

Introduction to HPC Using the New Cluster at GACRC

Georgia Advanced Computing Resource Center

University of Georgia

Zhuofei Hou, HPC Trainer

zhuofei@uga.edu

Outline

- What is GACRC?
- What is the new cluster at GACRC?
- How does it operate?
- How to work with it?

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)
- <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 at GACRC?

- Cluster Structural Diagram
- General Information
- Computing Resources

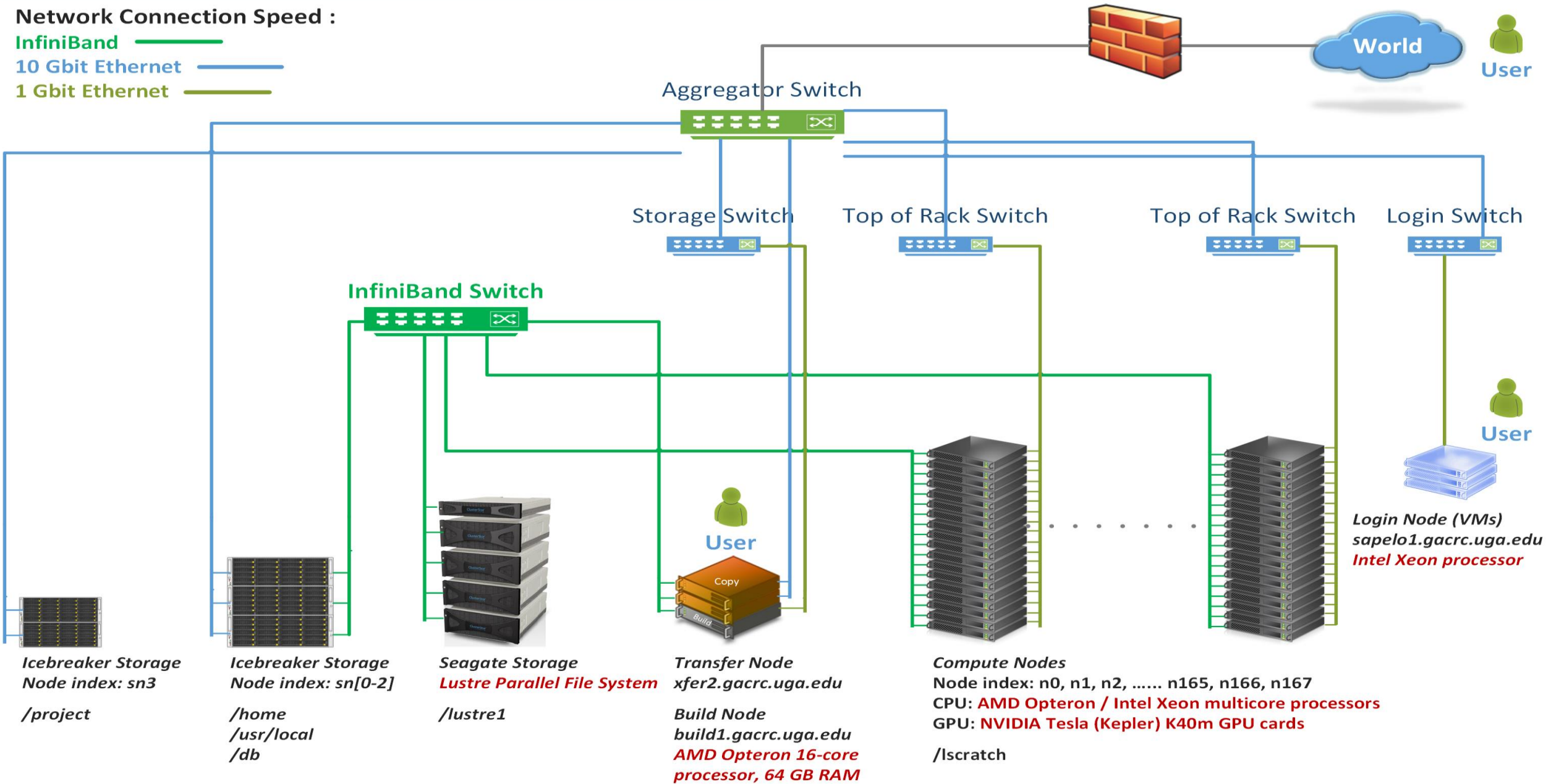
The New GACRC Linux HPC Cluster Structural Diagram

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
xfer2.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

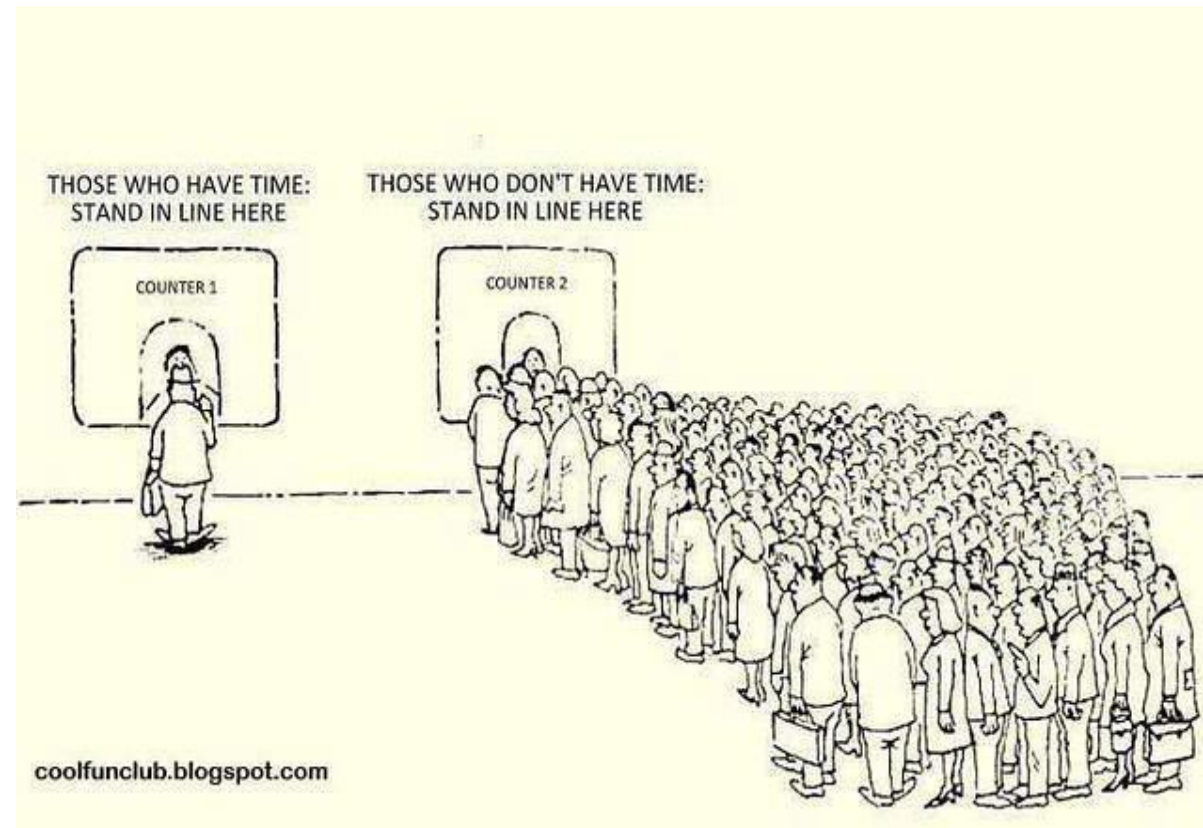
What is the new cluster – General Information

The new cluster is a Linux high performance computing (HPC) cluster:

- 64-bit CentOS 6.5 operating system
- User can login to:
 - Login node: sapelo1.gacrc.uga.edu (for login & job submission)
 - Transfer mode: xfer2.gacrc.uga.edu (for data transferring & compression)
 - Build node: build1.gacrc.uga.edu (for code compilation)
- **InfiniBand network** provides internodal communication:
 - compute nodes ↔ compute nodes
 - compute nodes ↔ storage systems, e.g., /home and /scratch

What is the new cluster – General Information

- 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 new cluster:
 - Torque** Resource Manager
 - Moab** Workload Manager



What is the new cluster – Computing Resources

Queue	Node Type	Total Nodes	Processor	Cores /Node	RAM (GB) /Node	Max RAM can be Request /Single-node Job	GPU	GPU Cards /Node	InfiniBand
batch	AMD	120	AMD Opteron	48	128	126	N/A	N/A	Yes
	HIGHMEM	3	AMD Opteron	48	512 (2)	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	

Peak Performance per Node: **500Gflops/Node**

Home directory: **100GB**

Scratch directory on /lustre1: **NO quota limit, auto-moved to /project if no modification in 30 days!**

New Cluster Storage Environment

Filesystem	Role	Quota	Accessible from	Intended Use	Notes
/home/username	Home	100GB	sapelo1.gacrc.uga.edu (Login) Interactive nodes (Interactive) xfer2.gacrc.uga.edu (Transfer) build1.gacrc.uga.edu (Build) compute nodes (Compute)	Highly static data being used frequently	Snapshots
/lustre1/username	Scratch	No Limit	Interactive nodes (Interactive) xfer2.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	xfer2.gacrc.uga.edu (Transfer)	Long-term data storage	Group sharing possible

- Note:
1. /usr/local/apps : Software installation directory
 /db : bioinformatics database installation directory
 2. To login to [Interactive](#) nodes, use [qlogin](#) from [Login](#) node

New Cluster Storage Environment

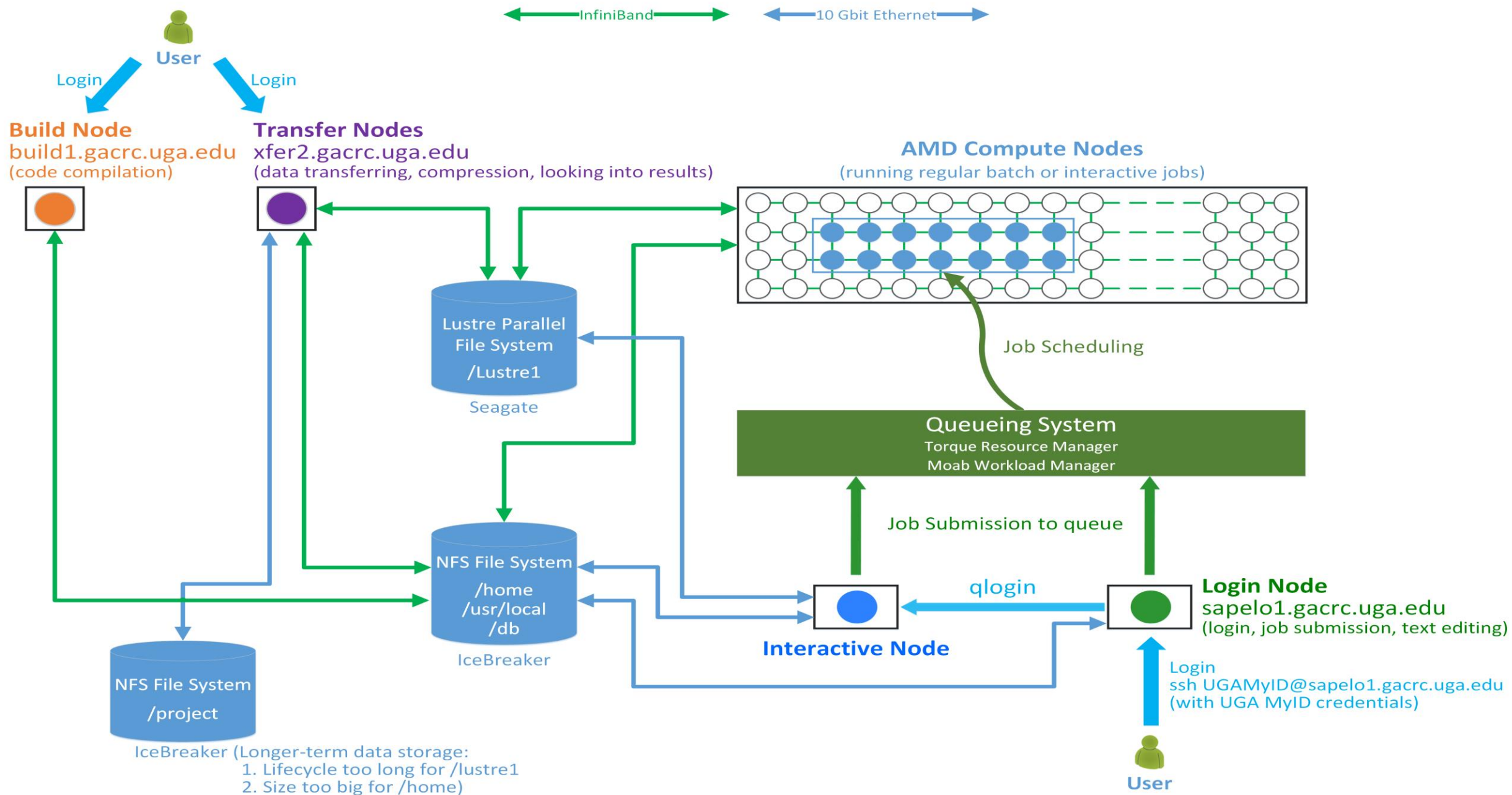
7 Main Functions	Related Filesystem	On/From-Node
Login Landing	/home/username (Home)	Login
Batch Job Submitting	/home/username (Home)	Login or Interactive
	/lustre1/username (Scratch)	Interactive
Interactive Job Running	/home/username (Home) /lustre1/username (Scratch)	Interactive
Data Archiving , Compressing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

How does it operate?

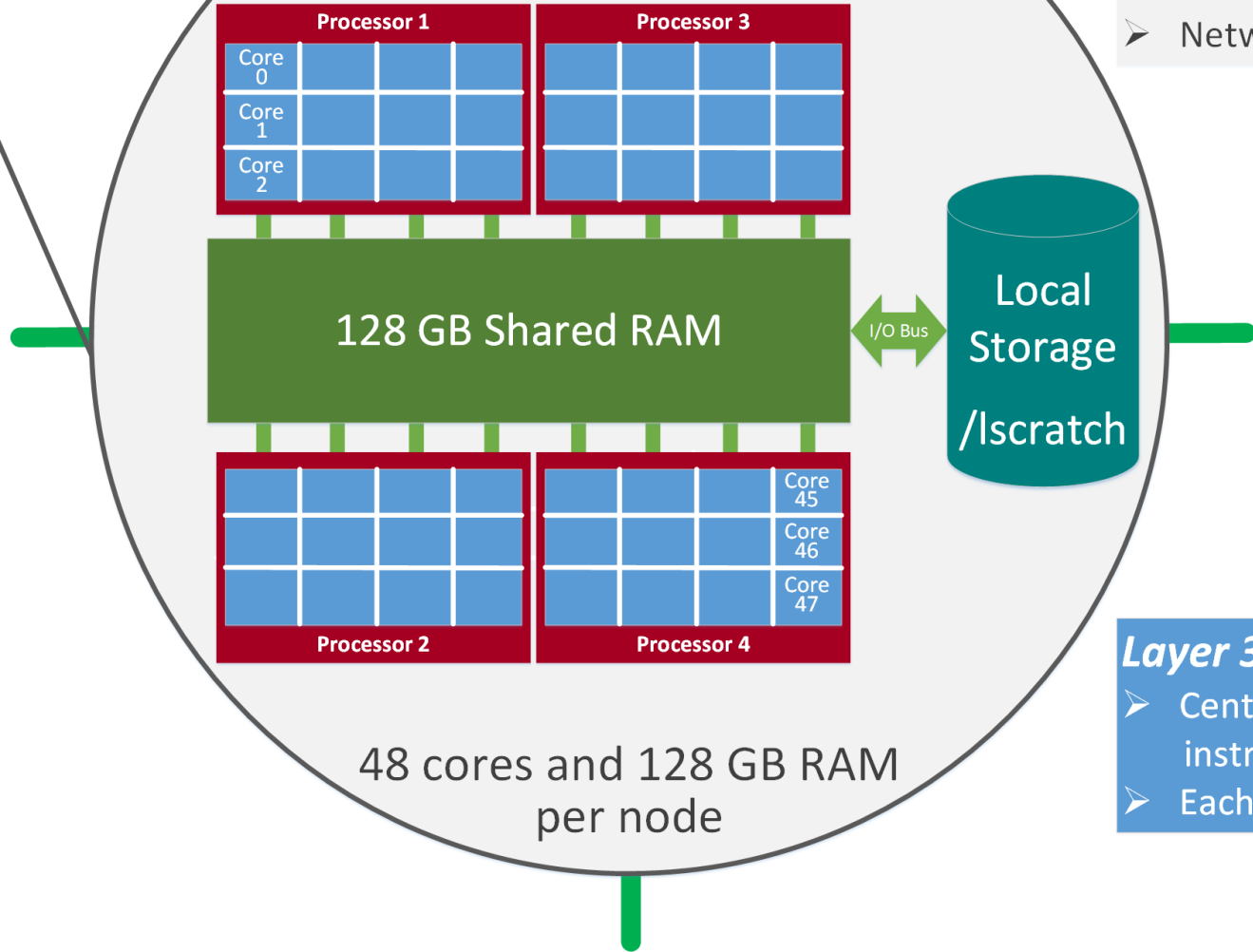
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The New GACRC Linux HPC Cluster Operational Diagram



Node 167



128 GB Shared RAM

I/O Bus

Local Storage
/lscratch

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

How to work with it?

Before we start:

- To get the new cluster to be your best HPC buddy, go to
GACRC Wiki (<http://wiki.gacrc.uga.edu>)
GACRC Web (<http://gacrc.uga.edu>)
- To get the most effective and qualified support from us, go to
GACRC Support (https://wiki.gacrc.uga.edu/wiki/Getting_Help)
- To work happily and productively, follow the new cluster's
Community Code of Conduct (**CCOC**)

How to work with it?

- Cluster's CCOC:

On cluster, you are not alone..... Each user is sharing finite resources, e.g., CPU cycles, RAM, disk storage, network bandwidth, with other researchers.

What you do may affect other researchers on the cluster.

6 rules of thumb:


- NO jobs running on login node
- NO multi-threaded job running with only 1 core requested
- NO large memory job running on regular nodes
- NO long job running on interactive node
- NO small memory job running on large memory nodes
- Use the copy node for file transfer and compression



How to work with it?

- Start with the Cluster
- Connect & Login
- Software Packages
- Run Jobs
 - How to submit a job
 - How to make a job submission script
 - How to check job status, cancel a job, etc.

How to work with it – Start with the Cluster

- You need a **User Account**: UGAMyID@sapelo1.gacrc.uga.edu
 To create your account correctly, you must provide us with your **official UGA MyID**, not a UGA MyID alias! 
- To get a user account, follow 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. We send you an **invitation letter** with instructions to start account initialization
 4. With Step 3 finished successfully, we send you a **welcome letter** with whole package of information about your account created successfully

How to work with it – Connect & Login

- Open a connection: Open a terminal 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 to be forwarded to your local machine

⁽²⁾ If using Windows, use **SSH client** to open connection, get from UGA download software 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
```

How to work with it – Software Packages

- The cluster uses **environment modules** to define the various paths for software packages
- Current number of modules installed is ~70 and expanding daily!
- **module avail** to list all modules available on the cluster:

```
[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 (D)	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
Data/system.txt	expat/2.0.1 (D)	lammps/16Aug13 (D)	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 it – 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
```

How to work with it – Run Jobs

- Components you need to run a job:
 - **Software** already loaded. If not, used `module load`
 - **Job submission script** to run the software, specifying 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` etc.

How to work with it – 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 it – 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 it – Run Jobs

- Example 2: **Threaded job script** *sub.sh* running NCBI Blast + with **4** threads

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

```
#PBS -q batch
```

```
#PBS -N testBlast
```

```
#PBS -l nodes=1:ppn=4:AMD
```

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

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

```
#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 4 [options] > outputfile
```

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

→ Email to receive a summary of computing resources used by the job

→ Receive an email when the job finishes (**e**)

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

→ Run blastn with 4 threads (**-num_threads 4**)

How to work with it – 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 it – 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 it – Run Jobs

- How to check computing resources? ***qstat -f JobID*** for a *running job* or a *finished job in 1 hour*)

```
[zhuofei@75-104 MPIs]$ qstat -f 481939
Job Id: 481939.pbs.scm
  Job_Name = testJob
  Job_Owner = zhuofei@uga-2f0f976.scm
  job_state = Q
  queue = batch
  .
  Error_Path = uga-2f0f976.scm:/home/zhuofei/MPIs/testJob.e481939
  .
  Join_Path = oe
  .
  Mail_Points = abe
```

How to work with it – Run Jobs

- How to check computing resources? ***showjobs JobID*** for a *finished job over 1 hour, but no longer than 7 days*)

```
[zhuofei@75-104 MPIs]$ qstat -f 481939
Job Id: 481939.pbs.scm
  Job_Name = testJob
  Job_Owner = zhuofei@uga-2f0f976.scm
  job_state = Q
  queue = batch
  .
  Error_Path = uga-2f0f976.scm:/home/zhuofei/MPIs/testJob.e481939
  .
  Join_Path = oe
  .
  Mail_Points = abe
```

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!