Georgia Advanced Computing Resource Center
UNIVERSITY OF GEORGIA

Using the Sapelo2 Cluster at the GACRC

Cluster New User Training Workshop

Georgia Advanced Computing Resource Center (GACRC)

EITS/University of Georgia

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Outline

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- Sapelo2 Cluster
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- Job Submission Workflow
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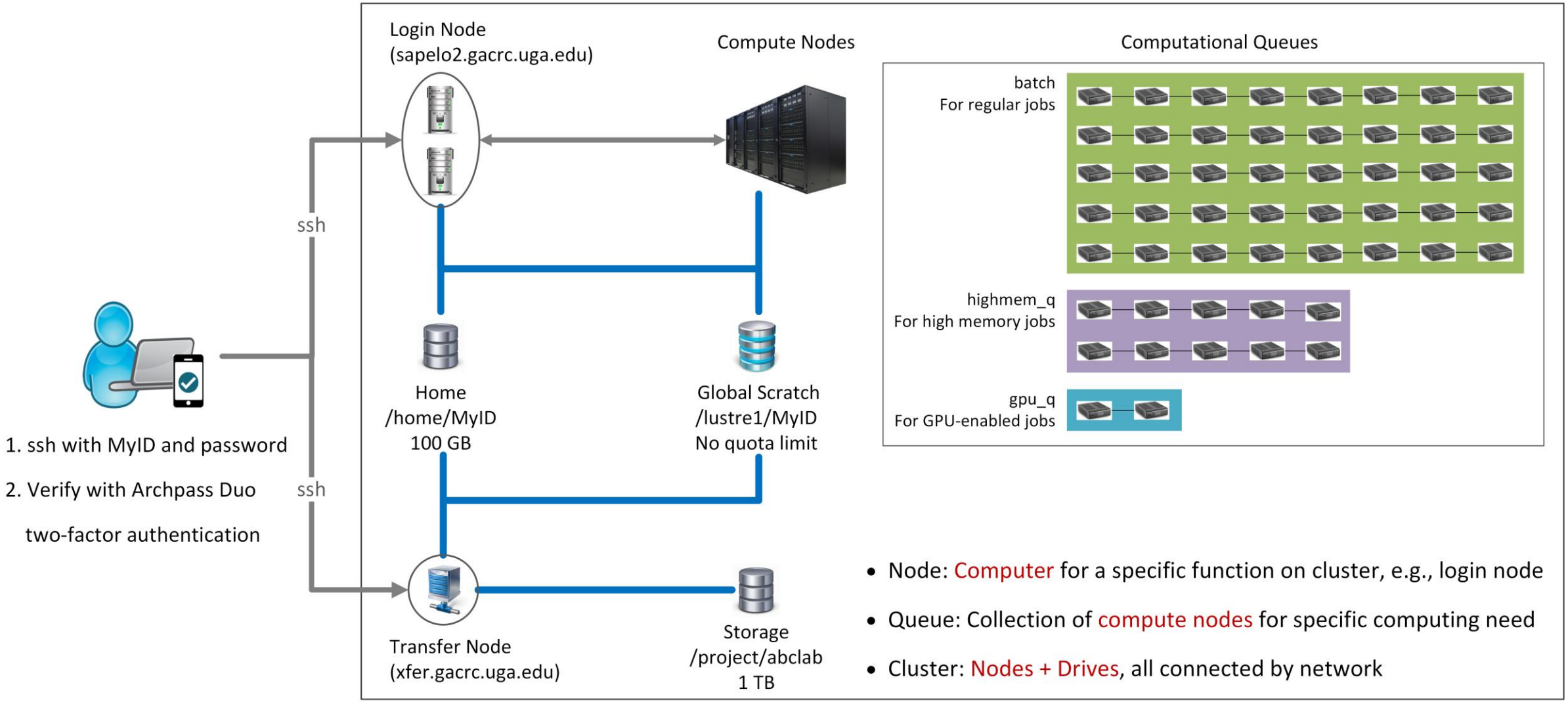
GACRC

- We are a high-performance-computing (HPC) center at UGA
- We provide to the UGA research and education community an advanced computing environment:
  - HPC computing and networking infrastructure located at the Boyd Data Center
  - Comprehensive collection of scientific, engineering and business applications
  - Consulting and training services
- http://wiki.gacrc.uga.edu (GACRC Wiki)
- https://wiki.gacrc.uga.edu/wiki/Getting_Help (GACRC Support)
- http://gacrc.uga.edu (GACRC Web)

Sapelo2 Cluster



- Node: Computer for a specific function on cluster, e.g., login node
- Queue: Collection of compute nodes for specific computing need
- Cluster: Nodes + Drives, all connected by network

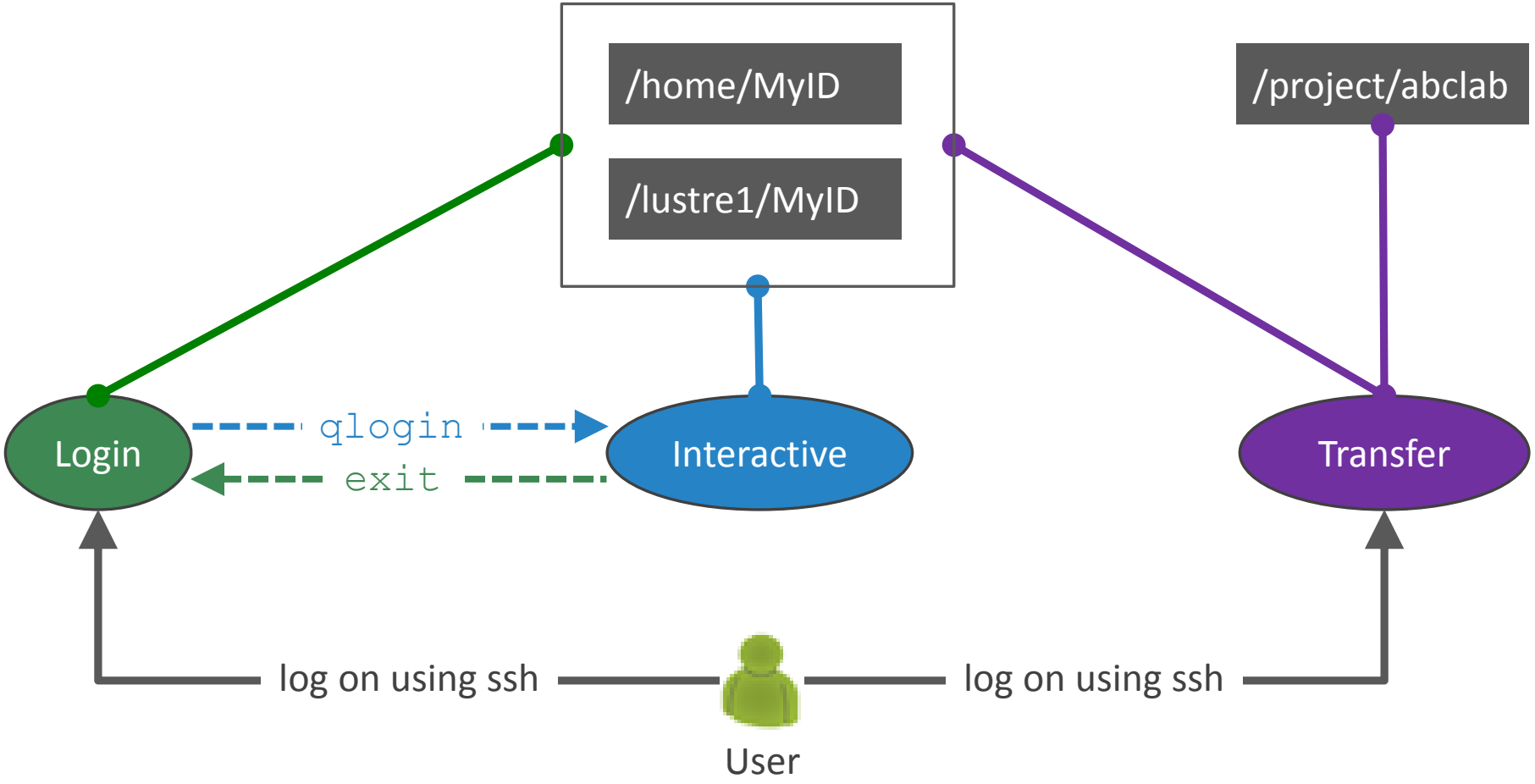
Sapelo2: A Linux HPC cluster (64-bit Centos 7)

- Two Nodes:
  1. Login node for batch job workflow: MyID@sapelo2.gacrc.uga.edu
  2. Transfer node for data transferring: MyID@xfer.gacrc.uga.edu
- Three Directories:
  1. Home: Landing spot; 100GB quota; Backuped
  2. Global Scratch: High performance job working space; NO quota; NOT backuped
  3. Storage: Temporary data parking; 1TB quota (for group); Backuped (**ONLY accessible from Transfer node!**)
- Three Computational Queues: batch, highmem_q, gpu_q

Three Directories

Role	Directory	Intended Use	Quota	Accessible from	Backuped	Notes
Home	**/home/MyID**	**Static data:** 1. Scripts, source codes 2. Local software	100GB	Login Transfer	Yes	
Global Scratch	**/lustre1/MyID**	**Current job data:** data being read/written by running jobs	No Limit		No	**User to clean up!** Subject to deletion in 30 days
Storage	**/project/abclab**	**Temporary data parking:** non-current active data	1TB (Initial)	Transfer	Yes	Group sharing possible

Three Directories (Cont.) – Accessing Directories from Nodes



Three Computational Queues

Queue	Node Feature	Total Nodes	Max RAM(GB) /Node	Cores /Node	Processor Type	GPU Cards /Node
batch	Intel	30	**62**	**28**	Intel Xeon	N/A
	AMD	25	**125**	**48**	AMD Opteron	
highmem_q	Intel	1	**997**	**28**	Intel Xeon	
gpu_q	GPU	2	**94**	**12**		7 NVIDIA K20Xm
PIMyID_q	variable					

Software on Cluster

1. Software names are long and have a Easybuild toolchain name associated to it, e.g., foss-2016b
2. Software names are case-sensitive!

- `ml avail`: List all available software modules installed on cluster
- `ml` *`moduleName`*: Load a module into your working environment
- `ml`: List modules currently loaded
- `ml unload` *`moduleName`*: Remove a module from your working environment
- `ml spider` *`pattern`*: Search module names matching a pattern (case-insensitive)

Job Submission Workflow

1. Log on to Login node using MyID and password, and two-factor authentication with Archpass Duo:

   `ssh MyID@sapelo2.gacrc.uga.edu`

2. On Login node, change directory to global scratch : `cd /lustre1/MyID`
3. Create a working subdirectory for a job : `mkdir ./workDir`
4. Change directory to workDir : `cd ./workDir`
5. Transfer data from local computer to workDir : use `scp` or SSH File Transfer to connect Transfer node

   Transfer data on cluster to workDir : log on to Transfer node and then use `cp` or `mv`
6. Make a job submission script in workDir : `nano ./sub.sh`
7. Submit a job from workDir : `qsub ./sub.sh`
8. Check job status : `qstat_me` or Cancel a job : `qdel JobID`

Step1: Log on to Login node - Mac/Linux using ssh

1. Open Terminal utility
2. Type command line: `ssh MyID@sapelo2.gacrc.uga.edu`
3. You will be prompted for your MyID password
4. Sapelo2 access requires ID verification using two-factor authentication with Archpass Duo.

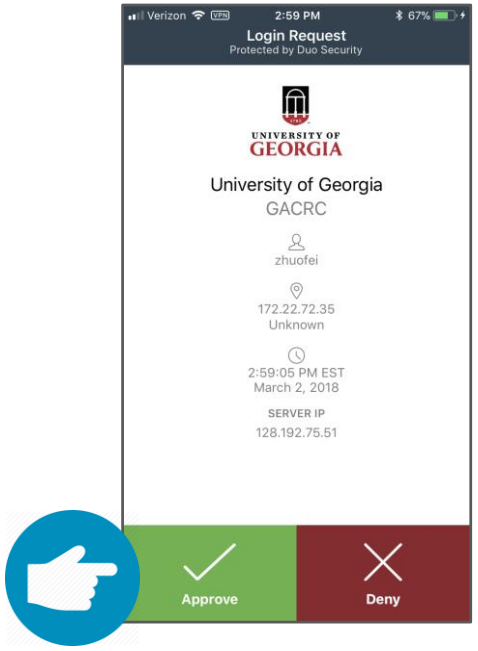
   If you are not enrolled in Archpass Duo, please refer to

   https://eits.uga.edu/access_and_security/infosec/tools/archpass_duo/ on how to enroll

https://wiki.gacrc.uga.edu/wiki/Connecting

Step1 (Cont.) - Mac/Linux

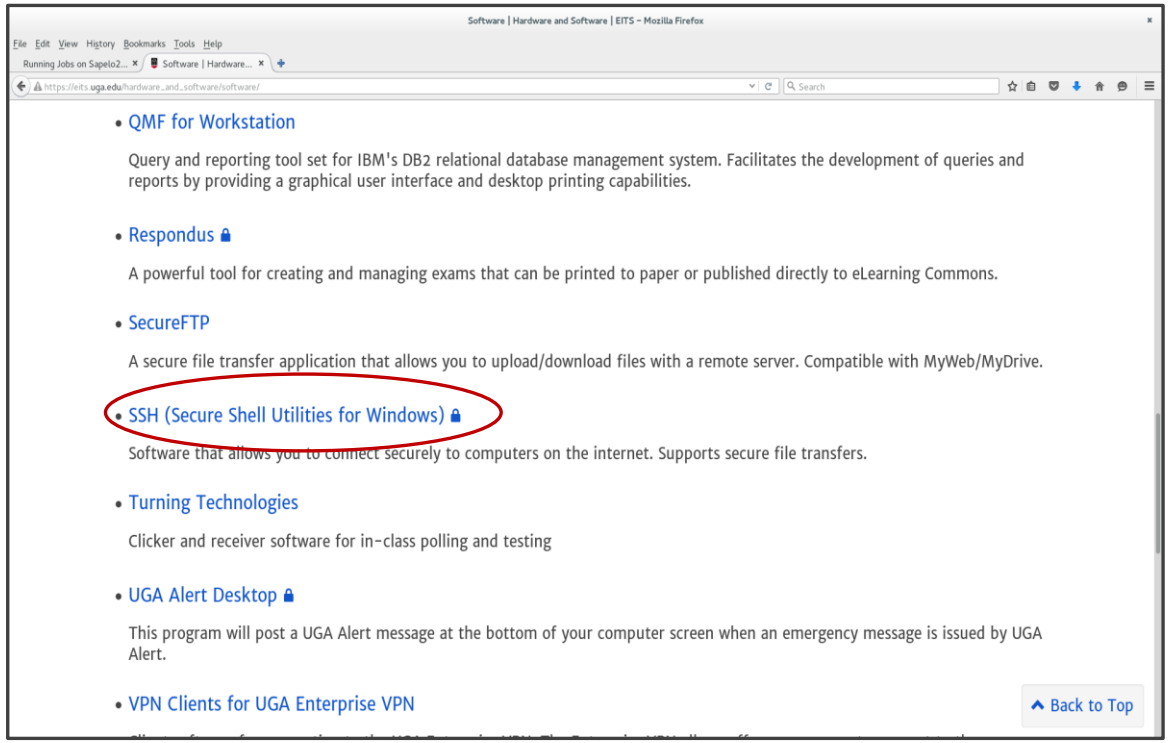
Use Terminal utility on Mac or Linux!

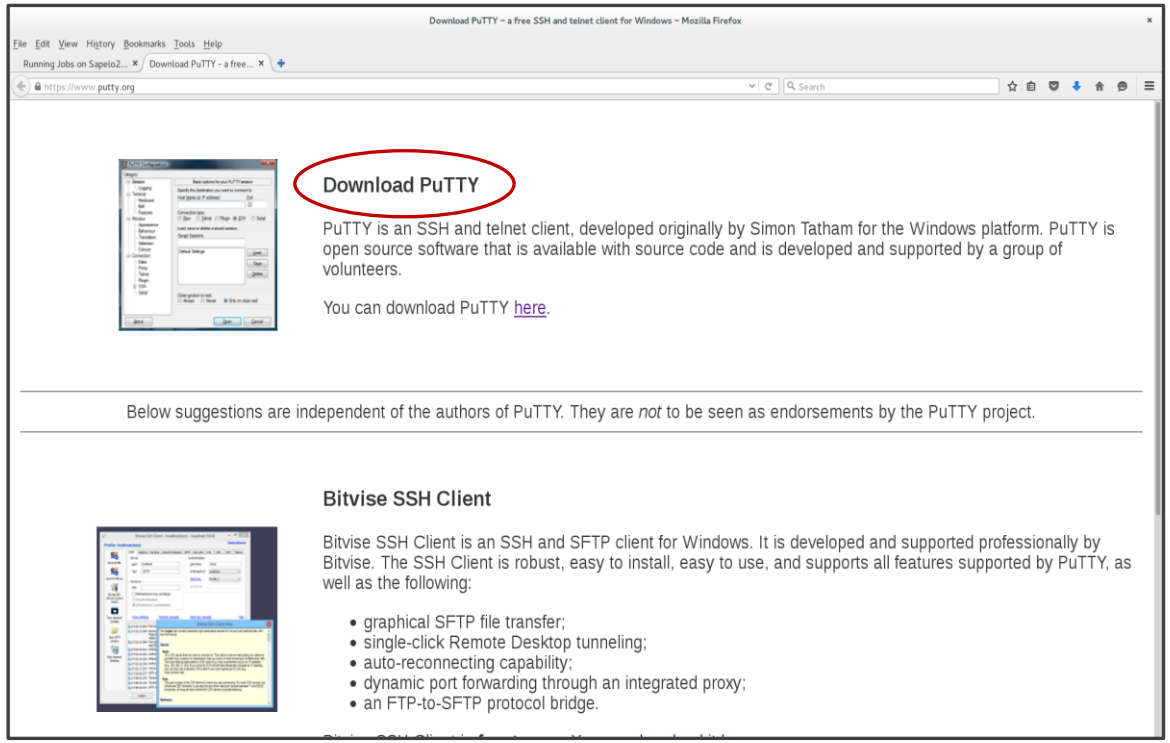



```
zhuofeihou — zhuofei@sapelo2-sub2:~ — ssh — 80×22
zhuofeihou@s172-20-19-h149:~$
zhuofeihou@s172-20-19-h149:~$
zhuofeihou@s172-20-19-h149:~$ssh zhuofei@sapelo2.gacrc.uga.edu   ← Log on
Password:                                                        ← Input MyID password!
Duo two-factor login for zhuofei

Enter a passcode or select one of the following options:

 1. Duo Push to XXX-XXX-5758
 2. Phone call to XXX-XXX-1925
 3. Phone call to XXX-XXX-5758
 4. SMS passcodes to XXX-XXX-5758

Passcode or option (1-4): 1                                      ← Select Duo login option!

Pushed a login request to your device...
Success. Logging you in...
zhuofei@sapelo2-sub2 ~$
zhuofei@sapelo2-sub2 ~$                                          ← I am on sapelo2-sub2!
```

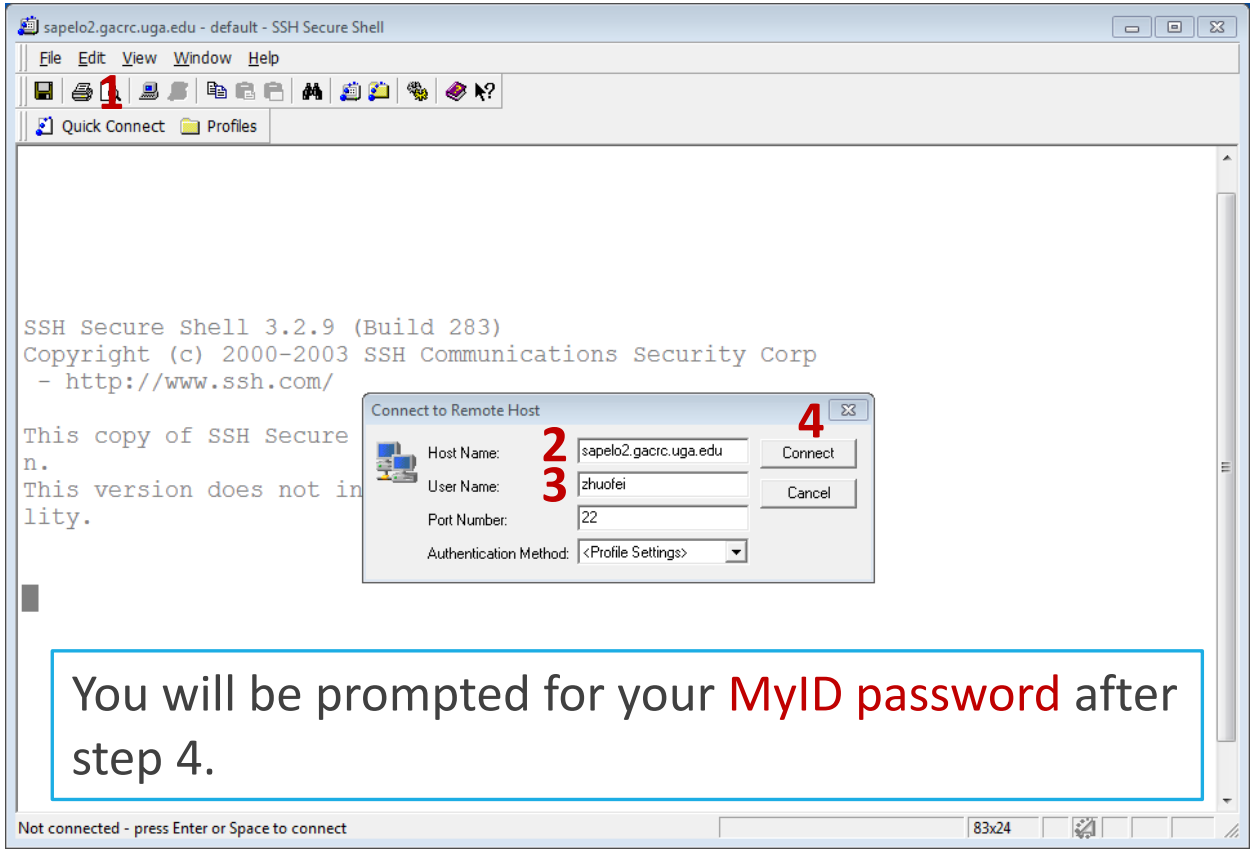
Step1 (Cont.) - Windows

1. Download and install SSH Secure Utilities: http://eits.uga.edu/hardware_and_software/software/
2. You can use PuTTY as an alternative: https://www.putty.org/

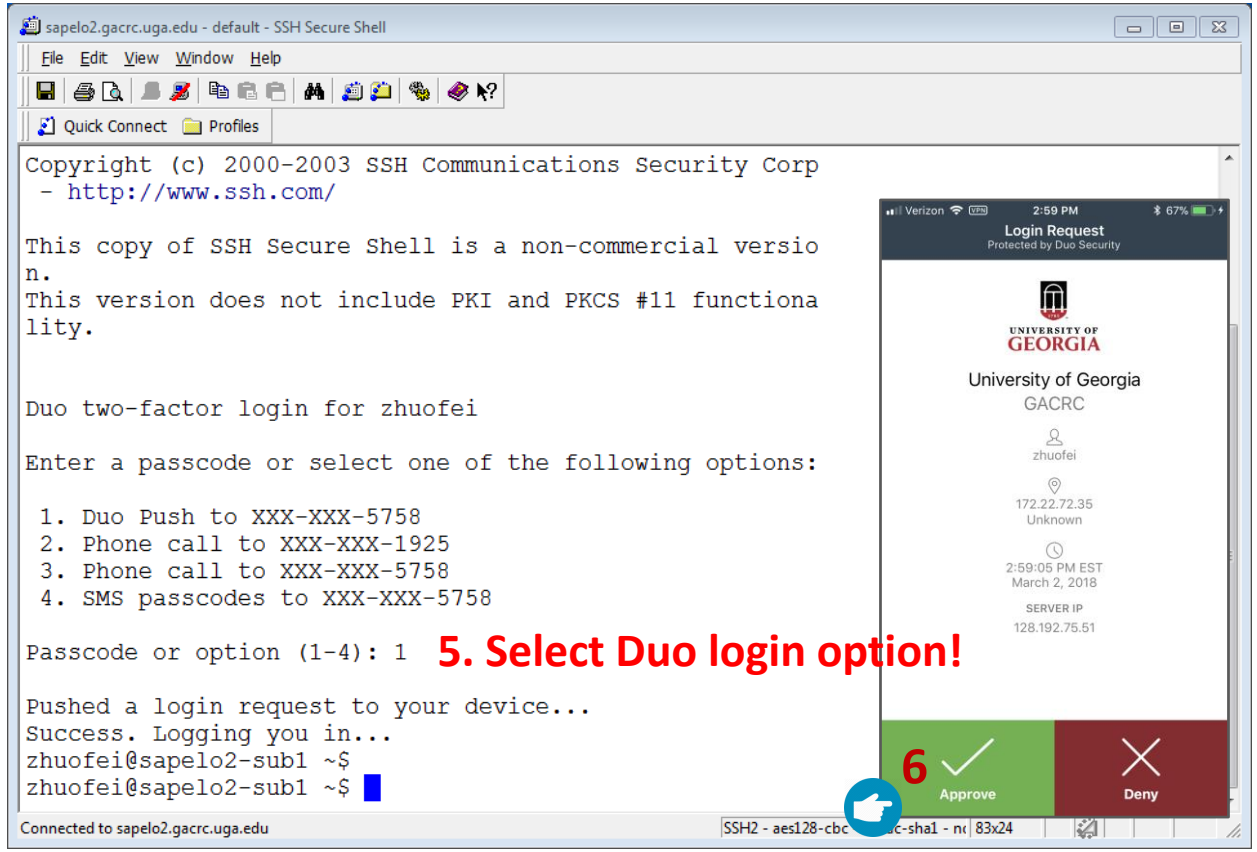




Step1 (Cont.) - Windows



You will be prompted for your MyID password after step 4.



Step2: On Login node change directory to global scratch

- Once you logged on, your current directory will be your home directory

```
zhuofei@sapelo2-sub2 ~$ pwd
/home/zhuofei                                    ← this is my home directory!
```

- Use `cd` command to change your current directory to /lustre1/MyID

```
zhuofei@sapelo2-sub2 /$ cd /lustre1/zhuofei
zhuofei@sapelo2-sub2 zhuofei$ pwd
/lustre1/zhuofei                                 ← this is my global scratch folder!
```

- Use `ls` command to take a look in /lustre1/MyID

```
zhuofei@sapelo2-sub2 zhuofei$ ls
user_test  workDir_Alex  workDir_bk
```

Step3 - 4: Create and cd to a working subdirectory

- Use `mkdir` command to make a subdirectory in /lustre1/MyID

```
zhuofei@sapelo2-sub2 zhuofei$ mkdir workDir
zhuofei@sapelo2-sub2 zhuofei$ ls
user_test   workDir   workDir_Alex   workDir_bk
```

- Use `cd` command to change your current directory to /lustre1/MyID/workDir

```
zhuofei@sapelo2-sub2 zhuofei$ cd workDir
zhuofei@sapelo2-sub2 workDir$ ls
zhuofei@sapelo2-sub2 workDir$                    ← it is empty!
```

Step5: Transfer data from local computer to workDir - Mac/Linux

1. You need to connect to cluster's Transfer node (xfer.gacrc.uga.edu)
2. Open Terminal utility on local computer to use scp (-r) [Source] [Target]

E.g. 1: working on local computer, from Local ➔ workDir on cluster

```
scp ./file zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/workDir/
```

```
scp -r ./folder/ zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/workDir/
```

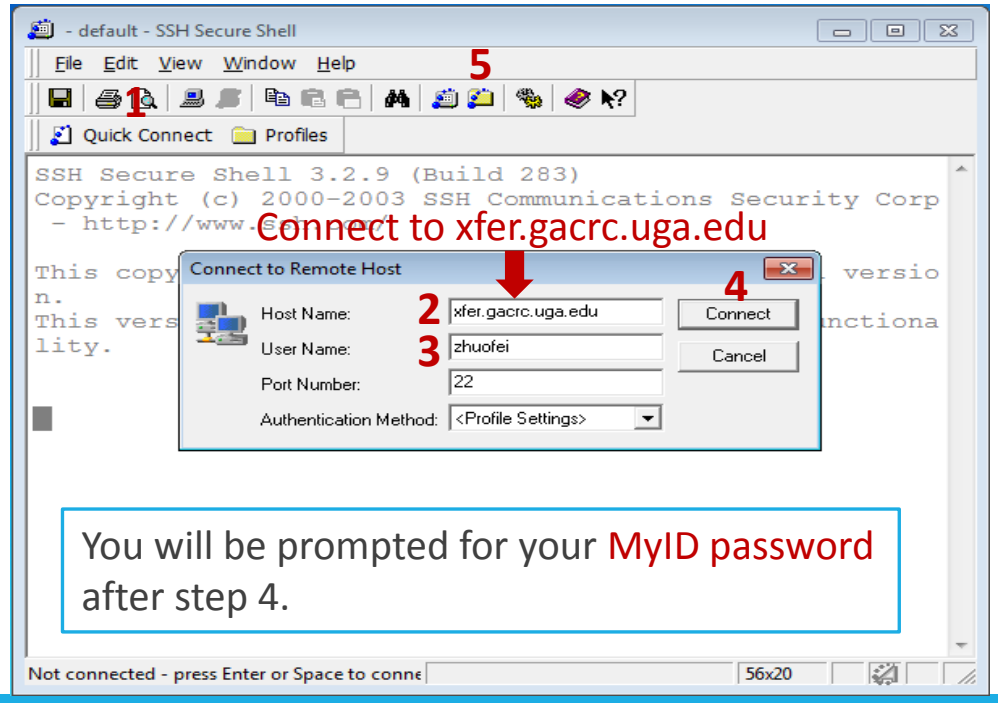
E.g. 2: working on local computer, from workDir on cluster ➔ Local

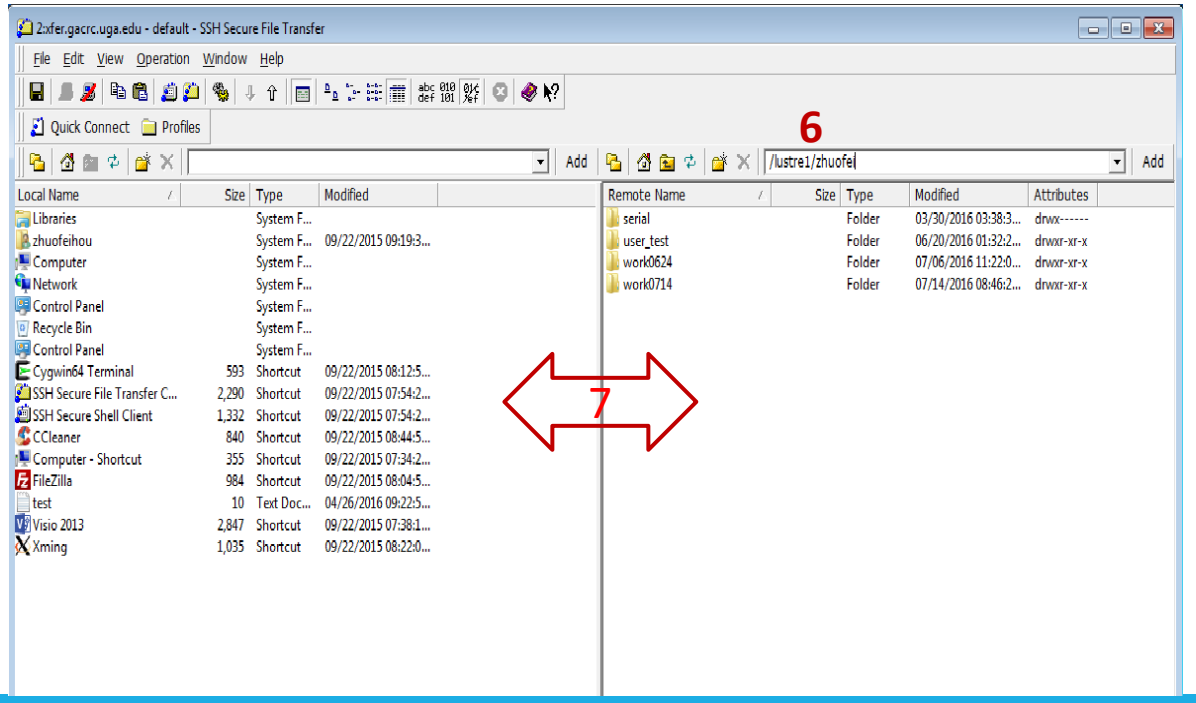
```
scp zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/workDir/file .
```

```
scp -r zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/workDir/folder/ .
```

Step5 (Cont.) - Windows

1. You need to connect to cluster's Transfer node (xfer.gacrc.uga.edu)
2. Use SSH File Transfer or FileZilla or WinSCP on local computer





Step5 (Cont.): Transfer data on cluster to workDir

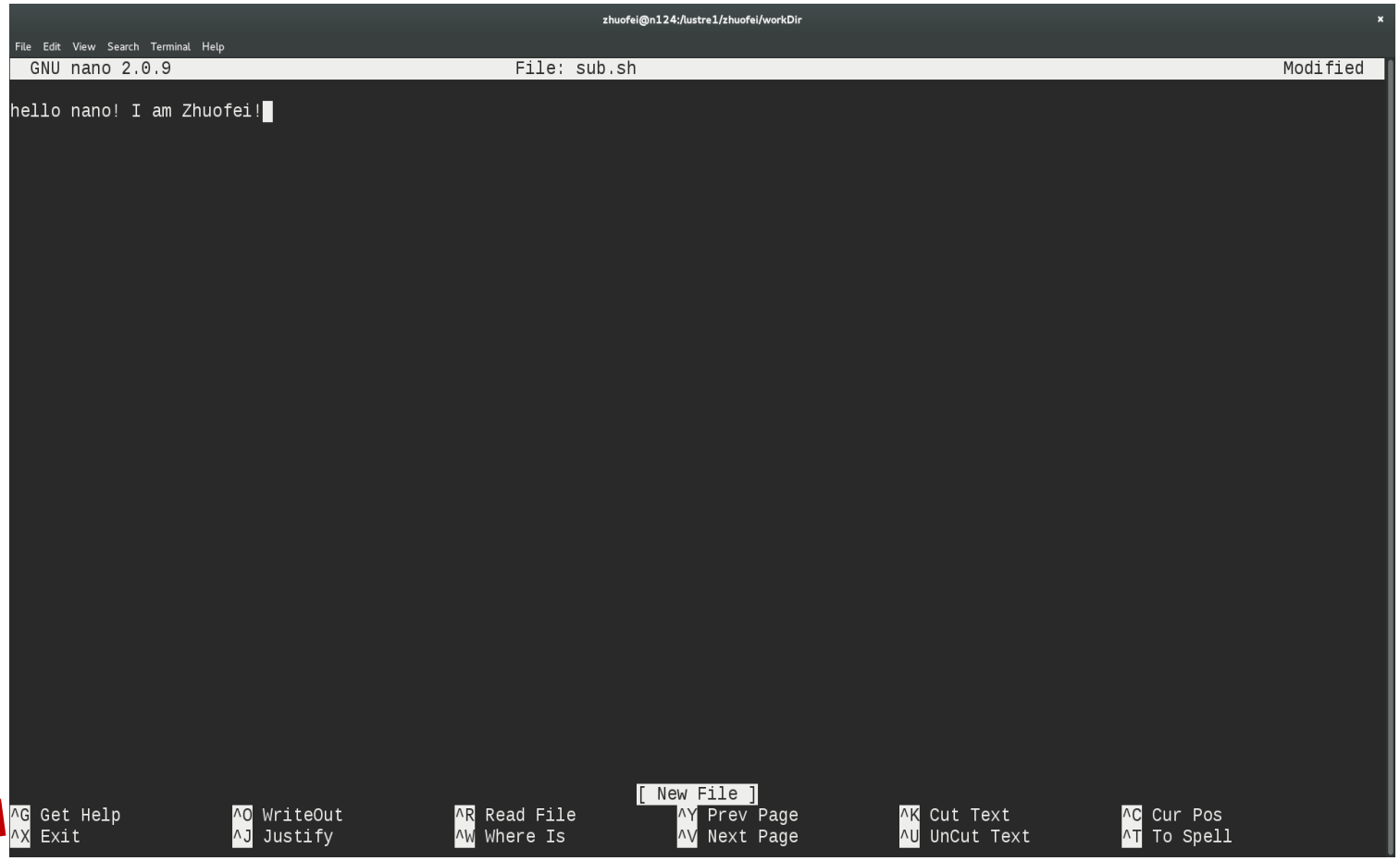
- Log on to Transfer node (xfer.gacrc.uga.edu)
  - ✓ Mac/Linux: ssh MyID@xfer.gacrc.uga.edu (page 12, 13)
  - ✓ Windows: use SSH Secure Client app (page 14, 15)
- Landing folder: /home/MyID (Home)
- Transfer data between folders on cluster using cp, mv
- Directories you can access using full path:
  1. /home/MyID
  2. /lustre1/MyID
  3. /project/abclab
- Most file systems on Transfer are *auto-mounted* upon *the first time full-path access*, e.g., cd /project/abclab/

Step6: Make a job submission script in workDir using nano

```
$ nano sub.sh
```

nano is a small and friendly text editor on Linux.

Ctrl-x to save file and quit from nano



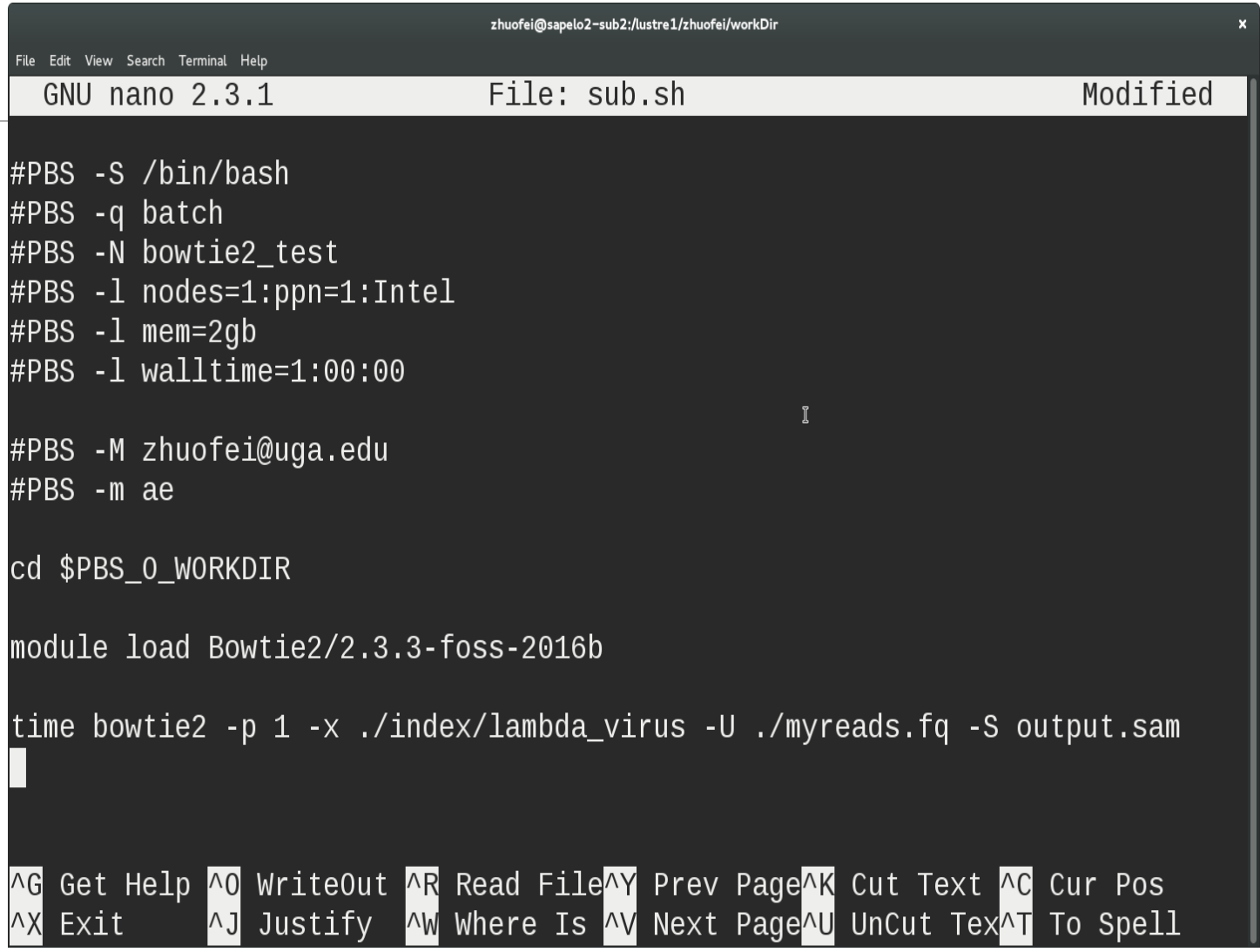
Step6 (Cont.)

1. Copy a sample script from GACRC Wiki Software: https://wiki.gacrc.uga.edu/wiki/Bowtie2-Sapelo2
2. Modify it as needed for your computing

To run this example, you need to copy input data to your current working folder:

cp -r /usr/local/training/index .

cp /usr/local/training/myreads.fq .



Step7: Submit a job from workDir using qsub

```
zhuofei@sapelo2-sub2 workDir$ pwd
/lustre1/zhuofei/workDir
zhuofei@sapelo2-sub2 workDir$ ls
index  myreads.fq  sub.sh
zhuofei@sapelo2-sub2 workDir$ qsub sub.sh
11943.sapelo2
```

sub.sh is job submission script to

1. specify computing resources:
2. load software using ml load
3. run any Linux commands you want to run
4. run the software

Step8: Check job status using qstat_me

```
zhuofei@sapelo2-sub2 workDir$ qstat_me
Job ID               Name             User      Time Use S Queue
-------------------- ---------------- --------- -------- - -----
11943.sapelo2        bowtie2_test     zhuofei   00:06:40 C batch
11944.sapelo2        bowtie2_test     zhuofei   00:05:17 R batch
11946.sapelo2        bowtie2_test     zhuofei   00:12:51 R batch
11947.sapelo2        bowtie2_test     zhuofei          0 R batch
11948.sapelo2        bowtie2_test     zhuofei          0 Q batch
```

R : job is running
C : job completed (or canceled or crashed) and is not longer running. Jobs stay in this state for 24 hour
Q : job is pending, waiting for resources to become available

Note: “Time Use” is the CPU time, instead of the wall-clock time of your job staying on cluster!

Step8 (Cont.): Cancel job using qdel

```
zhuofei@sapelo2-sub2 workDir$ qdel 11947
zhuofei@sapelo2-sub2 workDir$ qstat_me
Job ID                    Name             User            Time Use S Queue
------------------------- ---------------- --------------- -------- - -----
11943.sapelo2             bowtie2_test     zhuofei         00:06:40 C batch
11944.sapelo2             bowtie2_test     zhuofei         00:05:17 R batch
11946.sapelo2             bowtie2_test     zhuofei         00:12:51 R batch
11947.sapelo2             bowtie2_test     zhuofei         00:00:09 C batch
11948.sapelo2             bowtie2_test     zhuofei                0 Q batch
```

job 11947 status is changed from R to C

C status will stay in list for 24 hour

Step8 (Cont.): Check Job using qstat -n -u MyID

```
zhuofei@sapelo2-sub2 workDir$ qstat -n -u zhuofei

dispatch.ecompute:
                                                                  Req'd   Req'd       Elap
Job ID          Username  Queue  Jobname       SessID  NDS  TSK  Memory  Time      S  Time
--------------- --------  -----  ------------  ------  ---  ---  ------  --------  -  --------
12175.sapelo2 zhuofei   batch  bowtie2_test  132442  1    1    2gb     01:00:00  R  00:23:44
   n238/0  ← job is running on node238/CPU0
12176.sapelo2 zhuofei   batch  bowtie2_test  67226   1    1    2gb     01:00:00  R  00:20:44
   n237/0
12177.sapelo2 zhuofei   batch  bowtie2_test  119643  1    1    2gb     01:00:00  R  00:05:44
```

Note: “Elap Time” is the wall-clock time, instead of the CPU time, which qstat_me can give you!

Step8 (Cont.): Check all Jobs on cluster using qstat

```
zhuofei@sapelo2-sub2 workDir$ qstat
Job ID                    Name             User            Time Use S Queue
------------------------- ---------------- --------------- -------- - -----
11267.sapelo2              L80-500          jx57780          164:32:5 R batch
11269.sapelo2              L80-502          jx57780          164:55:5 C batch
11270.sapelo2              L80-503          jx57780          165:38:5 C batch
11607.sapelo2              canu             gd98309          3414:46: R bergman_q
11726.sapelo2              ..._3_constoptTS sm39091          3157:30: R wheeler_q
11729.sapelo2              ..._2_constoptTS sm39091          2731:29: R wheeler_q
11790.sapelo2              sp2_run19b_dye   castelao         4412:52: C batch
11804.sapelo2              ...e-4_Nnoise=64 cotter           98:26:20 R batch
11806.sapelo2              ...e-4_Nnoise=64 cotter           98:14:22 R batch
11987.sapelo2              ..._th_W18-T5-L4 qbcg             08:02:40 C batch
11989.sapelo2              matlabjob        zhyw86                  0 C batch
11990.sapelo2              ..._1_constoptTS sm39091          445:42:1 R wheeler_q
11991.sapelo2              ..._1_constoptTS sm39091          444:51:4 R wheeler_q
11992.sapelo2              ..._cl_W18-T3-D1 qbcg             03:04:21 C batch
.
.
```

Note: qstat command will give you a long list of all jobs from all users on cluster!

Workflow Diagram

1. Linux/Mac user:
`ssh MyID@sapelo1.gacrc.uga.edu`

Windows user:

Login

2. `cd /lustre1/MyID`

3. `mkdir ./workDir`
4. `cd ./workDir`

6. `nano ./sub.sh`

```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N bowtie2_test
#PBS -l nodes=1:ppn=1:Intel
#PBS -l mem=2gb
#PBS -l walltime=1:00:00

#PBS -M zhuofei@uga.edu
#PBS -m ae

cd $PBS_O_WORKDIR

module load Bowtie2/2.3.3-
foss-2016b……
```

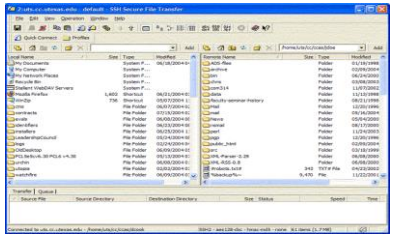
7. `$ qsub sub.sh`

8. `$ qstat_me or qdel JobID`

lustre1

5. Linux/Mac user:
`scp file MyID@xfer.gacrc.uga.edu:/lustre1/MyID/workDir`

Windows user:



Work on Sapelo2 - GACRC Wiki

Main Page: http://wiki.gacrc.uga.edu

Running Jobs: https://wiki.gacrc.uga.edu/wiki/Running_Jobs_on_Sapelo2

Software: https://wiki.gacrc.uga.edu/wiki/Software

Transfer File: https://wiki.gacrc.uga.edu/wiki/Transferring_Files

Linux Command: https://wiki.gacrc.uga.edu/wiki/Command_List

Training: https://wiki.gacrc.uga.edu/wiki/Training

User Account Request: https://wiki.gacrc.uga.edu/wiki/User_Accounts

Support: https://wiki.gacrc.uga.edu/wiki/Getting_Help

Get Help

➢ Job Troubleshooting:

Please tell us details of your question or problem, including but not limited to:

- ✓ Your user name
- ✓ Your job ID
- ✓ Your working directory
- ✓ The queue name and command you used to submit the job

➢ Software Installation:

- ✓ Specific name and version of the software
- ✓ Download website
- ✓ Supporting package information if have

Please note to make sure the correctness of datasets being used by your jobs!

GACRC's HelpDesk

The Georgia Advanced Computing Resource Center
A Collaborative Partnership between the *Vice President for Research* and the *Vice President for Information Technology*

Request Support

* indicates Required fields.

Your Name *	John smith
MyID *	jsmith
E-mail *	jsmith@uga.edu
Phone Number	411-555-1212
Brief Description	my job can not be started
Request Details *	(less than 2,000 characters)
Cluster	☐ zcluster ☐ sapelo ☑ sapelo2 ☐ other

Review

* For questions on cluster or software, please include the command/script used, working path and working nodes (interactive / queue name) if applicable.
* For software installation, please specify software name, version and include link to the software if applicable.
* Please review your message on the next page and then click the Submit button.

Appendix - Run Batch Jobs

- Components you need to run a job:
  - Software already installed (cluster software or the one installed by yourself)
  - Job submission script to
    1. specify computing resources:
       - ✓ number of nodes and cores
       - ✓ amount of memory
       - ✓ node's feature
       - ✓ maximum wallclock time
    2. load software using ml load (for cluster software)
    3. run any Linux commands you want to run, e.g., pwd, mkdir, cd, echo, etc.
    4. run the software
- Common queueing commands you need:
  - qsub, qstat_me, qstat, qdel
  - qstat -f, showq

Example 1: Serial job script running NCBI Blast+ using 1 CPU

```
#PBS -S /bin/bash                          → Linux default shell (bash)
#PBS -q batch                              → Queue name (batch)
#PBS -N testBlast                          → Job name (testBlast)
#PBS -l nodes=1:ppn=1:Intel                → Number of nodes (1), number of cores (1), node type (Intel)
#PBS -l mem=20gb                           → Maximum amount of RAM memory (20 GB) used by the job
#PBS -l walltime=48:00:00                  → Maximum wall-clock time (48 hours) for the job, default 6 minutes

cd $PBS_O_WORKDIR                          → Compute node will use the directory from which the job is submitted
                                             as the working directory, i.e., /lustre1/MyID/workDir

ml load BLAST+/2.6.0-foss-2016b-Python-2.7.14   → Load the module of ncbiblast+, version 2.6.0

time blastn [options] …                    → Run blastn with 'time' command to measure the amount of time it
                                             takes to run the application
```

https://wiki.gacrc.uga.edu/wiki/BLAST%2B-Sapelo2

*Example 2: Threaded job script running NCBI Blast+ using 4 CPUS

```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testBlast
#PBS -l nodes=1:ppn=4:Intel
#PBS -l mem=20gb
#PBS -l walltime=480:00:00

#PBS -M jsmith@uga.edu
#PBS -m ae
#PBS -j oe

cd $PBS_O_WORKDIR

ml load BLAST+/2.6.0-foss-2016b-Python-2.7.14

time blastn -num_threads 4 [options] …
```

➔ Number of nodes (1), number of cores (4), node type (AMD)
Number of cores requested (4) = Number of threads (4)

➔ Email address to receive a notification for computing resources
➔ Send email notification when job aborts (a) or terminates (e)
➔ Standard error file (testBlast.e12345) will be merged into standard out file (testBlast.o12345)

➔ Run blastn with 4 threads (-num_threads 4)

*Example 3: MPI job script running RAxML using 2 full nodes

```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testRAxML
#PBS -l nodes=2:ppn=28:Intel
#PBS -l walltime=120:00:00
#PBS -l mem=100gb

cd $PBS_O_WORKDIR

ml load RAxML/8.2.11-foss-2016b-mpi-avx

mpirun –np 50 raxmlHPC-MPI-AVX [options]
```

➔ Number of nodes (2), number of cores (28), node type (Intel)
Total cores requested = 2 × 28 = 56
We suggest, Number of MPI Processes (50) ≤ Number of cores requested (56)

➔ To run raxmlHPC-MPI-AVX, MPI version using OpenMPI

➔ Run raxmlHPC-MPI-AVX with 50 MPI processes (–np 50), default 56

Thank You!