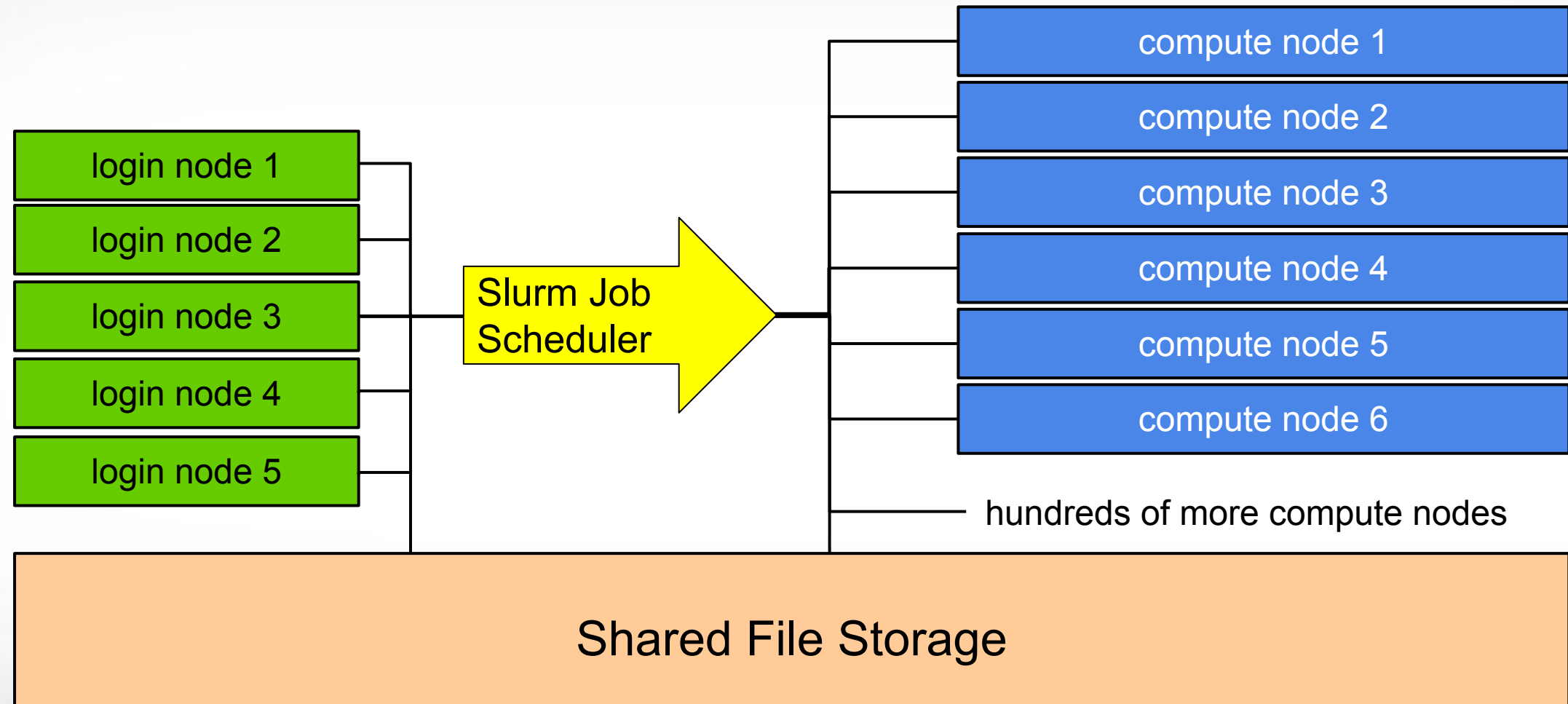


# Introduction to Grace



# HPC Diagram



Grace Compute nodes on HPRC clusters are not connected to the internet but you can connect using 'module load WebProxy'

# Grace Clusters Specs

	Grace
Compute Nodes	925
Total Cores	44,654
64GB memory nodes	-
384 GB memory nodes	800 (48 cores/node @ 3.00 GHz)
1TB memory nodes	-
2TB memory nodes	-
3TB memory nodes	8 (80 cores/node)
GPU nodes	117
login nodes	5
Production Date	Spring 2021

<https://hprc.tamu.edu/resources>

# Accessing Grace

- SSH command is required for accessing Grace:
  - On campus:
    - `ssh -X netid@grace.hprc.tamu.edu`
    - `-X` enables viewing of image files and GUI applications
  - Off campus:
    - Set up and start VPN (Virtual Private Network):
      - <http://u.tamu.edu/VPnetwork>
    - Then: `ssh -X netid@grace.hprc.tamu.edu`
- SSH programs for Windows:
  - MobaXTerm (preferred, includes SSH and X11)
- Access through <https://portal.hprc.tamu.edu>
  - Menu “Clusters” => “Grace Shell Access”
- Grace has 5 login nodes. Check the bash prompt to see which you log into.
  - `[netid@grace2 ~]$`

<https://hprc.tamu.edu/wiki/HPRC:Access>

# Grace Usage

- Login sessions that are idle for **60** minutes will be closed automatically
- Processes run longer than **60** minutes on login nodes will be stopped.
  - use data transfer nodes for large copy jobs
- **Do not use more than 8 cores on the login nodes!**
- Contact us for assistance installing software or install it yourself in your \$SCRATCH directory.
  - **Do not use the sudo command.**
- HPRC applications must be renewed each fiscal year which ends August 31 each year.
  - <https://hprc.tamu.edu/apply>      <https://hprc.tamu.edu/policies>
  - SUs expire at the end of each fiscal year
    - if you do not renew, you can still access your files on the clusters but you cannot submit any jobs
- Do not share your HPRC account with anyone



# File Transfers with Grace

- Simple File Transfers:
  - scp: command line (Linux, MacOS)
  - rsync: command line (Linux, MacOS); ***can resume transfer***
  - MobaXterm: GUI (Windows)
  - WinSCP: GUI (Windows)
  - Portal: <https://portal.hprc.tamu.edu>
- Use data transfer nodes for bulk data transfers (many large files):
  - scp and rsync data transfer processes will not timeout at 60 minutes
    - `ssh grace-dtn1.hprc.tamu.edu`
    - `ssh grace-dtn2.hprc.tamu.edu`
  - Globus Connect
    - <https://hprc.tamu.edu/wiki/SW:GlobusConnect>
  - GridFTP

<https://hprc.tamu.edu/wiki/HPRC:FileTransfers>

# 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.
/scratch/user/\$USER	\$SCRATCH	1 TB	250,000	Temporary storage of files for on-going computations. Not intended to be a long-term storage area.

- **\$HOME** and **\$SCRATCH** directories are not shared between HPRC clusters.
- View usage and quota limits using the command: **showquota**
- Quota and file limit increases will only be considered for scratch directory
- Request a group directory for sharing files.
- **Do not share your home, or scratch directory.**

# Software

- See the Software wiki page for instructions and examples
  - <https://hprc.tamu.edu/wiki/SW>
  - <https://hprc.tamu.edu/software/grace>
  - <https://hprc.tamu.edu/wiki/Bioinformatics>
- License-restricted software
  - Contact license owner for approval
- Contact us for software installation help/request
  - User can install software in their \$SCRATCH dir
  - **Do not use "*sudo*" command when installing software**



# Software Modules

- Installed software applications are available as modules which are available to all users
  - (except for restricted modules)
- It's a good habit to purge unused modules before loading new modules.
- It is highly recommended to load a specific software version instead of the defaults
- **Avoid loading modules in your `~/ .bashrc`**

```
module avail
```

```
# list all available modules (sometimes it is very slow)
# space bar down, page up/down, q to quit
# / for case sensitive search (similar to a UNIX man page)
```

```
module spider trinity
```

```
# case insensitive search for modules with 'boost' in name
```

```
module keyword assembly
```

```
# search module descriptions for keyword "assembly"
# some assembly software modules may be missed if
# keyword is not found in description (case insensitive)
```

# Computing Environment

- Almost all software, applications, libraries, etc. are available as a module.
  - Module names have the format:

software\_name / version - [Python-version]  
Trinity/2.12.0-Python-3.8.2

- Some software is installed as an Anaconda environment

```
module load Anaconda3/2020.07
conda env list
source activate qiime2-2021.2
```

- Grace uses a modulefile hierarchy so library dependencies must be loaded prior to loading the software module

# Module Loading Exercise

1. `module list` # list all loaded modules
2. `module spider trinity` # search for available module names matching trinity  
# not case sensitive unless an exact match is found
3. `module spider Trinity/2.12.0-Python-3.8.2` # search a specific module version  
  
# see message about what additional modules need to be loaded first  
You will need to load all module(s) on any one of the lines below before the "Trinity/2.12.0-Python-3.8.2" module is available to load.  
GCC/9.3.0 OpenMPI/4.0.3
4. `module load GCC/9.3.0 OpenMPI/4.0.3 Trinity/2.12.0-Python-3.8.2`
5. `module avail bwa` # show software with toolchain compatible with currently  
# loaded modules
6. `module load BWA/0.7.17` # load a toolchain-compatible module
7. `module purge` # unload all modules

# Computing Resources

- Resources specified in a job file:
  - Processor cores, memory, wall time
- Service Unit (SU) - defined as one CPU core usage for one hour
  - Use "myproject" to see your balance
  - SUs expire at the end of each fiscal year; Aug 31 and must be renewed <https://hprc.tamu.edu/apply>

myproject

=====						
List of YourNetID's Project Accounts						
-----						
Account	FY	Default	Allocation	Used & Pending SUs	Balance	PI
-----						
1228000223136	2020	N	10000.00	0.00	10000.00	Doe, John
-----						
1428000243716	2020	Y	5000.00	-71.06	4928.94	Doe, Jane
-----						

[https://hprc.tamu.edu/wiki/HPRC:AMS:Service\\_Unit](https://hprc.tamu.edu/wiki/HPRC:AMS:Service_Unit)

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

A Service Unit (SU) on Grace is equivalent to one core or **7.5** GB memory usage for one hour.

	Number of Cores	Total Memory (GB)	Hours	SUs charged
1.	1	7.5	1	1
2.	1	7.6	1	2
3.	1	360	1	48
4.	48	360	1	48

- SUs are charged at job submit time and the job's unused SUs are reimbursed if job finishes early

[https://hprc.tamu.edu/wiki/HPRC:AMS:Service\\_Unit](https://hprc.tamu.edu/wiki/HPRC:AMS:Service_Unit)

# See the HPRC Wiki on how to request all cores and all memory on a compute node

- Use all cores if the software you are using supports multi-core unless the software recommends fewer cores
- Use all cores if you are using all the memory even if the software only supports running on a single core
- When your job is complete, use the 'seff jobid' command to see job efficiency and use fewer cores and memory next time if efficiency was low.

1.1.2 How do I request all the cores and all the memory on a single compute node?

1.1.2.1 Grace

1.1.2.1.1 For a 384 GB memory Grace compute node

1.1.2.1.2 For a 3 TB memory Grace compute node

1.1.2.1.3 For a A100 GPU 384 GB memory Grace compute node

<https://hprc.tamu.edu/wiki/Bioinformatics:FAQ>



# Historical HPRC Cluster Usage

[hprc.tamu.edu](https://hprc.tamu.edu)

## Cluster Status

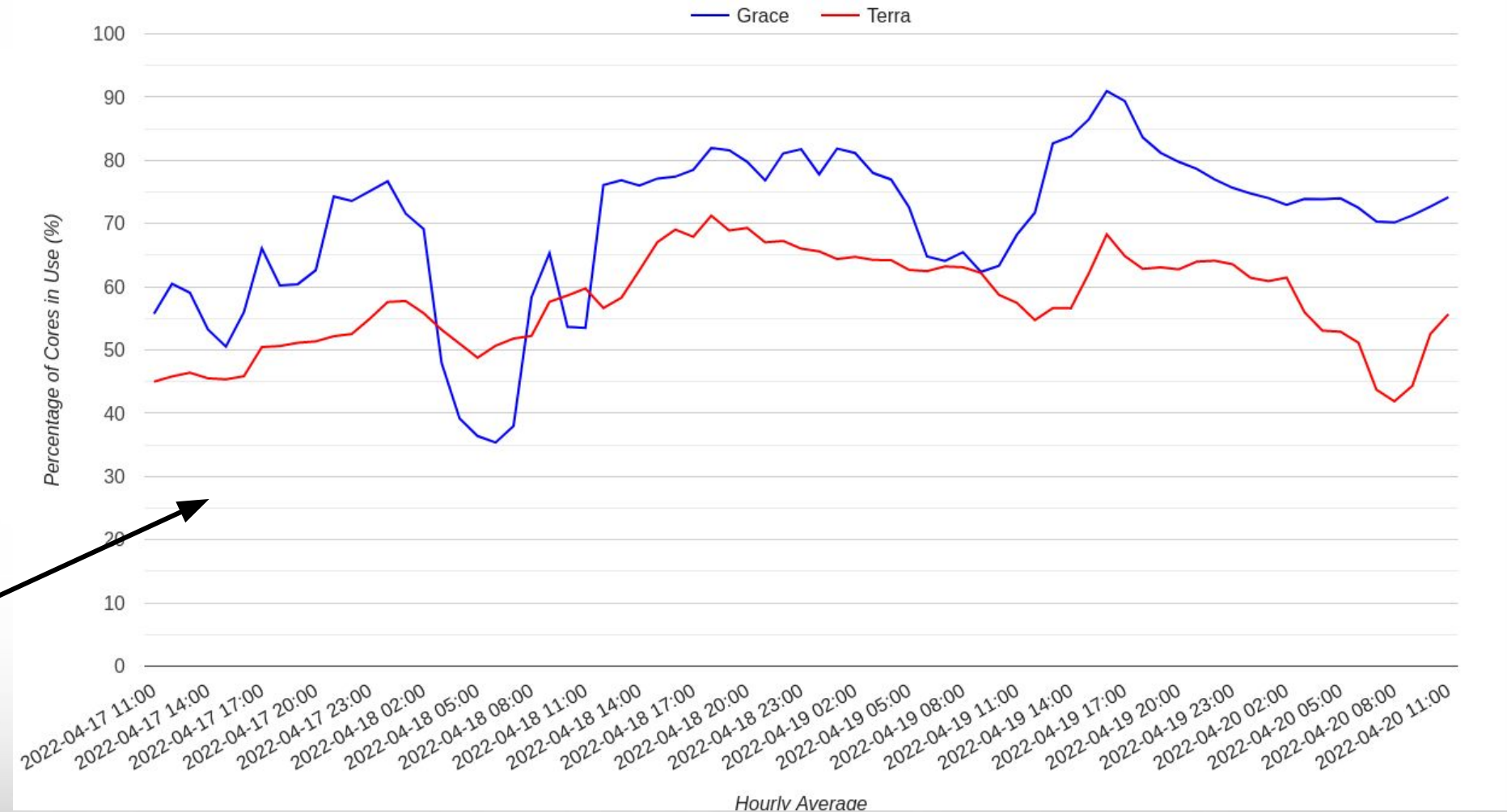
### Grace

Nodes 799/850 (94%)  
Cores 29839/40928 (73%)  
Jobs 904R-41Q

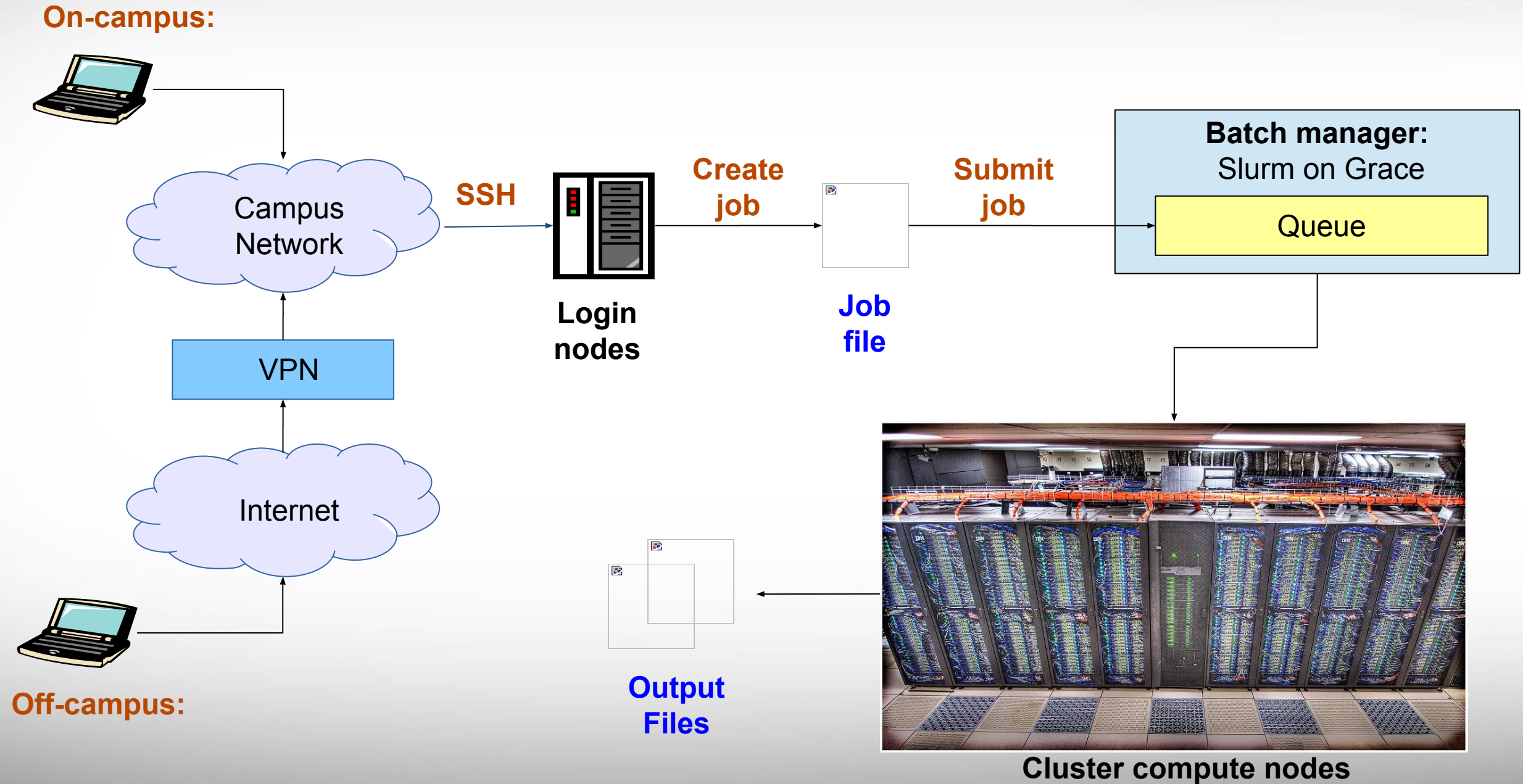
### Terra

Nodes 249/304 (82%)  
Cores 4911/8932 (55%)  
Jobs 176R-207Q

Historical Status



# Batch Computing on HPRC Clusters



# Slurm Job Scheduling

[https://hprc.tamu.edu/files/training/2022/Spring/Slurm\\_Job\\_Scheduling\\_2022\\_spring.pdf](https://hprc.tamu.edu/files/training/2022/Spring/Slurm_Job_Scheduling_2022_spring.pdf)

# Batch Job Scripts

# Sample Slurm Job Script Structure

## # NECESSARY JOB SPECIFICATIONS

```
#!/bin/bash
```

```
#SBATCH --export=NONE
```

```
#SBATCH --job-name=my_job
```

```
#SBATCH --time=7-00:00:00
```

```
#SBATCH --ntasks-per-node=1
```

```
#SBATCH --cpus-per-task=48
```

```
#SBATCH --mem=360G
```

```
#SBATCH --output=stdout.%j
```

```
#SBATCH --error=stderr.%j
```

```
# do not export current env to the job
```

```
# job name
```

```
# max job run time dd-hh:mm:ss
```

```
# tasks (commands) per compute node
```

```
# CPUs (threads) per command
```

```
# total memory per node
```

```
# save stdout to file
```

```
# save stderr to file
```

These parameters describe your job to the job scheduler

## # OPTIONAL JOB SPECIFICATIONS

```
#BSUB -P 123456
```

```
#BSUB -u email_address
```

```
#BSUB -B -N
```

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

Load the required module(s) first

```
# load required module(s)
```

```
module load GCC/9.3.0 OpenMPI/4.0.3 Trinity/2.12.0-Python-3.8.2
```

```
Trinity
```

This is a command (task) that is executed by the job

# Submitting Your Job and Check Job Status

## Submit job

```
sbatch run_trinity_grace.sh
```

```
Verifying job submission parameters...
Verifying project account...
  Account to charge: 082792010838
    Balance (SUs): 4871.5983
    SUs to charge: 24.000
Job <2470599> is submitted to default queue <sn_short>.
```

## Check status

```
squeue -u $USER
```

```
====Tue Jun 15 12:54:09 CDT 2021=====
JOBID PARTITION              NAME          USER      STATE      TIME TIME_LIMI  NODES NODELIST(REASON)
8249345  long                i-tasser-parallel  my_netid  RUNNING    8:23  7-00:00:00    1 tnxt-0742
```

[https://hprc.tamu.edu/files/training/2021/Spring/Slurm\\_Job\\_Scheduling\\_2021\\_spring.pdf](https://hprc.tamu.edu/files/training/2021/Spring/Slurm_Job_Scheduling_2021_spring.pdf)



# See Completed Job Efficiency Stats

- **seff JOBID**

- will show CPU and Memory efficiency based on selected resources

```
Job ID: 836933
Cluster: grace
User/Group: mynetid/mynetid
State: COMPLETED (exit code 0)
Nodes: 1
Cores per node: 48
CPU Utilized: 00:29:36
CPU Efficiency: 26.81% of 01:50:24
core-walltime
Job Wall-clock time: 00:02:18
Memory Utilized: 40.60 GB
Memory Efficiency: 11.28% of 360.00 GB
```

CPU load was at 100% for 27% of the run time or CPU load at 27% for 100% of the run time

max memory utilized was 11% of requested memory

# Check your Service Unit (SU) Balance

- List the SU Balance of your Account(s)

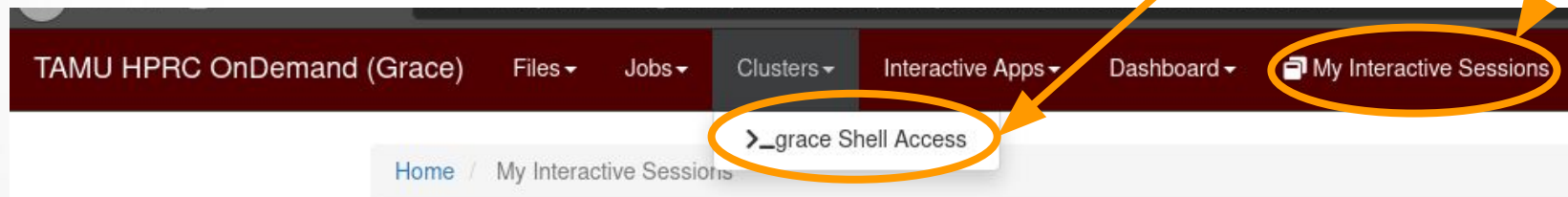
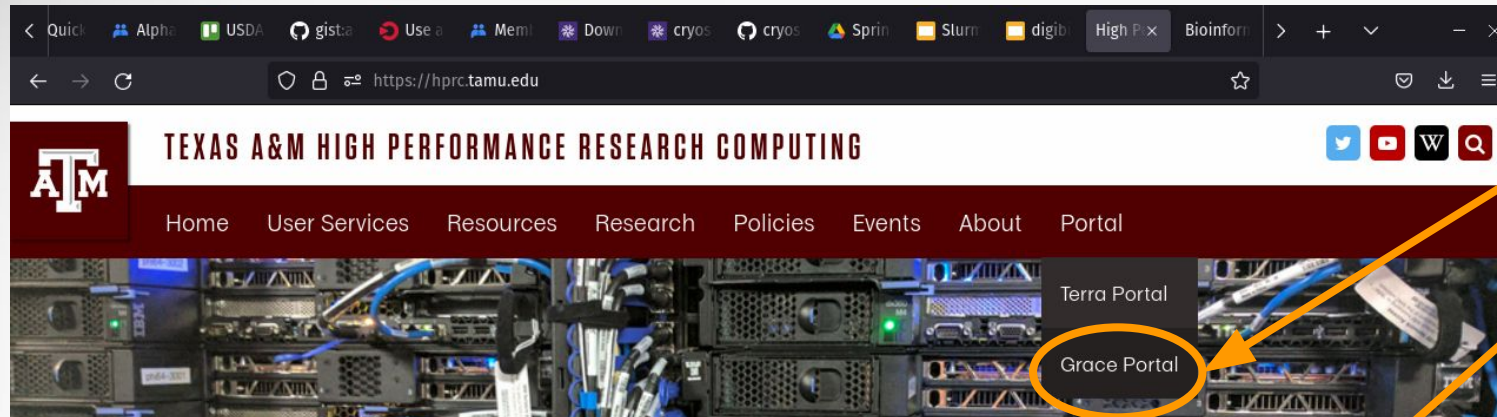
`myproject`

```
=====
                        List of YourNetID's Project Accounts
-----
| Account | FY | Default | Allocation | Used & Pending SUs | Balance | PI |
-----
| 1228000223136 | 2019 | N | 10000.00 | 0.00 | 10000.00 | Doe, John |
-----
| 1428000243716 | 2019 | Y | 5000.00 | -71.06 | 4928.94 | Doe, Jane |
-----
| 1258000247058 | 2019 | N | 5000.00 | -0.91 | 4999.09 | Doe, Jane |
-----
```

- To specify a project ID to charge in the job file
  - `#BSUB -P Account#`
- Run `"myproject -d Account#"` to change default project account
- Run `"myproject -h"` to see more options

[https://hprc.tamu.edu/wiki/HPRC:AMS:Service\\_Unit](https://hprc.tamu.edu/wiki/HPRC:AMS:Service_Unit)  
<https://hprc.tamu.edu/wiki/HPRC:AMS:UI>

# HPRC Portal



The HPRC portal allows users to do the following

- Browse files on the Grace filesystem
- Access the Grace UNIX command line
  - no SUs charged for using command line
- Launch jobs
  - SUs charged
- Compose job scripts
- Launch interactive GUI apps (SUs charged)
  - Grace
    - IGV
    - MATLAB
    - VNC
    - Jupyter Notebook
    - JupyterLab
    - RStudio
- Monitor and stop running jobs and interactive sessions

# HPRC Cluster Usage Notes

- Can test software on the login nodes but do not use more than 8 cores
  - processes get automatically killed on login node when they reach 60 minutes
  - login session gets automatically disconnected when idle for 60 minutes
- Transfer large data between HPRC clusters using the login nodes
  - transfer large data between HPRC clusters and sites off campus using the data transfer nodes
- Carefully read the stdout and stderr files for completed and failed jobs
  - most causes of failed jobs can be found in the log files
- Search the wiki and look at the FAQ pages for a solution before sending a helpdesk request
  - <https://hprc.tamu.edu/wiki/HPRC:CommonProblems>
  - <https://hprc.tamu.edu/wiki/Bioinformatics:FAQ>

# Need Help?

- First check the FAQ <https://hprc.tamu.edu/wiki/HPRC:CommonProblems>
  - Grace User Guide <https://hprc.tamu.edu/wiki/Grace>
- Email your questions to [help@hprc.tamu.edu](mailto:help@hprc.tamu.edu).
  - Managed by a ticketing system
- Help us, help you -- we need more info
  - Which Cluster
  - UserID/NetID (*UIN is not needed!*)
  - Job id(s) if any
  - Location of your jobfile, input/output files
  - Software module(s) used if any
  - Error messages
  - Steps you have taken, so we can reproduce the problem
- Or visit us @ 114A Henderson Hall
  - Making an appointment is recommended.



**HIGH PERFORMANCE  
RESEARCH COMPUTING**  
TEXAS A&M UNIVERSITY

**Thank you.**

*Any question?*