu   drain* 0     96    0.00    500000   489374  gpu:h100:2
ac039                 gpu   idle   0     96    0.00    500000   511650  gpu:h100:2
ac040                 gpu   idle   0     96    0.00    500000   463374  gpu:h100:2
ac046                 gpu   mix    0     96    0.00    500000   442789  gpu:h100:2
ac047                 gpu   alloc  96    96    1.97*   500000   489464  gpu:h100:2  <jobid>
ac064                 gpu   idle   0     96    0.00    500000   509287  gpu:a30:6
```

Could also check specifically your own jobs with: `pestat -u $USER`

Checking Maximum Allowed Resources

If you ask for too many resources, your job won't run.

Check the maximum with: **maxconfig**

```
  Grace partitions:   short  medium  long  xlong  vnc  gpu  bigmem  special  gpu-a40
  Grace GPUs in gpu partition:  a100:2  a40:3  rtx:2  t4:4

  Showing max parameters (cores, mem, time) for partition long

  CPU-billing * hours * nodes =   SUs
       48 *   168 *  1 = 8,064
```

```
#!/bin/bash
#SBATCH --job-name=my_job
#SBATCH --time=7-00:00:00
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=48
#SBATCH --mem=360G
#SBATCH --output=stdout.%x.%j
#SBATCH --error=stderr.%x.%j
```

Check specific partitions with:

maxconfig -p <partitionName>

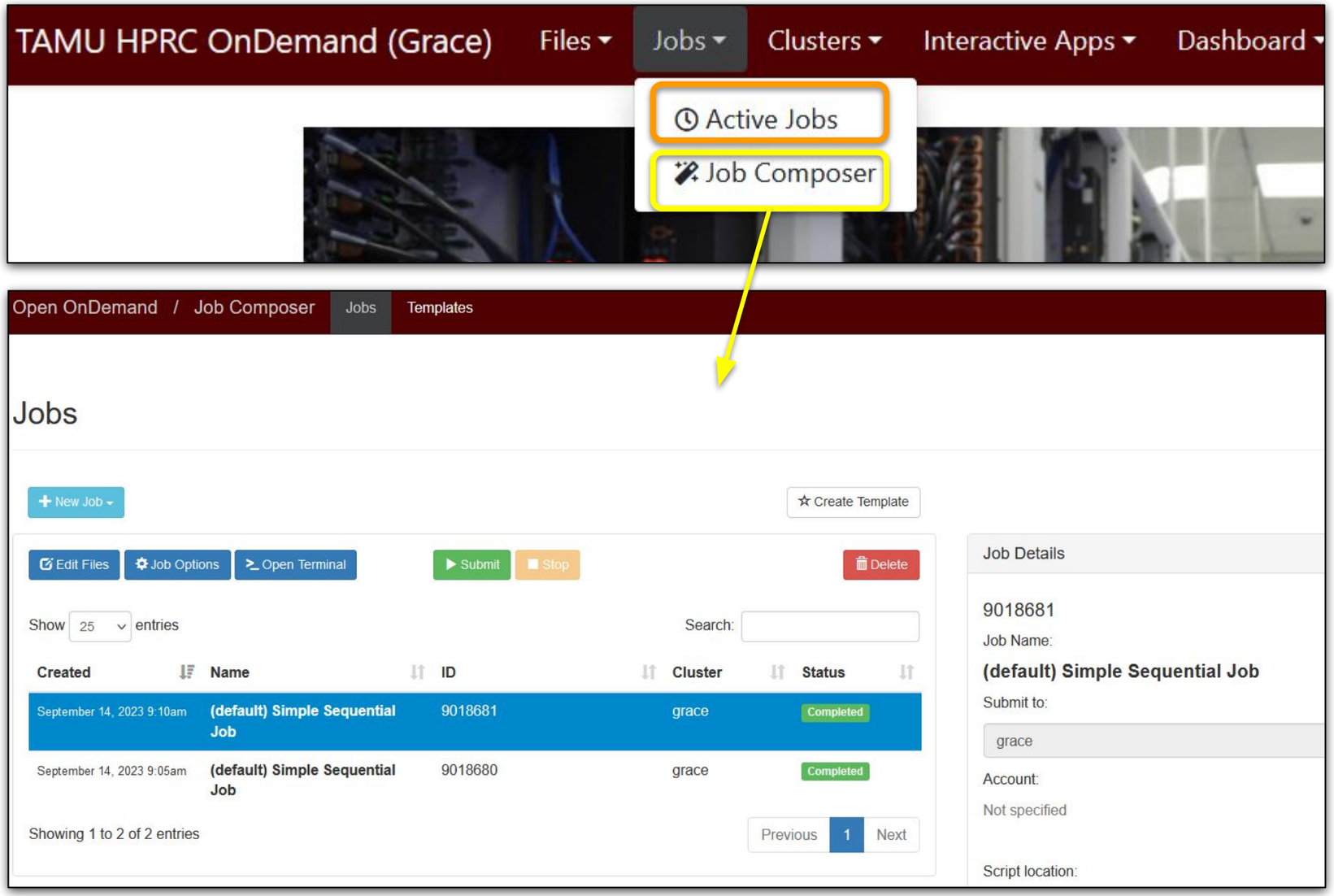
Estimate the SUs a job with require with:

maxconfig -f <jobScriptName>

Portal Job Composer

Some job management can also be done from the Portal

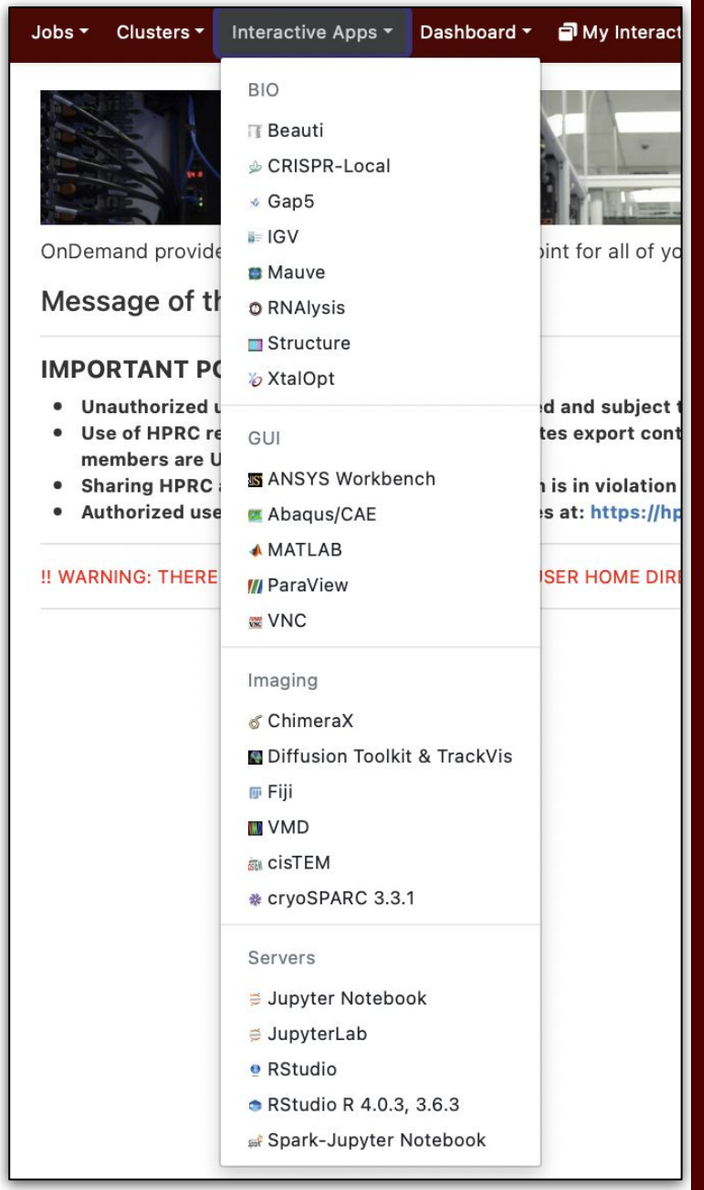
- "Active Jobs" is like squeue
- "Job Composer" lets you:
  - Create job scripts
  - Save job templates
  - Monitor your own jobs



Other Type of Jobs

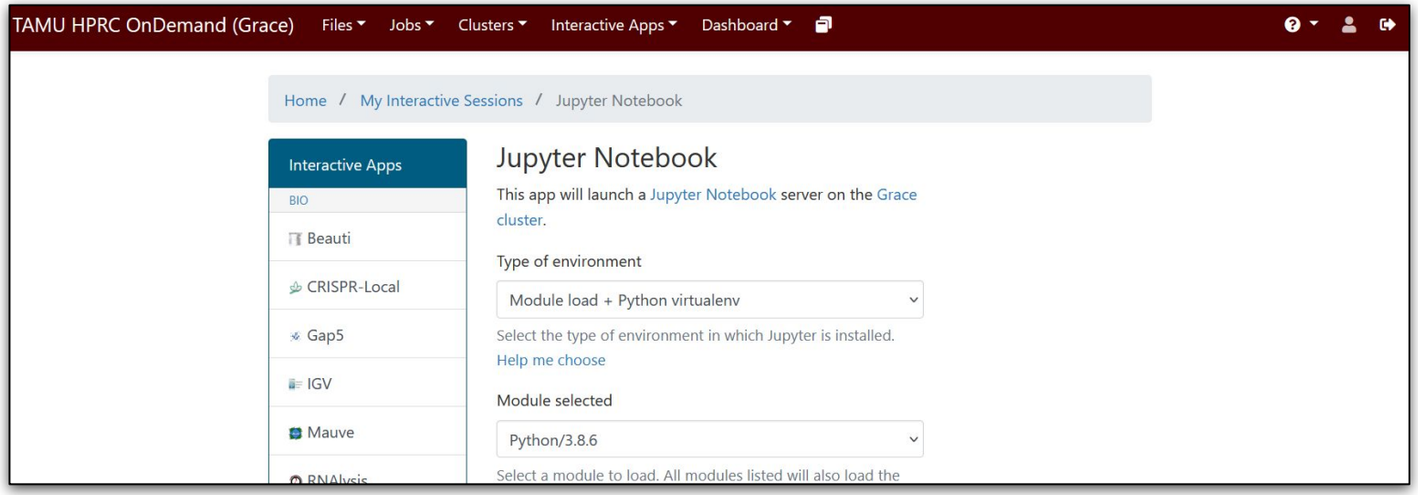
- Visualization:
  - portal.hprc.tamu.edu
  - Interactive Apps > choose application

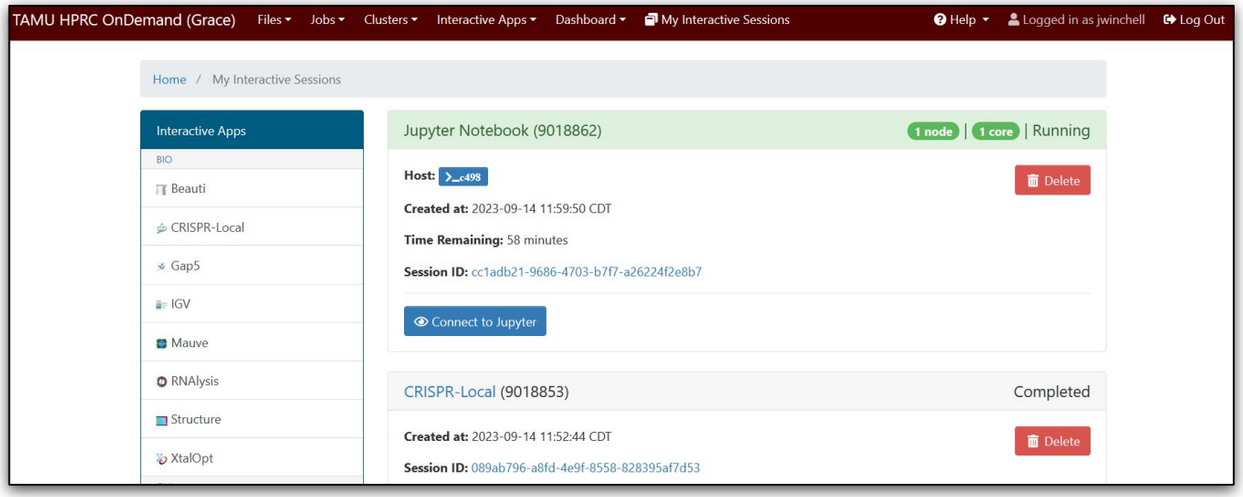
- Large number of concurrent single-core jobs
  - Check out *tamulauncher*
    - Useful for running many single core commands concurrently across multiple nodes within a job
    - Can be used with serial or multi-threaded programs
    - Can only be used in batch jobs
    - If a tamulauncher job gets killed, you can resubmit the same job to complete the unfinished commands in the input file
    - https://hprc.tamu.edu/kb/Software/tamulauncher/



Interactive Apps

1. Select an app from the dropdown menu
2. Specify environment and resources
3. Hit “Launch” at the bottom
4. On the “My Interactive Sessions” screen:
   a. wait for box to turn green
   b. connect to app
   c. quit from the app when you’re done
   d. box should turn grey





Need Help?

First check the FAQ https://hprc.tamu.edu/kb/FAQ/Accounts/

- FASTER User Guide https://hprc.tamu.edu/kb/User-Guides/Grace/
- Email your questions to help@hprc.tamu.edu

Help us help you -- we need more info:

- Which Cluster
- Username
- Job id(s) if any
- Location of your jobfile, input/output files
- Application used if any
- Module(s) loaded if any
- Error messages
- Steps you have taken, so we can reproduce the problem

High Performance
Research Computing
DIVISION OF RESEARCH

Thank you

Questions?

Batch Job Examples

Slurm Job File (Serial Example)

```
#!/bin/bash

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=JobExample1        #Set the job name to "JobExample1"
#SBATCH --time=01:30:00               #Set the wall clock limit to 1hr and 30min
#SBATCH --ntasks=1                    #Request 1 task
#SBATCH --mem=2560M                   #Request 2560MB (2.56GB) per node
#SBATCH --output=Example1Out.%j       #Send stdout/err to "Example1Out.[jobID]"

##OPTIONAL JOB SPECIFICATIONS
##CHANGE ACCOUNT NUMBER AND EMAIL ADDRESS BEFORE USING
##SBATCH --account=123456             #Set billing account to 123456
##SBATCH --mail-type=ALL              #Send email on all job events
##SBATCH --mail-user=email_address    #Send all emails to email_address

# this intel toolchain is just an example.  recommended toolchain is TBD
module purge
module load intel/2022a

# run your program
./helloworld.omp.C.exe
```

SUs = 1.5

Slurm Job File (multi core, single node)

```
#!/bin/bash

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=JobExample2         # Set the job name to "JobExample2"
#SBATCH --time=6:30:00                    # Set the wall clock limit to 6hr and 30min
#SBATCH --nodes=1                      # Request 1 node
#SBATCH --ntasks-per-node=8            # Request 8 tasks(cores) per node
#SBATCH --mem=8G                       # Request 8GB per node
#SBATCH --output=Example2Out.%j        # Send stdout/err to "Example2Out.[jobID]"

##OPTIONAL JOB SPECIFICATIONS
##CHANGE ACCOUNT NUMBER AND EMAIL ADDRESS BEFORE USING
##SBATCH --account=123456     # Set billing account to 123456  #find your account with "myproject"
##SBATCH --mail-type=ALL              # Send email on all job events
##SBATCH --mail-user=email_address    # Send all emails to email_address

# load required module(s)
module purge
module load intel/2022a

# run your program
mpirun ./helloworld.mpi.C.exe
```

SUs = 52

Slurm Job File (multi core, multi node)

```
#!/bin/bash

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=JobExample3          # Set the job name to "JobExample3"
#SBATCH --time=1-12:00:00               # Set the wall clock limit to 1 Day and 12hr
#SBATCH --ntasks=8                      # Request 8 tasks (cores)
#SBATCH --ntasks-per-node=2             # Request 2 tasks(cores) per node
#SBATCH --mem=4096M                     # Request 4096MB (4GB) per node
#SBATCH --output=Example3Out.%j         # Send stdout and stderr to "stdout.[jobID]"

##OPTIONAL JOB SPECIFICATIONS
##CHANGE ACCOUNT NUMBER AND EMAIL ADDRESS BEFORE USING
##SBATCH --account=123456      # Set billing account to 123456 #find your account with "myproject"
##SBATCH --mail-type=ALL               # Send email on all job events
##SBATCH --mail-user=email_address    # Send all emails to email_address

# this intel toolchain is just an example.  recommended toolchain is TBD
module purge
module load intel/2022a

# run program with MPI
mpirun ./helloworld.mpi.C.exe
```

SUs = 288

Slurm Job File (serial GPU)

```
#!/bin/bash

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=JobExample4          # Set the job name to "JobExample4"
#SBATCH --time=01:00:00                 # Set the wall clock limit to 1hr
#SBATCH --ntasks=1                      # Request 1 task (core)
#SBATCH --mem=2560M                     # Request 2560MB (2.5GB) per node
#SBATCH --output=Example4Out.%j         # Send stdout and stderr to "Example4Out.[jobID]"
#SBATCH --gres=gpu:a100:1               # Request 1 A100 GPUs
#SBATCH --partition=gpu                 # Request the GPU partition/queue

##OPTIONAL JOB SPECIFICATIONS
##CHANGE ACCOUNT NUMBER AND EMAIL ADDRESS BEFORE USING
##SBATCH --account=123456     # Set billing account to 123456  #find your account with "myproject"
##SBATCH --mail-type=ALL              # Send email on all job events
##SBATCH --mail-user=email_address    # Send all emails to email_address

# load required module(s)
module purge
module load CUDA/11.8.0

# run your program
my_cuda_enabled_program
```

SUs = 73

Slurm Job File (multi GPU)

```
#!/bin/bash

##NECESSARY JOB SPECIFICATIONS
#SBATCH --job-name=JobExample5          # Set the job name to "JobExample4"
#SBATCH --time=01:00:00                 # Set the wall clock limit to 1hr
#SBATCH --ntasks=2                      # Request 1 task (core)
#SBATCH --mem=250G                      # Request 250GB per node
#SBATCH --output=Example4Out.%j         # Send stdout and stderr to "Example4Out.[jobID]"
#SBATCH --gres=gpu:a100:2               # Request 2 A100 GPUs
#SBATCH --partition=gpu                 # Request the GPU partition/queue

##OPTIONAL JOB SPECIFICATIONS
##CHANGE ACCOUNT NUMBER AND EMAIL ADDRESS BEFORE USING
##SBATCH --account=123456     # Set billing account to 123456  #find your account with "myproject"
##SBATCH --mail-type=ALL              # Send email on all job events
##SBATCH --mail-user=email_address    # Send all emails to email_address

# load required module(s)
module purge
module load CUDA/11.8.0

# run your program
my_cuda_enabled_program
```

SUs = 192