

Introduction to HPC Using the New Cluster (Sapelo) at GACRC

Georgia Advanced Computing Resource Center

University of Georgia

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Outline

- What is GACRC?
- What is the new cluster (Sapelo) at GACRC?
- How does Sapelo operate?
- How to work with Sapelo?

What is GACRC?

Who Are We?

- Georgia **A**dvanced **C**omputing **R**esource **C**enter
- Collaboration between the Office of Vice President for Research (**OVPR**) and the Office of the Vice President for Information Technology (**OVPI**T)
- Guided by a faculty advisory committee (GACRC-AC)

Why Are We Here?

- To provide computing hardware and network infrastructure in support of high-performance computing (**HPC**) at UGA

Where Are We?

- <http://gacrc.uga.edu> (Web) <http://wiki.gacrc.uga.edu> (Wiki)
- <http://gacrc.uga.edu/help/> (Web Help)
- https://wiki.gacrc.uga.edu/wiki/Getting_Help (Wiki Help)

GACRC Users September 2015

Colleges & Schools	Depts	PIs	Users
Franklin College of Arts and Sciences	14	117	661
College of Agricultural & Environmental Sciences	9	29	128
College of Engineering	1	12	33
School of Forestry & Natural Resources	1	12	31
College of Veterinary Medicine	4	12	29
College of Public Health	2	8	28
College of Education	2	5	20
Terry College of Business	3	5	10
School of Ecology	1	8	22
School of Public and International Affairs	1	3	3
College of Pharmacy	2	3	5
	40	214	970
Centers & Institutes	9	19	59
TOTALS:	49	233	1029

GACRC Users September 2015

Centers & Institutes	PIs	Users
Center for Applied Isotope Study	1	1
Center for Computational Quantum Chemistry	3	10
Complex Carbohydrate Research Center	6	28
Georgia Genomics Facility	1	5
Institute of Bioinformatics	1	1
Savannah River Ecology Laboratory	3	9
Skidaway Institute of Oceanography	2	2
Center for Family Research	1	1
Carl Vinson Institute of Government	1	2
	19	59

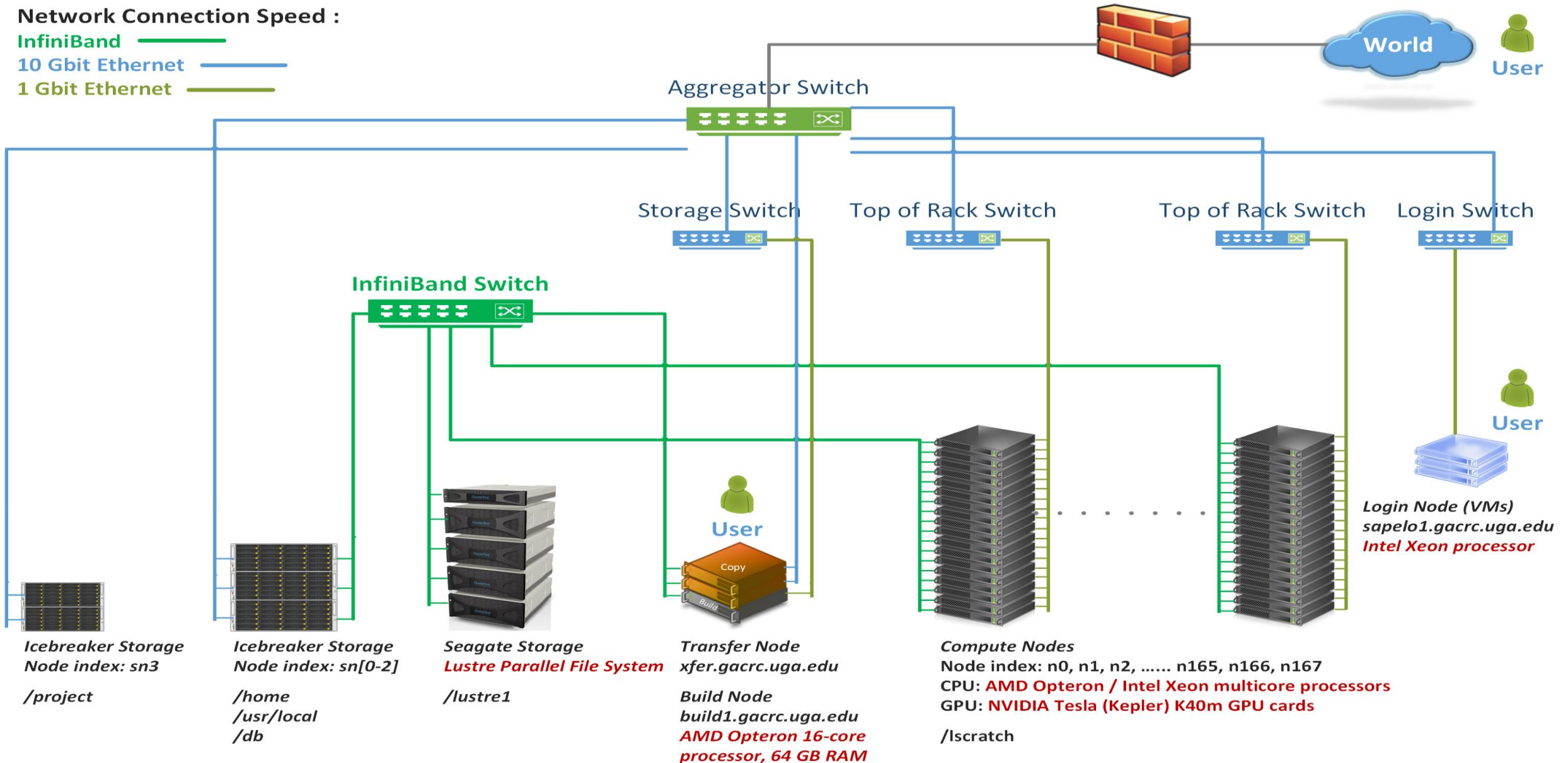
What is the new cluster (Sapelo) at GACRC?

- Cluster Structural Diagram
- Cluster Overview
- Computing Resources
- Storage Environment

The New GACRC Linux HPC Cluster Structural Diagram

Network Connection Speed :

- InfiniBand** —
- 10 Gbit Ethernet** —
- 1 Gbit Ethernet** —



Icebreaker Storage
Node index: sn3
/project

Icebreaker Storage
Node index: sn[0-2]
/home
/usr/local
/db

Seagate Storage
Lustre Parallel File System
/lustre1

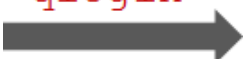
Transfer Node
xfer.gacrc.uga.edu
Build Node
build1.gacrc.uga.edu
AMD Opteron 16-core processor, 64 GB RAM

Compute Nodes
Node index: n0, n1, n2, n165, n166, n167
CPU: AMD Opteron / Intel Xeon multicore processors
GPU: NVIDIA Tesla (Kepler) K40m GPU cards
/lscratch

Login Node (VMs)
sapelo1.gacrc.uga.edu
Intel Xeon processor

What is the new cluster – Cluster Overview

Sapelo is a Linux high-performance computing (HPC) cluster:

- OS: 64-bit CentOS Linux 6.5
- You can log on to:
 - Login** (username@sapelo1.gacrc.uga.edu) : login, edit script, submit jobs
 - Transfer** (username@xfer.gacrc.uga.edu) : transfer, compress, package data
 - Build** (username@build1.gacrc.uga.edu) : compile, test
- **Login** ^{qlogin}  **Interactive Node** : run job interactively, edit script, submit jobs
- Internodal Communication: **InfiniBand network**
 compute nodes ↔ compute nodes ↔ storage systems, e.g., /home and /lustre1

What is the new cluster – Cluster Overview

- Batch-queueing System:
 - Jobs can be started (submitted), monitored, and controlled
 - Determine which compute node is the best place to run a job
 - Determine appropriate execution priority for a job to run
- On Sapelo:
 - **Torque** Resource Manager + **Moab** Workload Manager
 - Queueing commands: `qsub`, `qstat`, `qdel`
`showjobs`, `showq`



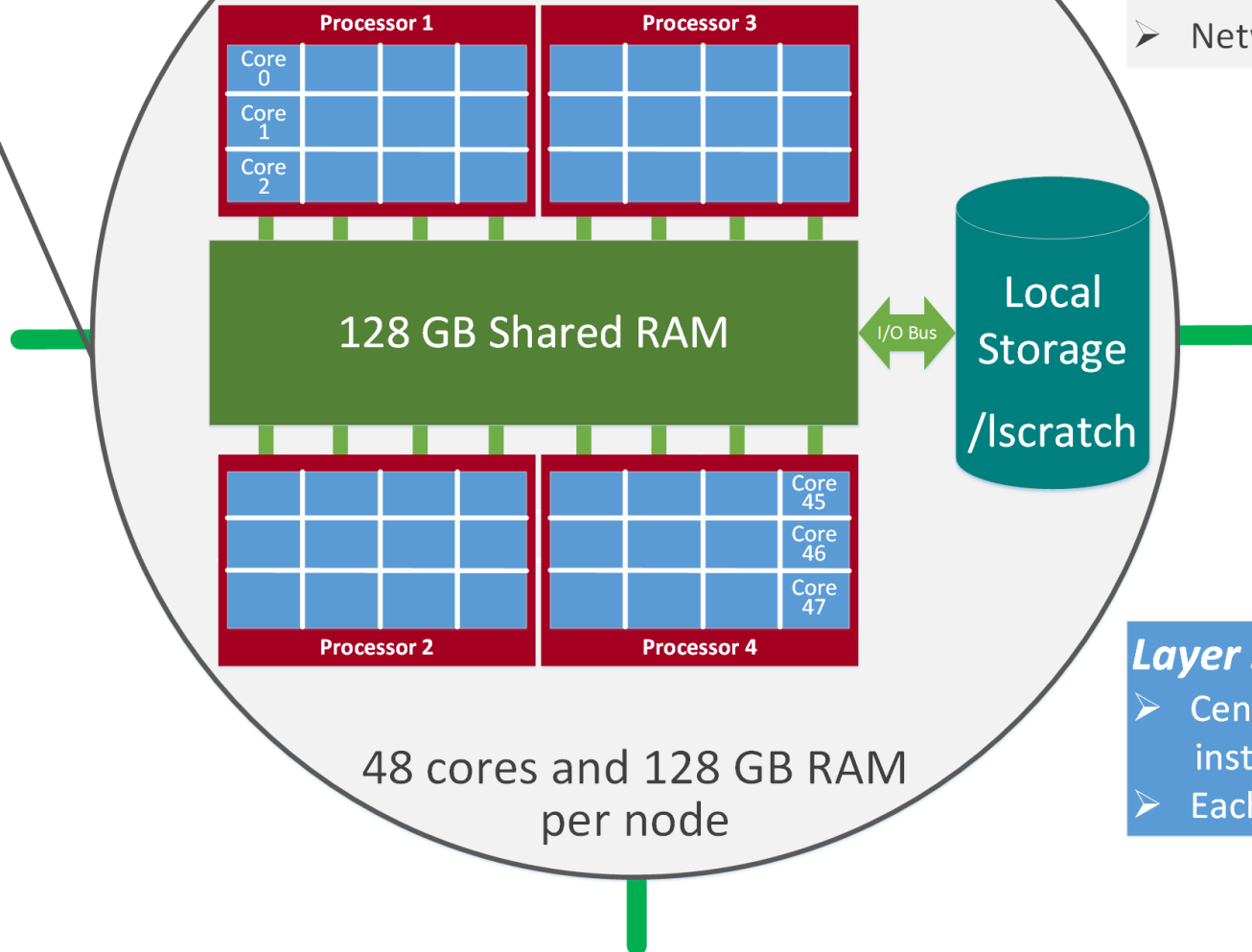
What is the new cluster – Computing Resources

Queue	Node Feature	Total	Processor	Cores /Node	RAM (GB) /Node	Max RAM (GB) /Single-node Job	GPU	GPU Cards /Node	InfiniBand
→ batch	AMD	112	AMD Opteron	48	128	126	N/A	N/A	Yes
		4			256	252			
	HIGHMEM	7	AMD Opteron	48	512 (6)	504	N/A	N/A	Yes
					1024 (1)	997			
	GPU	2	Intel Xeon	16	128	126	NVIDIA K40m	8	Yes
	abcnode (buy-in)	2	AMD Opteron	48	256	252	N/A	N/A	Yes

Home: /home/username: **100GB**

Global scratch: /lustre1/username: **NO quota limit, auto-moved to /project if no modification in 30 days!**

Node 167



Layer 1: Node

- A standalone “computer in a box”
- Multiple processors, e.g. 4, sharing memory
- Local disk storage, network interface, etc.
- Networked into a cluster

Layer 2: Processor

- A single computing component
- Multicore processor, e.g. 12 cores

Layer 3: Core

- Central processing unit (CPU) reading and executing instructions independently
- Each core is assigned to a software thread

What is the new cluster – Storage Environment

4 Filesystems	Role	Quota	Accessible from	Intended Use	Notes
→ /home/username	Home	100GB	sapelo1.gacrc.uga.edu (Login) Interactive nodes (Interactive) xfer.gacrc.uga.edu (Transfer) build1.gacrc.uga.edu (Build) compute nodes (Compute)	Highly static data being used frequently	Snapshots
→ /lustre1/username	Global Scratch	No Limit	Interactive nodes (Interactive) xfer.gacrc.uga.edu (Transfer) compute nodes (Compute)	Temporarily storing large data being used by jobs	Auto-moved to /project if 30 days no modification
/lscratch/username	Local Scratch	250GB	Individual compute node	Jobs with heavy disk I/O	User to clean up
→ /project/abclab	Storage	Variable	xfer.gacrc.uga.edu (Transfer)	Long-term data storage	Group sharing possible

Note: /usr/local/apps : Software installation directory
/db : Bioinformatics database installation directory

What is the new cluster – Storage Environment

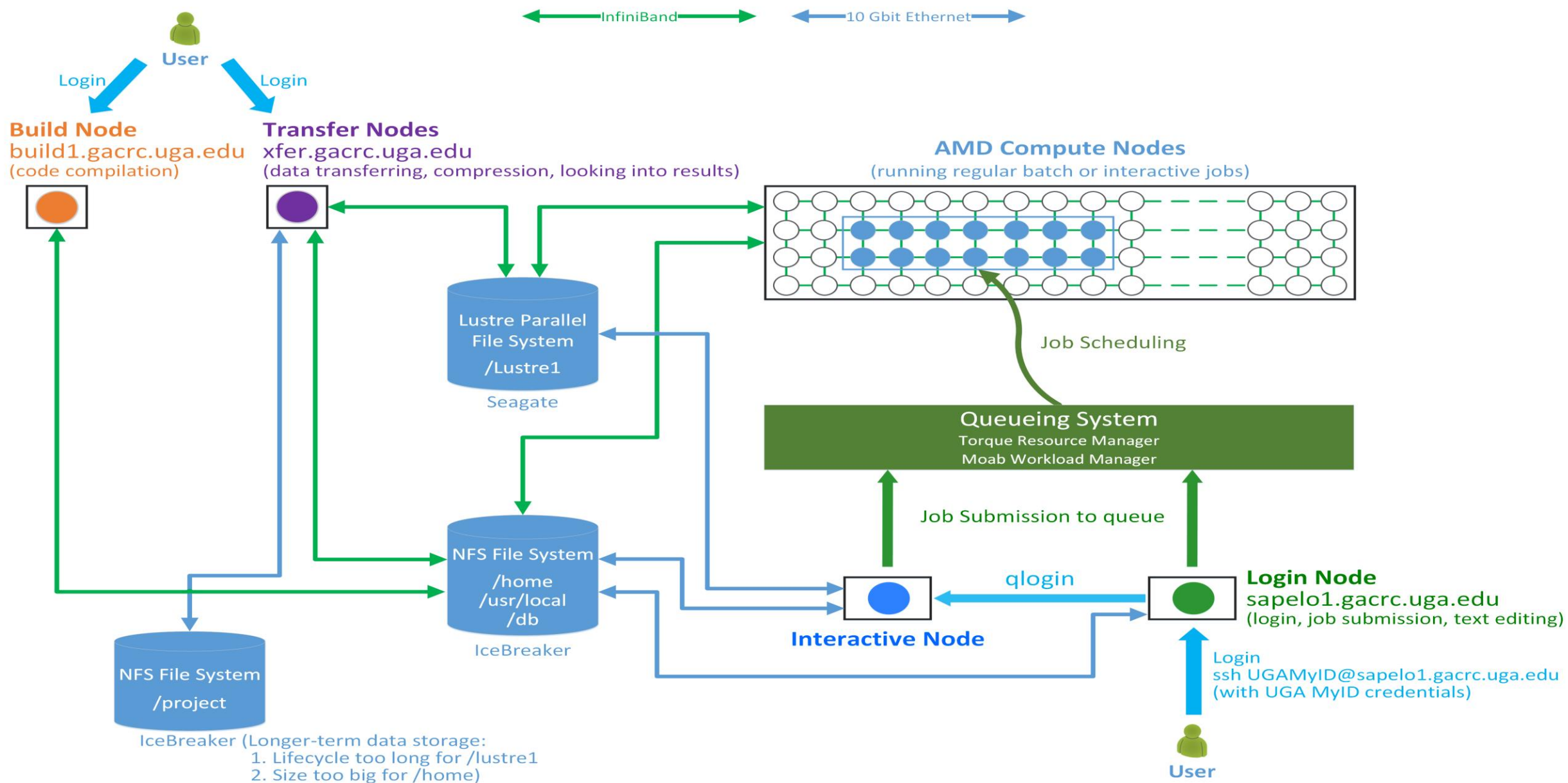
	7 Main Functions	On/From-Node	Related Filesystem
➔	Login Landing	Login or Transfer or Build	/home/username (Home) (Always!)
		Login	/home/username (Home)
➔	Batch Job Submitting	Interactive	/lustre1/username (Scratch) (Suggested!) /home/username (Home)
	Interactive Job Running	Interactive	/lustre1/username (Scratch) /home/username (Home)
➔	Data Transferring, Archiving, and Compressing	Transfer	/lustre1/username (Scratch) /home/username (Home)
	Job Data Temporarily Storing	Compute	/lscratch/username (Local Scratch) /lustre1/username (Scratch)
➔	Long-term Data Storing	Transfer or Copy	/project/abclab
	Code Compilation	Build	/home/username (Home)

How does Sapelo operate?

Next Page



The New GACRC Linux HPC Cluster Operational Diagram



Workflow 1 – Home as Job Working Space

1. Linux/Mac user:

`ssh userID@sapel01.gacrc.uga.edu`



Windows user:



Login



2. `mkdir ./workDir`

3. `cd ./workDir`

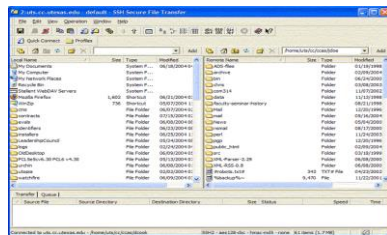


4. Linux/Mac user:

`scp input userID@xfer.gacrc.uga.edu:~/workDir`



Windows user:



5. `nano ./sub.sh`

```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testBlast
#PBS -l nodes=1:ppn=1:AMD
#PBS -l mem=20gb
#PBS -l walltime=48:00:00
cd $PBS_O_WORKDIR
module load ncbiblast+/2.2.29
time blastn [options] > outputfile
```

6.

```
$ qsub sub.sh
```

Useful PBS headers:

`#PBS mem=200gb` : use 256GB AMD nodes)
`ppn=24` : request 24 cores for 24 threads

Note: inputDate could be files or data folder (`scp -r`)

Workflow 1 – Home as Job Working Space

1. Log on to Sapelo **Login** node: `ssh userID@sapelol.gacrc.uga.edu`
2. Create a working subdirectory in home: `mkdir ./workDir`
3. Change directory to `workDir`: `cd ./workDir`
4. Transfer data to `workDir` using `scp` or **SSH Client File Transfer** (with `tar` or `gzip`)
5. Make a Sapelo job submission script: `nano ./sub.sh`
6. Submit job: `qsub ./sub.sh`

Useful PBS headers: `#PBS -l mem=200gb` : use 256GB high-RAM AMD nodes

`#PBS -l nodes=1:ppn=24:AMD` : request 24 cores for 24 threads, max **48!**

Workflow 2 – Global Scratch as Job Working Space

1. Linux/Mac user:

`ssh userID@sapel01.gacrc.uga.edu`



Windows user:



Login



Interactive



2. `qlogin`

3. `cd /lustre1/userID`

4. `mkdir ./workDir`

5. `cd ./workDir`

7. `nano ./sub.sh`



lustre1

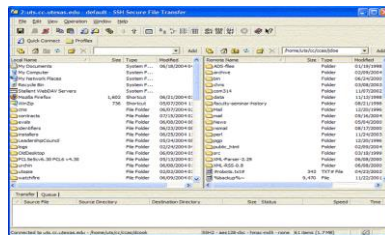
```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testBlast
#PBS -l nodes=1:ppn=1:AMD
#PBS -l mem=200gb
#PBS -l walltime=48:00:00
cd $PBS_O_WORKDIR
module load ncbiblast+/2.2.29
blastn [options] > outputfile
```

6. Linux/Mac user:

`scp input userID@xfer.gacrc.uga.edu:/lustre1/userID/workDir`



Windows user:



```
8.
$ qsub sub.sh
```

Useful PBS headers:

`#PBS mem=200gb : use 256GB AMD nodes)`
`ppn=24 : request 24 cores for 24 threads`

Note: inputDate could be files or data folder (`scp -r`)

Workflow 2 – Global Scratch as Job Working Space

1. Log on to Sapelo **Login** node: `ssh userID@sapelol1.gacrc.uga.edu`
2. From Sapelo **Login** node, transfer to **Interactive** node by issuing the command: `qlogin`
3. From **Interactive** node: Change directory to global scratch: `cd /lustre1/userID`
4. Create a working subdirectory on global scratch: `mkdir ./workDir`
5. Change directory to `workDir`: `cd ./workDir`
6. Transfer data to `workDir` using `scp` or **SSH Client File Transfer** (with `tar` or `gzip`)
7. Make a Sapelo job submission script: `nano ./sub.sh`
8. Submit job: `qsub ./sub.sh`

Useful PBS headers: `#PBS -l mem=200gb` : use 256GB high-RAM AMD nodes

`#PBS -l nodes=1:ppn=24:AMD` : request 24 cores for 24 threads, max **48!**

How to work with Sapelo?

Before we start:

- To get zcluster to be your best HPC buddy

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

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

How to work with Sapelo?

To submit a ticket to us?

➤ **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

Note:

It's **USER's** responsibility to make sure the **correctness of datasets** being used by jobs!



How to work with Sapelo?



- You are not alone on cluster... Each user is sharing finite computing resources, e.g., CPU cycles, RAM, disk storage, network bandwidth, with other researchers:

What you do may affect others on the cluster!

- Do NOT run jobs on login node → use the queues or the interactive nodes
- Do NOT use login node to move data into/out of cluster → use Transfer xfer.gacrc.uga.edu
- NO multi-threaded job running with only 1 core requested → threads # = cores # requested
- NO large memory job running on regular nodes → HIGHMEM node on batch queue
- NO long job running on interactive node → 12 hours
- NO small memory job running on large memory nodes → Saving memory for others

How to work with Sapelo?

- Start with the Cluster
- Connect and Login
- Transfer Files Using Transfer Node
- Software Packages
- Run Interactive Jobs
- Run Jobs
 - ✓ How to submit a job
 - ✓ Job submission scripts for *serial*, *threaded*, and *MPI* batch jobs
 - ✓ How to check job status, and cancel a job
 - ✓ How to check memory usage of a job

How to work with Sapelo – Start with the Cluster

- Sapelo User Account: UGAMyID@sapelo1.gacrc.uga.edu

A **valid official UGA MyID** is a MUST to create a user account!



- To get a user account, 4 steps:

1. New user training (<http://gacrc.uga.edu/help/training/>)
2. Tell us your **Name**, **UGA MyID**, **Lab name** and **PI's name**, via GACRC Support (https://wiki.gacrc.uga.edu/wiki/Getting_Help)
3. **Invitation letter** with instructions to start account initialization
4. **Welcome letter** with whole package of information about your Sapelo user account

Connect and Login

- On Linux/Mac: use Terminal utility and `ssh` to your account:

```
ssh zhuofei@sapel01.gacrc.uga.edu
```

or

```
ssh -X zhuofei@sapel01.gacrc.uga.edu
```

⁽¹⁾ `-X` is for *X windows application* running on the cluster with its UGI to be forwarded to local

⁽²⁾ On Windows, use a *SSH client* to open the connection (next page))

- Logging in: You will be prompted for your **UGA MyID password**:

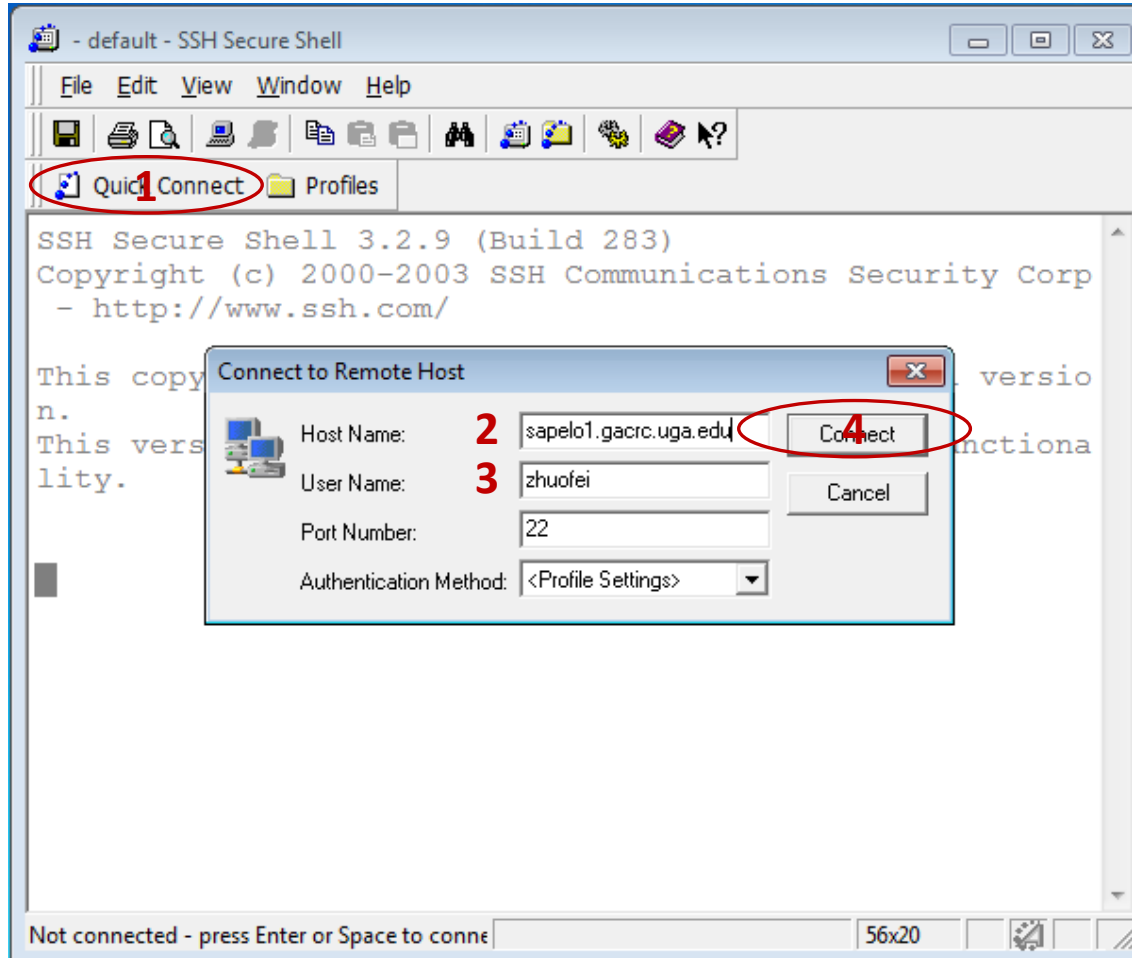
```
zhuofei@sapel01.gacrc.uga.edu's password: █
```

⁽³⁾ On Linux/Mac, when you type in the password, the prompt blinks and does not move)

- Logging out: `exit` to leave the system:

```
[zhuofei@75-104 ~]$ exit
```

Connect and Login



1. To download:

http://eits.uga.edu/hardware_and_software/software/

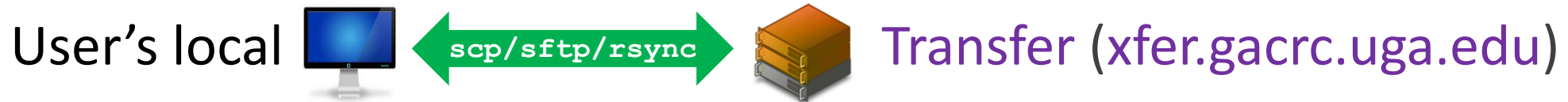
with your UGA MyID and password

2. After connection is built, working environment is Linux, same as Linux/Mac users'

Transfer Files Using Transfer Node xfer.gacrc.uga.edu

- ✓ `ssh username@xfer.gacrc.uga.edu` with your **UGA MyID password**
- ✓ Landing directory: `/home/username` (Sapelo home)
- ✓ Move data into/out of Sapelo (`scp`, `sftp`, `rsync`, **SSH Secure Shell File Transfer**, **FileZilla**)
- ✓ Compress or package data on Sapelo (`tar`, `gzip`)
- ✓ Transfer data between Sapelo and zcluster (`cp`, `mv`)
- ✓ Filesystems you can access:
 - `/home/username/` : Sapelo home (landing spot)
 - `/lustre1/username/` : Sapelo global scratch
 - `/panfs/pstor.storage/home/abclab/username/` : zcluster home
 - `/escratch4/username/` : zcluster scratch
 - `/project/abclab/` : long-term active data storage
- ✓ Most file systems on Transfer are *auto-mounted* upon *the first time full-path access*, e.g.,
`cd /project/abclab/`

Transfer Files Using Transfer Node xfer.gacrc.uga.edu



- On Linux, Mac or cygwin on Windows : `scp (-r) [Source] [Target]`

E.g. 1: working on local machine, from Local → Sapelo global scratch

```
scp ./file zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/work_Jul_1/
```

```
scp -r ./folder/ zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/work_Jul_1/
```

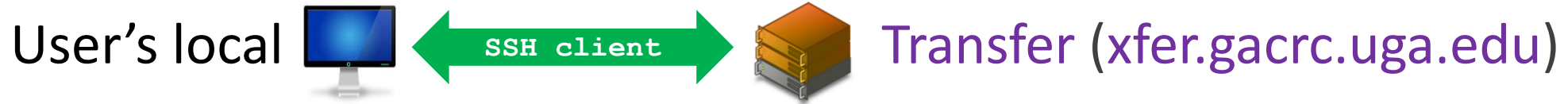
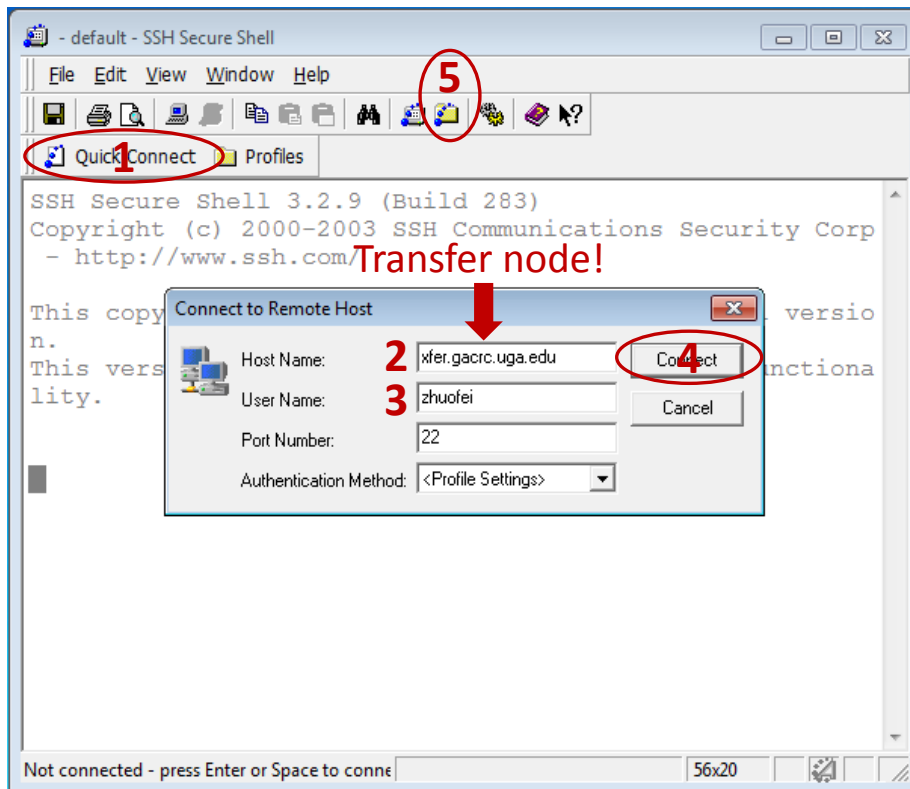
E.g. 2: working on local machine, from Sapelo global scratch → Local

```
scp zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/work_Jul_1/file ./
```

```
scp -r zhuofei@xfer.gacrc.uga.edu:/lustre1/zhuofei/work_Jul_1/folder/ ./
```

- On Window: **SSH Secure Shell File Transfer**, **FileZilla**, **WinSCP** (next page)

Transfer Files Using Transfer Node xfer.gacrc.uga.edu

SSH Secure Shell 3.2.9 (Build 283)
Copyright (c) 2000-2003 SSH Communications Security Corp
- <http://www.ssh.com>

Transfer node!

Connect to Remote Host

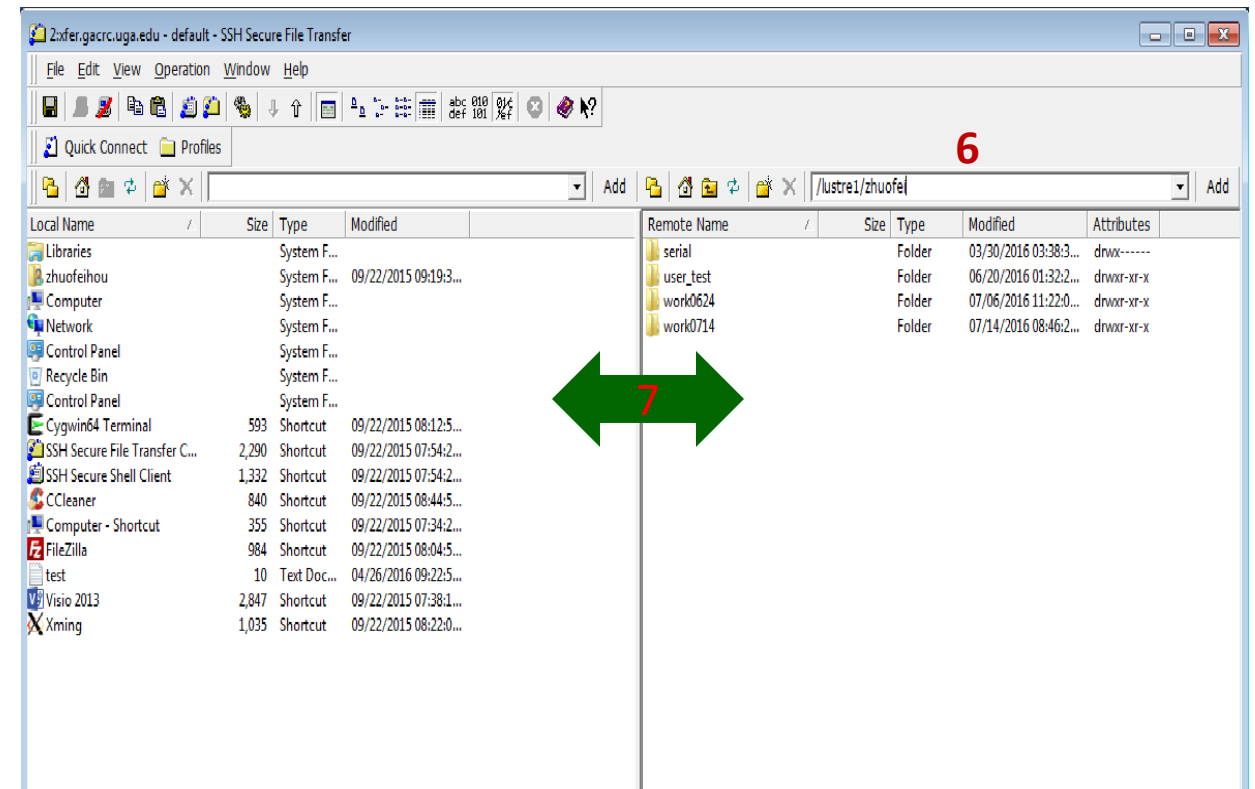
Host Name: 2 xfer.gacrc.uga.edu **4** Connect

User Name: 3 zhuofei Cancel

Port Number: 22

Authentication Method: <Profile Settings>

Not connected - press Enter or Space to connect 56x20



2xfer.gacrc.uga.edu - default - SSH Secure File Transfer

Quick Connect Profiles 6

Local Name	Size	Type	Modified	Remote Name	Size	Type	Modified	Attributes
Libraries		System F...		serial		Folder	03/30/2016 03:38:3...	drwx-----
zhuofei		System F...	09/22/2015 09:19:3...	user_test		Folder	06/20/2016 01:32:2...	drwxr-xr-x
Computer		System F...		work0624		Folder	07/06/2016 11:22:0...	drwxr-xr-x
Network		System F...		work0714		Folder	07/14/2016 08:46:2...	drwxr-xr-x
Control Panel		System F...						
Recycle Bin		System F...						
Control Panel		System F...						
Cygwin64 Terminal	593	Shortcut	09/22/2015 08:12:5...					
SSH Secure File Transfer C...	2,290	Shortcut	09/22/2015 07:54:2...					
SSH Secure Shell Client	1,332	Shortcut	09/22/2015 07:54:2...					
CCleaner	840	Shortcut	09/22/2015 08:44:5...					
Computer - Shortcut	355	Shortcut	09/22/2015 07:34:2...					
FileZilla	984	Shortcut	09/22/2015 08:04:5...					
test	10	Text Doc...	04/26/2016 09:22:5...					
Visio 2013	2,847	Shortcut	09/22/2015 07:38:1...					
Xming	1,035	Shortcut	09/22/2015 08:22:0...					

How to work with Sapelo – Software Packages

- The cluster uses **environment modules** to define the various paths for software packages
- Current number of modules installed is **~300** and expanding daily!
- **module avail** to list all available modules (centralized installation):

```
[zhuofei@75-104 ~]$ module avail
----- /usr/local/modulefiles -----
Core/StdEnv                exabayes/1.4.1                java/jdk1.8.0_20              openmpi/1.6.5/gcc/4.4.7      rsem/latest
Data/cache/moduleT.new    examl/3.0.11                  java/latest                   openmpi/1.6.5/pgi/14.9      rsem/1.2.20 (D)
Data/cache/moduleT (D)   expat/latest                  lammps/5Sep14                openmpi/1.8.3/gcc/4.4.7      samtools/latest (D)
Data/system.txt          expat/2.0.1 (D)             lammps/16Aug13              openmpi/1.8.3/gcc/4.7.4      samtools/0.1.19
R/3.1.2                  fastqc/latest                 moab/7.2.10                 openmpi/1.8.3/gcc/4.8.0 (D)  samtools/1.1
bedops/latest            fastqc/0.11.3 (D)          moab/8.1.1 (D)              openmpi/1.8.3/intel/14.0    samtools/1.2 (D)
bedops/2.4.14 (D)       gcc/4.7.4                    moabs/1.3.2                 openmpi/1.8.3/intel/15.0.2 (D)  scripture/latest
boost/1.47.0/gcc447      gcc/4.8.0 (D)                mvapich2/2.0.0/gcc/4.4.7    openmpi/1.8.3/pgi/14.9      scripture/03202015 (D)
boost/1.57.0/gcc447      gmap-gsnap/latest            mvapich2/2.0.0/pgi/14.9    orca/3.0.3                  sparsehash/latest
boost/1.57.0_thread/gcc447  gmap-gsnap/2014-12-24 (D)  ncbiblast+/2.2.29          perl/latest                  sparsehash/2.0.2 (D)
bowtie/latest           gnuplot/5.0.0                netcdf/3.6.3/gcc/4.4.7     perl/5.20.1                 tophat/latest
bowtie/1.1.1 (D)        gsl/1.16/gcc/4.4.7           netcdf/3.6.3/intel/14.0    perl/5.20.2 (D)            tophat/2.0.13 (D)
bowtie2/latest          hdf5/1.8.14/gcc/4.4.7        netcdf/3.6.3/intel/15.0.2 (D)  pgi/14.9                    trinity/latest
bowtie2/2.2.4 (D)       hdf5/1.8.14/intel/15.0.2    netcdf/4.1.3/gcc/4.4.7     pgi/14.10 (D)              trinity/r20140717
cuda/5.0.35/gcc/4.4.7    hdf5/1.8.14/pgi/14.9        netcdf/4.1.3/intel/15.0.2  python/2.7.8-ucs4           trinity/2.0.6 (D)
cuda/6.5.14/gcc/4.4.7   imb/3.2                      netcdf/4.1.3/pgi/14.10     python/2.7.8                zlib/gcc447/1.2.8
cufflinks/latest       intel/14.0                   netcdf/4.3.2/gcc/4.4.7     python/3.4.3 (D)
cufflinks/2.2.1 (D)    intel/15.0.2 (D)            netcdf/4.3.2/pgi/14.9     raxml/8.1.20
```

How to work with Sapelo – Software Packages

- `module list` to list which modules currently loaded:

```
[zhuofei@75-104 ~]$ module list
Currently Loaded Modules:
  1) StdEnv   2) moab/7.2.10
```

- `module load` to load the needed modules:

```
[zhuofei@75-104 ~]$ module load ncbiblast+/2.2.29
[zhuofei@75-104 ~]$ module load python/2.7.8
[zhuofei@75-104 ~]$ module load R/3.1.2
[zhuofei@75-104 ~]$ module list
Currently Loaded Modules:
  1) StdEnv   2) moab/7.2.10   3) ncbiblast+/2.2.29   4) python/2.7.8   5) R/3.1.2
```

- `module unload` to remove the specific module:

```
[zhuofei@75-104 ~]$ module unload R/3.1.2
[zhuofei@75-104 ~]$ module list
Currently Loaded Modules:
  1) StdEnv   2) moab/7.2.10   3) ncbiblast+/2.2.29   4) python/2.7.8
```

Run Interactive Jobs

- To run an interactive job, using `qlogin` command from **Login** node:

```
[zhuofei@75-104 ~]$ qlogin
qsub: waiting for job 1058157.pbs.scm to start
qsub: job 1058157.pbs.scm ready
[zhuofei@n14 ~] ← Now I am on n14, which is an interactive node
[zhuofei@n14 ~]$ module load R/3.2.3
[zhuofei@n14 ~]$ R

R version 3.2.3 (2015-12-10) -- "Wooden Christmas-Tree"
Copyright (C) 2015 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

...
[Previously saved workspace restored]

>
```

- When you are done, remember to `exit` the session

How to work with Sapelo – Run Jobs

- Components you need to run a job:
 - **Software** already loaded. If not, used `module load`
 - **Job submission script** to run the software, and specify computing resources:
 - ✓ Number of nodes and cores
 - ✓ Amount of memory
 - ✓ Type of nodes
 - ✓ Maximum wallclock time, etc.
- Common commands you need:
 - `qsub, qdel`
 - `qstat -f, showjobs, showq`

How to work with Sapelo – Run Jobs

- How to submit a job? **Easy!**

```
[zhuofei@75-104 MPIs]$ qsub sub.sh
```

qsub is to
submit a job

sub.sh is your **job submission script**
specifying:

- ✓ Number of nodes and cores
- ✓ Amount of memory
- ✓ Type of nodes
- ✓ Maximum wallclock time, etc.

- How to make a job submission script? **Next Page!**

How to work with Sapelo – Run Jobs

- Example 1: **Serial job script** *sub.sh* running NCBI Blast +

<code>#PBS -S /bin/bash</code>	→ Linux shell (bash)
<code>#PBS -q batch</code>	→ Queue name (batch)
<code>#PBS -N testBlast</code>	→ Name of the job (testBlast)
<code>#PBS -l nodes=1:ppn=1:AMD</code>	→ Number of nodes (1), number of cores/node (1), node type (AMD)
<code>#PBS -l mem=20gb</code>	→ Maximum amount of physical memory (20 GB) used by the job
<code>#PBS -l walltime=48:00:00</code>	→ Maximum wall clock time (48 hours) for the job, default 6 minutes
 <code>cd \$PBS_O_WORKDIR</code>	 → Use the directory from which the job is submitted as the working directory
 <code>module load ncbiblast+/2.2.29</code>	 → Load the module of ncbiblast+, version 2.2.29
 <code>time blastn [options] > outputfile</code>	 → Run blastn with ‘time’ command to measure the amount of time it takes to run the application

How to work with Sapelo – Run Jobs

- Example 1: **Serial job script** *sub.sh* running NCBI Blast +

```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testBlast
#PBS -l nodes=1:ppn=1:AMD
#PBS -l mem=200gb
#PBS -l walltime=48:00:00

cd $PBS_O_WORKDIR

module load ncbiblast+/2.2.29

time blastn [options] > outputfile
```

→ Job will be dispatched to run on AMD **256GB** node

How to work with Sapelo – Run Jobs

- Example 2: **Threaded job script** *sub.sh* running NCBI Blast+ with **24** threads

```
#PBS -S /bin/bash
```

```
#PBS -q batch
```

```
#PBS -N testBlast
```

```
#PBS -l nodes=1:ppn=24:AMD
```

```
#PBS -l mem=200gb
```

```
#PBS -l walltime=480:00:00
```

```
#PBS -M jSmith@uga.edu
```

```
#PBS -m ae
```

```
#PBS -j oe
```

```
cd $PBS_O_WORKDIR
```

```
module load ncbiblast+/2.2.29
```

```
time blastn -num_threads 24 [options] > outputfile
```

→ Number of nodes (**1**), number of cores/node (**24**), node type (**AMD**)
Number of threads (24) = Number of cores requested (24)

→ Email address to receive a notification for computing resources

→ Send email notification when job aborts (**a**) or terminates (**e**)

→ Standard error file (**testBlast.e1234**) will be merged into standard out file (**testBlast.o1234**)

→ Run blastn with 24 threads (**-num_threads 24**)

How to work with Sapelo – Run Jobs

- Example 3: **MPI job script** *sub.sh* running RAxML with **50** MPI processes

```
#PBS -S /bin/bash
```

```
#PBS -q batch
```

```
#PBS -N testRAxML
```

```
#PBS -l nodes=2:ppn=48:AMD
```

→ Number of nodes (**2**), number of cores/node (**48**), node type (**AMD**)

```
#PBS -l walltime=480:00:00
```

Total cores requested = $2 \times 48 = 96$

```
#PBS -l mem=20gb
```

We suggest, Number of MPI Processes (50) ≤ Number of cores requested (96)

```
#PBS -j oe
```

```
cd $PBS_O_WORKDIR
```

```
module load raxml/8.1.20
```

→ To run raxmlHPC-MPI-AVX, MPI version using OpenMPI 1.8.3/Intel 15.0.2

```
module load intel/15.0.2
```

```
module load openmpi/1.8.3/intel/15.0.2
```



```
mpirun -np 50 raxmlHPC-MPI-AVX [options] > outputfile
```

→ Run raxmlHPC-MPI-AVX with 50 MPI processes (**-np 50**)

```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testRAxML
#PBS -l nodes=2:ppn=27:AMD
#PBS -l walltime=480:00:00
#PBS -l mem=20gb
#PBS -j oe
```

→ ppn number (27) fewer than 48 MUST be a multiplier of 3!

```
cd $PBS_O_WORKDIR
```

```
# Context Sharing
CONTEXTS=$(/usr/local/bin/set_contexts.sh $PBS_NUM_PPN)
if [[ "$?" -eq "0" ]]; then
    export PSM_SHAREDCONTEXTS_MAX=$CONTEXTS
fi
```

} New lines copied from GACRC Wiki

```
module load raxml/8.1.20
module load intel/15.0.2
module load openmpi/1.8.3/intel/15.0.2
```

```
mpirun -np 50 raxmlHPC-MPI-AVX [options] > outputfile → Run raxmlHPC-MPI-AVX with 50 MPI processes (-np 50)
```

How to work with Sapelo – Run Jobs

- How to check job status? **qstat**

```
[jSmith@75-104 MPIs]$ qstat
Job ID          Name           User           Time Use  S Queue
-----
481929.pbs     testJob1       jSmith         900:58:0  C batch
481931.pbs     testJob2       jSmith         04:00:03  R batch
481934.pbs     testJob3       jSmith          0 Q batch

Job status:
R : job is running
C : job completed (or crashed) and is not longer running. Jobs stay in this state for 1h
Q : job is pending, waiting for resources to become available
```

- How to cancel *testJob3* with jobID 481934? **qdel**

```
[zhuofei@75-104 MPIs]$ qdel 481934
[jSmith@75-104 MPIs]$ qstat
Job ID          Name           User           Time Use  S Queue
-----
481929.pbs     testJob1       jSmith         900:58:0  C batch
481931.pbs     testJob2       jSmith         04:00:03  R batch
481934.pbs     testJob3       jSmith          0 C batch
← Stay on list 1 hr
```


How to work with Sapelo – Run Jobs

- How to check computing resources?

Option 1: `qstat -f JobID` for *running jobs* or *finished jobs in 1 hour*

Option 2: `showjobs JobID` for *finished jobs over 1 hour, but ≤ 7 days*

Option 3: Email notification from *finished jobs (completed, canceled, or crashed)*,
if using:

```
#PBS -M jSmith@uga.edu
```

```
#PBS -m ae
```

How to work with it – Run Jobs

- **qstat -f JobID** for *running jobs* or *finished jobs in 1 hour*

```
[zhuofei@75-104 MPIs]$ qstat -f 699847
Job Id: 699847.pbs.scn
  Job_Name = testJob
  Job_Owner = zhuofei@uga-2f0f976.scn
resources_used.cput = 00:11:55
resources_used.energy_used = 0
resources_used.mem = 411572kb
resources_used.vmem = 6548528kb
resources_used.walltime = 07:01:36
job_state = C
queue = batch

.
Error_Path = uga-2f0f976.scn:/home/zhuofei/MPIs/testJob.e699847
exec_host = n165/0-23
Output_Path = uga-2f0f976.scn:/home/zhuofei/MPIs/testJob.o699847

.
Resource_List.mem = 5gb
Resource_List.nodect = 1
Resource_List.nodes = 1:ppn=24:AMD
Resource_List.walltime = 10:00:00

.
Variable_List = PBS_O_QUEUE=batch,PBS_O_HOME=/home/zhuofei, ..... ,
                PBS_O_WORKDIR=/home/zhuofei/MPIs,
```

How to work with it – Run Jobs

- **showjobs JobID** for *finished jobs over 1 hour, but ≤ 7 days*

```
[zhuofei@75-104 MPIs]$ showjobs 699847
Job Id       : 699847.pbs.scn
Job Name     : testJob
Output File  : uga-2f0f976.scn:/home/zhuofei/MPIs/testJob.o699847
Error File   : uga-2f0f976.scn:/home/zhuofei/MPIs/testJob.e699847
Working Directory : /home/zhuofei/MPIs
Home Directory  : /home/zhuofei
Submit Arguments : sub.sh
User Name     : zhuofei
Group Name    : rccstaff
Queue Name    : batch
Wallclock Limit : 10:00:00
Wallclock Duration: 07:01:36
CPUTime      : 00:11:55
Memory Used   : 401.9Mb
Memory Limit  : 5gb
vmem Used    : 6.2Gb
Submit Time   : Wed Nov  4 12:02:22 2015
Start Time    : Wed Nov  4 12:03:41 2015
End Time      : Wed Nov  4 12:04:45 2015
Exit Code     : 0
Master Host   : n165
```

How to work with it – Run Jobs

- Email notification from *finished jobs* (**completed**, **canceled**, or **crashed**)

```

PBS Job Id: 700009.pbs.scm
Job Name:   testJob
Exec host:  n1/4-27
Execution terminated
Exit_status=0
resources_used.cput=00:05:12
resources_used.energy_used=0
resources_used.mem=410984kb
resources_used.vmem=6548516kb
resources_used.walltime=04:00:59
Error_Path: uga-
2f0f976.scm:/home/zhuofei/MPIs/testJob.o700009
Output_Path: uga-
2f0f976.scm:/home/zhuofei/MPIs/testJob.o700009
    
```

```

PBS Job Id: 700097.pbs.scm
Job Name:   testJob
Exec host:  n1/4-27
Execution terminated
Exit_status=271
resources_used.cput=00:11:22
resources_used.energy_used=0
resources_used.mem=412304kb
resources_used.vmem=6548524kb
resources_used.walltime=05:00:41
Error_Path: uga-
2f0f976.scm:/home/zhuofei/MPIs/testJob.o700097
Output_Path: uga-
2f0f976.scm:/home/zhuofei/MPIs/testJob.o700097
    
```

How to work with it – Run Jobs

- How to check queue status?
showq

```
[zhuofei@75-104 MPIs]$ showq
active jobs-----
JOBID                USERNAME           STATE  PROCS   REMAINING          STARTTIME
481914                brant              Running  1      20:46:21   Fri Jun 12 11:32:23
481915                brant              Running  1      20:48:56   Fri Jun 12 11:34:58
481567                becton             Running 288    2:04:15:48 Wed Jun 10 15:01:50
481857                kkim              Running  48     9:18:21:41 Fri Jun 12 09:07:43
481859                kkim              Running  48     9:18:42:21 Fri Jun 12 09:28:23
.
108 active jobs      5141 of 5740 processors in use by local jobs (89.56%)
                    121 of 122 nodes active          (99.18%)
eligible jobs-----
481821                joykai             Idle    48     50:00:00:00 Thu Jun 11 13:41:20
481813                joykai             Idle    48     50:00:00:00 Thu Jun 11 13:41:19
481811                joykai             Idle    48     50:00:00:00 Thu Jun 11 13:41:19
481825                joykai             Idle    48     50:00:00:00 Thu Jun 11 13:41:20
.
50 eligible jobs
blocked jobs-----
JOBID                USERNAME           STATE  PROCS   WCLIMIT          QUEUETIME
0 blocked jobs
Total jobs: 158
```

Thank You!