

User Environment on Super Mike II

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User Services HPC @ LSU



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Outline

- User environment
 - System access and file systems
 - Software stack
 - Compiling programs on Super Mike II GPU-accelerated code and Open MPI
 - Job management
- Applications benchmark results







SuperMikell

- Ranked 250 in Nov 2012 Top 500 list
- 440 nodes, dual 8-core Intel Sandy Bridge Xeon processors
 @ 2.6GHz, including
 - 382 nodes with 32 GB RAM
 - 50 GPU nodes with 64 GB RAM and dual NVIDIA Tesla M2090 GPUs
 - 8 nodes with 256 GB RAM, capable of aggregation into a single virtual symmetric multiprocessing (vSMP) using ScaleMP
- 146 CPU TFLOPS and 66 GPU TFLOPS (double-precision)
- 364 TB of storage space
- Mellanox Infiniband network







Accessing the Clusters

- Host name: *mike.hpc.lsu.edu*
- Use ssh to connect
 - Unix-alike and Mac: "ssh <host name>" in a terminal window
 - Windows: use **Putty** or other ssh clients
- The default log in shell is bash
 - Supported: bash, tcsh, csh, ksh and sh







Connection with X11 Forwarding

- Some software packages have GUI, which requires X11 forwarding to be established with the ssh connection
- Unix/Linux users
 - Use the "-X" option of ssh
- Mac users
 - Use the "X11" application
- Windows users
 - Install X server for Windows (e.g. Xming)
 - Enable X11 forwarding in the ssh client







File Systems

	Distributed	Throughput	File life time	Best used for
Home	Yes	Low	Unlimited	Code in development, compiled executable
Work/Scratch	Yes	High	30 or 60 days	Job input/output
Local scratch	No		Job duration	Temporary files

- Tips
 - Never let you job write output to your home directory
 - Do not write temporary files to /tmp
 - Write to the local scratch or work space
 - The work space is not for long-term storage
 - Files are purged periodically
 - Use "rmpurge" to delete large amount of files







Disk Quota

Cluster	Home		Work		Local scratch
Cluster	Access point	Quota	Access Point	Quota	Access point
SuperMikell	/home/\$USER	5 GB	/work/\$USER	None	/var/scratch

- No quota is enforced on the /work space on Super Mike II (146TB total)
 - Again, it is subject to a purge every 30 to 60 days
- The work directory is created within an hour after the first login
- Command to check current disk usage: showquota







Storage Allocation on /project

- One can apply for extra disk space on the /project volume (218TB total on Super Mike II) if
 - your research requires some files to remain on the cluster for a fairly long period of time; and
 - their size exceeds the quota of the /home
- The unit is 100 GB
- Storage allocations are good for 6 months, but can be extended based on the merit of the request
- Examples of valid requests
 - I am doing a 6-month data mining project on a large data set
 - The package I am running requires 10 GB of disk space to install
- Examples of invalid requests
 - I do not have time to transfer the data from my scratch space to my local storage and I need a temporary staging area







File Transfer

- From/to a Windows machine
 - Use a client that supports the scp protocol (e.g. WinSCP, Filezilla)
- From/to a Unix/Linux/Mac machine (including between the clusters)
 - scp command
 - Syntax:scp <options> <source> <destination>
 - rsync command
 - Syntax:rsync <options> <source> <destination>







Software Stack

- Similar to other LSU HPC Linux clusters
 - Installed under /usr/local/packages
- Compiler
 - Default: Intel 13.0.0
 - Also available: Intel 12.1.4, PGI-12.8, PGI-11.5, GCC-4.7.2, GCC 4.4.6
- MPI
 - Default: OpenMPI 1.6.2
 - Also available: Mvapich2 1.8.1, Mvapich2 1.9a2







Software Stack Cont'd

- Script language
 - Python 2.7.3
 - Perl 5.10.1
 - Ruby 1.9.3
- Application software
 - NAMD, Matlab, Mathematica, DDT...
- A complete list available at <u>http://www.hpc.lsu.edu/docs/guides/index.php#Supermike2</u>
 - Or use the <code>softenv</code> command to find out
- User requested software will be installed in the user's home space
 - Unless requested by multiple users, in which case it will be installed under /usr/local/packages







Using SOFTENV

- Environment variables
 - PATH: where to look for executables
 - LD_LIBRARY_PATH: where to look for shared libraries
 - Other custom environment variables needed by various software
- **SOFTENV** is a software that helps users set up environment variables properly to use software packages
 - Much more convenient than setting environment variables in .bashrc or .cshrc







Listing All Packages

 Command "softenv" lists all packages that are managed by SOFTENV

[lyan1@mike1 ~]\$ softenv
SoftEnv version 1.6.2

•••

These are the keywords explicitly available:

+ImageMagick-6.7.9-gcc-4.4.6	<pre>@types: library @name: ImageMagick @version: 6.7.9 @build: ImageMagick-6.7.9-gcc-4.4.6</pre>
	@internal: @external:
	http://www.imagemagick.org @about: A
	software suite to create, edit, and compose
	bitmap images.
+Intel-12.1.4	@types: Compiler @name: Intel compiler suite
	@version: 12.1.4 @build: Binary
	installation @internal: @external:
	http://software.intel.com/en-





Searching A Specific Package

• Use "-k" option with "softenv"

[lyan1@mike1 ~]\$ **softenv -k fftw**

These are the keywords explicitly available:

+fftw-3.3.2-Intel-13.0.0

+fftw-3.3.3-Intel-13.0.0

@types: library @name: fftw @version: 3.3.2 @build: Intel-13.0.0 @internal: @external: www.fftw.org @about: A fast, free C FFT library; includes real-complex, multidimensional, and parallel transforms. @types: library @name: fftw @version: 3.3.3 @build: Intel-13.0.0 @internal: @external: www.fftw.org @about: A fast, free C FFT library; includes real-complex, multidimensional, and parallel transforms.







Setting up Environment via Softenv – permanent change

- Set up the environment variables to use a certain software package
 - First add the key to \$HOME/.soft
 - Then execute resoft at the command line
 - The environment will be the same next time you log in

```
[lyan1@mike1 ~]$ cat .soft
#
# This is the .soft file.
+portland-12.8
@default
[lyan1@mike1 ~]$ resoft
[lyan1@mike1 ~]$ which pgf90
/usr/local/compilers/pgi/linux86-
64/12.8/bin/pgf90
```









Setting up Environment via Softenv – one time change

- Set up the environment variables to use a certain software package in the current login session only
 - Add a package: soft add <key>
 - Remove a package: soft delete <key>

```
[lyan1@mike1 ~]$ which gcc
/usr/bin/gcc
[lyan1@mike1 ~]$ gcc --version
gcc (GCC) 4.4.6 20110731 (Red Hat 4.4.6-3)
[lyan1@mike1 ~]$ soft add +gcc-4.7.2
[lyan1@mike1 ~]$ which gcc
/usr/local/compilers/GNU/gcc-4.7.2/bin/gcc
[lyan1@mike1 ~]$ gcc --version
gcc (GCC) 4.7.2
```







Querying a Softenv key

 Command "soft-dbq" shows which variables are set by a SOFTENV key

[lyan1@mike1 ~]\$ soft-dbq +portland-12.8

Name: +portland-12.8 Description: @types: Compiler @name: The Portland Group Compilers @version: 12.8 @about: Portland Group's high-performance compilers and tools.

On the Linux architecture, the following will be done to the environment:

```
The following environment changes will be made:

CUDA_NIC_INTEROP = 1

LD_INCLUDE_PATH = ${LD_INCLUDE_PATH}:/usr/local/compilers/pgi/linux86-64/12.8/include

LD_LIBRARY_PATH = ${LD_LIBRARY_PATH}:/usr/local/compilers/pgi/linux86-64/12.8/lib

MANPATH = ${MANPATH}:/usr/local/compilers/pgi/linux86-64/12.8/man

PATH = ${PATH}:/usr/local/compilers/pgi/linux86-64/12.8/bin

PGI = /usr/local/compilers/pgi

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Compilers

	Vendor				
Language	Intel	PGI	GNU	NVIDIA	
Fortran	ifort	pgf77, pgf90	gfortran		
С	icc	pgcc	gcc		
C++	ісрс	pgCC	g++		
CUDA				nvcc	

- Usage: <compiler> <options> <your_code>
 - Example: icc -03 -o myexec mycode.c







Compiling CUDA Programs

- Add the softenv keys for CUDA and NVIDIA driver
 Currently +cuda-4.2.9 and +nvidiadriver-default
- Use the nvcc command to compile

```
[lyan1@mike401 asyncAPI]$ nvcc -I../../common/inc/ asyncAPI.cu
[lyan1@mike401 asyncAPI]$ ./a.out
[./a.out] - Starting...
GPU Device 0: "Tesla M2090" with compute capability 2.0
```

CUDA device [Tesla M2090] time spent executing by the GPU: 22.31 time spent by CPU in CUDA calls: 0.04 CPU executed 132214 iterations while waiting for GPU to finish







Compiling CUDA Fortran Programs

CUDA Fortran

- Fortran interface to CUDA
- PGI v12.8 is the only compiler that supports it on Super Mike II

```
[lyan1@mike405 cudaFortran]$ which pgf90
              /usr/local/compilers/pgi/linux86-64/12.8/bin/pgf90
              [lyan1@mike405 cudaFortran]$ pgf90 matmul.CUF
              [lyan1@mike405 cudaFortran]$ ./a.out
                arrays sized
                                       512 by
                                                         1024 by
                                                                            512
               calling mmul
               Kernel time excluding data xfer:
                                                    2665.000
                                                                  microseconds
               Megaflops excluding data xfer:
                                                    100726.3
               Total time including data xfer:
                                                    219162.0
                                                                  microseconds
                                                    1224.827
               Megaflops including data xfer:
                C(1,1) = 3.5791874E+11
                C(2,2) = 3.5739933E+11
                No errors found
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```



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Compiling OpenACC Programs

- OpenACC
 - Directive-based programming for code running on accelerators with syntax similar to OpenMP
 - Available in Fortran, C and C++
- Supported via PGI 12.8

```
[lyanl@mike401 openacc]$ pgf90 vecadd.f90 -ta=nvidia -Minfo
vector_add:
    11, Generating copyout(c(1:10))
    Generating copyin(a(1:10))
    Generating compute capability 1.0 binary
    Generating compute capability 2.0 binary
    12, Loop is parallelizable
    Accelerator kernel generated
    12, !$acc loop gang, vector(32) ! blockidx%x threadidx%x
        CC 1.0 : 7 registers; 52 shared, 12 constant, 0 local memory bytes
        CC 2.0 : 14 registers; 0 shared, 68 constant, 0 local memory bytes
```

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SHOC Benchmark

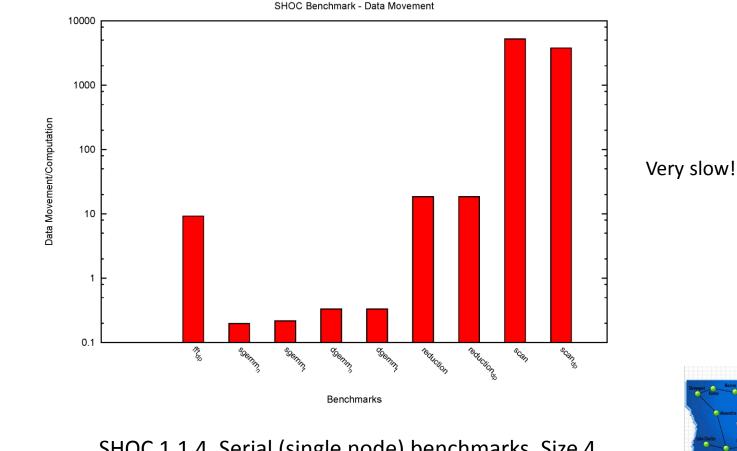
- Scalable HeterOgeneous Computing Benchmark Suite
 - Multiple benchmarks in both CUDA and OpenCL
 - Supports multiple devices per node
 - Inter-node parallel benchmarks with MPI
 - Both performance tests and stability tests







SHOC – Data Movement over PCIe





SHOC 1.1.4, Serial (single node) benchmarks, Size 4

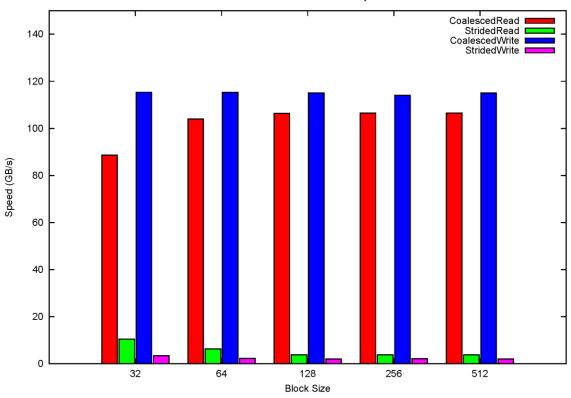
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SHOC – Coalesced vs Strided Memory Access



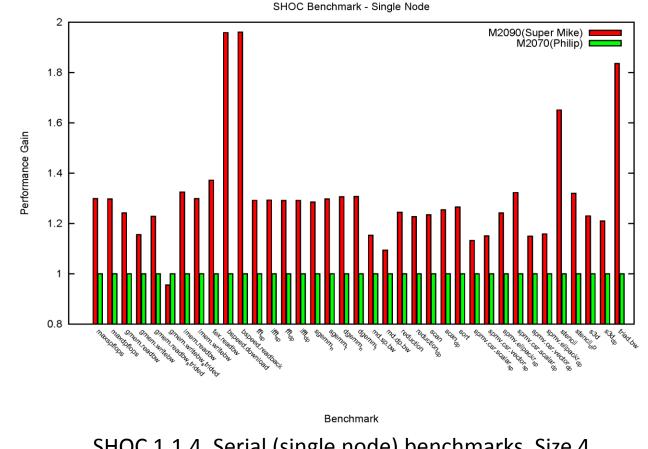
SHOC Benchmark - Global Memory Access







SHOC - Tesla M2090 vs M2070





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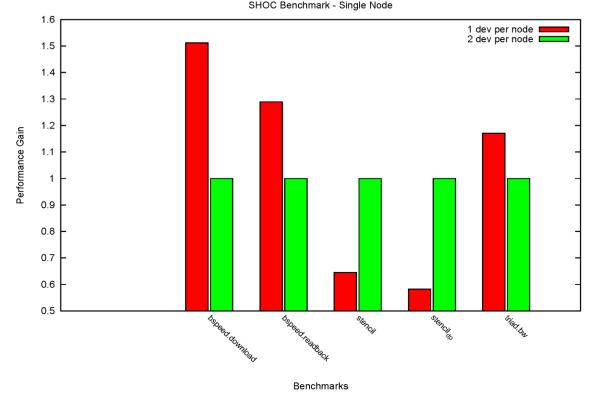
SHOC 1.1.4, Serial (single node) benchmarks, Size 4



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SHOC – Single vs Multiple Devices





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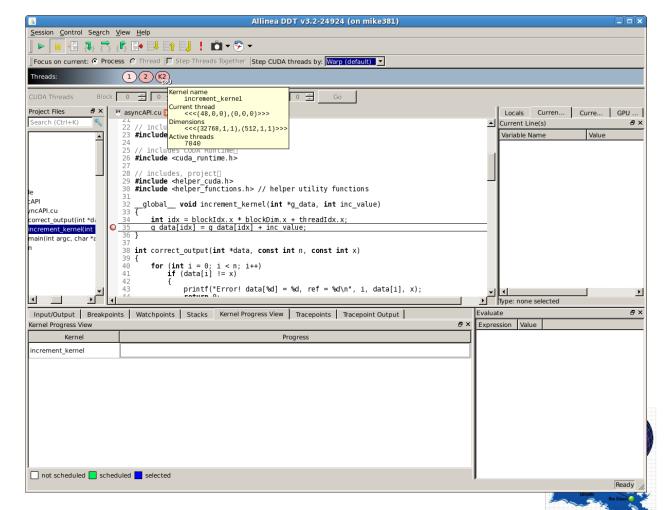
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SHOC 1.1.4, Parallel (MPI) benchmarks, Size 4



Debugging GPU Programs

- NVIDIA cuda-gdb
 - Command line debugger that comes with CUDA toolkit
 - CUDA only
- DDT
 - Parallel debugger that supports CUDA
 - Step through CUDA kernel
 - Examine data in GPU memory



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MPI Compilers (1)

Language	Compiler command
Fortran	mpif77, mpif90
С	mpicc
C++	mpiCC

- Usage: similar to what we have seen
 - Example: mpif90 -02 -o myexec mycode.f90
- On Super Mike II
 - The default MPI is OpenMPI 1.6.2
 - Keys:

```
+openmpi-1.6.2-Intel-13.0.0
+openmpi-1.6.2-gcc-4.4.6
+openmpi-1.6.2-gcc-4.7.2
+openmpi-1.6.2-pgi-12.8
```





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MPI Compilers (2)

- The MPI compilers are wrappers
 - They still use the compilers we've seen on the previous slide
 - Intel, PGI or GNU
 - They take care of everything we need to build MPI codes
 - Head files, libraries etc.
 - What they actually do can be reveal by the --show option
- It's extremely important that you compile and run your code with the same version of MPI
 - Use the default version (+openmpi-1.6.2-Intel-13.0.0) if possible







OpenMPI - mpirun

- Use mpirun or mpiexec (identical for OpenMPI) to run
- Options
 - np: number of processes
 - -hostfile (or -machinefile): name of the host file
 - --mca <parameter> <value>: specify run-time
 environment
 - Back-end network, resource manager support etc.
 - Ex: "--mca btl ^tcp" prevents tcp from being used for pointto-point communication







OpenMPI – mpirun (cont'd)

- Options (cont'd)
 - --bind-to-core: bind processes to specific cores
 (default is not to)
 - Performance consideration mainly for MPI-OpenMP hybrid programs
 - --byslot: assign processes round-robin by slot (default)
 - --bysocket: assign processes round-robin by socket
 - --bynode: assign processes round-robin by node







OpenMPI Commands

- Useful commands other than mpirun
 - ompi_info: tells everything about the OpenMPI
 installation
 - Ex:ompi_info -param btl all
 - ompi-top: Diagnostic to provide process info similar to the popular "top" program
 - ompi-ps: Displays information about the active jobs and processes in Open MPI







OpenMPI Configuration

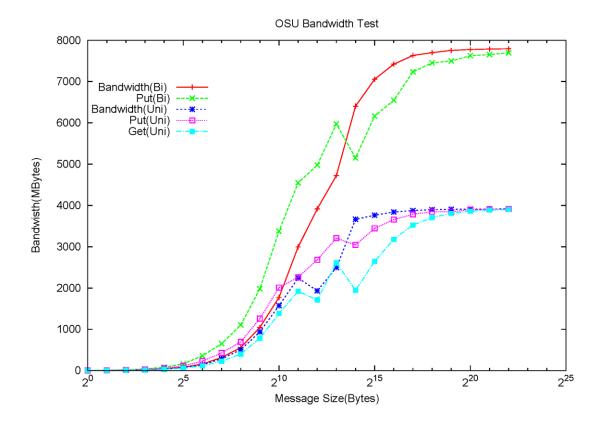
- Determined by (in the given order)
 - mpirun command line
 - Environment variables
 - File
 - \$HOME/.openmpi/mca-params.conf
 - <OpenMPI installation path>/etc/openmpi-mca-params.conf
 - Default
- Defined by openmpi-mca-params.conf on Super Mike II
 - FCA is turned off by default
 - Because of firmware issues, but
 - Consider to turn it on to reduce latency when you have many collective MPI calls with large message size (--mca coll coll_fca_enable 1)
 - MPI_LEAVE_PINNED is turned off by default
 - May hang multi-threaded MPI programs, but
 - Consider to turn it on to sustain high bandwidth when you have lots of large MPI messages (--mca mpi leave pinned 1)







OSU MPI Benchmarks – Bandwidth







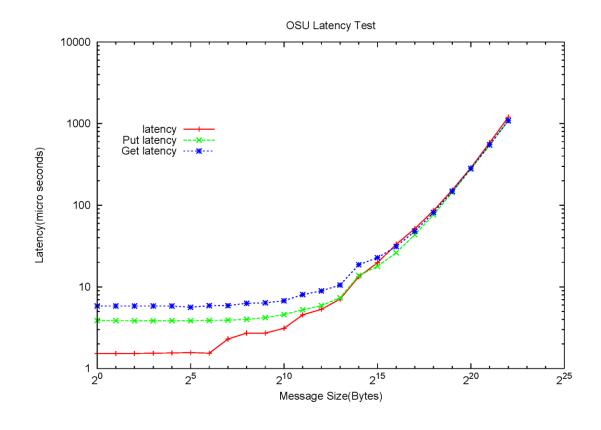
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OSU MPI Benchmark – Latency







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Batch Queuing System

- A software that manages resources (CPU time, memory etc.) and schedules job execution
 - Super Mike II: Torque (PBS)/Moab
- The batch queuing system determines
 - The order jobs are executed
 - On which node(s) jobs are executed







Job Queues

- There are more than one job queue
- The main purpose is group similar jobs to maximize utilization
- Each job queue differs in
 - Number of available nodes
 - Max run time
 - Max running jobs per user
 - Node characteristics
 - ...







Job Queues on Super Mike II

Machine	Queue	Max Runtime	# of nodes	Max running jobs per user	Max nodes per job	Use	
SuperMikell	workq	3 days	346	48	128	Unpreemptable	
	checkpt		262		200	Preemptable	
	bigmem	2 days	8		2	Big memory	
	gpu	1 day	50		32	Job using GPU	
	single	3 days	2	8	1	Serial jobs	
	Mwfa						
	Lasigma	Only open to certain users					
	Priority						
	Admin						







Job Types

- Interactive job
 - Set up an interactive environment on compute nodes for users
 - Advantage: can run programs interactively
 - Disadvantage: must be present when the job starts
 - Purpose: testing and debugging
 - Do not run on the head node!!!
 - Try not to run interactive jobs with large core count, which is a waste of resources)
- Batch job
 - Executed without user intervention using a job script
 - Advantage: the system takes care of everything
 - Disadvantage: can only execute one sequence of commands which cannot changed after submission
 - Purpose: production run







Basic Commands

- Queue querying
 - Check how busy the cluster is
- Job submission
 - Submit a job to run
- Job monitoring
 - Check job status (estimated start time, remaining run time etc.)
- Job manipulation
 - Cancel/hold jobs







Queue Querying

- Command: qfree
 - Show the number of free, busy and queued nodes

[lyan1@mike1 ~]\$ qfree
PBS total nodes: 453, free: 118, busy: 315, down: 20, use: 69%
PBS workq nodes: 168, free: 30, busy: 31, queued: 0
PBS checkpt nodes: 252, free: 30, busy: 17, queued: 248







Submitting Jobs

- Interactive job
 - qsub -I -V -l walltime=<hh:mm:ss>,nodes=<# of nodes>:ppn=16 -A <your allocation> -q <queue name>
 - Add -X to enable X11 forwarding
 - Limited to a maximum of 12 hours on Super Mike II
- Batch job
 - qsub <job script>
- On Super Mike II ppn must be 16 except for serial jobs







PBS Job Script – Parallel Jobs

#!/bin/bash					
<pre>#PBS -l nodes=4:ppn=16</pre>	Number of nodes and processor				
# PBS -1 walltime=24:00:00	Maximum wall time				
#PBS -N myjob	Job name				
#PBS -o <file name=""></file>	File name for standard output				
#PBS -e <file name=""></file>	File name for standard error				
#PBS -q checkpt	Queue name				
#PBS -A <hpc_allocation></hpc_allocation>	Allocation name				
#PBS −m e	Send mail when job ends				
#PBS -M <email address=""></email>	Send mail to this address				
<shell commands=""></shell>					
<pre>mpirun -machinefile \$PBS_NODEFILE -np 16 <path_to_executable> <options></options></path_to_executable></pre>					
<shell commands=""></shell>					







Running GPU-enabled Applications

- One needs to specify
 - How many devices per node
 - How many CPU cores per device
- Varies from one application to another
 - Ex: NAMD will automatically use all devices on the node(s) if built with CUDA
 - The user needs to determine how many CPU cores to use by
 - Creating an appropriate host file (with mpirun) or
 - Using the "+p<n>" and "+ppn<n>" option (with charmrun)
 - The user can indicate which device(s) to use with the "+devices" option (whith charmrun)







Example: Running NAMD on GPU

• Running NAMD on 16 nodes with 2 devices per node and 1 CPU process for device:

– With mpirun

mpirun -np 32 -hostfile \$newhostfile <path to namd
executable> apoal.namd

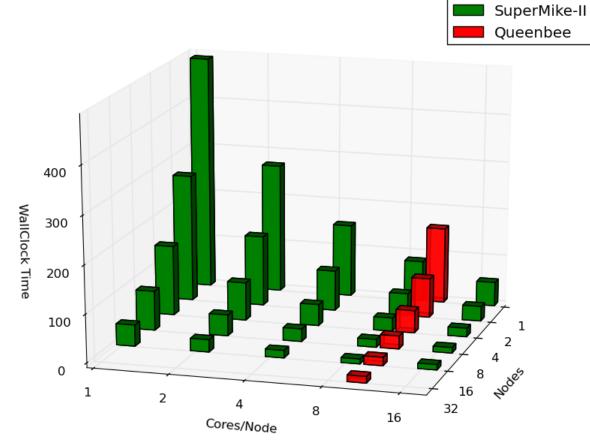
– With charmrun

charmrun +p32 ++nodelist <path to host file> <path to namd excutable> apoal.namd ++ppn 2 +idlepoll ++remote-shell ssh





NAMD Benchmark – CPU Only





NAMD 2.9, Apoa1 benchmark

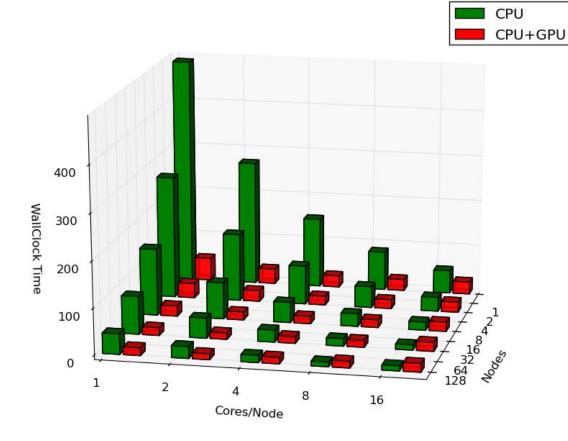
http://www.ks.uiuc.edu/Research/namd/performance.html



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NAMD Benchmark – With GPU





NAMD 2.9, Apoa1 benchmark

http://www.ks.uiuc.edu/Research/namd/performance.html



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Job Monitoring

- Command: showstart <job_id>
 - Check when a job is estimated to start
- Things that can change the estimated start time
 - Higher priority jobs are submitted
 - Running jobs terminate earlier than the system expects
 - The system has trouble starting your job







Job Monitoring cont'd

- Command:qstat <options> <job_id>
 - Show information on job status
 - All jobs are displayed if <job_id> is omitted
 - Show jobs submitted by a specific user: qstat -u <username>
 - Display in the alternative format: qstat -a <job_id>
- Command: qshow <job_id>
 - Show information on a running job
 - On which node(s) the job is running
 - CPU load
 - Memory usage







Job Manipulation

- Command: qdel <job_id>
 - Cancel a running or queued job
 - May take some time depending on the size of the job
- Command: qhold <job_id>
 - Put a queued job on hold
- Command:qrls <job_id>
 - Resume a held job





Benchmark Results on Super Mike II



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NAS Parallel Benchmarks

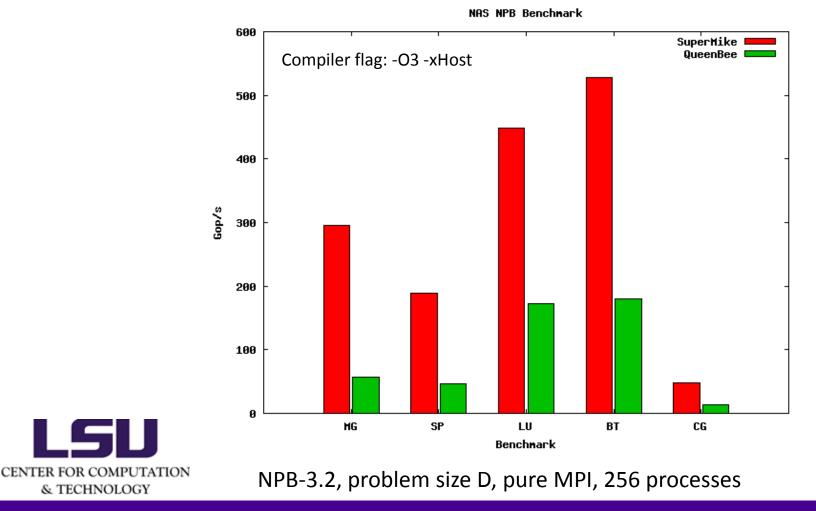
- Developed by NASA Advanced Supercomputing (NAS)
- Derived from CFD applications
 - MG: Multi-grid method for a 3D Poisson problem
 - CG: Conjugate-gradient solver for an unstructured sparse linear system
 - BT: Block tri-diagonal solver
 - Scalar penta-diagonal solver
 - LU: Lower-upper Gauss-Seidel solver







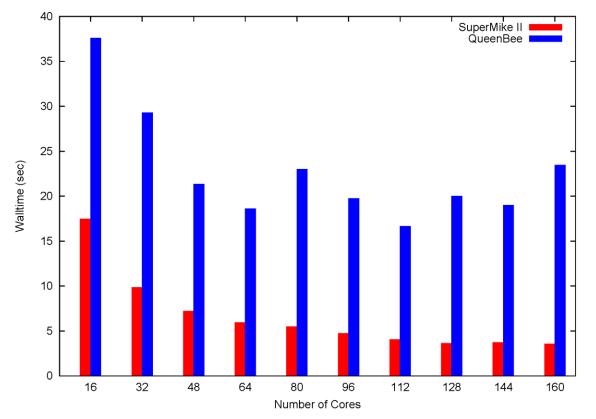
NAS Parallel Benchmarks



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LAMMPS Benchmark – CPU Only



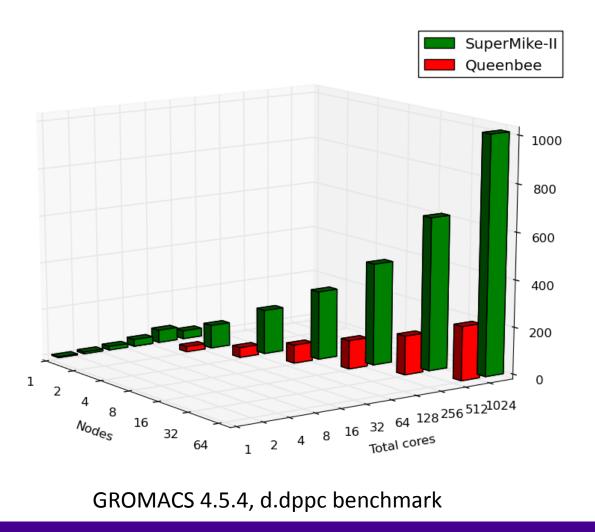




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GROMACS Benchmark





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Questions?





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