



Introduction to HPC Using Sapelo at GACRC

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Slides courtesy: Zhuofei Hou



Outline

- GACRC
- Sapelo Cluster at GACRC
- Job Submission Workflow
- Work with Sapelo Cluster
- Guideline and Practical Tips



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 (**OVPIIT**)
- 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)
- https://wiki.gacrc.uga.edu/wiki/Getting_Help (Wiki Help)



Sapelo cluster at GACRC

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

What is a Cluster?

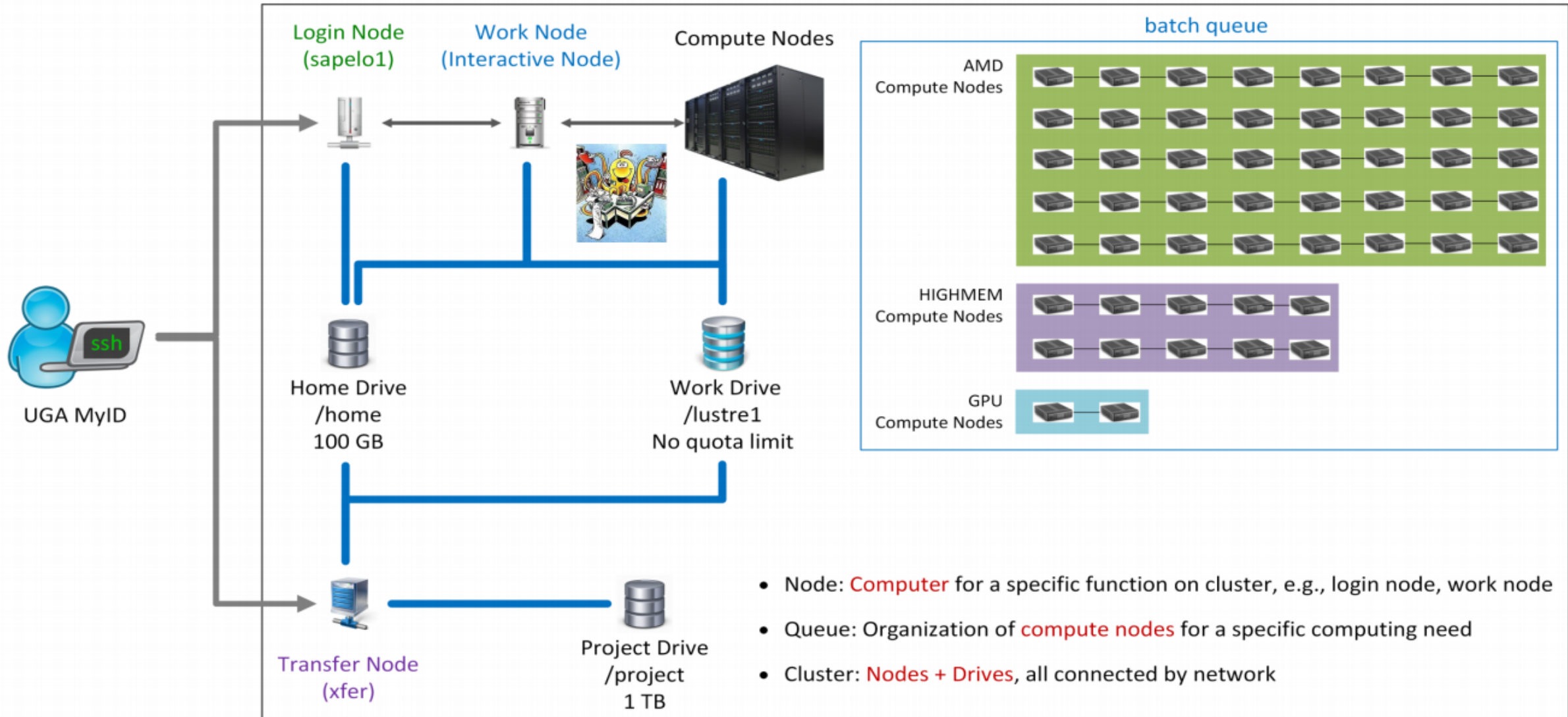
When you work on cluster, **3** roles are working:

- User: to submit a job
- Queueing system: to dispatch a job to run on cluster
- Cluster: to run a job





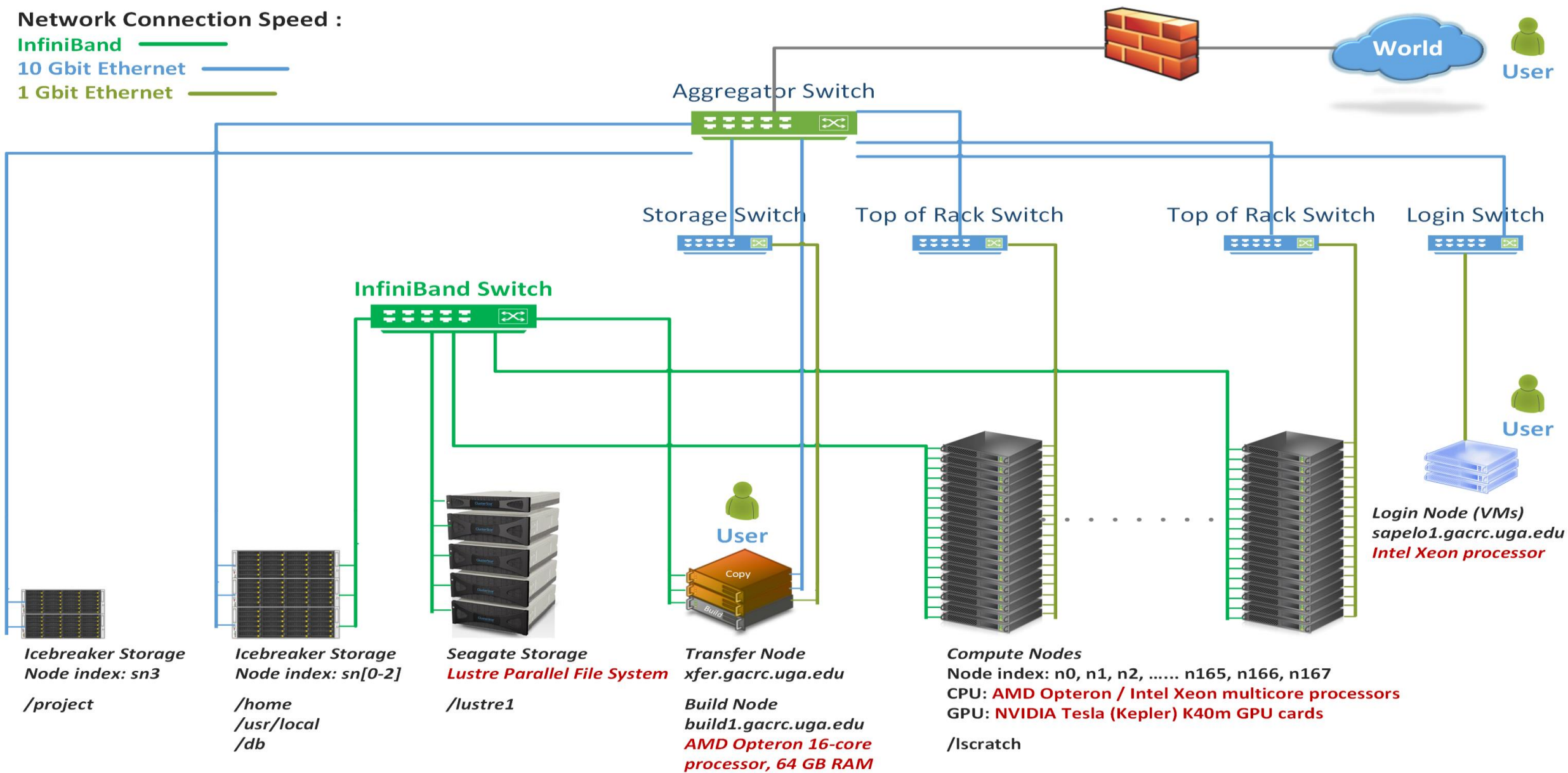
Sapelo cluster Diagram



The New GACRC Linux HPC Cluster Structural Diagram

Network Connection Speed :

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





Sapelo 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

Transfer (username@xfer.gacrc.uga.edu) : transfer, compress, package data

*Build (username@build1.gacrc.uga.edu) : compile, test

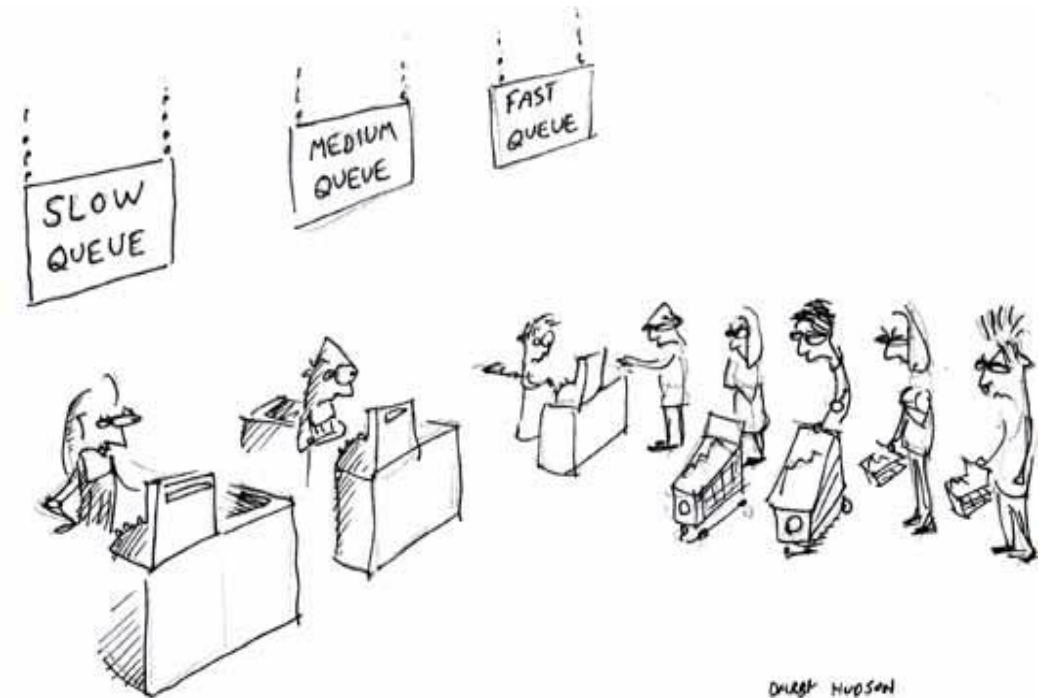
➤ Login  [Interactive Node](#) : run job interactively, edit script, submit jobs

➤ Internodal Communication: **InfiniBand network**

compute nodes ↔ compute nodes ↔ storage systems, e.g., /home and /lustre1

Sapelo 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`





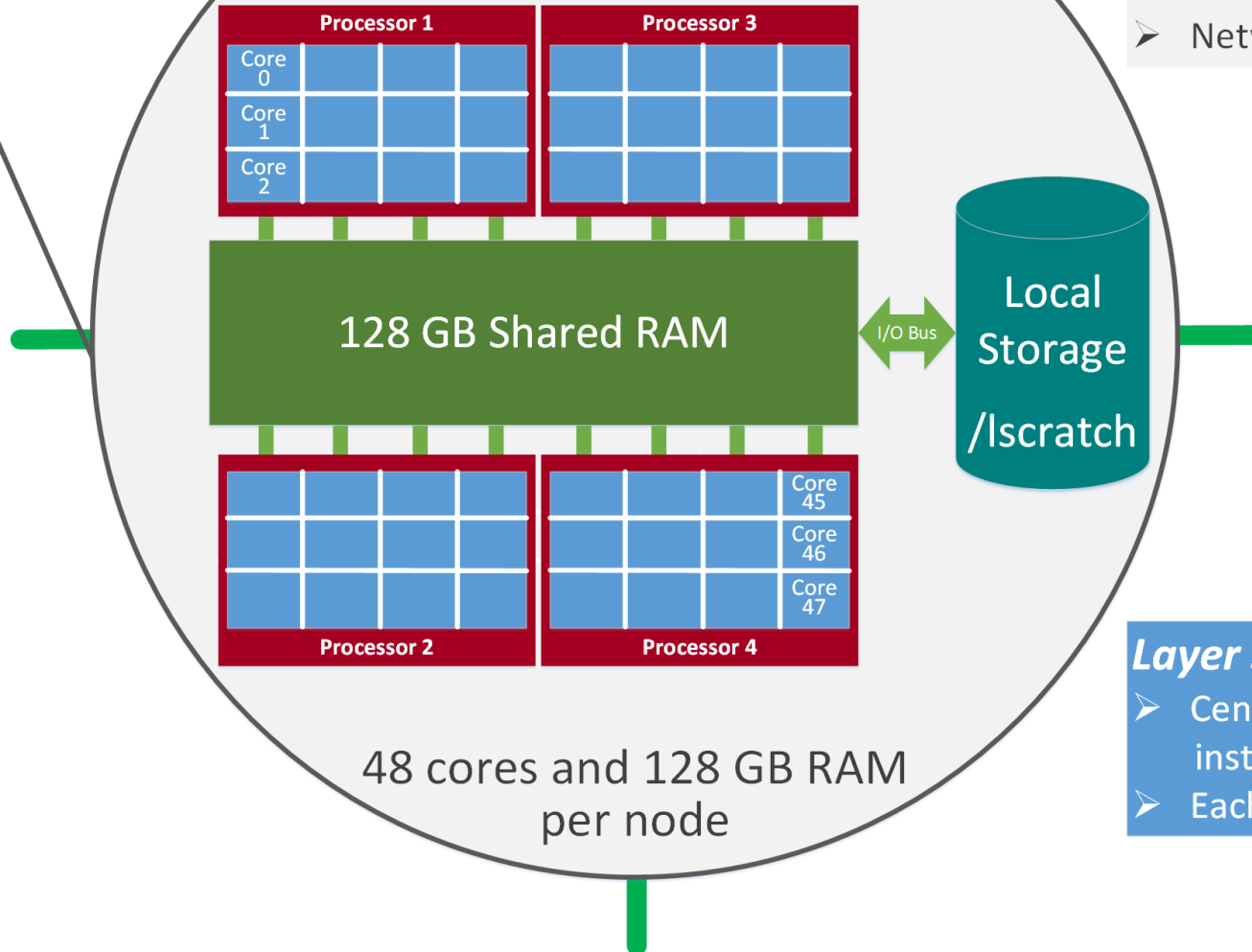
Computing Resources

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	8			512 (4)	504			
					1024 (4)	997			
	GPU	2	Intel Xeon	16	128	126	NVIDIA K40m	8	
	abcnode (buy-in)	variable	variable	variable	variable	variable	variable	variable	

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

Global scratch: /lustre1/username: **NO quota limit, User's responsibility for cleanup!**

Node 167



128 GB Shared RAM

Local Storage
/lscratch

I/O Bus

48 cores and 128 GB RAM
per node

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

Storage Environment

Mainly, there are 3 different storage locations

- **Home directory** → */home/username*
 - With a quota of **~100GB**
 - Any directory on /home has **snapshot** backups
- **Global Scratch directory** → */lustre1/username*
 - “**No quota limit**”
 - **No snapshot backup**
 - User’s responsibility to clean up data
- **Group project Storage directory** → */project/abclab/*
 - Created for a lab, e.g., abclab
 - Temporary data parking for non-current active data



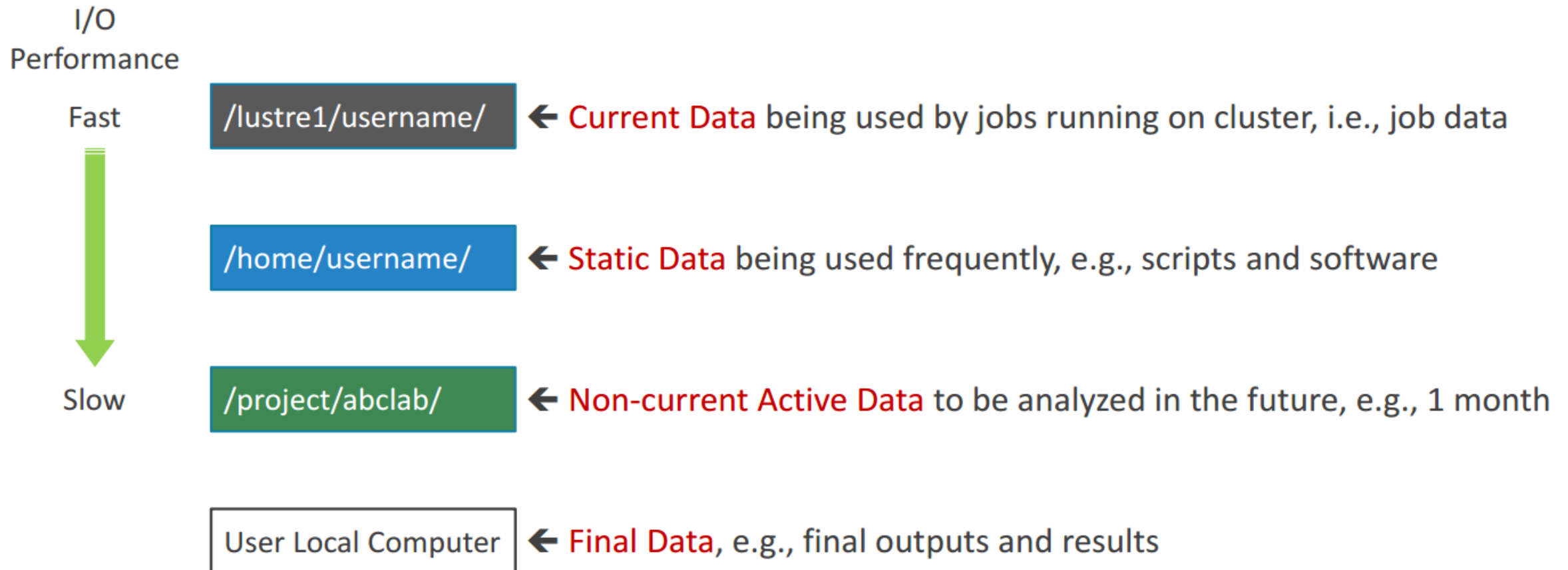
Storage Environment

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	User to clean up
/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

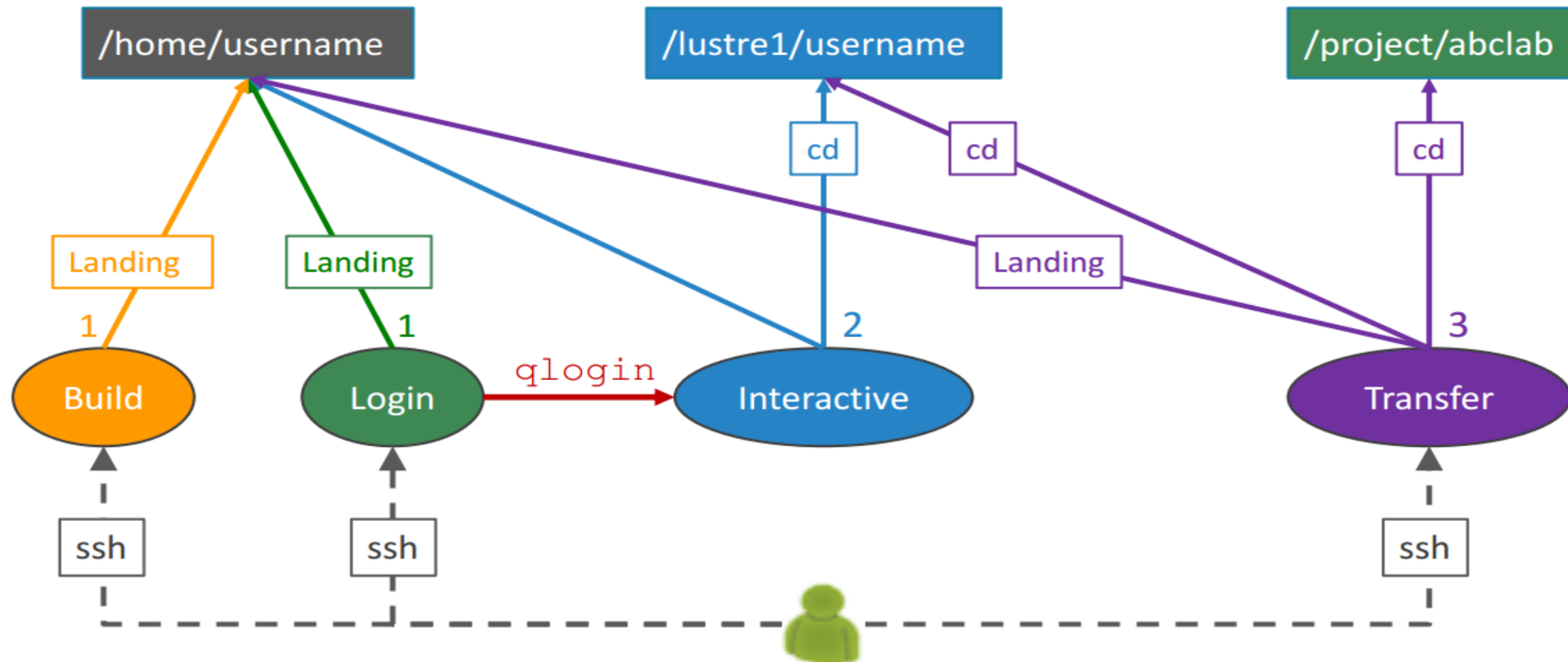
Note: /usr/local/apps : Software installation directory
/db : Bioinformatics database installation directory



Storage Environment – Data Storing Rule



Storage Environment – Accessing Rule 123





Storage Environment

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

Note: * denotes component or policy to be implemented in the future

Job Submission Workflow

Job Working Space is Global Scratch: `/lustre1/username/`

- **Why?**

No quota limit + The I/O fastest filesystem

- **How to access?**

From **Interactive Node**, `cd /lustre1/username/`

- **What need to pay attention?**

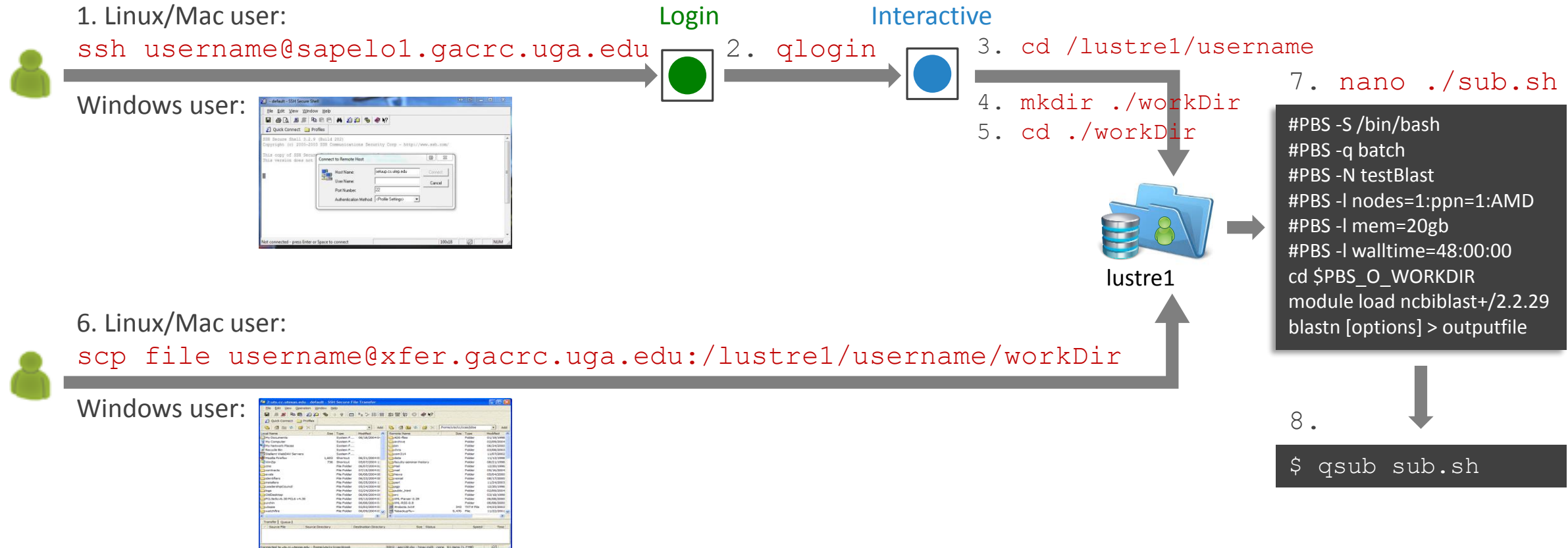
Clean up! Non-current Active Data → `/project/abclab/`

Non-active Data → local storage

} using **Transfer Node**



Job Submission Workflow



Note: `-r` option of `scp` command will recursively copy a directory



Job Submission Workflow

1. Log on to Sapelo **Login** node: `ssh username@sapelo1.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 /lustrel/username`
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 File Transfer** (with `tar` or `gzip`)
7. Make a Sapelo job submission script: `nano ./sub.sh`
8. Submit job: `qsub ./sub.sh`



Working With Sapelo

Before we start:

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

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



Working 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

User Account

- 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:

1. Computing Lab Registration: <http://help.gacrc.uga.edu/labAcct.php> (for PI of a new group)
2. User Account Request: <http://help.gacrc.uga.edu/userAcct.php> (for PI of an existing group)
3. New User Training: <http://gacrc.uga.edu/help/training/>
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 pakala@sapelo1.gacrc.uga.edu
```

or

```
ssh -x pakala@sapelo1.gacrc.uga.edu
```

⁽¹⁾ `-X` is for *X windows application* running on the cluster with its GUI 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**:

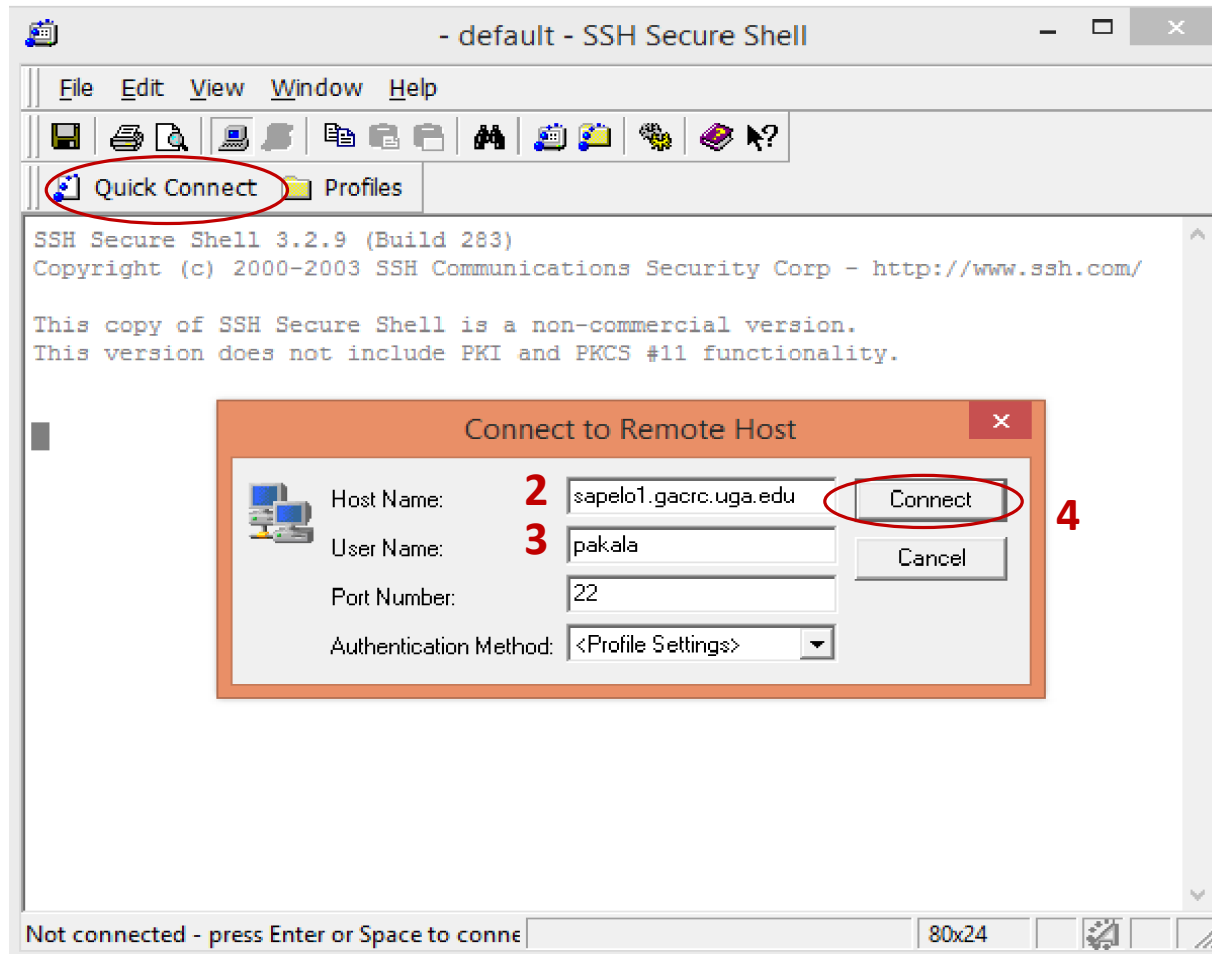
```
pakala@sapelo1.gacrc.uga.edu's password :
```

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

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

```
[pakala@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'

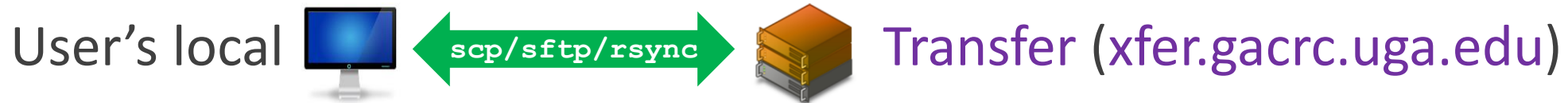


Transfer Files Using Transfer Node xfer.gacrc.uga.edu

- ✓ `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 [Source] [Target]`

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

```
scp ./file pakala@xfer.gacrc.uga.edu:/lustre1/pakala/suchi_Sept_14/
```

```
scp -r ./folder/ pakala@xfer.gacrc.uga.edu:/lustre1/pakala/suchi_Sept_14/
```

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

```
scp pakala@xfer.gacrc.uga.edu:/lustre1/pakala/suchi_Sept_14/file ./
```

```
scp -r pakala@xfer.gacrc.uga.edu:/lustre1/pakala/suchi_Sept_14/folder/ ./
```

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

SSH Secure Client: Connecting to Transfer

The screenshot shows the SSH Secure File Transfer application window. The 'Quick Connect' button is circled in red and labeled with a red '1'. A 'Connect to Remote Host' dialog box is open, with the 'Host Name' field containing 'xfer.gacrc.uga.edu' (labeled with a red '2'), the 'User Name' field containing 'pakala' (labeled with a red '3'), and the 'Connect' button circled in red (labeled with a red '4'). The dialog box also shows 'Port Number' as 22 and 'Authentication Method' as '<Profile Settings>'. The background window shows a file list with columns for Local Name, Size, Type, Modified, Remote Name, Size, Type, Modified, and Attributes. The status bar at the bottom indicates 'Not connected - press Enter or Space to connect'.

Local Name	Size	Type	Modified	Remote Name	Size	Type	Modified	Attributes
OneDrive		System F...	07/05/2016 02:19:3...					
Homegroup		System F...						
suchitra pakala		System F...	05/22/2016 03:37:5...					
My Computer		System F...						
Libraries		System F...						
Network		System F...						
Control Panel		System F...						
Recycle Bin		System F...						
Control Panel		System F...						
Foxit Reader	1,382	Shortcut	11/19/2015 04:57:1...					
Google Chrome	2,214	Shortcut	06/20/2016 10:12:1...					
Lenovo Solution Center	2,018	Shortcut	02/08/2016 11:15:0...					
Skype	2,713	Shortcut	03/08/2016 02:12:0...					
SSH Secure File Transfer C...	2,321	Shortcut	11/11/2015 10:17:3...					
SSH Secure Shell Client	1,363	Shortcut	11/11/2015 10:17:3...					

Source File	Source Directory	Destination Directory	Size	Status	Speed	Time
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SSH Secure Client: Connecting to Transfer Node

The screenshot shows the SSH Secure File Transfer client window titled "xfer.gacrc.uga.edu - default - SSH Secure File Transfer". The interface includes a menu bar (File, Edit, View, Operation, Window, Help), a toolbar, and a main pane divided into "Local Name" and "Remote Name" sections. A red dialog box titled "Enter Password" is overlaid on the main pane, with a red circle around the "Password:" label and a red number "5" to its left. The dialog box contains a text input field with asterisks, "OK", and "Cancel" buttons. The status bar at the bottom indicates "Connecting to xfer.gacrc.uga.edu...".

Local Name	Size	Type	Modified	Remote Name	Size	Type	Modified	Attributes
OneDrive		System F...	07/05/2016 02:19:3...					
Homegroup		System F...						
suchitra pakala		System F...	05/22/2016 03:37:5...					
My Computer		System F...						
Libraries		System F...						
Network		System F...						
Control Panel		System F...						
Recycle Bin		System F...						
Control Panel		System F...						
Foxit Reader	1,382	Shortcut	11/19/2015 04:57:1...					
Google Chrome	2,214	Shortcut	06/20/2016 10:12:1...					
Lenovo Solution Center	2,018	Shortcut	02/08/2016 11:15:0...					
Skype	2,713	Shortcut	03/08/2016 02:12:0...					

Transfer	Queue					
Source File	Source Directory	Destination Directory	Size	Status	Speed	Time

SSH Secure : Connected to Home

The screenshot shows the SSH Secure File Transfer application window. The title bar reads "xfer.gacrc.uga.edu - default - SSH Secure File Transfer". The interface includes a menu bar (File, Edit, View, Operation, Window, Help), a toolbar, and a "Quick Connect" section. The address bar shows the path "home/pakala", with a red arrow pointing to it and the text "Home Directory" above. The main area is divided into two panes: "Local Name" and "Remote Name".

Local Name	Size	Type	Modified	Remote Name	Size	Type	Modified	Attributes
OneDrive		System F...	09/13/2016 04:49:0...	AF293		Folder	09/14/2016 02:06:4...	drwxr-xr-x
Homegroup		System F...		fastqc		Folder	09/12/2016 01:35:3...	drwxr-xr-x
suchitra pakala		System F...	05/22/2016 03:37:5...	for_suman		Folder	03/02/2016 08:15:1...	drwxr-xr-x
My Computer		System F...		RNA_SEQ		Folder	09/13/2016 03:07:5...	drwxr-xr-x
Libraries		System F...						
Network		System F...						
Control Panel		System F...						
Recycle Bin		System F...						
Control Panel		System F...						
Foxit Reader	1,382	Shortcut	11/19/2015 04:57:1...					
Google Chrome	2,214	Shortcut	09/14/2016 10:16:2...					
Lenovo Solution Center	2,018	Shortcut	02/08/2016 11:15:0...					
Skype	2,713	Shortcut	03/08/2016 02:12:0...					
SSH Secure File Transfer C...	2,321	Shortcut	11/11/2015 10:17:3...					
SSH Secure Shell Client	1,363	Shortcut	11/11/2015 10:17:3...					

At the bottom, the status bar shows "Connected to xfer.gacrc.uga.edu - /home/pakala" and "SSH2 - aes128-cbc - hmac-md5 - nc 4 items (0 Bytes)".



SSH Secure : Navigated to /lustre1/pakala

The screenshot shows the SSH Secure File Transfer interface. The title bar reads "xfer.gacrc.uga.edu - default - SSH Secure File Transfer". The address bar shows the path "/lustre1/pakala". A red arrow points to this path with the text "lustre1 directory". The main pane displays a table of remote files and folders.

Remote Name	Size	Type	Modified	Attributes
fastq_YH		Folder	12/31/2016 04:55:3...	drwxr-xr-x
for_suman		Folder	03/07/2017 02:11:0...	drwxrwxr...

At the bottom, the status bar indicates "Connected to xfer.gacrc.uga.edu - /lustre1/pakala" and "SSH2 - aes128-cbc - hmac-md5 - n... 2 items (0 Bytes)".



Software Packages

- The cluster uses **environment modules** to define the various paths for software packages
- Current number of modules installed is ~**600** and expanding daily!
- `module avail` to list all available modules (centralized installation)



Software Packages

```
[pakala@75-104 ~]$ module avail
```

```
-----/usr/local/modulefiles-----
Core/StdEnv          fftw/3.3.4/pgi149-omp183      (D)  mcscanx/0.8                python/2.7.8-del
Data/cache/moduleT.new  find_cns/07212016           mcscanx-transposed/0.8      python/2.7.8-ucs4
Data/cache/moduleT      (D)  flash/1.2.11                megahit/latest              python/2.7.8
Data/system.txt         flex/2.6.0/gcc/4.7.4        megahit/1.0.0                (D)  python/3.4.3                (D)
R/3.1.2                 flex/2.6.0/pgi/14.10        megan/6.4.3                  qiime/1.9.1
R/3.2.1                 freebayes/1.0.1             meme/4.10.2                   quast/4.1
R/3.2.3                 gam-ngs/1.1b                meme/4.11.0                   (D)  quast/4.2                    (D)
R/3.3.1                 (D)  gamess/5Dec2014-1node        meraculous/2.0.5            quota-alignment/07142016
abyss/1.5.2              gatk/latest                  mercurial/3.9                 raxml/8.1.20
abyss/1.9.0              (D)  gatk/3.3.0                   metabat/0.26.1              raxml/8.2.4                  (D)
allmaps/0.6.6            gatk/3.4.0                   metavelvet/latest            ray/2.3.1-kmer32
amber/14-at15            gatk/3.5                      (D)  metavelvet/1.2.02          ray/2.3.1-kmer121           (D)
amber/14                 gatk/3.6                      (D)  metavelvetsl/latest        rdptools/2.0.2
amber/14-20160315        (D)  gblocks/0.91b                metavelvetsl/1.0            (D)  reademption/0.3.7
anaconda/2-4.1.1         gcc/4.7.4                     methylpy/08252016            repeatmasker/4.0.5_perl_threaded
anaconda/2.2.0-fix       gcc/4.8.0                     miinconda2/07152016          repeatmasker/4.0.5          (D)
-----/usr/local/modulefiles/Core-----
```

```
StdEnv
```

```
-----/usr/local/apps/lmod/5.8/modulefiles/Core-----
```

```
lmod/5.8      settarg/5.8
```

```
Where:
```

```
(D): Default Module
```

Use "module spider" to find all possible modules.

Use "module keyword key1 key2 ..." to search for all possible modules matching any of the "keys".



Software Packages

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

```
[pakala@75-104 ~]$ module list
Currently Loaded Modules:
  1) moab/8.1.1   2) StdEnv
```

- `module load` to load the needed modules:

```
[pakala@75-104 ~]$ module load ncbiblast/2.2.26
[pakala@75-104 ~]$ module load bamtools/2.4.0
[pakala@75-104 ~]$ module list
Currently Loaded Modules:
  1) moab/8.1.1   3) ncbiblast/2.2.26
  2) StdEnv      4) bamtools/2.4.0
```

- `module unload` to remove the specific module:

```
[pakala@75-104 ~]$ module unload bamtools/2.4.0
[pakala@75-104 ~]$ module list
Currently Loaded Modules:
  1) moab/8.1.1   2) StdEnv   3) ncbiblast/2.2.26
```



Run Interactive Jobs

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

```
[pakala@75-104 ~]$ qlogin
qsub: waiting for job 1329698.pbs.scm to start
qsub: job 1329698.pbs.scm ready
[pakala@n15 ~]$ ← Now connected to n15, which is an interactive node
[pakala@n15 ~]$ pwd
/home/pakala
[pakala@n15 ~]$ cd /lustre1/pakala
[pakala@n15 pakala]$ module load ncbiblast+/2.2.29
[pakala@n15 pakala]$ module load bowtie/1.1.1
[pakala@n15 pakala]$ module list

Currently Loaded Modules:
  1) moab/8.1.1      3) ncbiblast/2.2.26  5) ncbiblast+/2.2.29
  2) StdEnv         4) bamtools/2.4.0   6) bowtie/1.1.1
```

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



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 **module 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, qdel**
 - **qstat, showjobs, checkjob, showq**



Submit Batch Jobs

```
[pakala@n15 AF293]$ pwd                ← n15: interactive node
/lustre1/pakala/AF293                 ← /lustre1/pakala/: global scratch
[pakala@n15 AF293]$
[pakala@n15 AF293]$ qsub sub.sh
1412941.pbs.scm
```

qsub is to
submit a job

sub.sh is the 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



Job Submission Script

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

```
#PBS -S /bin/bash           → Linux shell (bash)
#PBS -q batch               → Queue name (batch)
#PBS -N testBlast          → Name of the job (testBlast)
#PBS -l nodes=1:ppn=1:AMD  → Number of nodes (1), number of cores/node (1), node type (AMD)
#PBS -l mem=20gb           → Maximum amount of physical 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          → Use the directory from which the job is submitted as the working
                           directory

module load ncbiblast+/2.2.29 → Load the module of ncbiblast+, version 2.2.29

time blastn [options] > outputfile 2>&1 → Run blastn with 'time' command to measure the amount of time it
                                           takes to run the application
```



Job Submission Script

- 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
```

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

```
cd $PBS_O_WORKDIR
```

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

```
time blastn [options] > outputfile 2>&1
```



Job Submission Script

- 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
cd $PBS_O_WORKDIR

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

module load ncbiblast+/2.2.29

time blastn -num_threads 24 [options] > outputfile 2>&1
```

→ 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)



Job Submission Script

- Example 3: **MPI job script** *sub.sh* running RAxML with **94** 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 × 48 = 96
#PBS -l mem=20gb              We suggest, Number of MPI Processes (94) ≤ 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 94 raxmlHPC-MPI-AVX [options] > outputfile → Run raxmlHPC-MPI-AVX with 94 MPI processes (-np 94)
```




```
#PBS -S /bin/bash
#PBS -q batch
#PBS -N testRAxML
#PBS -l nodes=2:ppn=27:AMD → ppn number (27) fewer than 48 MUST be a multiplier of 3!
#PBS -l walltime=480:00:00
#PBS -l mem=20gb
#PBS -j oe

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

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)
```

} New lines copied from GACRC Wiki



Check Job Status (`qstat`) and Cancel a Job (`qdel`)

```
$ 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 canceled or crashed) and is not longer running. Jobs stay in this state for 1h

Q : job is pending, waiting for resources to become available

```
$ qdel 481934
```

```
$ 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



Check Computing Resources Used by a Job

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*

➤ “**showjobs**” command should be run in a “**qlogin**” session, not on the login node.

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

if using: `#PBS -M pakala@uga.edu`

`#PBS -m ae`



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

```
$ qstat -f 1426778
Job Id: 1426778.pbs.scm
  Job_Name = BS2_GFF_range_methylator5-10.py
  Job_Owner = gent@uga-2f0f976.scm
  resources_used.cput = 76:54:46
  resources_used.energy_used = 0
  resources_used.mem = 44136kb
  resources_used.vmem = 90200kb
  resources_used.walltime = 76:50:04
  job_state = C
  queue = batch
.
Error_Path = uga-2f0f976.scm:/home/gent/scripts/BS2_GFF_range_methylator5-10.py.e1426778
exec_host = n2/7
Output_Path = uga-2f0f976.scm:/home/gent/scripts/BS2_GFF_range_methylator5-10.py.o1426778
.
Resource_List.mem = 2gb
Resource_List.nodect = 1
Resource_List.nodes = 1:ppn=1:AMD
Resource_List.walltime = 480:00:00
.
Variable_List = PBS_O_QUEUE=batch,PBS_O_HOME=/home/zhuofei, ..... ,
                PBS_O_WORKDIR=/home/zhuofei/MPIs,
```



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

```
$ showjobs 1426778
Job Id      : 1426778.pbs.scm
Job Name    : BS2_GFF_range_methylator5-10.py
Output File : uga-2f0f976.scm:/home/gent/scripts/BS2_GFF_range_methylator5-10.py.o1426778
Error File  : uga-2f0f976.scm:/home/gent/scripts/BS2_GFF_range_methylator5-10.py.e1426778
Working Directory : /home/gent/scripts
Home Directory : /home/gent
Submit Arguments : BS2_GFF_range_methylator5-10.py.sh
User Name    : gent
Group Name   : krdlab
Queue Name   : batch
Wallclock Limit : 20:00:00:00
Wallclock Duration: 3:04:50:04
CPUtime      : 3:04:54:46
Memory Used  : 43.1Mb
Memory Limit : 2gb
vmem Used    : 88.1Mb
Submit Time  : Mon Mar 27 20:51:01 2017
Start Time   : Tue Mar 28 03:06:41 2017
End Time     : Fri Mar 31 15:24:32 2017
Exit Code    : 0
Master Host  : n2
```



Email notification from finished jobs

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: n5/4-27
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



Check Queue Status

```
[pakala@n15 for_suman]$ showq
```

active jobs--

JOBID	USERNAME	STATE	PROCS	REMAINING		STARTTIME
1412927	gent	Running	4	19:22:58:29	Tue Mar 7	13:35:02
1412931	jl03308	Running	4	19:23:03:11	Tue Mar 7	13:39:44
1412944	pakala	Running	1	19:23:37:33	Tue Mar 7	14:14:06
1412945	jl03308	Running	4	19:23:38:19	Tue Mar 7	14:14:52

```
370 active jobs          4306 of 7472 processors in use by local jobs (57.63%)  
                          114 of 170 nodes active          (67.06%)
```

eligible jobs--

JOBID	USERNAME	STATE	PROCS	WCLIMIT		QUEUETIME
1410619	rzzmh	Idle	12	30:00:00:00	Thu Mar 2	17:02:57
1411044	apjaeger	Idle	42	28:00:00:00	Fri Mar 3	13:30:32
1412702	mesbahi	Idle	24	41:04:00:00	Tue Mar 7	10:08:01

```
81 eligible jobs
```

blocked jobs--

JOBID	USERNAME	STATE	PROCS	WCLIMIT		QUEUETIME
1409386	lferreri	BatchHold	1	20:00:00:00	Tue Feb 28	13:16:59

```
1 blocked job
```

```
Total jobs: 452
```



Guideline Tips

- Do NOT use Login Node to run jobs → Interactive Node or the queue
 - Do NOT use Login Node upload or download data to/from cluster
 - Do NOT use Login Node to transfer data to the home dir
- } Transfer Node
- NO large memory job running on AMD nodes → HIGHMEM nodes
 - NO small memory job running on HIGHMEM nodes → AMD nodes
 - As a general rule, threads # = cores # requested

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!





Practical Tips

- Job name should have a specific computational meaning

Good Examples: `#PBS -N blastn_dataSet1_trail2 ; #PBS -N M-10-1121`

Bad Examples: `#PBS -N job1 ; #PBS -N bowtie ; #PBS -N 20160930`

- The stdout .o file and stderr .e file are to be written into files at the finishing time of a job.

Redirect standard output and error of the application to a file, instead of letting it be written in the stdout .o file and stderr .e file of the job, e.g.:

```
time application >file 2>&1
```

- Monitor job progress from time to time, to catch if a job gets stuck

How to Submit Tickets to GACRC

- For Installation/Downloading Software:
 - User needs to provide the name, version (or latest), and website
 - Applications need to be compatible with Linux
 - Note – only **FREE** software will be installed
- For Troubleshooting:
 - List the path of the working directory, path of the script that is producing errors, Job ID, and the command sent to the queue or interactive node
 - No need to attach the script or huge error messages
- For Testing:
 - Please have a sample dataset at your working directory, so that it can be used for debugging
- These steps will help us in responding quickly and efficiently



Useful Links

- GACRC Wiki: https://wiki.gacrc.uga.edu/wiki/Main_Page
- GACRC Software: <https://wiki.gacrc.uga.edu/wiki/Software>
- GACRC Support: <http://gacrc.uga.edu/help/>
- GACRC Training: <https://wiki.gacrc.uga.edu/wiki/Training>

*Georgia Advanced Computing Resource Center
4098C Stegeman Coliseum
University of Georgia*

Telephone Support

EITS HELPDESK: 706-542-3106

MONDAY – THURSDAY: 8AM – 10PM

FRIDAY: 8AM – 6PM

SATURDAY – SUNDAY: 1PM – 7PM



THANK YOU for your
patience

