



Introduction to High Performance Computing (HPC) Resources at GACRC

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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 Advanced Computing Resource Center
- Collaboration between the Office of Vice President for Research (OVPR) and the Office of the Vice President for Information Technology (OVPIT)
- 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)

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

GACRC Users September 2015

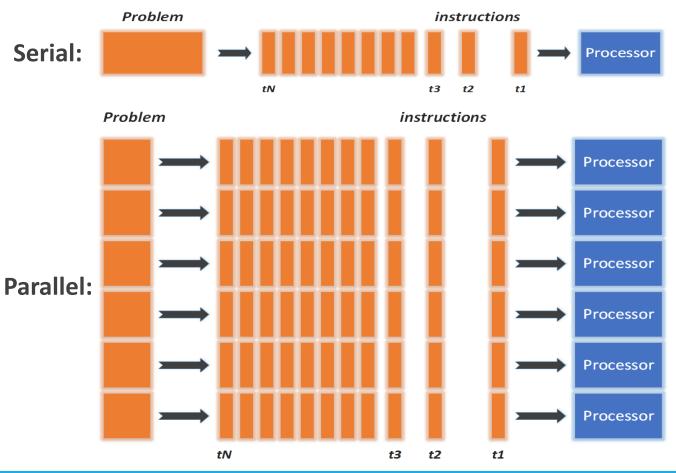
Colleges & Schools	Depts	Pls	Users
Franklin College of Arts and Sciences	14	117	661
College of Agricultural & Environmental Sciences	9	29	128
College of Engineering	1	12	33
School of Forestry & Natural Resources	1	12	31
College of Veterinary Medicine	4	12	29
College of Public Health	2	8	28
College of 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	Pls	Users
	115	03013
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)

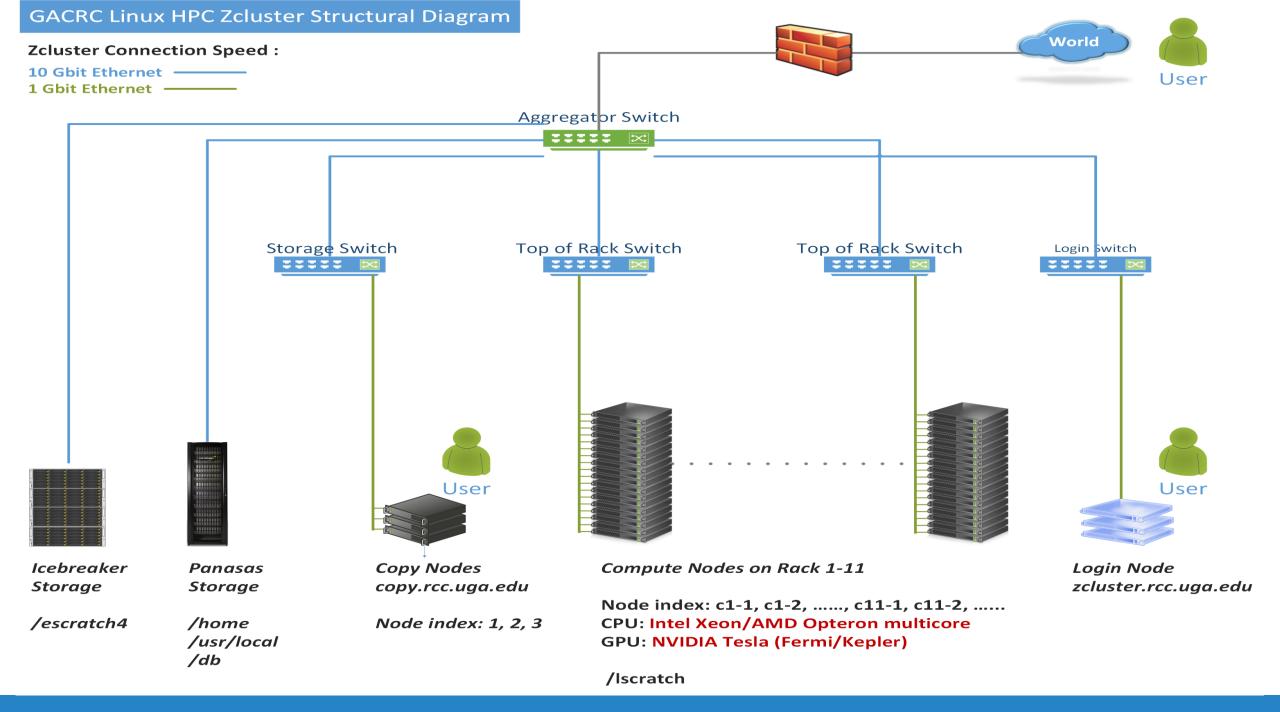


- ✓ Serial problem can not be broken
- ✓ *Discrete* instructions executed *sequentially*
- Only 1 instruction executed at any moment on a single processor
- Problem broken into *parallel* parts can be solved concurrently
- ✓ Instructions executed *simultaneously* on *multiply* processors
- ✓ Synchronization/communication employed
- ✓ Shared-memory multithreaded or MPI



What is GACRC zcluster?

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



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

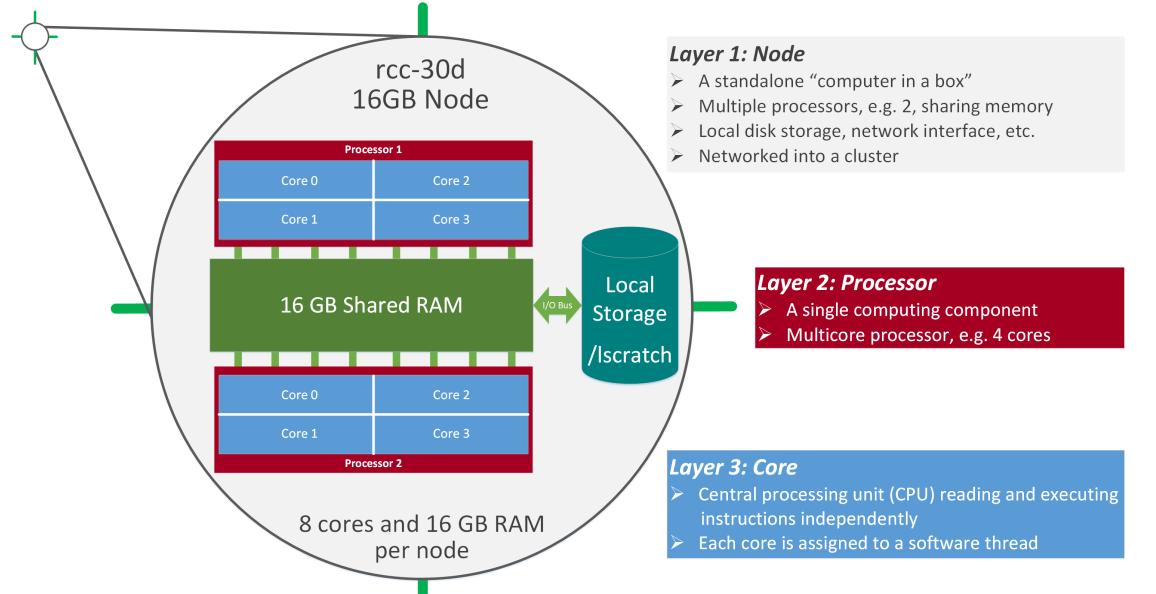


zcluster Computing Resources

	Queue Type	Queue Name	Nodes	Processor	Cores/Node	RAM(GB)/Node	Cores	NVIDIA GPU	
⇒	Dogular	rcc-30d	45	Intel Xeon	12	48	540	N/A	
	Regular		150		8	16	1200		
		rec m128 20d	4		8	192	32		
	High Memory	rcc-m128-30d	10	Intel Xeon	12	256	120	N/A	
		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	
		rcc-sgpu-30d	2		8	48	16	4 Tesla S1070 cards	
	GPU	rcc-mgpu-30d	2	Intel Xeon	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

ÎGACRC





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

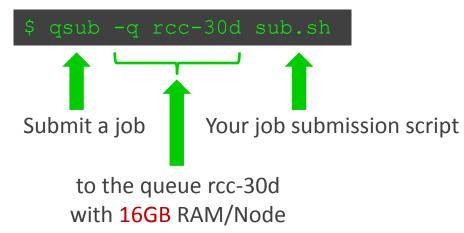
• **Step 1**: Create a job submission script *sub.sh* running *Samtools*:

#!/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:

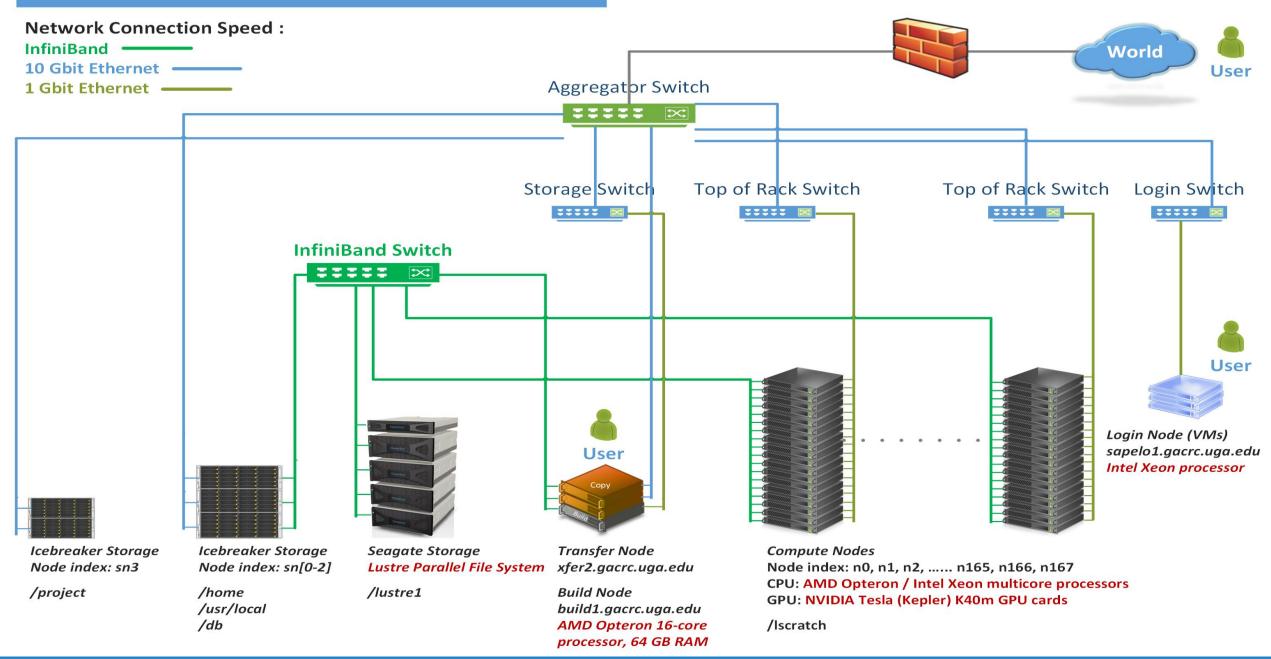




What is GACRC Sapelo

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

The New GACRC Linux HPC Cluster Structural Diagram





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 \Leftrightarrow compute nodes compute nodes \Leftrightarrow storage systems, e.g., /home and /scratch

• Queueing System: Torque + Moab with qsub, qstat, qdel, etc. commands

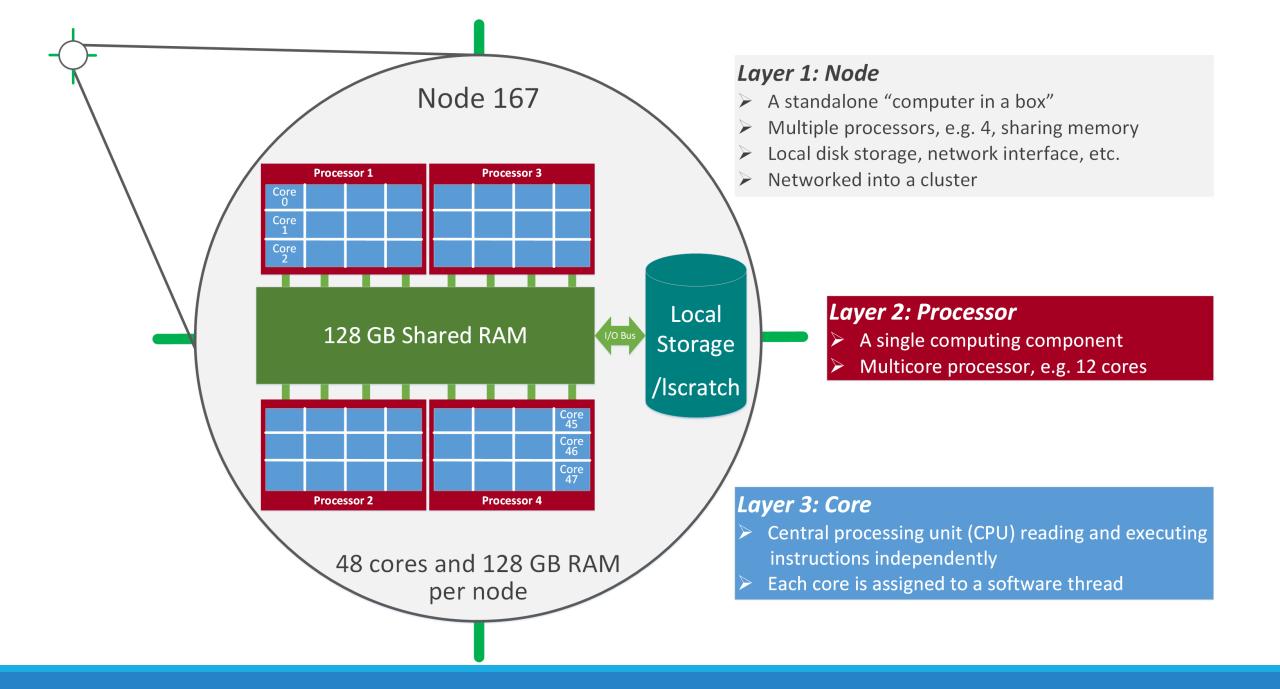


Sapelo Computing Resources

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





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 load → Load modules needed



huofei@75-104 ~] 🤇 module avail j

			- Zusr	/local/modulefiles			
Core/StdEnv		fftw/2.1.5/pgi149-omp183	(D)	metavelvet/latest		python/2.7.8-ucs4	
Data/cache/moduleT.new		fftw/3.3.4/gcc447-mvapich200		metavelvet/1.2.02	(D)	python/2.7.8	
	(D)	fftw/3.3.4/gcc447-ompi183		metavelvetsl/latest		python/3.4.3	(D)
		fftw/3.3.4/pgi149-mvapich200			(D)	raxm1/8.1.20	
Data/system.txt					(0)		
R/3.1.2			(U)	moab/7.2.10		rsem/latest	
R/3.2.1	(D)	gamess/5Dec2014-1node			(D)		(D)
amber/14		gatk/latest				salmon/latest	
anaconda/2.2.0		gatk/3.3.0		mpfr/3.1.2/gcc/4.4.7_gmp431			(D)
anaconda/3-2.2.0	(D)		(D)		(D)	samtools/latest	
apache-ant/1.9.6						samtools/0.1.19	
aspera/latest			(D)	mvapich2/2.0.0/pgi/14.9		samtools/1.1	
aspera/3.6.0.106805	(D)	gmap-gsnap/latest		mvapich2/2.1/gcc/4.4.7			(D)
astalavista/3.2		gmap-gsnap/2014-12-24	(D)	mvapich2/2.1/intel/14.0		scripture/latest	
bam-read/latest		gmp/6.0.0/gcc/4.4.7		mvapich2/2.1/pgi/14.10		scripture/03202015	(D)
bam-read/1.0.0	(D)	gmpfrxx/20081116/gcc447-mpfr312-gmp431		mysql/5.6.23		snap-aligner/latest	
bamtools/2.4.0		gmpfrxx/20081116/gcc447-mpfr312-gmp600	(D)	ncbiblast+/2.2.29			(D)
bedops/latest		gnuplot/5.0.0		netcdf/3.6.3/gcc/4.4.7		sparsehash/latest	
bedops/2.4.14	(D)			netcdf/3.6.3/intel/14.0			(D)
binf/core1		grads/2.1a3/gcc/4.7.4			(D)	sratoolkit/latest	
binf/latest	(D)	gsl/1.16/gcc/4.4.7		netcdf/4.1.3-v4/gcc/4.4.7	(0)		(D)
boost/1.47.0/gcc447		hdf5/1.8.14/gcc/4.4.7			(D)	structure/latest	
boost/1.57.0/gcc447		hdf5/1.8.14/intel/15.0.2		netcdf/4.1.3-v4/pgi/14.10			(D)
boost/1.57.0_thread/gcc447		hdf5/1.8.14/pgi/14.9		netcdf/4.1.3/gcc/4.4.7		suntans/20150923	(0)
boost/1.59.0/gcc447		hdf5/1.8.6/gcc/4.4.7		netcdf/4.1.3/intel/14.0		suppa/latest	
boost/gcc447/1.47.0			(D)		(D)		
			(0)		(U)	suppa/06122015	(D)
boost/gcc447/1.57.0_thread		hdf5/1.8.6/pgi/14.10		netcdf/4.1.3/pgi/14.10		tophat/latest	
	(D)	hmmer/3.1b2		netcdf/4.3.2/gcc/4.4.7			(D)
bowtie/latest		htsjdk/latest		netcdf/4.3.2/pgi/14.9		transrate/1.0.1	
bowtie/1.1.1	(D)		(D)			triangle/1.6	
bowtie2/latest		imb/3.2		openldap/2.4.42		trinity/latest	
bowtie2/2.2.4	(D)	intel/14.0		openmpi/1.6.5/gcc/4.4.7		trinity/r20140717	
cmake/3.0.2			(D)	openmpi/1.6.5/pgi/14.9		trinity/2.0.6-UGA	
cuda/5.0.35/gcc/4.4.7				openmpi/1.8.3/gcc/4.4.7			(D)
cuda/6.5.14/gcc/4.4.7				openmpi/1.8.3/gcc/4.7.4		ucsc/latest	
cufflinks/latest		jasper/1.900.1/pgi/14.10			(D)		(D)
cufflinks/2.2.1	(D)			openmpi/1.8.3/intel/14.0		udunits/2.2.19/gcc/4.7.4	
detect-nahr/20150916		java/jdk1.8.0_20		openmpi/1.8.3/intel/15.0.2	(D)	vcftools/0.1.12b	
exabayes/1.4.1		java/latest	(D)	openmpi/1.8.3/pgi/14.9		velvet/1.2.10	
examl/3.0.11		jellyfish/latest				wps/3.7/pgi/14.10/openmpi/1.8.3	
expat/latest		jellyfish/2.2.3	(D)	parallel/20150622		wrf/3.7/pgi/14.10/openmpi/1.8.3	
expat/2.0.1	(D)	ĺammps/5Sep14		parmetis/4.0.3/mvapich2/2.1/intel/14.0		yaggo/latest	
fastgc/latest		lammps/10Aug15		perl/latest			(D)
fastqc/0.11.3	(D)		(D)	perl/5.20.1		zlib/1.2.5/gcc/4.4.7	
fftw/2.1.5/gcc447-mvapich200		lapack/3.5.0/gcc447			(D)		(D)
fftw/2.1.5/gcc447-ompi183		megahit/latest		pgi/14.9	~ /	zlib/1.2.5/pgi/14.10	
fftw/2.1.5/pgi149-mvapich200			(D)		(D)	zlib/gcc447/1.2.8	
i i in critio pyri io mruprenzoo							

StdEnv

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

lmod/5.8 settarg/5



```
[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)

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!*

qsub is to

submit a job



Submit Batch Jobs on Sapelo

• Example: Serial job submission 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=20gb
#PBS -l walltime=48:00:00

cd \$PBS_O_WORKDIR

module load ncbiblast+/2.2.29

time blastn [options] > outputfile

- → Linux shell (bash)
- ➔ Queue name (batch)
- → Name of the job (testBlast)
- → Number of nodes (1), number of cores/node (1), node type (AMD)
- → Maximum amount of physical memory (20 GB) used by the job
- → Maximum wall clock time (48 hours) for the job, default 6 minutes
- ➔ Use the directory from which the job is submitted as the working directory
- → Load the module of ncbiblast+, version 2.2.29
- Run blastn with 'time' command to measure the amount of time it takes to run the application



Where to Find Useful Information?

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

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MONDAY – THURSDAY: 8AM – 10PM
FRIDAY: 8AM – 6PM
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Thank You!