



Introduction to High Performance Computing (HPC) Resources at GACRC

Georgia Advanced Computing Resource Center
University of Georgia
Zhuofei Hou, HPC Trainer
zhuofei@uga.edu

Outline

- What is GACRC?
- Concept of High Performance Computing (HPC)
- What is GACRC zcluster?
- What is GACRC New Cluster – 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 (**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)

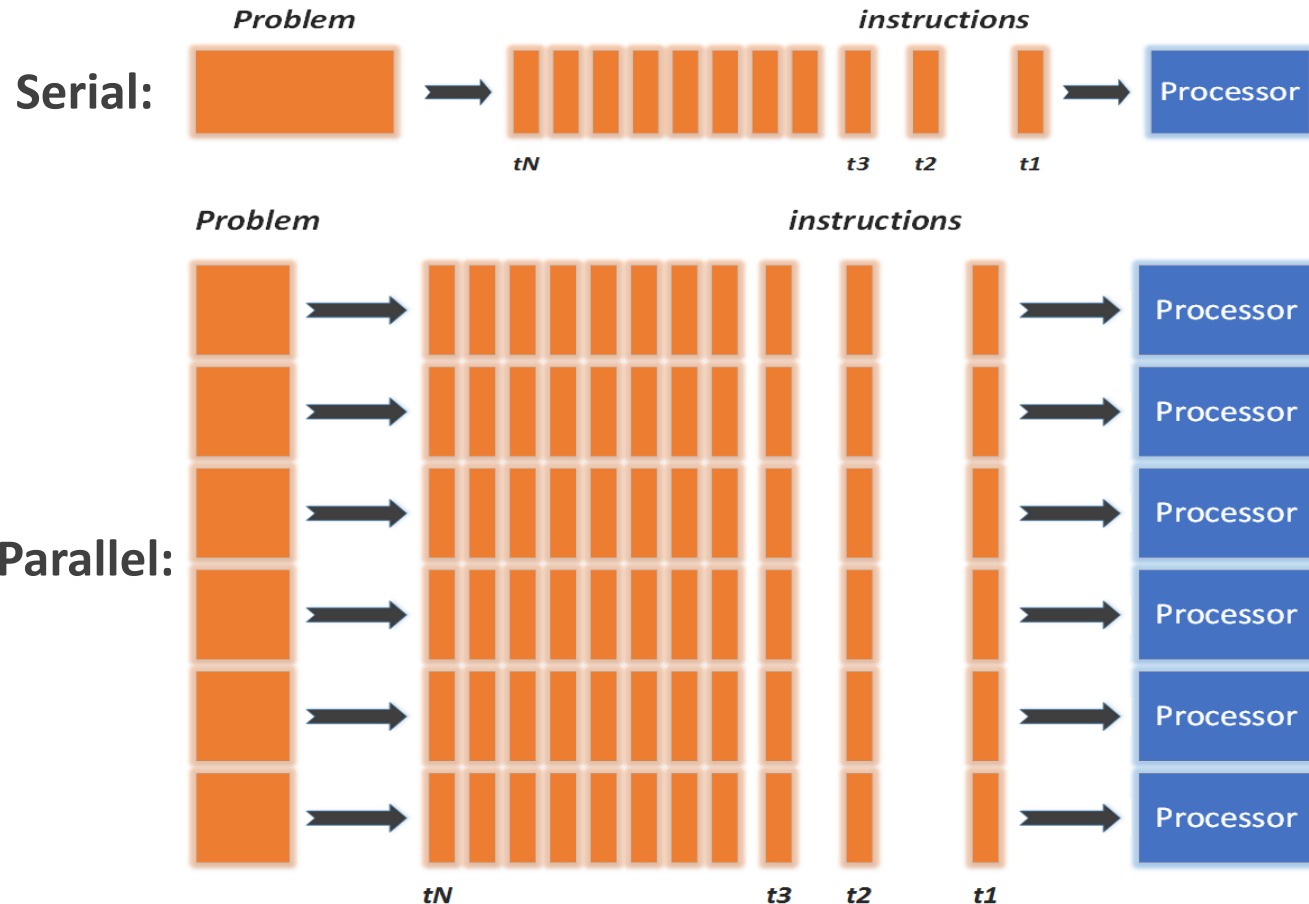
GACRC Users September 2015

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

Concept of High Performance Computing (HPC)



- ✓ **Serial** problem can not be broken
- ✓ *Discrete* instructions executed *sequentially*
- ✓ Only 1 instruction executed at any moment on a *single* processor

- ✓ Problem broken into *parallel* parts can be solved *concurrently*
- ✓ Instructions executed *simultaneously* on *multiply* processors
- ✓ Synchronization/communication employed
- ✓ **Shared-memory multithreaded job** or **MPI job** (Message Passing Interface)

What is GACRC zcluster?

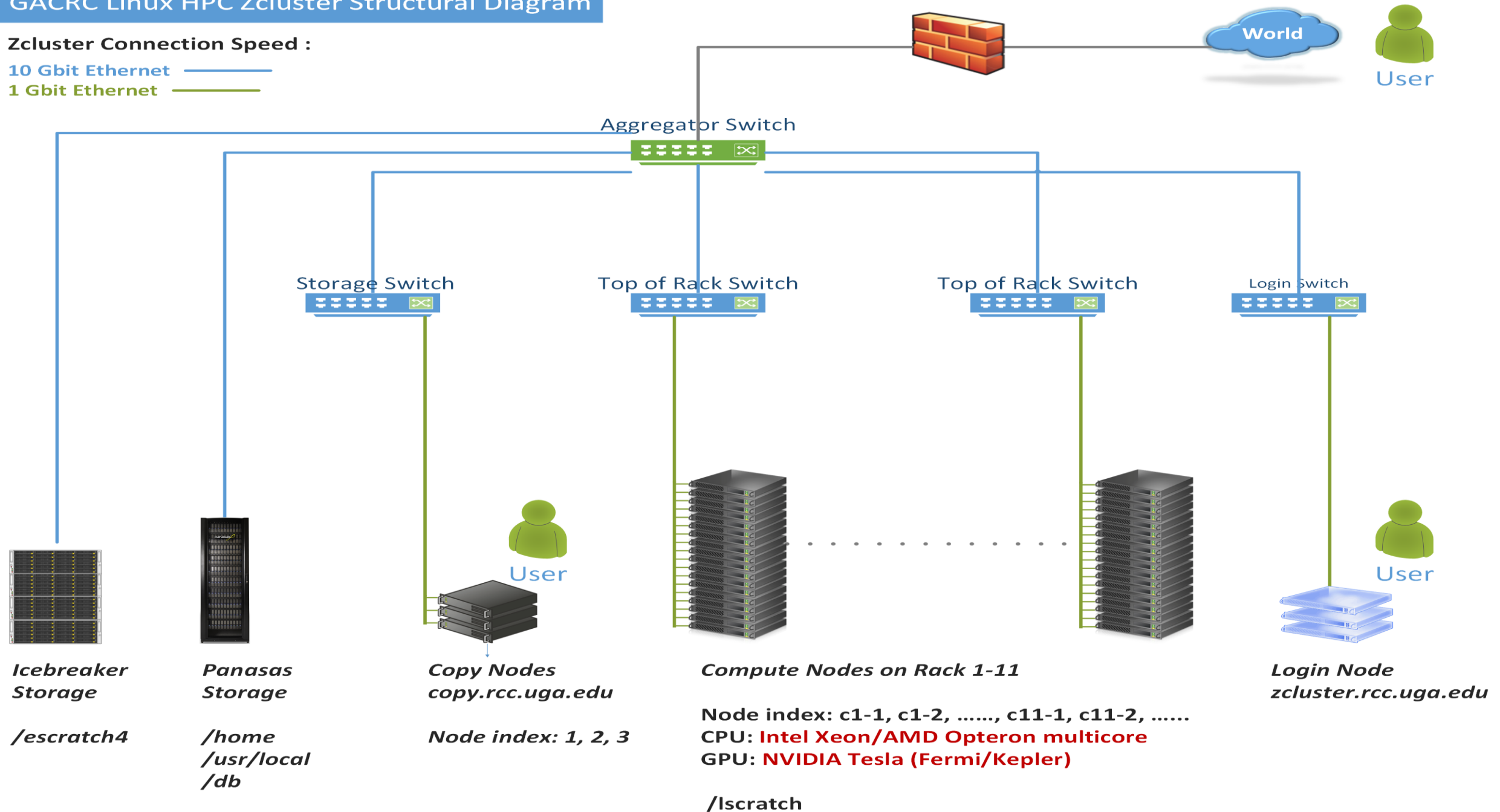
- Cluster Structural Diagram
- General Information
- Computing Resources
- Software Installed
- Submit Jobs

GACRC Linux HPC Zcluster Structural Diagram

Zcluster Connection Speed :

10 Gbit Ethernet —————

1 Gbit Ethernet —————



zcluster General Information

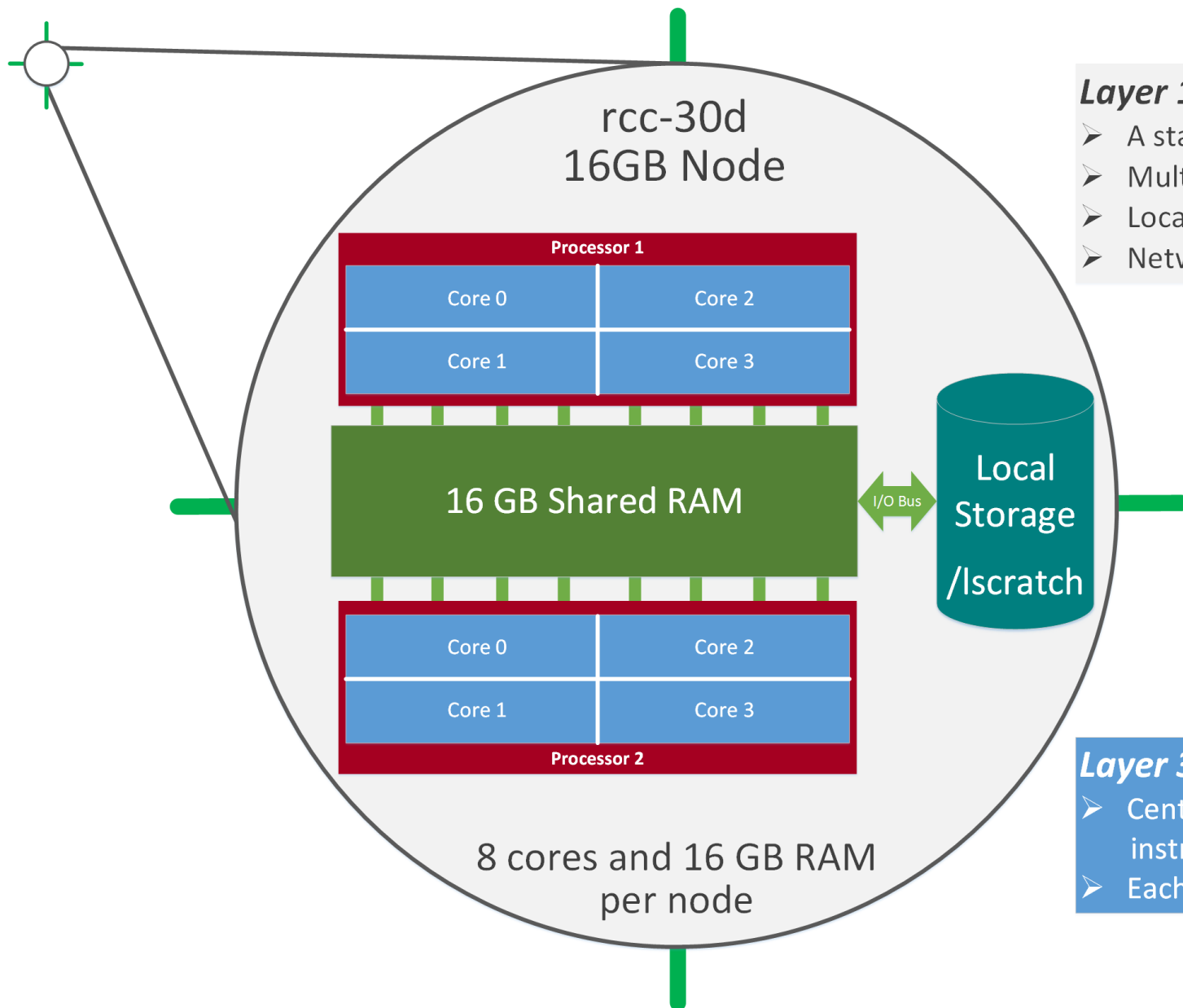
zcluster is a Linux high performance computing (HPC) cluster:

- Operating System: **64-bit Red Hat Enterprise Linux 5 (RHEL 5)**
- User can login to:
 - Login node: **zcluster.rcc.uga.edu** (for login & job submission)
 - Copy node: **copy.rcc.uga.edu** (for data transferring & compression)
- Internodal Communication: **1Gbit** network
 - compute nodes ↔ compute nodes
 - compute nodes ↔ storage systems
- Queueing System: **Sun Grid Engine (SGE)** with **qsub**, **qstat**, **qdel**, etc. commands

zcluster Computing Resources

Queue Type	Queue Name	Nodes	Processor	Cores/Node	RAM(GB)/Node	Cores	NVIDIA GPU
Regular	rcc-30d	45	Intel Xeon	12	48	540	N/A
		150		8	16	1200	
High Memory	rcc-m128-30d	4	Intel Xeon	8	192	32	N/A
		10		12	256	120	
	rcc-m512-30d	2		32	512	64	
Multi Core	rcc-mc-30d	6	AMD Opteron	32	64	192	N/A
Interactive	interq	2	AMD Opteron	48	132	96	N/A
GPU	rcc-sgpu-30d	2	Intel Xeon	8	48	16	4 Tesla S1070 cards
	rcc-mgpu-30d	2		12	48	24	9 Tesla (Fermi) M2070 cards
	rcc-kgpu-30d	4		12	96	24	32 Tesla (Kepler) K20Xm cards

Total peak performance: 23 Tflops



Layer 1: Node

- A standalone “computer in a box”
- Multiple processors, e.g. 2, sharing memory
- Local disk storage, network interface, etc.
- Networked into a cluster

Layer 2: Processor

- A single computing component
- Multicore processor, e.g. 4 cores

Layer 3: Core

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

Software Installed on zcluster

- Perl, Python, Java, awk, sed, C/C++ and Fortran compilers
- Matlab, Maple, R
- Many Bioinformatics applications: NCBI Blast+, Velvet, Trinity, TopHat, MrBayes, SoapDeNovo, Samtools, RaxML, etc.
- RCCBatchBlast (RCCBatchBlastPlus) to distribute NCBI Blast (NCBI Blast+) searches to multiple nodes.
- Many Bioinformatics Databases: NCBI Blast, Pfam, uniprot, etc.
- For a complete list of applications installed:
<https://wiki.gacrc.uga.edu/wiki/Software>

Submit Jobs on zcluster

- To submit a batch job, you need:
 - **Software** installed
 - **Job submission script** to run the software,
 - ✓ Specifying working directory
 - ✓ Exporting environment variables, e.g.,
 - OMP_NUM_THREADS (OpenMP threads number)
 - LD_LIBRARY_PATH (searching paths for shared libraries)
- Job queueing commands:
 - **qsub** with specifying **queue name**
 - **qstat, qdel**
 - **qacct, qsj**, etc.

Submit Jobs on zcluster

- **Step 1:** Create a job submission script *sub.sh* running *Samtools*:

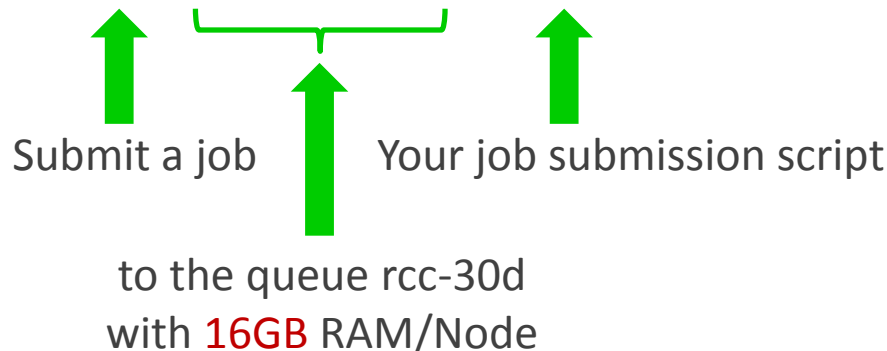
```
#!/bin/bash           → Linux shell (bash)

cd ${HOME}/testdir    → Specify and enter (cd) the working directory (${HOME}/testdir)

time /usr/local/samtools/latest/samtools <command> [options] → Run samtools with 'time' command to measure amount of
                                                                time it takes to run the application
```

- **Step 2:** Submit it to the queue:

```
$ qsub -q rcc-30d sub.sh
```



Submit a job

to the queue rcc-30d
with **16GB** RAM/Node

Your job submission script

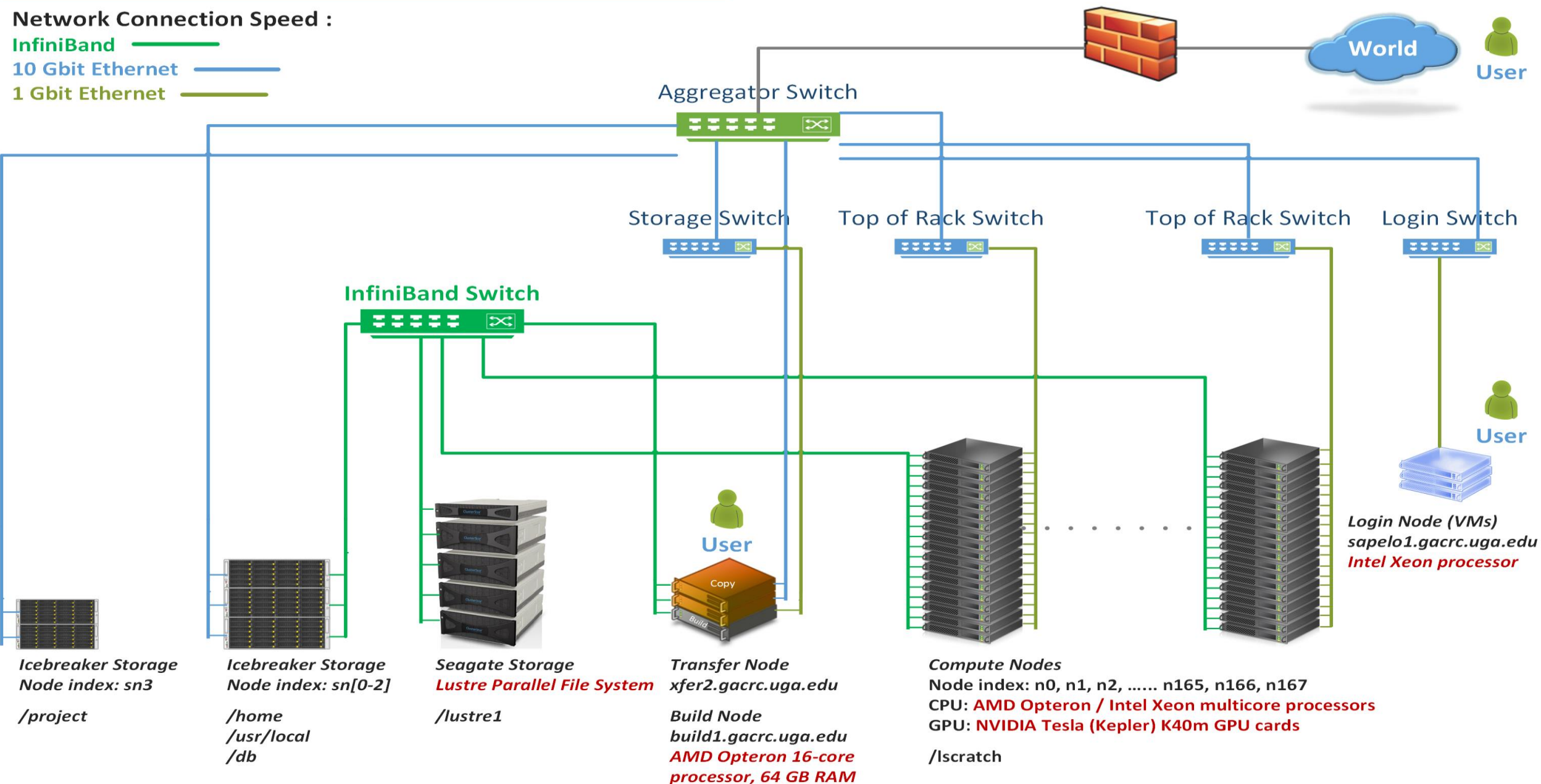
What is GACRC Sapelo

- Cluster Structural Diagram
- General Information
- Computing Resources
- Software installed
- Submit Jobs

The New GACRC Linux HPC Cluster Structural Diagram

Network Connection Speed :

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



Sapelo General Information

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

- Operating System: [64-bit CentOS Linux 6.5](#)
- 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)
- Internodal communication: [InfiniBand network](#)
 - compute nodes ↔ compute nodes
 - compute nodes ↔ storage systems, e.g., /home and /scratch
- Queueing System: [Torque + Moab](#) with [qsub](#), [qstat](#), [qdel](#), etc. commands

Sapelo Computing Resources



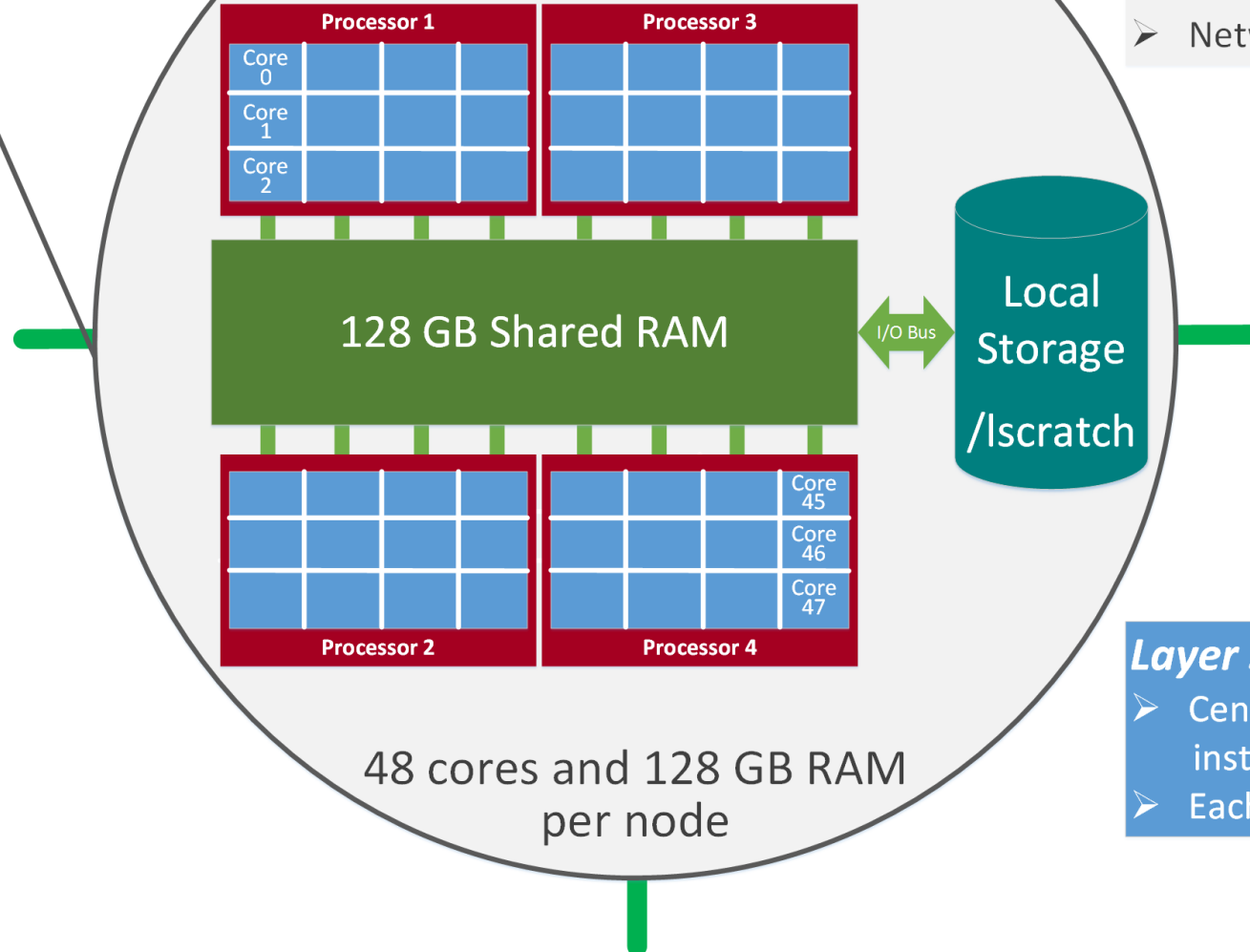
Queue	Node Type	Total Nodes	Processor	Cores / Node	RAM (GB) / Node	GPU	GPU Cards / Node	InfiniBand
batch	AMD	120	AMD Opteron	48	128	N/A	N/A	Yes
	HIGHMEM	3	AMD Opteron	48	512 (2)	N/A	N/A	Yes
					1024 (1)			
	GPU	2	Intel Xeon	16	128	NVIDIA K40m	8	Yes

Peak Performance per Node: 500 Gflops/Node

Home directory : **100 GB**

Scratch directory on /lustre1 : **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

Software Installed on Sapelo

- Sapelo uses **environment modules** to define paths for software
- Current number of modules installed is **~90** and expanding daily!
- `module avail` → List all modules available on Sapelo
- `module list` → List modules currently being loaded for use
- `module load` → Load modules needed
- `module unload` → Unload modules not needed

[zhuoifei@75-104 ~] % module avail

```
----- /usr/local/modulefiles -----
Core/StdEnv                                (D)  metavelvet/latest
Data/cache/moduleT.new                    (D)  metavelvet/1.2.02
Data/cache/moduleT                          (D)  metavelvetsl/latest
Data/system.txt                            (D)  metavelvetsl/1.0
R/3.1.2                                    (D)  moab/7.2.10
R/3.2.1                                    (D)  moab/8.1.1
amber/14                                  (D)  moabs/1.3.2
anaconda/2.2.0                             (D)  mpfr/3.1.2/gcc/4.4.7_gmp431
anaconda/3-2.2.0                           (D)  mpfr/3.1.2/gcc/4.4.7
apache-ant/1.9.6                           (D)  mvapich2/2.0.0/gcc/4.4.7
aspera/latest                             (D)  mvapich2/2.0.0/pgi/14.9
aspera/3.6.0.106805                         (D)  mvapich2/2.1/gcc/4.4.7
astalavista/3.2                           (D)  mvapich2/2.1/intel/14.0
bam-read/latest                           (D)  mvapich2/2.1/pgi/14.10
bam-read/1.0.0                             (D)  mysql/5.6.23
bamtools/2.4.0                             (D)  ncbiblast+/2.2.29
bedops/latest                             (D)  netcdf/3.6.3/gcc/4.4.7
bedops/2.4.14                             (D)  netcdf/3.6.3/intel/14.0
binf/core1                                (D)  netcdf/3.6.3/intel/15.0.2
binf/latest                               (D)  netcdf/4.1.3-v4/gcc/4.4.7
boost/1.47.0/gcc447                         (D)  netcdf/4.1.3-v4/gcc/4.7.4
boost/1.57.0/gcc447                         (D)  netcdf/4.1.3-v4/pgi/14.10
boost/1.57.0_thread/gcc447                 (D)  netcdf/4.1.3/gcc/4.4.7
boost/1.59.0/gcc447                         (D)  netcdf/4.1.3/intel/14.0
boost/gcc447/1.47.0                         (D)  netcdf/4.1.3/intel/15.0.2
boost/gcc447/1.57.0_thread                 (D)  netcdf/4.1.3/pgi/14.10
boost/gcc447/1.57.0                         (D)  netcdf/4.3.2/gcc/4.4.7
bowtie/latest                             (D)  netcdf/4.3.2/pgi/14.9
bowtie/1.1.1                               (D)  nwchem/6.5
bowtie2/latest                             (D)  openldap/2.4.42
bowtie2/2.2.4                             (D)  openmpi/1.6.5/gcc/4.4.7
cmake/3.0.2                                (D)  openmpi/1.6.5/pgi/14.9
cuda/5.0.35/gcc/4.4.7                      (D)  openmpi/1.8.3/gcc/4.4.7
cuda/6.5.14/gcc/4.4.7                      (D)  openmpi/1.8.3/gcc/4.7.4
cufflinks/latest                           (D)  openmpi/1.8.3/gcc/4.8.0
cufflinks/2.2.1                             (D)  openmpi/1.8.3/intel/14.0
detect-nahr/20150916                       (D)  openmpi/1.8.3/intel/15.0.2
exabayes/1.4.1                             (D)  openmpi/1.8.3/pgi/14.9
examl/3.0.11                               (D)  orca/3.0.3
expat/latest                               (D)  parallel/20150622
expat/2.0.1                                (D)  parmetis/4.0.3/mvapich2/2.1/intel/14.0
fastqc/latest                             (D)  perl/latest
fastqc/0.11.3                              (D)  perl/5.20.1
fftw/2.1.5/gcc447-mvapich200                (D)  perl/5.20.2
fftw/2.1.5/gcc447-mpi183                    (D)  pgi/14.9
fftw/2.1.5/pgi149-mvapich200                (D)  pgi/14.10

----- /usr/local/modulefiles/Core -----
StdEnv

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

Where:
(D):  Default Module
```

```
[zhuofei@75-104 ~]$  
[zhuofei@75-104 ~]$ module list  
  
Currently Loaded Modules:  
  1) StdEnv    2) moab/7.2.10  
  
[zhuofei@75-104 ~]$ module load python/2.7.8  
[zhuofei@75-104 ~]$  
[zhuofei@75-104 ~]$ module list  
  
Currently Loaded Modules:  
  1) StdEnv    2) moab/7.2.10    3) python/2.7.8  
  
[zhuofei@75-104 ~]$ exit  
logout  
Connection to sapelo1.gacrc.uga.edu closed.  
zhuofei@zcluster:~$ ssh zhuofei@sapelo1.gacrc.uga.edu  
zhuofei@sapelo1.gacrc.uga.edu's password:  
  
The following have been reloaded with a version change:  
  1) moab/8.1.1 => moab/7.2.10  
  
[zhuofei@75-104 ~]$ module list  
  
Currently Loaded Modules:  
  1) StdEnv    2) moab/7.2.10
```

Submit Batch Jobs on Sapelo

- To submit a batch job, you need:
 - **Software** loaded. If not, used `module load`
 - **Job submission script** to run the software, specifying working directory and computing resources:
 - ✓ Number of nodes and cores
 - ✓ Amount of memory
 - ✓ Type of nodes
 - ✓ Maximum wallclock time, etc.
- Job queueing commands:
 - `qsub`, `qstat`, `qdel`
 - `showq`, `checkjob`, etc.

Submit Batch Jobs on Sapelo

- 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!*

Submit Batch Jobs on Sapelo

- Example: **Serial job submission 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

Where to Find Useful Information?

- GACRC Web: <http://gacrc.uga.edu/>
- GACRC Wiki: https://wiki.gacrc.uga.edu/wiki/Main_Page
- GACRC Help : <http://gacrc.uga.edu/help/>
- GACRC Training: <https://wiki.gacrc.uga.edu/wiki/Training>
- GACRC User Account: https://wiki.gacrc.uga.edu/wiki/User_Accounts
- GACRC Software: <https://wiki.gacrc.uga.edu/wiki/Software>

*Georgia Advanced Computing Resource Center
4098C Stegeman Coliseum
University of Georgia
Athens, GA 30602*

Telephone Support

EITS HELPDESK: 706-542-3106

MONDAY – THURSDAY: 8AM – 10PM

FRIDAY: 8AM – 6PM

SATURDAY – SUNDAY: 1PM – 7PM

Thank You!