

# Guide to W&M Computational Resources



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September 21st, 2023

# RC/HPC Staff



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# Research Computing / HPC Training

1. Thursday – September 14th 5-6pm Zoom – Introduction to Linux command line
2. **Thursday – September 21st 5-6pm Zoom – Introduction to HPC at W&M/VIMS**
3. Thursday – September 28th 5-6pm Zoom – Linux in the HPC environment

2023 September						
SUNDAY	MONDAY	TUESDAY	WEDNESDAY	THURSDAY	FRIDAY	SATURDAY
					1	2
3	4	5	6	7	8	9
10	11	12	13	14 1.	15	16
17	18	19	20	21 2.	22	23
24	25	26	27	28 3.	29	30

- <https://www.wm.edu/it/rc> - shortcut to RC/HPC web
- [hpc-help@wm.edu](mailto:hpc-help@wm.edu) - help desk email – **best way to reach us**
- [hpc-announce@wm.edu](mailto:hpc-announce@wm.edu) - list for announcements from RC (auto-subscribed)
- Office hours: by appointment – email [hpc-help@wm.edu](mailto:hpc-help@wm.edu)

# Using HPC / Web Docs

## Using HPC

### Obtaining an account

Unlike many other IT services, HPC access is by request only. If you have not yet obtained an account, or your account has expired, please [submit an account request](#).

### Prerequisites

You will need to be comfortable using a [Unix/Linux command-line](#) after logging in with [SSH](#).

### Logging in

The [subcluster pages](#) will tell you which "front-end" server to log in to, depending on which hardware you want to use. Generally, you must log in to the HPC systems from the campus network (at W&M or VIMS), via the College's [VPN](#), or via a host that is on the campus network (such as [stat.wm.edu](#), accessible from off-campus with your WMuserid and password) or you will see errors like `Connection timed out` or `Network is unreachable`. Chesapeake is behind VIMS' (more restrictive) firewall and from W&M must be accessed via `stat` or by first logging into SciClone.

### Running calculations

The login servers are called "front-ends" because you do not run your calculations there, but rather on back-end "compute" servers that the front-end server provides access to. Access compute servers via the [batch system](#), using the `qsub` command.

In order to use installed software, you must generally "load" it using [Environment Modules](#), or you will see errors like `Command not found`. We have specific guidance for users of MATLAB, Python, and other software under our [Tutorials](#) and [Software](#) pages, as well as for users [compiling](#) software themselves.

If you need to work with or produce more than a few gigabytes of data, familiarize yourself with [filesystems](#) other than your home directory, and with [preventing your disk usage from disrupting others' work](#).

### When you are finished

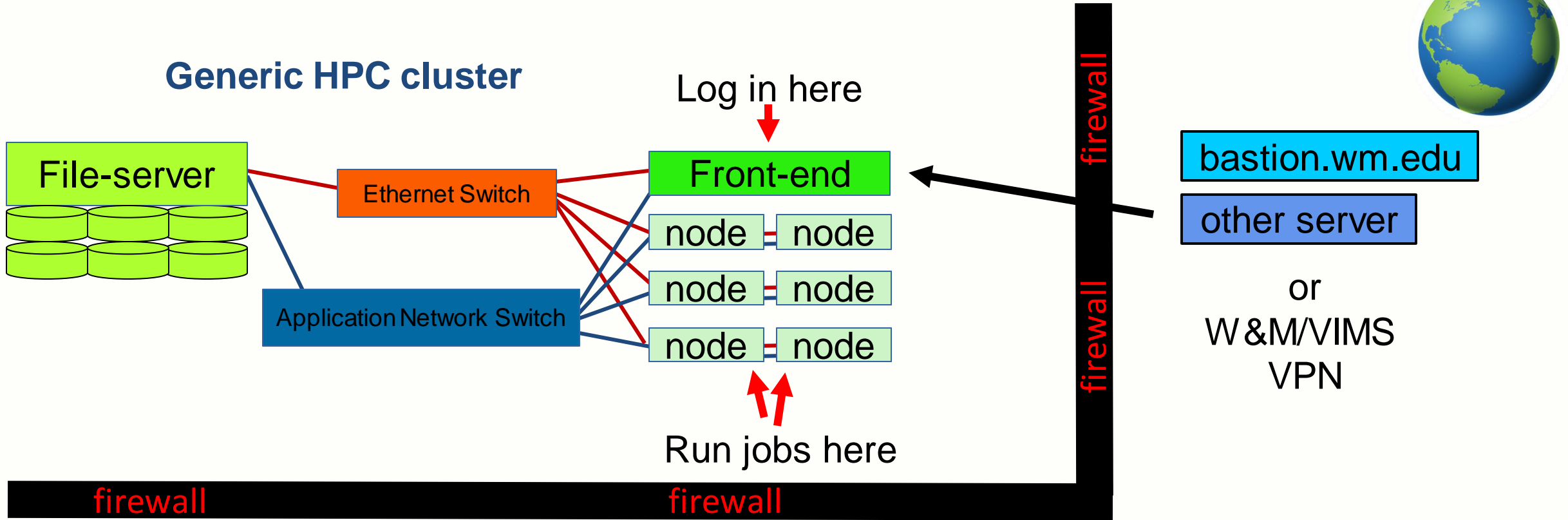
The HPC systems cannot provide archival or long-term storage. If files no longer need to be available for work on the system, [copy them off](#) and delete them so that the space can be used for active projects. **All files will be completely and permanently deleted after your HPC account expires**, so if your files need to remain available for work on the system, keep track of when your account will expire, and before it expires either [renew](#) your account or [contact us](#) to arrange to have your files reassigned to another user.

## What you need to get started

1. Getting an account
2. Linux command line / text editors
3. Logging into the clusters
4. Selecting/installing/requesting software
5. How to use file-systems effectively
6. How to use to use the batch system(s)
7. Compiling / installing your own applications
8. Saving your own files/projects

# Cluster Nomenclature

## Generic HPC cluster



Must get through **W&M/VIMS firewall** to get to cluster resources  
On campus you are already within firewall  
Otherwise use **bastion.wm.edu**, another server, or VPN

# Cluster Resources

	Cluster	Front-end	# Nodes	# Cores/Node	# Total Cores	Memory/Node (GB)	
HTC	vortex	vortex	31	12	372	32/128	} ALL
HTC	hima	bora	7	32*	224	256	
HTC	gust	gust	2	128	256	512	
HPC	bora	bora	49	20	980	128	
HTC	meltemi	meltemi	88	64	5632	192	} AUTH
HPC	cyclops	cyclops	30	24	720	32	
HPC	femto	femto	30	32	960	96	
HPC	james	james	26	20	520	64	} VIMS
HTC	potomac	chesapeake	13	12	156	32	
HTC	pamunkey	james	2	64	128	256	

**High Throughput Computing (HTC)** – serial or small core count jobs  
**High Performance Computing (HPC)** – parallel jobs with 10's-100's cores

VIMS has their own policies: email [hpc@vims.edu](mailto:hpc@vims.edu) if need more than 10 nodes for more than 48 hrs.

- W&M on [.sciclone.wm.edu](http://.sciclone.wm.edu) network (e.g.: vortex.sciclone.wm.edu)
- VIMS on [.hpc.vims.edu](http://.hpc.vims.edu) network (e.g.: james.hpc.vims.edu)

## Main campus cluster policy:

- ALL** – resources available for all
- AUTH** – must get authorization
- VIMS** – must be a VIMS fac/staff/student

# Connecting to W&M HPC

## Must connect via Secure Shell Client (ssh)

- Linux / Mac can use built-in *terminal / console*
- Windows – powershell/run or *SSH Secure Shell Client / PuTTY*
- **ssh keys are allowed**

## Am I on or off campus?

- On campus: can ssh right into HPC servers

```
15 [mycomputer] ssh vortex.sciclone.wm.edu
```

- Off campus, must jump through bastion host

```
15 [mycomputer] ssh -J bastion.wm.edu vortex.sciclone.wm.edu
```

## Is my username the same on my local machine?

If it is different use: `ssh <username>@<host>.<domain>`

## Do I need graphics?

If yes, must log in with `-Y`

# Linux command-line / Text editors

Web documentation: <https://www.wm.edu/offices/it/services/researchcomputing/using/prereqs/index.php>

Intro to Linux slides / recording: <https://www.wm.edu/offices/it/services/researchcomputing/using/tutorials/index.php>

## Common Linux Commands

**cd** – change directory  
**ls** – list files  
**ls -l** – list files (long)  
**cp** – copy file  
**mv** – move file  
**pwd** – print working directory  
**mkdir** – make directory  
**rmdir** – remove directory  
**df** – list disks  
**ps -fu <user>** – list <user> process ids  
**kill <pid>** – kill processes  
**cat <file>** – dump file to screen  
**less <file>** – page file on screen

## Text Editors

**nano** : easiest / least powerful

<https://www.howtogeek.com/42980/the-beginners-guide-to-nano-the-linux-command-line-text-editor/>

**vi/vim** : advanced / powerful

**emacs** : advanced / powerful

**vscode** on local computer :

supports ssh for remote editing

- Linux session is called a “**shell**”
- ‘.’ means current directory ; ‘..’ parent directory
- ‘~’ mean home directory
- <tab> for file-completion
- <up-arrow> mean “last command”
- bash/tcsh common shell flavor

All users get **tcsh** by default on W&M cluster / can request **bash**



# Environment Modules / Software

Sets up environment for particular software packages

```
12 [vortex] module list
Currently Loaded Modulefiles:
  1) modules          2) maui/r156-GRes   3) torque/6.1.1.1   4) intel/2018       5) intel/2018-mpi
13 [vortex] module avail

----- /usr/local/Modules/versions -----
--
3.2.10 3.2.6

----- /usr/local/Modules/modulefiles -----
--
abcluster/2.0          matlab/R2020a
ampl/20210531(default) maui/r156-GRes
anaconda2/2019.10     mumps/5.4.0/gcc-4.8.5
anaconda3/2020.02     mvapich2-ib/2.3.1/gcc-9.3.0
anaconda3/2021.05     mvapich2-ib/2.3.1/intel-2018
anaconda3/2021.05n    nciplot/4.0
boost/1.74.0/gcc-9.3.0 nco/4.9.3-intel-2018_intel-mpi
.                      .
.                      .
.                      .
```

Can change modules on demand: [module load/unload](#)

Also list what the module sets: [module show](#)

Can even write your own modules to make custom environments

# Startup Modules / Environment

In user home directories, there are startup files which control default modules (bash users use `.bashrc.XXX`)

## Start-up file

```
.cshrc  
.cshrc.vortex  
.cshrc.e17-xeon  
.cshrc.gust  
.cshrc.e17-phi  
.cshrc.femto  
.cshrc.cyclops  
  
.cshrc.e17-x86_64  
.cshrc.potomac  
.cshrc.rhel17-opteron
```

## Controls modules for

```
all front-ends  
Vortex  
Bora & Hima  
Gust  
Meltemi  
Femto  
Cyclops  
  
James  
Potomac  
Pamunkey
```

Be careful when modifying start-up files

***User shell cannot have output when invoked  
(PBS/Torque)***

`$PLATFORM` variable:

```
11 [vortex] echo $PLATFORM  
vortex
```

This means that startup is controlled by `.cshrc.vortex` for *vortex cluster*



# Paths, ENV variables, symbolic links

**PATH** – environmental variable ; list of directories which are searched for executable

```
22 [vortex] echo $PATH
/sciclone/home10/ewalter/bin:/usr/local/intel-2018/compilers_and_libraries_2018/linux/mpi/intel64/bin:/usr/local/intel-2018/compilers_and_libraries_2018.5.274/linux/bin/intel64:/usr/local/torque-6.1.1.1/bin:/usr/local/torque-6.1.1.1/sbin:/usr/local/maui-r156-GRes/bin:/usr/local/Modules/3.2.10/bin:/usr/local/torque-6.1.1.1/bin:/usr/local/torque-6.1.1.1/sbin:/usr/lib64/qt-3.3/bin:/usr/lib64/ccache:/usr/local/bin:/bin:/usr/bin:/usr/local/sbin:/usr/sbin:/sbin:/opt/ibutils/bin:/opt/puppetlabs/bin:/usr/local/bin:/usr/local/sbin:/usr/sbin:/usr/local/intel-2018/parallel_studio_xe_2018.4.057/bin
```

**Current directory (.) is usually not in path – (must type ./<executable>)**

**Symbolic link** – allows an alias for another file/directory

```
23 [vortex] ls -l
lrwxrwxrwx 1 ewalter hpcf    24 Apr  9  2012 data10 -> /sciclone/data10/ewalter
lrwxrwxrwx 1 ewalter hpcf    18 Apr  9  2012 lscr -> /local/scr/ewalter
.
```

**ln -s <PATH> <TARGET>**

# Files & I/O

## Web Documentation

<https://www.wm.edu/offices/it/services/hpc/using/files/index.php>

- There are multiple files-systems available
- Some are for ongoing / project storage  
**data, home**
- Some are for running jobs (90 day purge)  
**scrXX, pscr, /local/scr**
- **Only** data/home/home00 backed up
- Use **local scratch** when possible (every node has some)
- Users are responsible for using disk space **responsibly**
- Misue can disturb other jobs / cause **administrative action**
- Don't use home/data10 for writing or large reads
- Use scratch space for jobs
- Lustre (pscr) best practices:

<https://www.wm.edu/offices/it/services/researchcomputing/using/files/lustre/index.php>

Name	Appropriate for	Backups	Purged	Per- formance
/sciclone/home /ches/home00	Source code, executables, configuration files, scripts, and small (<100MB total) data files. Unless we have directed you otherwise, <b>you should not have a job read or write any substantial amount of data to your home directory</b> , as doing so is extremely likely to impact others' interactive work.	Weeknightly, on-site only		
/sciclone/data10 /ches/data10	Input data files that are needed on an ongoing basis for active projects on the cluster and cannot be easily re-created or re-uploaded. <b>Please do not have jobs write a substantial amount to data filesystems.</b> Please use the scratch filesystems (below) for job output unless already given permission from HPC staff.	Weekly, on-site only	After account expiration.	Low
/local/scr /ches/scr10 /sciclone/scr10 /sciclone/scr20 /sciclone/scr-mlt /sciclone/pscr	<b>Scratch space:</b> job outputs and working data that can be easily re-created or re-uploaded, or which will be copied elsewhere for longer-term storage.	<b>Never</b>	<b>Any files not accessed for 90 days, and after account expiration.</b>	Medium  High

# Transferring Files

## Web Documentation

<https://www.wm.edu/offices/it/services/researchcomputing/using/files/xfers/index.php>

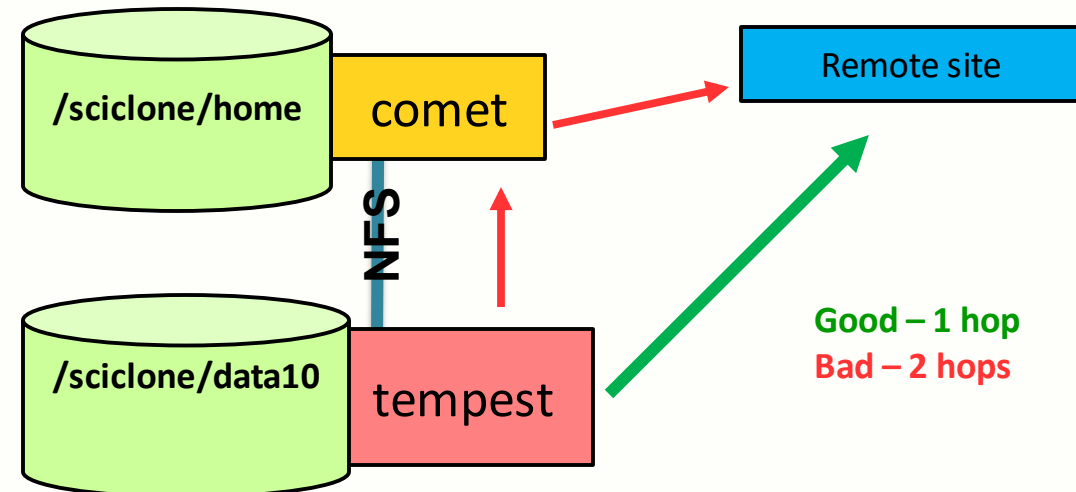
Filesystem	Recommended node and Endpoint Display Name
/sciclone/* (New endpoint to be used for all sciclone transfers once Globus V4 is deprecated)	io.sciclone.wm.edu W&M RC/HPC/IO Collection
/sciclone/home	comet.sciclone.wm.edu Sciclone Cluster at W&M, home (Comet)
/sciclone/pscr	bora.sciclone.wm.edu Sciclone Cluster at W&M, pscr (Bora)
/sciclone/data10	tempest.sciclone.wm.edu Sciclone Cluster at W&M, data10 (Tempest)
/sciclone/scr10	polar.sciclone.wm.edu Sciclone Cluster at W&M, scr10 (Polar)
/ches/home00	james.hpc.vims.edu VIMS Cluster at W&M, home00 (James)
/ches/data10	choptank.hpc.vims.edu VIMS Cluster at W&M, data10 (Choptank)
/ches/scr10	rappahannock.hpc.vims.edu VIMS Cluster at W&M, scr10 (Rappahannock)

Globus - <https://www.globus.org/>  
We have endpoints for all file-systems

Each file-system has a server that runs it  
For direct access you are **STRONGLY** encouraged to use the recommended node

e.g. : Logged into **comet**; cd'd into data10 ; transfer off-site

Do this from **tempest** since files won't have to hop through **comet** to get off-site.



# Permissions / sharing files

Want to allow users in the VASP group to read my results file (out)

```
44 [vortex] pwd                                     (where am I?)
/sciclone/home10/ewalter

45 [vortex] ls -ld results                          (long list just <dir>)
drwx----- 2 ewalter hpcf 4096 May  6 12:27 results

46 [vortex] ls -l results                          (long list <dir> contents)
total 28
-rw----- 1 ewalter hpcf 25905 May  6 12:27 out

47 [vortex] groups ewalter                        (what group am I in?)
ewalter : hpcf wheel hpcfstaff hpcfadmin sysadmin www seadas
vasp wm wmall hugepage

48 [vortex] chgrp vasp -R results/                (change group)

49 [vortex] ls -ld results
drwx----- 2 ewalter vasp 4096 May  6 12:27 results

50 [vortex] ls -l results
total 28
-rw----- 1 ewalter vasp 25905 May  6 12:27 out

51 [vortex] chmod g+rX -R results                 (change group
permissions
recursively)

52 [vortex] ls -ld results
drwxr-x--- 2 ewalter vasp 4096 May  6 12:27 results

53 [vortex] ls -l results
total 28
-rw-r----- 1 ewalter vasp 25905 May  6 12:27 out
```

```
drwx----- 2 ewalter hpcf 4096 May  6 12:27 results
```

user group other

user group

**d**-directory

**r**-read

**w**-write

**x**-execute/enter

**pwd** – print working directory

**groups** – print groups that user is in

**chgrp** – change **group** ownership

**chmod** – change **permissions**

**chown** – **change user ownership**

**umask** – controls default permissions

- change in .cshrc/.bashrc

**Whole path needs to be accessible to share!**

**William & Mary** see <http://linuxcommand.org/lc3Its0090.php> for more information

# Software

**There are many software packages available on the HPC systems!**

Common packages are all available: [Python](#), [R](#), [Gaussian16](#), [Matlab](#), etc.

- Check the modules on a particular cluster with: “module avail”
- Install it yourself
- Email [hpc-help@wm.edu](mailto:hpc-help@wm.edu)

We encourage **users to install their own software** in their home directory if possible

We can help install, but we get **LOTS** of requests so try not to abuse

Packages used by multiple users can be considered for installing globally

# Compilers and Installing

Web docs: <https://www.wm.edu/offices/it/services/researchcomputing/using/compiling/index.php>  
<https://www.wm.edu/offices/it/services/researchcomputing/using/software/index.php>

- All clusters are equipped with GNU and Intel compilers – some have older PGI
- All popular flavors of MPI supported (Intel, Mvapich2, OpenMPI)
- Also (for PBS/Torque nodes) special wrapper mvp2run available for easier MPI use:  
<https://www.wm.edu/offices/it/services/researchcomputing/using/jobs/mvp2run/index.php>

Compiler web page lists suggested compiler flags for each node type and best practices guides. It is **extremely** important to check the validity of results.

**Don't assume if the job runs correctly, it has correct results!**



# Batch system & Jobs

Web documentation: <https://www.wm.edu/offices/it/services/researchcomputing/using/jobs/index.php>

Cluster	Front-end	Max Walltime (hrs)	Batch System
vortex	vortex	180	PBS/Torque
hima	bora	72	PBS/Torque
bora	bora	72	PBS/Torque
gust	gust	72	SLURM
meltemi	meltemi	72	PBS/Torque
cyclops	cyclops	72	SLURM
femto	femto	72	SLURM
james	james	72	PBS/Torque
potomac	chesapeake	180	PBS/Torque
pamunkey	james	180	PBS/Torque

ALL

AUTH

VIMS

Only newer resources use SLURM (gust)

**PBS/Torque** vs. **SLURM** ; both share same concepts  
Commands are different

**PBS/Torque clusters -**

Vortex/hima/bora all share batch system

e. g. can submit/query jobs from

bora front-end to vortex/bora/hima cluster

vortex front-end to bora vortex/bora/hima cluster

Same with james/potomac/pamunkey

Meltemi uses a separate batch system from these two

**DON'T SUBMIT JOBS longer than 72hrs to hima,bora, or james – they won't start running.**

**SLURM clusters -**

Submit from cluster front-end only

**Front-end** – same architecture as **cluster** used for compiling, preparing jobs, analyzing data, etc.

# Batch system: Interactive Jobs

Cluster	Front-end	Max Walltime (hrs)	node spec
vortex	vortex	180	vortex,c18a,c18b
hima	bora	72	Hima,hima:gpu,hima:nogpu
bora	bora	72	bora
gust	gust	72	N/A
james	james	72	james
potomac	chesapeake	180	potomac
pamunkey	james	180	pamunkey

**special node subsets**

- c18a** – 32GB nodes
- c18b** – 128GB nodes
- hima:gpu** – want node with gpu
- hima:nogpu** – want node without gpu

For PBS/Torque nodes are selected via the *node spec*  
*qsub* – submits the job to the batch system

```
1 [vortex] qsub -I -l walltime=30:00 -l nodes=1:vortex:ppn=1
qsub: waiting for job 10274099 to start
qsub: job 10274099 ready

2 [vx03] python prog.py
```

SLURM front-ends are tied to a single cluster  
--- no need for node-spec.

Use *salloc* (*srun* on on femto,cyclops)

All slurm clusters have 72hr max walltime

```
1 [gust] salloc -N1 -n1
salloc: Granted job allocation 388
salloc: Waiting for resource configuration
salloc: Nodes gt01 are ready for job

2 [gt01]$ python prog.py
```

**Interactive** job puts you on a node ready to work

# Batch Jobs PBS/Torque

You can also submit a *batch* job which does not run interactively

First you must write a *batch script*:

```
34 [vortex] cat run
#!/bin/tcsh
#PBS -N test
#PBS -l nodes=1:vortex:ppn=1
#PBS -l walltime=0:10:00

cd $PBS_O_WORKDIR

python prog.py >& prog.out
```

```
#!/bin/tcsh           interpret the following in tcsh syntax
-N                   name of the job
-l                   job specifications (walltime ; nodespec)
```

PBS/Torque start session on node in user home directory!  
cd \$PBS\_O\_WORKDIR *cd to where I submitted the job*

```
35 [vortex] qsub run
```

most widely used batch commands

- qsub** <script> – submit job / interactive job
- qdel** <jobid> – delete job
- qstat** – list jobs
- qsu** – list my jobs

Generates *test.o<jobid>* and *test.e<jobid>*  
- batch stdout & stderr output files

# Batch Jobs SLURM

Just like any batch system, you must write a *batch script*:

```
22 [gust] cat run

#!/bin/tcsh
#SBATCH -J test
#SBATCH -N 1 -n 1
#SBATCH -t 0:10:00

python prog.py >& prog.out
```

```
24 [gust] sbatch run
```

most widely used batch commands  
**sbatch** <script> – submit job script  
**scancel** <jobid> – delete job  
**squeue** – list jobs  
**squeue -u** <userid> – list my jobs

```
#!/bin/tcsh           interpret the following in tcsh syntax
-J                   name of the job
-N                   # nodes
-n                   # cores
-t                   walltime hh:mm:ss
```

SLURM starts session on node in *submission directory*

Generates *slurm-<jobid>.out*  
- batch stdout & stderr output file

# Batch system & Jobs Example

## PBS/Torque MATLAB example

```
107 [vortex] cat run
#!/bin/tcsh
#PBS -N test
#PBS -l nodes=1:vortex:ppn=12
#PBS -l walltime=12:00:00
#PBS -q matlab

cd $PBS_O_WORKDIR
module load matlab

matlab -nodisplay -r "readMatrix" >& OUT
```

must add -q matlab for matlab jobs  
(PBS/Torque only)

load matlab module (if needed)  
PBS/Torque starts node session with default environment.  
If modules are not loaded in module startup file (.cshrc.vortex,  
e.g.), must load in batch script

redirect stdout and stderr

file for stdout and stderr

- Submit job with **qsub**
- Once job starts, check 'OUT' for output
- Check batch **stdout/stderr** files for issues -  
named *test.o<jobid>* and *test.e<jobid>*

```
108 [vortex] cat readMatrix.m
tic
%parpool(8)
syms a b c d;
meshpoints = meshgenerator();
eigfile = fopen('eigfile.txt', 'wt');
count = 1;
.
```

# Batch system & Jobs Example

## SLURM / MATLAB example

```
107 [gust] cat run
#!/bin/tcsh
#SBATCH -J test
#SBATCH -N 1 -n 1
#SBATCH -t 0:10:00
```

```
module load matlab
```

```
matlab -nodisplay -r "readMatrix" >& OUT
```

load matlab module (if needed)

**SLURM starts node session with current environment and in directory where you typed `sbatch <script>`.**

**If modules aren't loaded when script is submitted or in module startup file, they must be loaded.**

redirect stdout and stderr

file for stdout and stderr

- Submit job with **`sbatch`**
- Once job starts, check '**OUT**' for output
- Check batch **stdout/stderr** file for issues - named **`slurm-<jobid>.out`**

```
108 [vortex] cat readMatrix.m
```

```
tic
```

```
%parpool(8)
```

```
syms a b c d;
```

```
meshpoints = meshgenerator();
```

```
eigfile = fopen('eigfile.txt', 'wt');
```

```
count = 1;
```

```
.
```

# Getting more help

HPC webpage: <https://www.wm.edu/it/rc>  
HPC ticket system: mail: [hpc-help@wm.edu](mailto:hpc-help@wm.edu)

*Using the ticket system is useful since it is **monitored by 5 of us***

# Thank you!