GACRC Sapelo2 Cluster New User Training

Georgia Advanced Computing Resource Center (GACRC)

Enterprise Information Technology Services(EITS)

The University of Georgia

Outline

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- Sapelo2 Cluster
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  - Five Directories
  - Four Computational Partitions
  - Software Environment
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- GACRC Wiki and User Support
- Appendices

GACRC

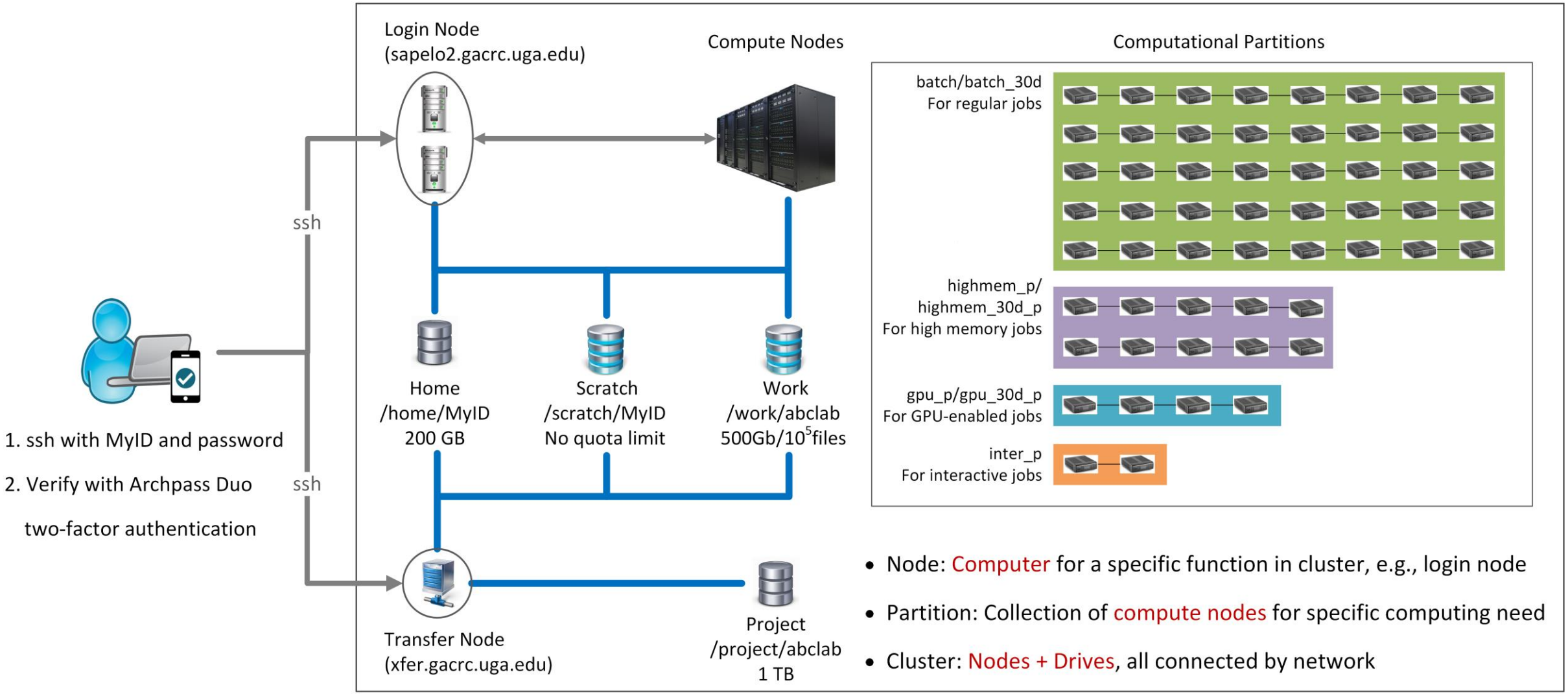
- A high-performance-computing (HPC) center at the UGA
- Provide to the UGA research and education community an advanced computing environment:
  - HPC computing and networking infrastructure located at the Boyd Data Center
  - Comprehensive collection of scientific, engineering and business applications
  - Consulting and training services

Wiki: http://wiki.gacrc.uga.edu

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

Web Site: http://gacrc.uga.edu

Sapelo2 Cluster



Note: You need to connect to the UGA network using VPN when accessing from outside of the **UGA main campus**.
UGA VPN: https://eits.uga.edu/access_and_security/infosec/tools/vpn/

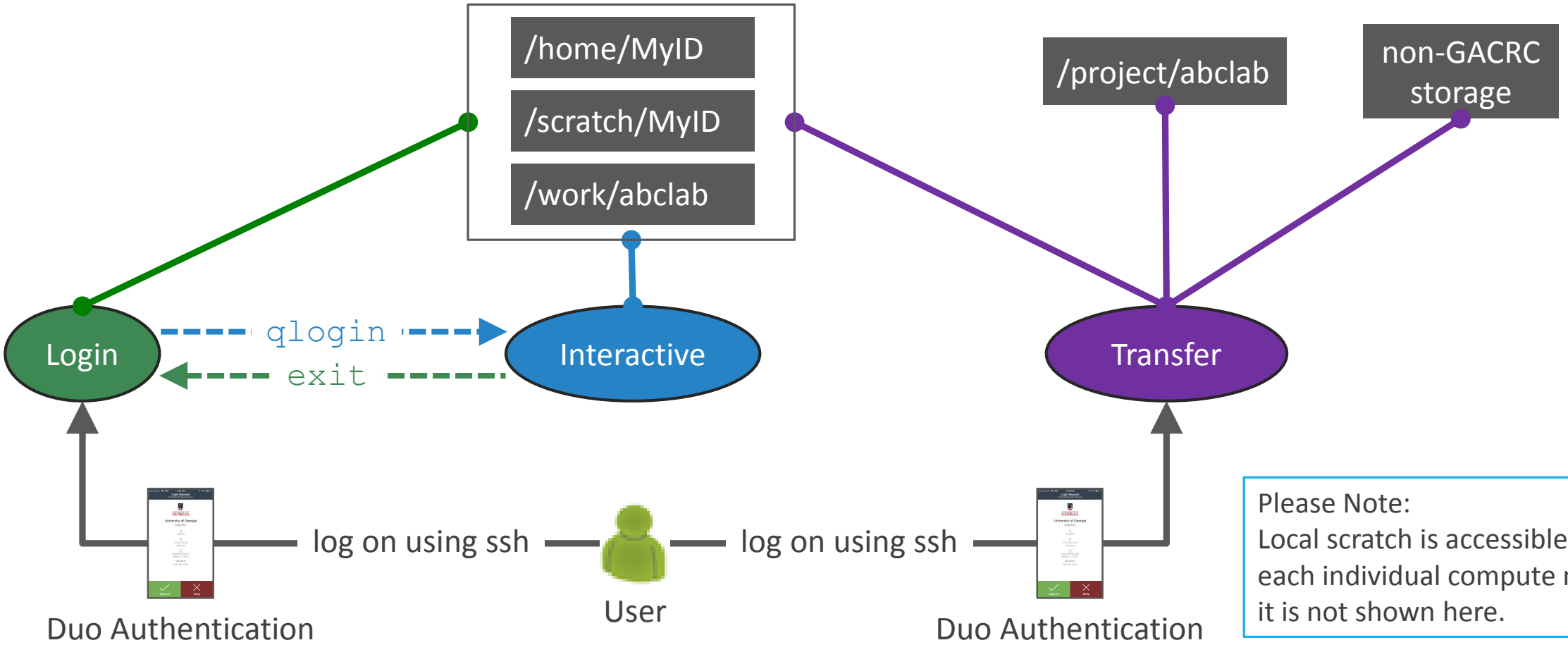
Overview

- Two nodes, your "username" is your MyID for both of them:
  1. For batch job workflow, the host to log into is sapelo2.gacrc.uga.edu
  2. For file transfers, the host to log into is xfer.gacrc.uga.edu
- Five Directories:
  1. Home: Login landing spot; 200GB quota; Backed-up
  2. Scratch: High-speed FS for temp files needed for current jobs; NO quota; NOT backed-up; 30-day purge
  3. Work: High-speed FS for input files needed for repeated jobs; per group quota of 500GB and max 100,000 single files; NOT backed-up
  4. Project: Temporary data parking; per group quota of 1TB; Backed-up (ONLY accessible from Transfer node!)
  5. Local Scratch: Local storage on each individual compute node; 200~800GB quota; NOT backed-up
- Five Computational Partitions: batch/batch_30d, highmem_p/highmem_30d, gpu_p/gpu_30d_p, inter_p, name_p

Five Directories https://wiki.gacrc.uga.edu/wiki/Disk_Storage

Directory	Name	Quota	Accessible from	Intended Use	Backed-up	Important Notes
/home/MyID	Home	200GB	Login Transfer Compute	Static data, e.g. 1. Scripts, source codes 2. Local software	Yes	Not for storing data of your jobs!
/scratch/MyID	Scratch	No Limit		Temporary files needed for current running jobs	No	Clean up when your job finishes! Subject to "30-day purge" policy
/work/abclab	Work	500GB 10^5 files		Input files needed for repeated jobs	No	Clean up when your job finishes! Group sharing is possible
/project/abclab	Project	1TB (initial)	Transfer	Temporary data parking	Yes	Group sharing is possible
/lscratch	Local Scratch	200GB	Compute	Jobs with heavy disk I/O operations	No	Clean up when job exits from node! Files generated are persistent

Accessing Directories from Nodes



Please Note:
Local scratch is accessible on each individual compute node; it is not shown here.

More about scratch file system "30-day purge" policy

https://wiki.gacrc.uga.edu/wiki/Disk_Storage#Scratch_file_system

Any file that is not accessed or modified by a compute job in a time period no longer than 30 days will be automatically deleted off the /scratch file system.

Measures circumventing this policy will be monitored and actively discouraged.

- You have a list of those purgeable files located at /usr/local/var/lustre_stats/$USER.over30d.files.lst
- You are suggested to copy files from /scratch to /project or outside of GACRC
- You should first move all unnecessary files and folders to /scratch/trash/$USER
- The fastest way to save old files is to copy them to /project area, using the fpsync utility on xfer.gacrc.uga.edu
- When you archive data using tar on /scratch, please do not use z option (compression option). After you achieved data by tar, you can use gzip to compress it.

Type	Partition	Time limit	Max jobs Running	Max jobs Submit	Notes
Regular	batch	7 days	50	20000	Regular nodes
	highmem_p		15	20	For high memory jobs
	gpu_p		5	20	For GPU-enabled jobs
Long-term	batch_30d	30 days	1	2	A given user can have up to one job running at a time here, plus one pending, or two pending and none running
	highmem_30d_p				
	gpu_30d_p				
Buy-in	name_p	variable			Partitions that target different groups' buy-in nodes. The name string is specific to each group

Partition	Total Nodes	RAM(GB) /Node	Max Mem(GB) /Single-node job	Cores /Node	Processor Type	GPU Cards /Node	InfiniBand
batch batch_30d	40	128	120	48	AMD Opteron	N/A	QDR
	24			64	AMD EPYC		EDR
	6			32			
	4	256	250	48	AMD Opteron		QDR
	1	192	180	32	Intel Skylake		EDR
	1	64	58	28	Intel Broadwell		
highmem_p highmem_30d_p	4	512	500	48	AMD Opteron		QDR
	2		490	32	AMD EPYC		EDR
gpu_p gpu_30d_p	1	192	180	32	Intel Xeon Skylake	1 NVDIA P100	
name_p	variable						

Software Environment

https://wiki.gacrc.uga.edu/wiki/Software_on_Sapelo2

- 700 software modules are installed (as of Nov. 2020)
- Most modules are compiled EasyBuild (EB) toolchains GCC-8.3.0 or foss-2019b.
- Name format: Name/Version-Toolchain, e.g., Python/3.8.2-GCCcore-8.3.0 (case-sensitive)
- Module commands:
  - ml spider *pattern* : Search module names matching a *pattern*
  - ml *moduleName* : Load a module into your working environment
  - ml av : List all available software modules installed on cluster
  - ml : List modules currently loaded
  - ml -*moduleName* : Remove a module from working environment

- Installation path of 3 kinds of Software on Sap2test:
  - /apps/eb : Software built by EasyBuild, e.g., RepeatModeler/2.0.1-foss-2019b, TensorFlow/2.2.0-fosscuda-2019b-Python-3.7.4
  - /apps/gb : Software built out of EasyBuild (no EB toolchain in software name), e.g., ansys/19.2, matlab/R2019b, CellProfiler/4.0.0rc5_pyenv
  - /apps/singularity-images : Singularity container, e.g., busco-4.0.5.simg, repeatmodeler-2.0.1.simg, trinity-2.8.5.simg
- Once software is loaded, its installation path is stored in EBROOTAPPNAME, where APPNAME needs to be replaced by the actual software name (all capital letters), for example,

```
zhuofei@b1-1 ~$ ml TensorFlow/2.2.0-fosscuda-2019b-Python-3.7.4
zhuofei@b1-1 ~$ echo $EBROOTTENSORFLOW
/apps/eb/TensorFlow/2.2.0-fosscuda-2019b-Python-3.7.4
```

Important Tip using Software

- When you load more than one software modules, toolchain compatibility is the most important thing you need to pay attention to
- Toolchain in included as a part of software name, if the software is built by Easybuild
- If you load more than one module and some toolchains are incompatible, you will end up with failing dependencies or Lmod errors, like this:

```
Lmod has detected the following error:
These module(s) exist but cannot be loaded as requested
```

- https://wiki.gacrc.uga.edu/wiki/Available_Toolchains_and_Toolchain_Compatibility

Job Submission Workflow

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

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

   `ssh MyID@sap2test.gacrc.uga.edu`
2. On Login node, change directory to your scratch space: `cd /scratch/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 : `sbatch ./sub.sh`
8. Check job status : `squeue --me` or Cancel a job : `scancel jobID`

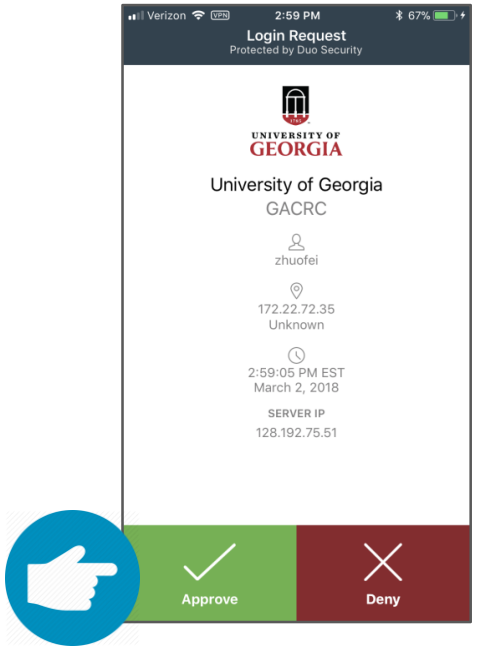
Step1: Log on to Login node - Mac/Linux using ssh

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

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

Step1 (Cont.) - Mac/Linux using ssh

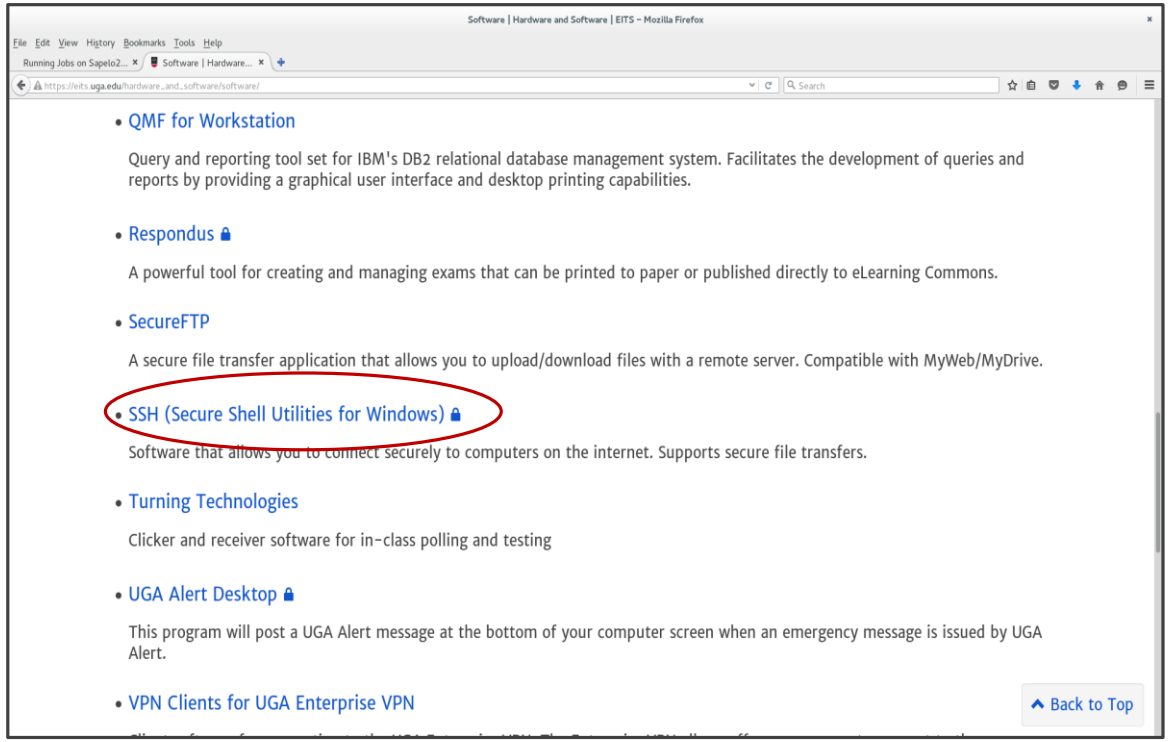
Use Terminal utility on Mac or Linux!

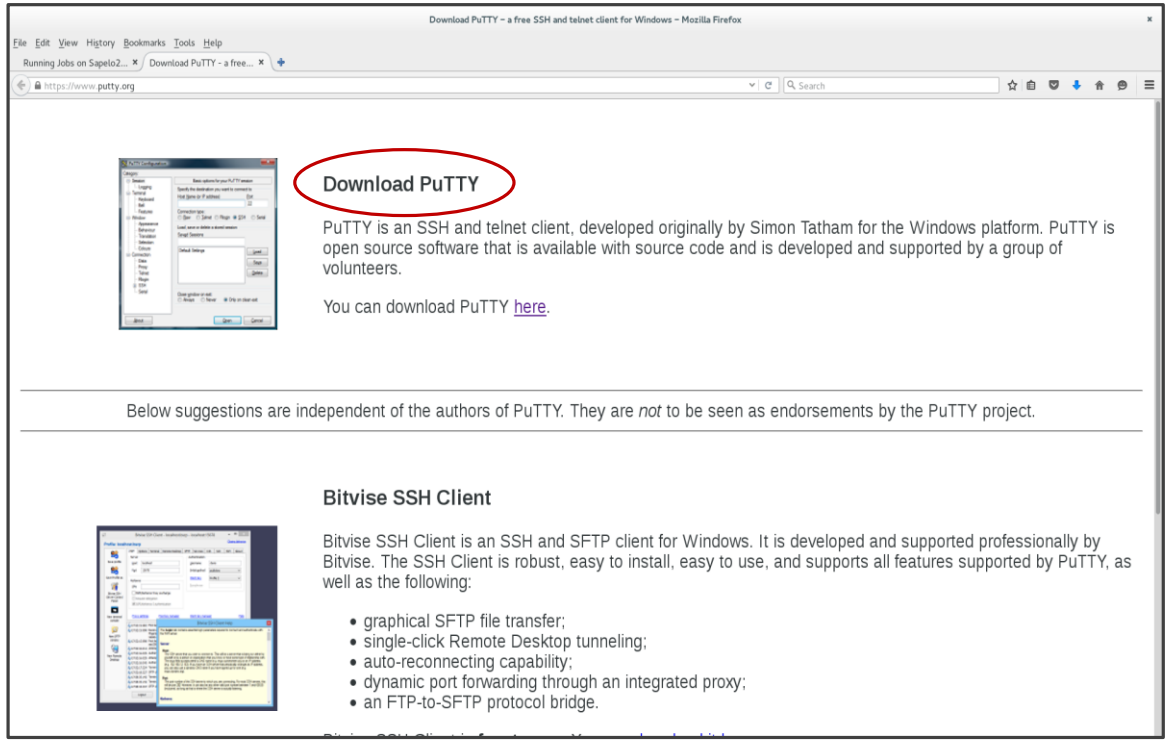



```
[zhuofei@localhost ~]$
[zhuofei@localhost ~]$ ssh zhuofei@sap2test.gacrc.uga.edu   ← Log on
Password:                                                   ← Input MyID password!
……
Enter a passcode or select one of the following options:
 1. Duo Push to XXX-XXX-5758
 2. Phone call to XXX-XXX-5758
 3. Phone call to XXX-XXX-1925
 4. SMS passcodes to XXX-XXX-5758

Passcode or option (1-5): 1        ← Select Duo authentication option!
Success. Logging you in...
Last login: Tue Sep 15 11:22:42 2020 from 128.192.75.65

zhuofei@ss-sub1 ~$                 ← I am on login node ss-sub1!
```

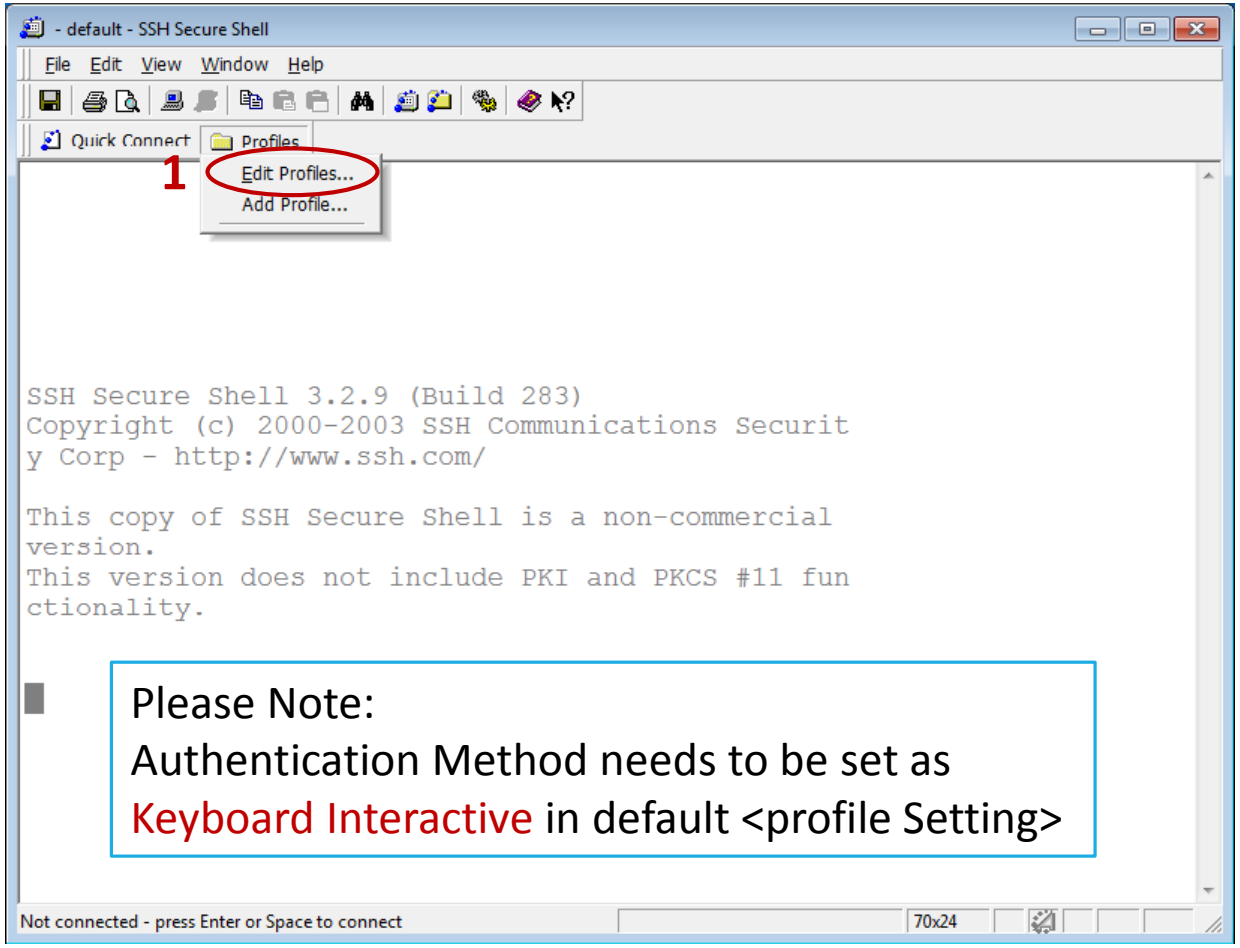
Step1 (Cont.) - Windows using SSH Secure Utilities

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/

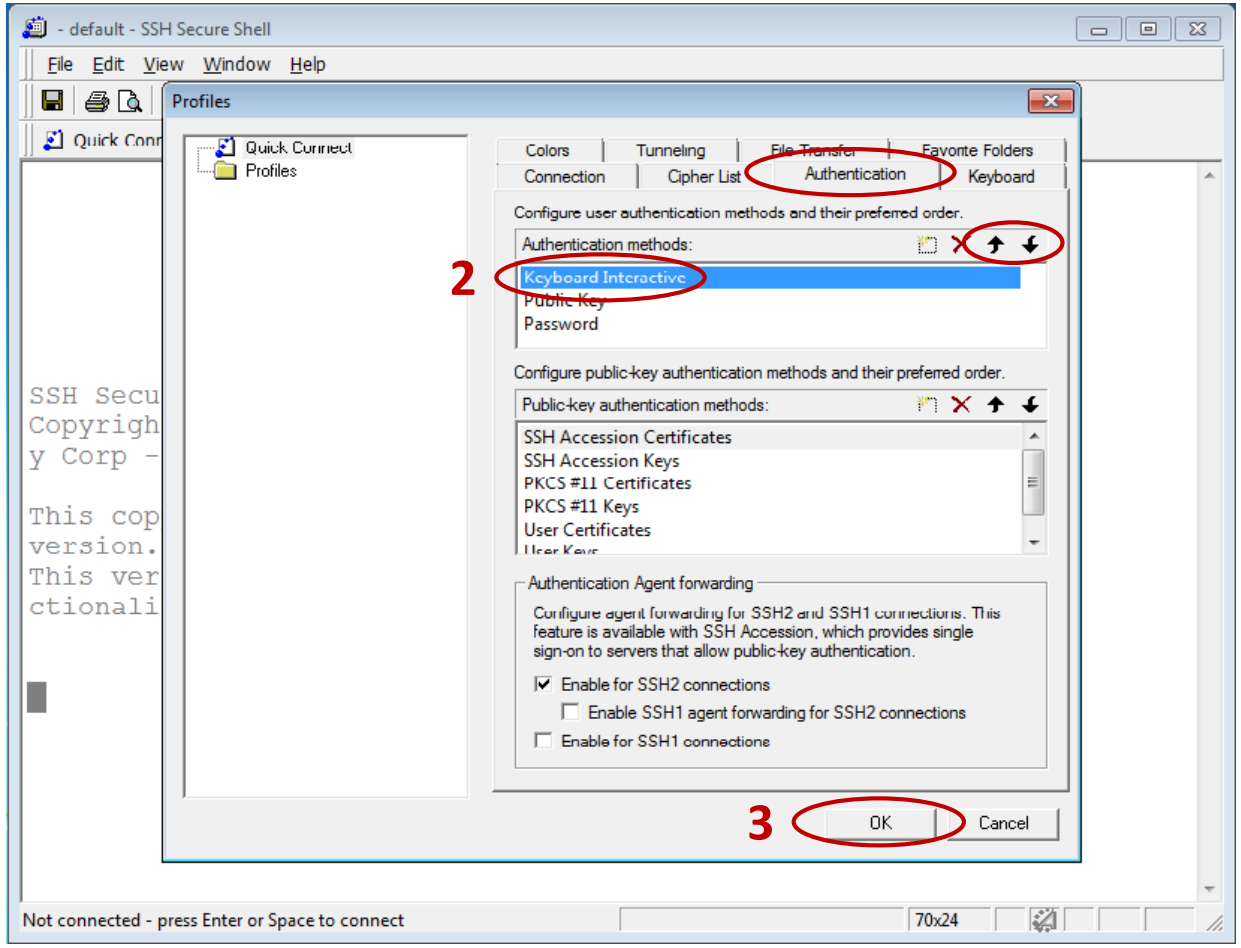




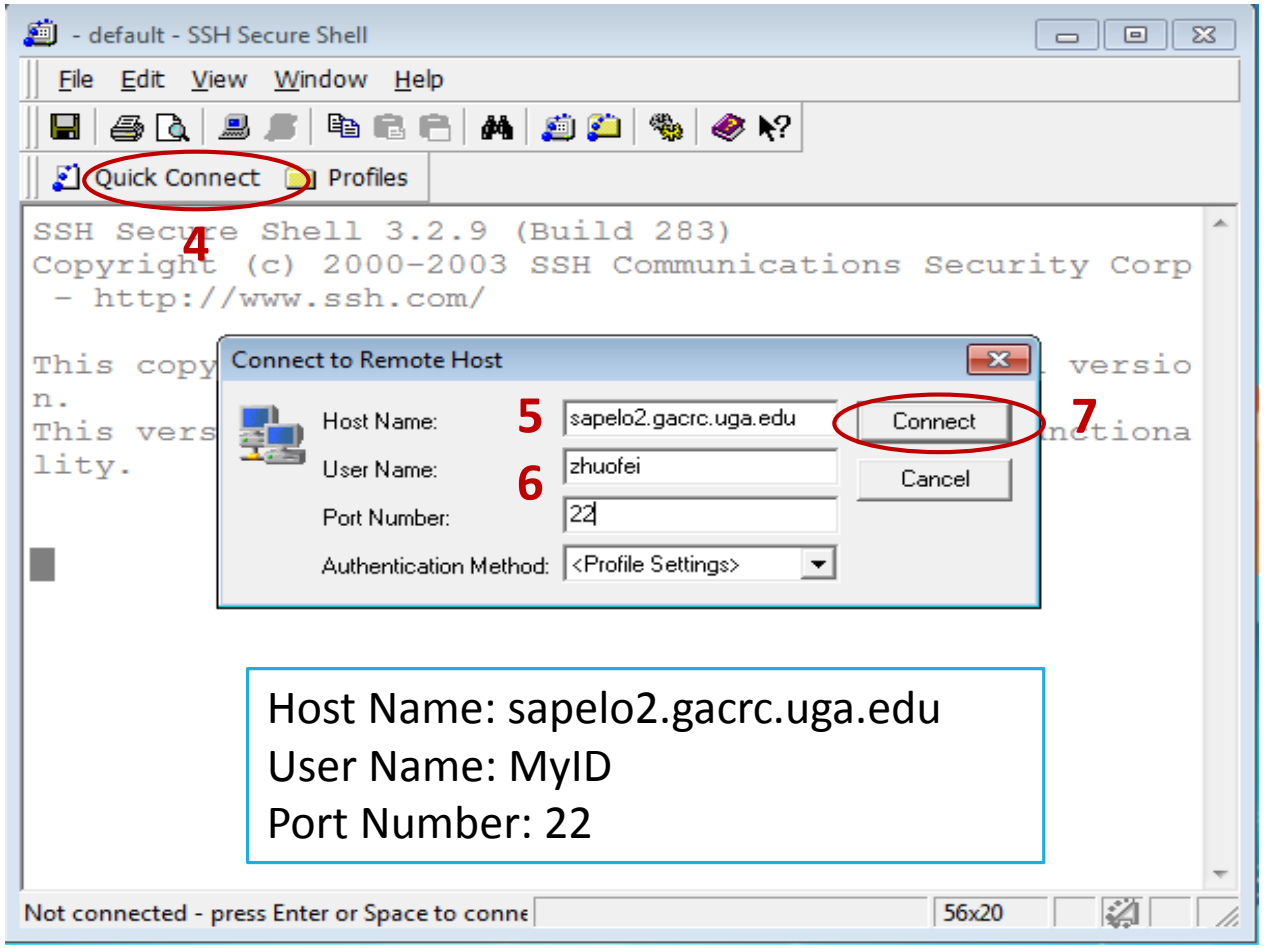
Step1 (Cont.) - Windows using SSH Secure Utilities



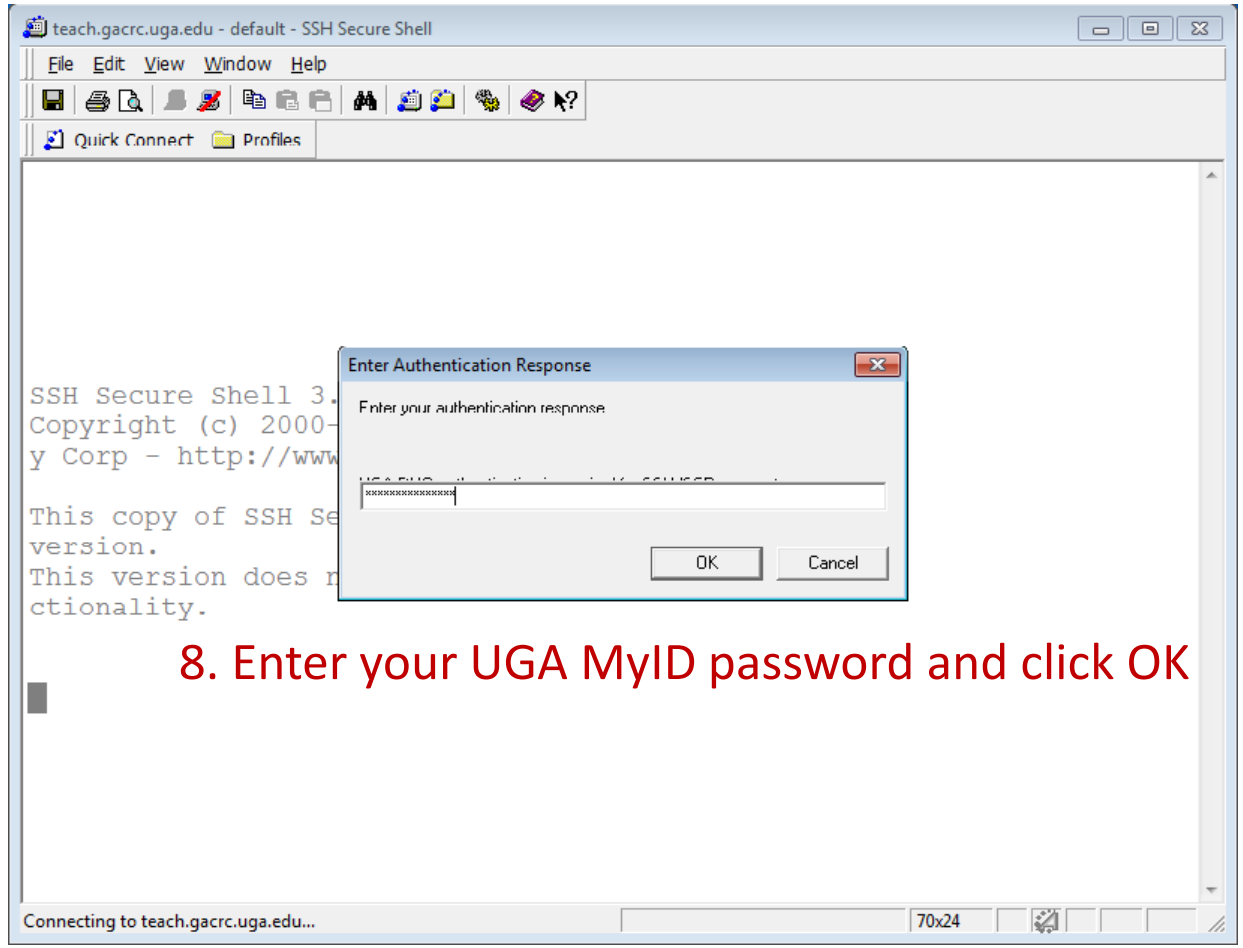
Please Note:
Authentication Method needs to be set as
Keyboard Interactive in default <profile Setting>



Step1 (Cont.) - Windows using SSH Secure Utilities

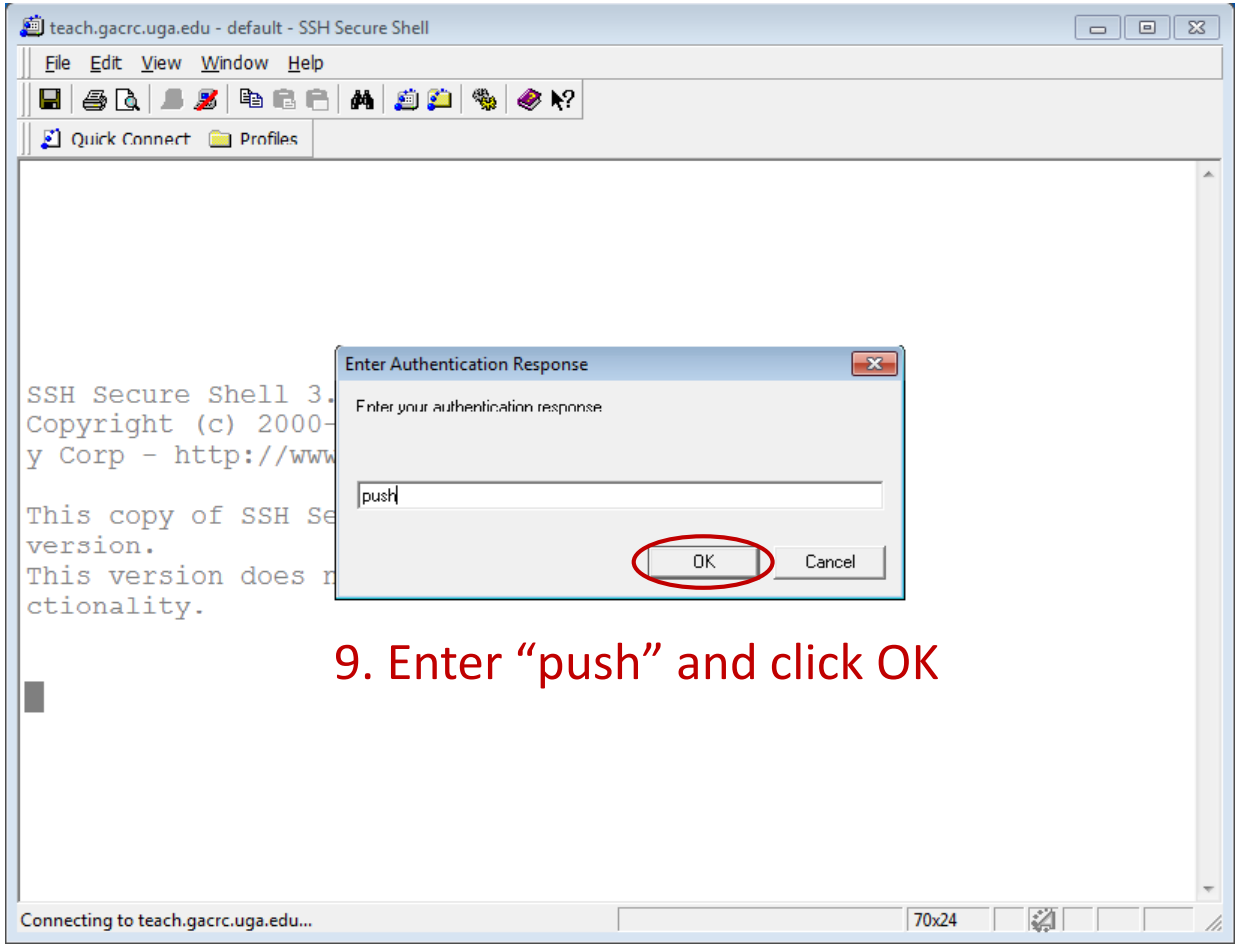


Host Name: sapelo2.gacrc.uga.edu
User Name: MyID
Port Number: 22

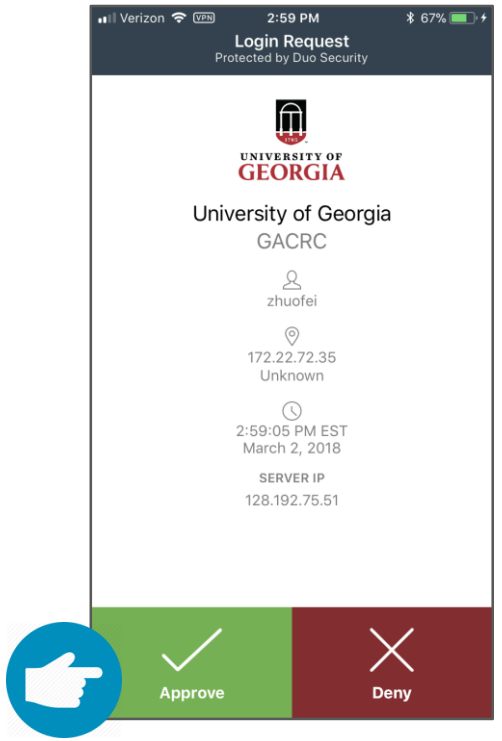


8. Enter your UGA MyID password and click OK

Step1 (Cont.) - Windows using SSH Secure Utilities



9. Enter “push” and click OK



10. Verify login using Duo, then you will log on!

Step2: On Login node change directory to global scratch

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

```
zhuofei@ss-sub1 ~$ pwd
/home/zhuofei                    ← this is my home directory!
```

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

```
zhuofei@ss-sub1 ~$ cd /scratch/zhuofei/
zhuofei@ss-sub1 zhuofei$ pwd
/scratch/zhuofei                 ← this is my scratch space!
```

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

```
zhuofei@ss-sub1 zhuofei$ ls
user_test
```

Step3 - 4: Create and cd to a working subdirectory

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

```
zhuofei@ss-sub1 zhuofei$ mkdir workDir
zhuofei@ss-sub1 zhuofei$ ls
user_test  workDir
```

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

```
zhuofei@ss-sub1 zhuofei$ cd workDir
zhuofei@ss-sub1 workDir$ pwd
/scratch/zhuofei/workDir
zhuofei@ss-sub1 workDir$ ls
```

← it is empty!

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

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

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:/scratch/zhuofei/workDir/
```

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

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

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

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

Step5 (Cont.) - Windows using SSH Secure Utilities

1. You need to connect to cluster's Transfer node (xfer.gacrc.uga.edu)

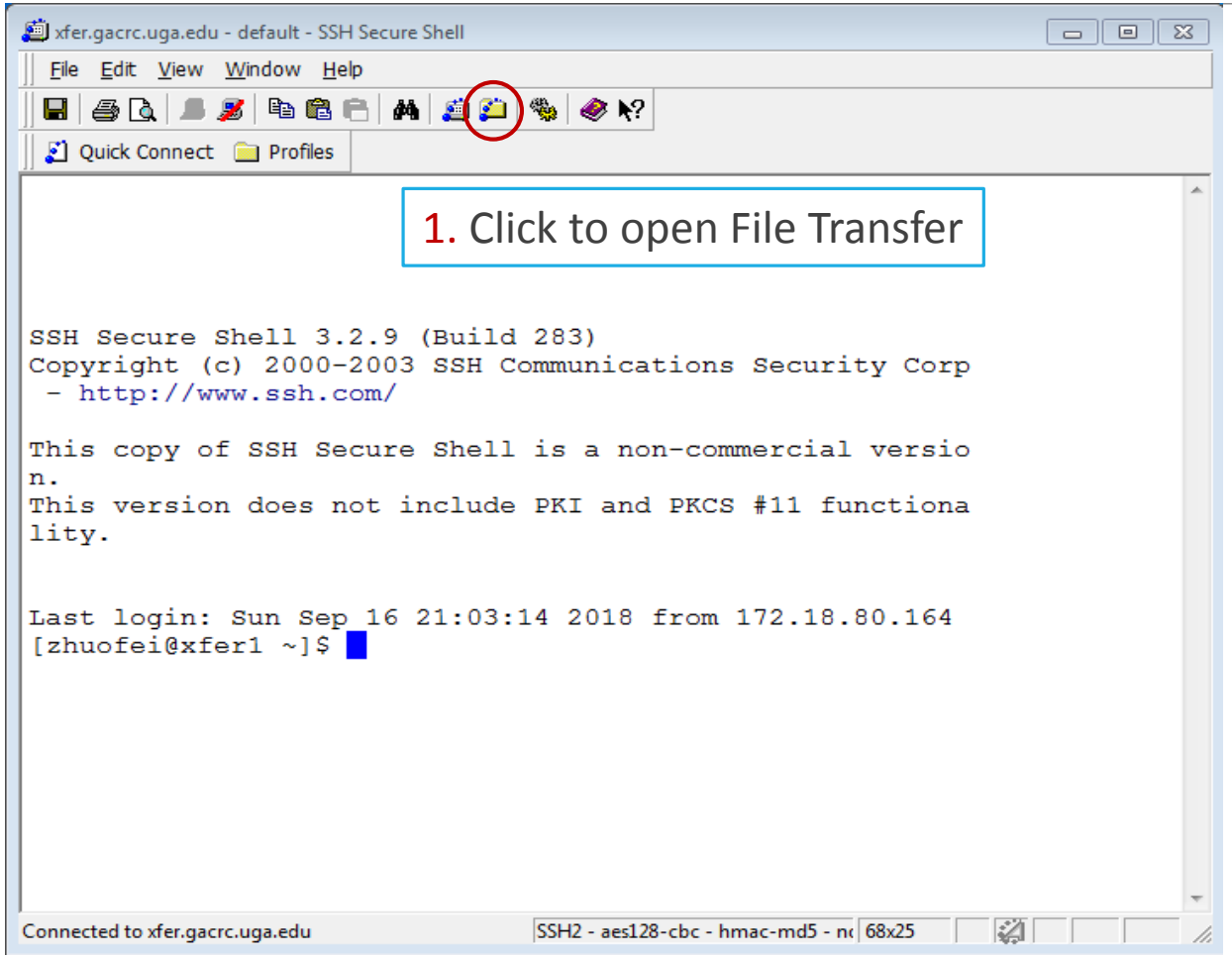
2. Use SSH File Transfer on local computer (alternative FileZilla or WinSCP)

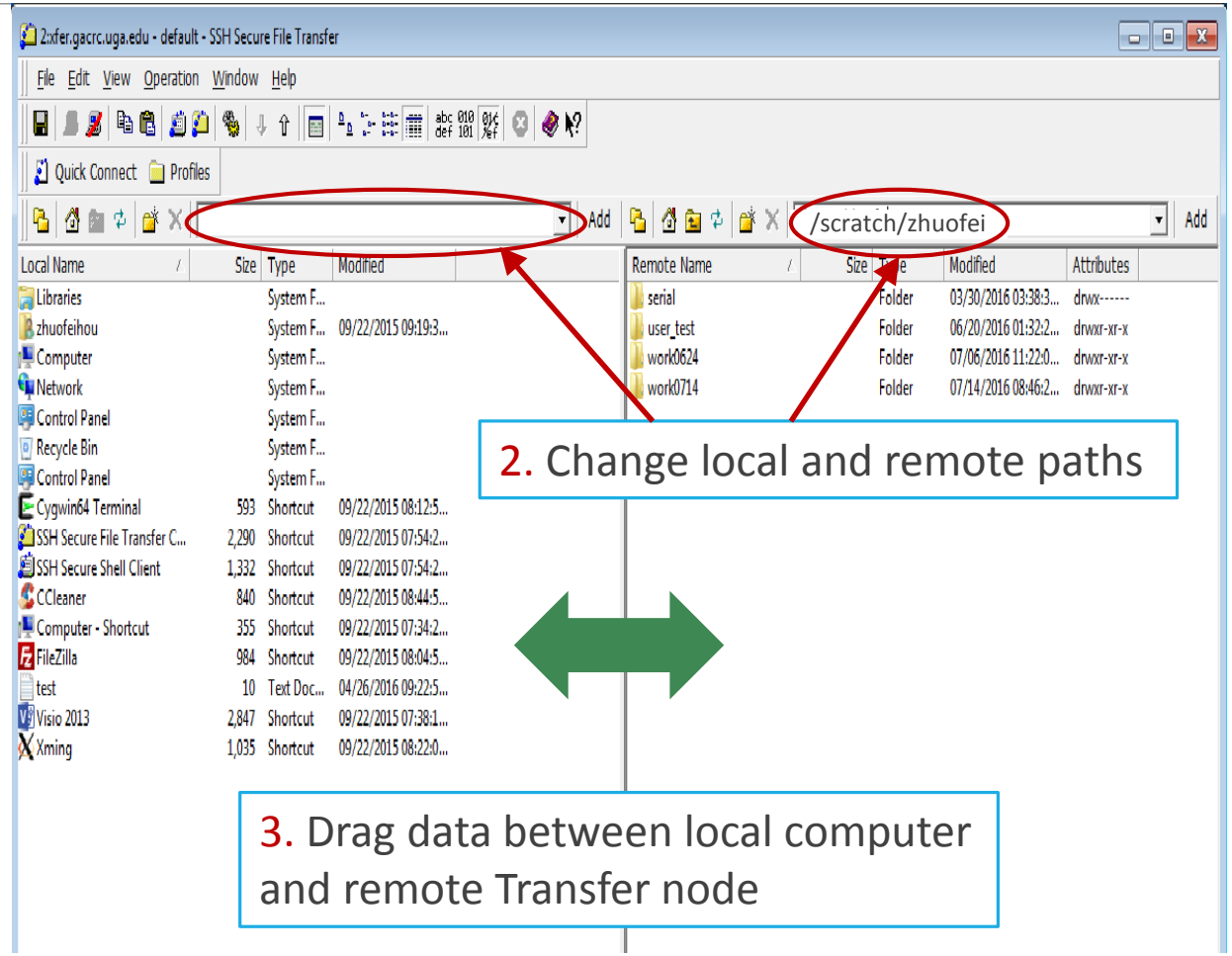
3. Steps 1-10 are the same as steps on page 14-15, except for Host Name in step 5:

   Host Name: xfer.gacrc.uga.edu

4. Once you log on, use File Transfer of SSH Secure Utilities, as shown on next page

Step5 (Cont.) - Windows using SSH Secure Utilities





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

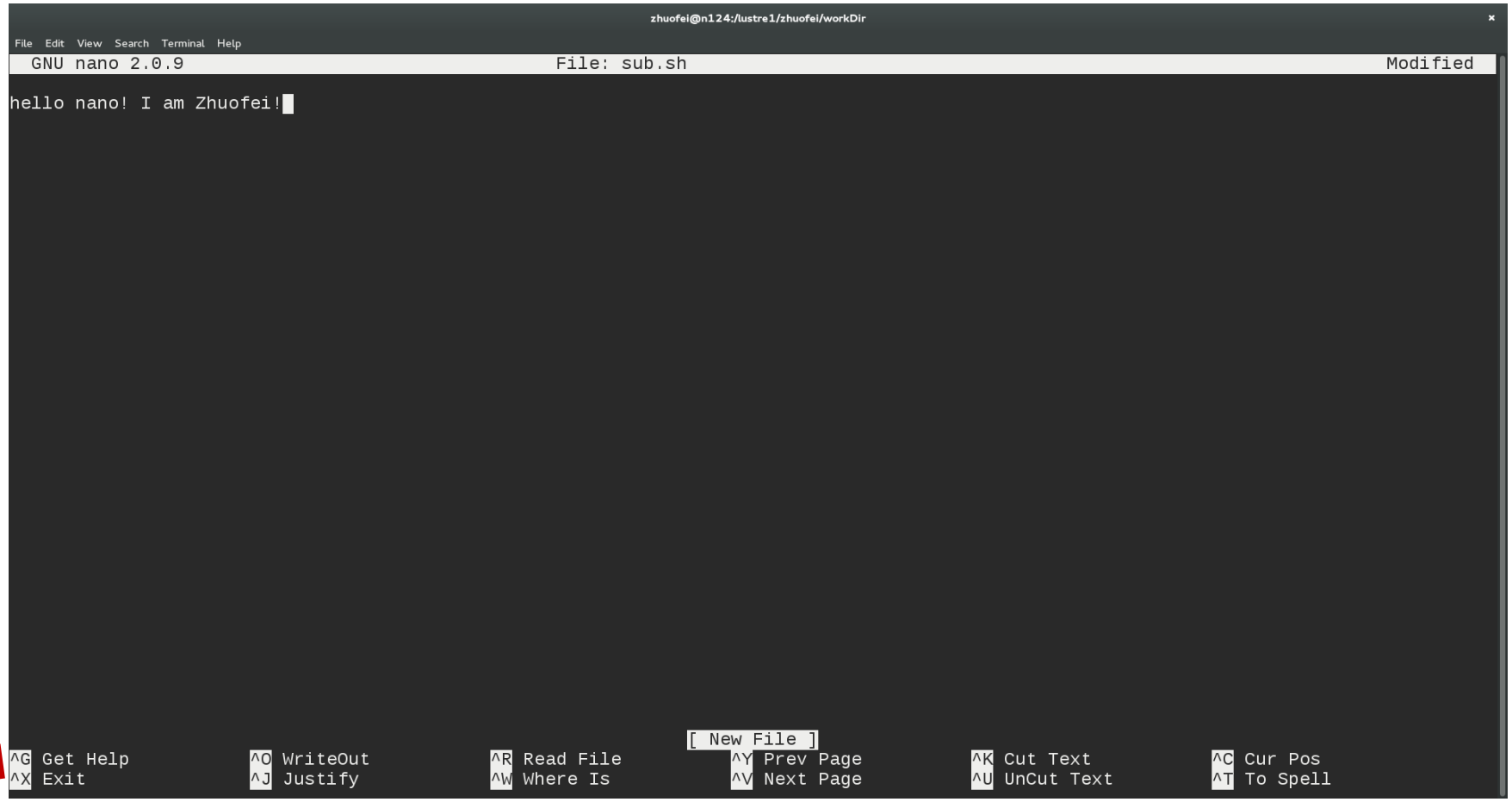
- Log on to Transfer node (xfer.gacrc.uga.edu)
  - ✓ Mac/Linux: ssh MyID@xfer.gacrc.uga.edu (page 12)
  - ✓ Windows: use SSH Secure Utilities (page 19)
- Landing folder: /home/MyID (Home)
- You can transfer data between following directories on cluster using cp or mv:
  1. /home/MyID (Home)
  2. /scratch/MyID (Scratch)
  3. /work/abclab (Work)
  4. /project/abclab (Project)
- 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

https://wiki.gacrc.uga.edu/wiki/Sample_batch_job_submission_scripts_on_Sapelo2

```
$ nano sub.sh
```

nano is a small and friendly text editor on Linux.



Ctrl-x to save file and quit from nano

```
  GNU nano 2.3.1                File: sub.sh                      Modified

#!/bin/bash
#SBATCH --job-name=testBowtie2          # Job name (testBowtie2)
#SBATCH --partition=batch               # Queue name (batch)
#SBATCH --ntasks=1                      # Run single task using one CPU core on a single node
#SBATCH --mem=4G                        # Job memory limit (4 GB)
#SBATCH --time=1:00:00                  # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --export=NONE                   # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.out              # Standard output, testBowtie2_1234.out
#SBATCH --error=%x_%j.err               # Standard error log, testBowtie2_1234.err
#SBATCH --mail-type=END,FAIL            # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu    # Where to send mail

cd $SLURM_SUBMIT_DIR                    # Change directory to job submission directory
ml Bowtie2/2.4.1-GCC-8.3.0              # Load software module and run bowtie2 below

bowtie2  -x  ./index/lambda_virus  -U  ./myreads.fq  -S  output.sam

^G Get Help     ^O WriteOut     ^R Read File    ^Y Prev Page    ^K Cut Tex
^X Exit         ^J Justify      ^W Where Is     ^V Next Page    ^U UnCut Te
```

To run demo example, please copy 3 files into your current working dir:

```
cp  /usr/local/training/sub.sh   .
cp  /usr/local/training/myreads.fq   .
cp  -r  /usr/local/training/index   .
```

Step7: Submit a job from workDir using sbatch

https://wiki.gacrc.uga.edu/wiki/Running_Jobs_on_Sapelo2#How_to_submit_a_job_to_the_batch_partition

```
zhuofei@ss-sub1 workDir$ pwd
/scratch/zhuofei/workDir
zhuofei@ss-sub1 workDir$ ls
index  myreads.fq  sub.sh
zhuofei@ss-sub1 workDir$ sbatch sub.sh
Submitted batch job 32860
```

sub.sh is a job submission script to

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

Step8: Check job status using squeue --me

https://wiki.gacrc.uga.edu/wiki/Monitoring_Jobs_on_Sapelo2

```
zhuofei@ss-sub1 workDir$ squeue --me
JOBID PARTITION     NAME     USER  ST      TIME  NODES     NODELIST(REASON)
32862     batch testBowt  zhuofei  PD      0:00      1     (None)
32861     batch testBowt  zhuofei   R      0:05      1     c5-19
32860     batch testBowt  zhuofei   R      4:37      1     c5-19
32859     batch testBowt  zhuofei  CD      9:29      1     b1-2
```

R : job is Running
PD : job is PenDing, waiting for resources to become available
CD : job is CompleteD and is not longer running
CA : job is CAnceled and is not longer running
F : job is Failed (crashed) on the node and is not longer running

Note: "TIME" is the elapsed wall-clock time of your job running on cluster, instead of the CPU time.

Step8: Check job status using squeue --me -l

https://wiki.gacrc.uga.edu/wiki/Monitoring_Jobs_on_Sapelo2

```
zhuofei@ss-sub1 workDir$ squeue --me -l
Tue Sep 15 15:00:51 2020
JOBID PARTITION     NAME     USER    STATE       TIME TIME_LIMI  NODES NODELIST(REASON)
32866     batch testBowt  zhuofei  RUNNING       0:14   1:00:00      1 rc6-10
32865     batch testBowt  zhuofei  RUNNING       0:30   1:00:00      1 rc6-10
32864     batch testBowt  zhuofei  RUNNING       0:33   1:00:00      1 rc6-10
```

Step8 (Cont.): Cancel job using scancel

https://wiki.gacrc.uga.edu/wiki/Running_Jobs_on_Sapelo2#How_to_cancel_.28delete.29_a_running_or_pending_job

```
zhuofei@ss-sub1 workDir$ squeue --me -l
Tue Sep 15 15:08:27 2020
JOBID PARTITION     NAME     USER    STATE       TIME TIME_LIMI  NODES NODELIST(REASON)
32869     batch testBowt  zhuofei  RUNNING       0:01   1:00:00      1 c5-19
32868     batch testBowt  zhuofei  RUNNING       0:05   1:00:00      1 c5-19
32867     batch testBowt  zhuofei  RUNNING       0:10   1:00:00      1 c5-19
zhuofei@ss-sub1 workDir$
zhuofei@ss-sub1 workDir$ scancel 32867
zhuofei@ss-sub1 workDir$ squeue --me -l
Tue Sep 15 15:08:45 2020
JOBID PARTITION     NAME     USER    STATE       TIME TIME_LIMI  NODES NODELIST(REASON)
32867     batch testBowt  zhuofei COMPLETI       0:26   1:00:00      1 c5-19
32869     batch testBowt  zhuofei  RUNNING       0:19   1:00:00      1 c5-19
32868     batch testBowt  zhuofei  RUNNING       0:23   1:00:00      1 c5-19
zhuofei@ss-sub1 workDir$ squeue --me -l
Tue Sep 15 15:08:50 2020
JOBID PARTITION     NAME     USER    STATE       TIME TIME_LIMI  NODES NODELIST(REASON)
32869     batch testBowt  zhuofei  RUNNING       0:19   1:00:00      1 c5-19
32868     batch testBowt  zhuofei  RUNNING       0:23   1:00:00      1 c5-19
```

```
zhuofei@ss-sub1 workDir$ scontrol show job 32870
JobId=32870 JobName=testBowtie2
   UserId=zhuofei(1772) GroupId=gacrc-instruction(21004) MCS_label=N/A
   Priority=1 Nice=0 Account=gacrc-appadmin QOS=normal
   JobState=RUNNING Reason=None Dependency=(null)
   Requeue=1 Restarts=0 BatchFlag=1 Reboot=0 ExitCode=0:0
   RunTime=00:00:21 TimeLimit=01:00:00 TimeMin=N/A
   SubmitTime=2020-09-15T15:30:41 EligibleTime=2020-09-15T15:30:41
   StartTime=2020-09-15T15:30:42 EndTime=2020-09-15T16:30:42 Deadline=N/A
   ……
   Partition=batch AllocNode:Sid=128.192.75.18:94107
   ReqNodeList=(null) ExcNodeList=(null)
   NodeList=c5-19
   BatchHost=c5-19
   NumNodes=1 NumCPUs=4 NumTasks=1 CPUs/Task=4 ReqB:S:C:T=0:0:*:*
   ……
   Command=/scratch/zhuofei/workDir/sub.sh
   WorkDir=/scratch/zhuofei/workDir
   StdErr=/scratch/zhuofei/workDir/testBowtie2_32870.err
   StdIn=/dev/null
   StdOut=/scratch/zhuofei/workDir/testBowtie2_32870.out
```

```
zhuofei@ss-sub1 workDir$ seff 37259
Job ID: 37259
Cluster: tc2
User/Group: zhuofei/gacrc-instruction
State: COMPLETED (exit code 0)
Cores: 1
CPU Utilized: 00:09:45
CPU Efficiency: 99.66% of 00:09:47 core-walltime
Job Wall-clock time: 00:09:47
Memory Utilized: 197.34 MB
Memory Efficiency: 4.82% of 4.00 GB
```

```
zhuofei@ss-sub1 workDir$ sacct-gacrc
```

JobID	JobName	User	Partition	NodeList	AllocNodes	NTasks	NCPUS	ReqMem	MaxVMSize	State	CPUTime	Elapsed	Timelimit	ExitCode	WorkDir
275	bowti+	zhuofei	batch	rc6-10	1		1	4Gn		COMPLETED	00:09:13	00:09:13	01:00:00	0:0	/scratch/zhu..
275.batch	batch			rc6-10	1	1	1	4Gn	396868K	COMPLETED	00:09:13	00:09:13		0:0	
275.extern	extern			rc6-10	1	1	1	4Gn	142616K	COMPLETED	00:09:13	00:09:13		0:0	
276	amberjob	shtsai	gpu_p	c4-23	1		1	10Gn		CANCELLED+	00:03:19	00:03:19	02:00:00	0:0	/scratch/sht..
276.batch	batch			c4-23	1	1	1	10Gn	221140K	CANCELLED	00:03:20	00:03:20		0:15	
276.extern	extern			c4-23	1	1	1	10Gn	169800K	COMPLETED	00:03:19	00:03:19		0:0	
277	mpitest	shtsai	batch	c2-[11-12]	2		24	600Mc		COMPLETED	04:01:12	00:10:03	02:00:00	0:0	/scratch/sht..
277.batch	batch			c2-11	1	1	12	600Mc	221268K	COMPLETED	02:00:36	00:10:03		0:0	
277.extern	extern			c2-[11-12]	2	2	24	600Mc	169800K	COMPLETED	04:01:12	00:10:03		0:0	
277.0	orted			c2-12	1	1	1	600Mc	265640K	COMPLETED	00:00:01	00:00:01		0:0	
278	bash	shtsai	inter_p	c2-4	1		1	2Gn		RUNNING	00:13:37	00:13:37	12:00:00	0:0	/scratch/sht..
278.extern	extern			c2-4	1	1	1	2Gn		RUNNING	00:13:37	00:13:37		0:0	
278.0	bash			c2-4	1	1	1	2Gn		RUNNING	00:13:37	00:13:37		0:0	

```
zhuofei@ss-sub1 workDir$ sacct-gacrc-v 47939

JobID           47939
JobName         testBowti+
User            zhuofei
Partition       batch
NodeList        c1-3
AllocNodes      1
State           RUNNING
CPUTime         00:00:28
Elapsed         00:00:28
Timelimit       01:00:00
ExitCode        0:0
WorkDir         /scratch/zhuofei/workDir_sap2test
NTasks          1
NCPUS           1
ReqMem          4Gn
```

```
zhuofei@ss-sub1 workDir$ sinfo-gacrc
```

PARTITION	NODELIST	STATE	CPUS	MEMORY(MB)	AVAIL_FEATURES	GRES
batch	ra3-19,ra4-12	down*	48	128914	AMD,Opteron,QDR	(null)
batch	b1-[3-23],d4-[6-10]	drained	32+	128596+	AMD,EPYC,EDR	(null)
batch	c1-3	drained	28	64205	Intel,Broadwell,EDR	(null)
batch	ra3-[1-18,20-24],ra4-[2-11,13-14,18-20]	drained	48	128914+	AMD,Opteron,QDR	(null)
batch	rc6-10	drained	28	64205	Intel,Broadwell,QDR	(null)
batch	b1-2,d4-5	idle	32+	128596+	AMD,EPYC,EDR	(null)
batch	c5-19	idle	32	192039	Intel,Skylake,EDR	(null)
gpu_p	c4-23	drained	32	192038	Intel,Skylake,EDR	gpu:P100:1
highmem_p	ra4-16	draining	48	128914	AMD,Opteron,QDR	(null)
highmem_p	d4-[11-12]	drained	32	515743	AMD,EPYC,EDR	(null)
highmem_p	ra4-[21-24]	drained	48	515986	AMD,Opteron,QDR	(null)
inter_p	ra4-16	draining	48	128914	AMD,Opteron,QDR	(null)
inter_p	ra4-17	drained	48	257938	AMD,Opteron,QDR	(null)

Obtain Job Details

https://wiki.gacrc.uga.edu/wiki/Monitoring_Jobs_on_Sapelo2#How_to_see_detailed_information_about_a_given_job

Option 1: `scontrol show job JobID` for details of a running or pending jobs

Option 2: `seff` for details of computing resource usage of a finished job

Option 3: `sacct-gacrc` or `sacct-gacrc-v` for details of computing resource usage of a running or finished job

Option 4: Email notification from finished jobs (completed, canceled, or crashed), if using:

```
#SBATCH --mail-user=username@uga.edu
#SBATCH --mail-type=END,FAIL
```

Interactive jobs

Description	Slurm Command
Start an interactive session	qlogin
Start an interactive session with X forwarding	xqlogin

qlogin	srun --pty -p inter_p --mem=2G --nodes=1 --ntasks-per-node=1 --time=8:00:00 --job-name=qlogin bash
xqlogin	srun --pty --x11 -p inter_p --mem=2G --nodes=1 --ntasks-per-node=1 --time=8:00:00 --job-name=xqlogin bash

https://wiki.gacrc.uga.edu/wiki/Running_Jobs_on_Sapelo2#How_to_open_an_interactive_session

GACRC Wiki http://wiki.gacrc.uga.edu

System: https://wiki.gacrc.uga.edu/wiki/Systems

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

Software: https://wiki.gacrc.uga.edu/wiki/Software_on_Sapelo2

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

Monitoring Jobs: https://wiki.gacrc.uga.edu/wiki/Monitoring_Jobs_on_Sapelo2

Sample scripts : https://wiki.gacrc.uga.edu/wiki/Sample_batch_job_submission_scripts_on_Sapelo2

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

GACRC Help and Support
https://wiki.gacrc.uga.edu/wiki/Getting_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

When you ask GACRC to test or troubleshoot your jobs, Please make sure of the correctness of your datasets being used!

GACRC Service Catalog

Georgia Advanced Computing Resource Center (GACRC) service catalog

Services (11)

Account Creation
For a research group's PI to request user accounts for group members on the GACRC computing systems.

Class Account Creation
For an instructor to request user accounts for students attending a course that will need to use GACRC computing systems.

Class Account Modification
For instructors to request changes to be made in previously requested class account.

Computing Lab Modification/Deletion

General Internal

General Support
Report issues and request help with GACRC systems, except for software installation requests and account/lab creation requests.

Lab Creation
For a research group's PI to register a computing lab on the GACRC computing systems

Modify/Delete Account
For PIs to request changes in or deletion of user accounts on GACRC computing systems.

Software Installation/Update
Request software and common application database (e.g. NCBI blast databases) installation and upgrade.

My Recent Requests

- home directory is not fully provisioned: ss57215
- GACRC Sapelo2 New Lab/Use Account Request 2018-11-14_preTraining
- GACRC Sapelo2 Cluster New Lab/Use Account Request 2018-11-05_preTraining
- provision 5 user accounts for ugahelpdesk group
- GACRC Sapelo2 New Lab/Use Account Request 2018-10-22_preTraining

View All Recent Requests >

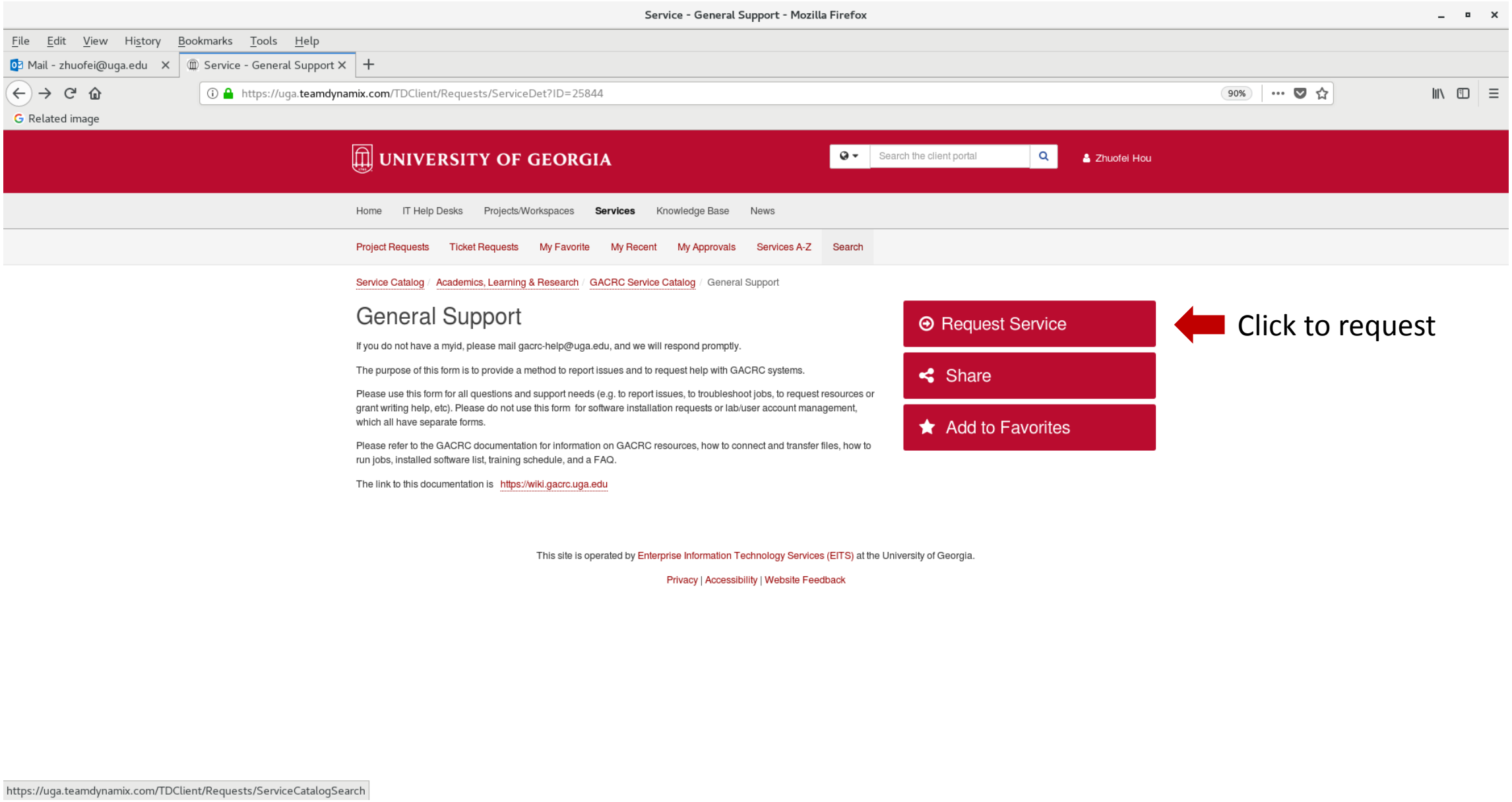
Popular Services

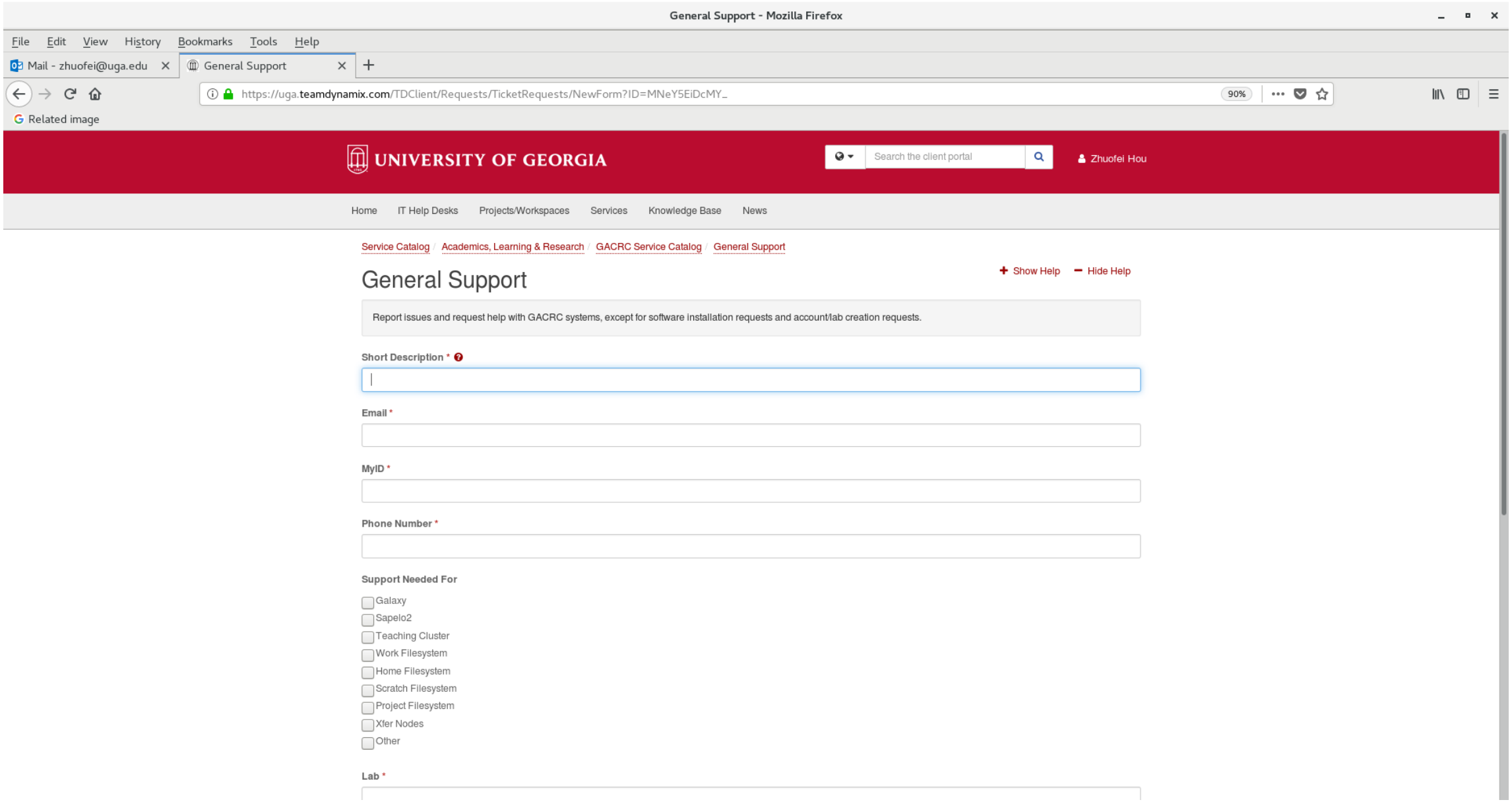
- EITS Help Desk Support Request
- MyID Account Request
- Change Request
- 02 Restricted VPN Access
- Terry Classroom & Meeting Room Support

View All Popular Services >

My Recently Visited Services

- Modify/Delete Account
- Class Account Creation


Service - General Support - Mozilla Firefox
File Edit View History Bookmarks Tools Help
Mail - zhuofei@uga.edu
Service - General Support
https://uga.teamdynamix.com/TDClient/Requests/ServiceDet?ID=25844
90%
Related image
UNIVERSITY OF GEORGIA
Search the client portal
Zhuofei Hou
Home IT Help Desks Projects/Workspaces Services Knowledge Base News
Project Requests Ticket Requests My Favorite My Recent My Approvals Services A-Z Search
Service Catalog / Academics, Learning & Research / GACRC Service Catalog / General Support
General Support
If you do not have a myid, please mail gacrc-help@uga.edu, and we will respond promptly.
The purpose of this form is to provide a method to report issues and to request help with GACRC systems.
Please use this form for all questions and support needs (e.g. to report issues, to troubleshoot jobs, to request resources or grant writing help, etc). Please do not use this form for software installation requests or lab/user account management, which all have separate forms.
Please refer to the GACRC documentation for information on GACRC resources, how to connect and transfer files, how to run jobs, installed software list, training schedule, and a FAQ.
The link to this documentation is https://wiki.gacrc.uga.edu
Request Service
Share
Add to Favorites
Click to request
This site is operated by Enterprise Information Technology Services (EITS) at the University of Georgia.
Privacy | Accessibility | Website Feedback
https://uga.teamdynamix.com/TDClient/Requests/ServiceCatalogSearch


General Support - Mozilla Firefox
File Edit View History Bookmarks Tools Help
Mail - zhuofei@uga.edu
General Support
https://uga.teamdynamix.com/TDClient/Requests/TicketRequests/NewForm?ID=MNeY5EiDcMY_
90%
Related image
UNIVERSITY OF GEORGIA
Search the client portal
Zhuofei Hou
Home
IT Help Desks
Projects/Workspaces
Services
Knowledge Base
News
Service Catalog / Academics, Learning & Research / GACRC Service Catalog / General Support
General Support
Show Help
Hide Help
Report issues and request help with GACRC systems, except for software installation requests and account/lab creation requests.
Short Description *
Email *
MyID *
Phone Number *
Support Needed For
Galaxy
Sapelo2
Teaching Cluster
Work Filesystem
Home Filesystem
Scratch Filesystem
Project Filesystem
Xfer Nodes
Other
Lab *

Slurm job states

Code	State	Meaning
R	Running	Job is running on compute node(s)
PD	Pending	Job is waiting for compute node(s)
CD	Completed	Job completed
CG	Completing	Job is completing
CA	Canceled	Job was canceled
F	Failed	Job terminated with non-zero exit code
NF	Node Fail	Job terminated due to failure of node(s)

Commands for submitting and canceling jobs

Description	Slurm Command
Submit a batch job to queue	sbatch sub.sh
Delete a job from queue	scancel <jobID>
Cancel all your job(s)	scancel -u <username>
Cancel all your pending job(s)	scancel -t PENDING -u <username>
Cancel your job(s) by job name	scancel --name <jobname>
Cancel an element (index) of an array job (jobID)	scancel <jobID>_<index>

Commands for monitoring jobs

Description	Slurm Command
Command	squeue or squeue -l
Job status of all your jobs	squeue --me or squeue --me -l
Job status of a job	squeue -j <jobID>
Job status of job(s) from a user	squeue -u <username>
Job status with details	scontrol show job <job ID> scontrol show job -dd <job ID>
Job's resource usage	sacct-gacrc
View job batch script	scontrol write batch_script <job ID> [filename]

Slurm headers for running a Serial (single-core) job

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

```
#!/bin/bash
#SBATCH --job-name=testBowtie2              # Job name (testBowtie2)
#SBATCH --partition=batch                   # Queue name (batch)
#SBATCH --ntasks=1                          # Run in a single task using one CPU core on a single node
#SBATCH --mem=4G                            # Job memory limit (4 GB)
#SBATCH --time=1:00:00                      # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --export=NONE                       # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.out                  # Standard output log, e.g., testBowtie2_1234.out
#SBATCH --error=%x_%j.err                   # Standard error log, e.g., testBowtie2_1234.err
#SBATCH --mail-type=END,FAIL                # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu        # Where to send mail

cd $SLURM_SUBMIT_DIR                        # Change directory to job submission directory
ml Bowtie2/2.4.1-GCC-8.3.0                  # Load software module and run bowtie2 below
bowtie2  -x  ./index/lambda_virus  -U  ./myreads.fq  -S  output.sam
```

Slurm headers for running a Threaded job


```
#!/bin/bash
#SBATCH --job-name=testBowtie2          # Job name (testBowtie2)
#SBATCH --partition=batch               # Queue name (batch)
#SBATCH --nodes=1                       # Run all processes on a single node
#SBATCH --ntasks=1                      # Run in a single task on a single node
#SBATCH --cpus-per-task=8               # Number of CPU cores per task (8)
#SBATCH --mem=10G                       # Job memory limit (10 GB)
#SBATCH --time=1:00:00                  # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --export=NONE                   # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.out              # Standard output log, e.g., testBowtie2_1234.out
#SBATCH --error=%x_%j.err               # Standard error log, e.g., testBowtie2_1234.err
#SBATCH --mail-type=END,FAIL            # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu    # Where to send mail

cd $SLURM_SUBMIT_DIR
ml Bowtie2/2.4.1-GCC-8.3.0
bowtie2  -p  8  -x  ./index/lambda_virus  -U  ./myreads.fq  -S  output.sam
```

Slurm headers for running an Array job


```
#!/bin/bash
#SBATCH --job-name=testBowtie2Array      # Job name (testBowtie2Array)
#SBATCH --partition=batch                # Queue name (batch)
#SBATCH --ntasks=1                       # Run in a single task using one CPU core on a single node
#SBATCH --mem=4G                         # Job memory limit (4 GB)
#SBATCH --time=1:00:00                   # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --export=NONE                    # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.out               # Standard output log, e.g., testBowtie2Array_1234.out
#SBATCH --error=%x_%j.err                # Standard error log, e.g., testBowtie2Array_1234.err
#SBATCH --array=0-9                      # Array element range from 0 to 9, i.e. 10 element jobs

cd $SLURM_SUBMIT_DIR
ml Bowtie2/2.4.1-GCC-8.3.0               # Original data is split into 10 pieces and run in each element job
bowtie2  -x  ./index/lambda_virus  -U  ./myreads_$SLURM_ARRAY_TASK_ID.fq \
-S  output_$SLURM_ARRAY_TASK_ID.sam
```

Slurm headers for running a Threaded (OpenMP) job


```
#!/bin/bash
#SBATCH --job-name=testOpenMP                # Job name (testOpenMP)
#SBATCH --partition=batch                    # Queue name (batch)
#SBATCH --nodes=1                            # Run all processes on a single node
#SBATCH --ntasks=1                           # Run in a single task on a single node
#SBATCH --cpus-per-task=12                   # Number of CPU cores per task (12)
#SBATCH --mem=10G                            # Job memory limit (10 GB)
#SBATCH --export=NONE                        # Do not load any users' explicit environment variables
#SBATCH --time=24:00:00                      # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --output=%x_%j.log                   # Standard output and error log, e.g., testOpenMP_1234.log
#SBATCH --mail-type=END,FAIL                 # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu         # Where to send mail

cd $SLURM_SUBMIT_DIR
export OMP_NUM_THREADS=$SLURM_CPUS_PER_TASK  # Sets the number of threads to use for OpenMP parallel regions
ml foss/2019b                                # Load toolchain module
./myProgram.x                                # Run your program binary compiled with OpenMP
```

Slurm headers for running a MPI job


```
#!/bin/bash
#SBATCH --job-name=testMPI                  #  Job name (tesMPI)
#SBATCH --partition=batch                   #  Queue name (batch)
#SBATCH --nodes=2                           #  Run on two nodes
#SBATCH --ntasks-per-node=16                #  How many tasks on each node; Number of tasks=32=MPI ranks
#SBATCH --cpus-per-task=1                   #  Number of CPU cores per task; 16 CPU cores per node
#SBATCH --mem-per-cpu=500M                  # Memory per allocated CPU; 8GB (500MB*16) memory per node
#SBATCH --time=24:00:00                     # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --export=NONE                       # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.log                  # Standard output and error log, e.g., testMPI_1234.log
#SBATCH --mail-type=END,FAIL                # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu        # Where to send mail

cd $SLURM_SUBMIT_DIR
ml foss/2019b                               # Load toolchain module
mpirun -n 32 ./myProgram.x                  # Run your program binary compiled with OpenMPI with 32 ranks
```

Slurm headers for running a Hybrid MPI/OpenMP job


```
#!/bin/bash
#SBATCH --job-name=testHybrid              #  Job name (testHybrid)
#SBATCH --partition=batch                  #  Queue name (batch)
#SBATCH --nodes=2                          #  Run on two nodes
#SBATCH --ntasks-per-node=8                #  How many tasks on each node; Number of tasks=16=MPI ranks
#SBATCH --cpus-per-task=4                  #  Number of CPU cores per task; 32 CPU cores per node
#SBATCH --mem-per-cpu=500M                 # Memory per allocated CPU; 16GB (500MB*32) memory per node
#SBATCH --time=24:00:00                    # Time limit hrs:min:sec or days-hours:minutes:seconds
#SBATCH --export=NONE                      # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.log                 # Standard output and error log
#SBATCH --mail-type=END,FAIL               # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu       # Where to send mail

cd $SLURM_SUBMIT_DIR                       # Change directory to job submission directory
export OMP_NUM_THREADS=$SLURM_CPUS_PER_TASK    # Sets the number of threads to use for OpenMP parallel regions
ml foss/2019b                              # Load toolchain module
mpirun -n 16 ./myProgram.x                 # Run your program binary compiled with OpenMPI with 16 ranks
```

Slurm headers for running a GPU job


```
#!/bin/bash
#SBATCH --job-name=amber                    # Job name
#SBATCH --partition=gpu_p                   # Partition (queue) name, i.e., gpu_p
#SBATCH --gres=gpu:1                        # Requests one GPU device; --gres=gpu:P100:1, --gres=gpu:K40:1
#SBATCH --ntasks=1                          # Run a single task
#SBATCH --cpus-per-task=2                   # Number of CPU cores per task
#SBATCH --mem=40gb                          # Job memory request
#SBATCH --time=10:00:00                     # Time limit hrs:min:sec
#SBATCH --export=NONE                       # Do not load any users' explicit environment variables
#SBATCH --output=%x_%j.out                  # Standard output and error log, e.g., amber_1234.out
#SBATCH --mail-type=END,FAIL                # Mail events (BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu        # Where to send mail

cd $SLURM_SUBMIT_DIR
ml Amber/18-fosscuda-2018b-AmberTools-18-patchlevel-10-8
mpiexec $AMBERHOME/bin/pmemd.cuda -O -i ./prod.in -o prod_c4-23.out  -p ./dimerFBP_GOL.prmtop -c ./restart.rst \
-r prod.rst -x prod.mdcrd
```

Slurm headers for running a Singularity container


```
#!/bin/bash
#SBATCH --job-name=test_sortmerna          # Job name
#SBATCH --partition=batch                  # Partition (queue) name
#SBATCH --ntasks=1                         # Run on a single CPU
#SBATCH --mem=8gb                          # Job memory request
#SBATCH --time=02:00:00                    # Time limit hrs:min:sec
#SBATCH --export=NONE                      # Do not load any users' explicit environment variables
#SBATCH --output=sortmerna.%j.out          # Standard output log, e.g., sortmerna.1234.out
#SBATCH --error=sortmerna.%j.err           # Standard error log, e.g., sortmerna.1234.err
#SBATCH --cpus-per-task=4                  # Number of CPU cores per task
#SBATCH --mail-type=END,FAIL               # Mail events (NONE, BEGIN, END, FAIL, ALL)
#SBATCH --mail-user=username@uga.edu       # Where to send mail

cd $SLURM_SUBMIT_DIR
singularity exec /apps/singularity-images/sortmerna-3.0.3.simg sortmerna --threads 4 --ref db.fasta,db.idx --reads file.fa \
--aligned base_name_output
```

Guideline Tips

- Do NOT use Login node to run CPU/memory intensive tasks directly ➔ submit job to queue!
- Do NOT use Login Node to transfer data between your local computer and cluster ➔ use Transfer node!
- Do NOT use Home for storing job data ➔ use /scratch/MyID
- Do NOT park data in Scratch or Local Scratch ➔ clean up when job finishes or exits from node
- Do NOT park data permanently in Project ➔ download data to your local drive
- NO large memory job running on batch partition ➔ use highmem_p
- NO small memory job running on highmem_p partition ➔ use batch
- In general, number of threads you want to run with a parallel job = number of cores requested
- When you archive data using tar on /scratch, please do not use z option (compression option). After you achieved data by tar, you can use gzip to compress it.

Practical Tips

- Each directory should not have too many files inside! A rule of thumb would be to try to keep no more than a few tens of thousands of files (<10000 would be even better) in any single directory which is accessed frequently

All files are in ONE single dir!

Files are organized in subdirs!

Thank You!

Telephone Support

EITS Help Desk: 706-542-3106

Monday – Thursday: 7:30 a.m. – 7:30 p.m.

Friday: 7:30 a.m. – 6 p.m.

Saturday – Sunday: 1 p.m. – 7 p.m.

Georgia Advanced Computing Resource Center

101-108 Computing Services building

University of Georgia

Athens, GA 30602

https://gacrc.uga.edu/