Introduction to High Performance Computing and Orchestra

HMS Research Computing Fall 2016



What is Orchestra?

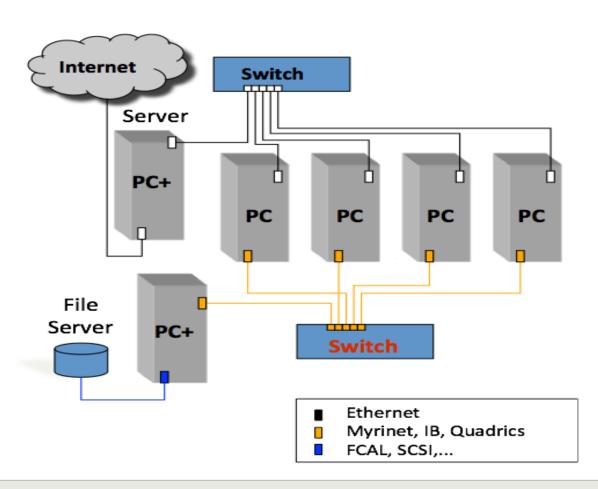


- Wiki page: https://wiki.med.harvard.edu/Orchestra
- Tech spec:
 - Over 550 compute nodes
 - Over 7500 cores
 - 10GigE interconnection
 - Over 40TB RAM
- CentOS 6 Linux
- LSF scheduler
- Total 28+PB storage





Generic Cluster Architecture



- Login nodes are for data management, job submission, code development, etc.
- Compute nodes are for production runs
- Your storage space is centralized network storage system
- Hundreds users are sharing the resources, so please be nice each other.
- Job scheduler works based on complex algorithms of fair-share, priority management, load balancing, etc.

Orchestra Compute Nodes

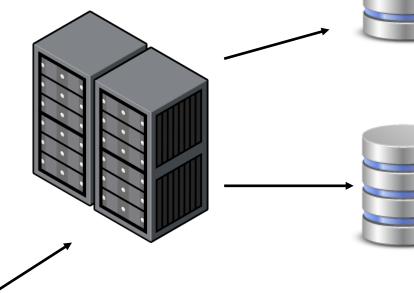
NODE CLASS	СРИ ТҮРЕ	Number of Nodes	Cores x Node	MEMORY x Node (~GB)	Total Cores
Flute	Opteron2216	25	4	32 (vary)	100
Bassoon	XeonE5345	43	8	32 (vary)	344
Bassoon	XeonE5430	12	8	32	96
Sax	XeonE74807	2	16	1024	32
Clarinet	XeonE5530	21	8	vary	168
Clarinet	XeonL5640	294	12	96 (vary)	3528
Fife	XeonE52680	16	20	190	320
Piccolo	XeonE5266v2	40	20	128	800
Ocarina	Opteron6376	8	32	512	512
Ottavino	XeonE52697	16	28	252	448

Orchestra Primary Storage



Orchestra Cluster

- 7500+ cores
- LSF batch system



Your computer

/home

- /home/user_id
- quota: 100GB per user
- Backup: extra copy & snapshots:
- daily to 14 days, weekly up to 60 days

/n/data1, /n/data2, /groups

- /n/data1/institution/dept/lab/your dir
- quota: expandable
- Backup: extra copy & snapshots:
- daily to 14 days, weekly up to 60 days



https://rc.hms.harvard.edu/



Temporary "Scratch" storage



- /n/scratch2
- For data only needed temporarily during analyses.
- Each account can use up to 5 TB and 1 million files/directories

- **Lustre** --> a high-performance parallel file system running on DDN Storage.
- More than 1 PB of total shared disk space.
- No backups! Files are automatically deleted after unaccessed for 15 days, to save space.
- More info at: https://wiki.med.harvard.edu/Orchestra/LustreScratch







- /n/nobackup
- used for large data sets not requiring backups
- limited to only a few labs with large data requirements

- **GPFS** --> a high-performance clustered file developed by IBM.
- 2 PB of disk space.
- No backups, but files are not purged on a schedule like "scratch" storage.
- More info at: https://wiki.med.harvard.edu/Orchestra/NoBackupGPFS



Checking Storage Usage

To check your storage available:

mfk8@loge:~\$ quota

Home directory: you get 100 GB, total.

Group directories: space varies, can increase.

/groups/groupname

/n/data1

/n/data2



Checking Storage Usage: scratch2

- mfk8@loge:~\$ Ifs quota -h /n/scratch2
- Quota is on user basis, not group basis
- Users are entitled to 5TB and up to 1 million files/directories

Storage Policies

- /home: 14 day snapshots + 60 day full backup
- /groups, /n/data1, /n/data2: 14 day snapshots + 60 day full backup
- /n/scratch2: 15 day retention, no backups
- New tape system for Long Term Storage

Snapshots

- Snapshots (static) are retained for up to 60 days: recover data
- mfk8@clarinet001:~\$ cd .snapshot
- mfk8@clarinet001:~\$ Is

Orchestra_home_daily_2015-10-02-02-00

Orchestra_home_daily_2015-10-01-02-00

- mfk8@clarinet001:~\$ cd Orchestra_home_daily_2015-10-02-02-00
- mfk8@clarinet001:~\$ cp MyRetreivedFile ~

Create an Orchestra Account

- http://rc.hms.harvard.edu/#orchestra
 - Click the red button and fill out the form!
- Your username will be your eCommons ID, with your eCommons password.

Account Request

LSF: Fair Sharing

- Load Sharing Facility: distributes jobs across Orchestra fairly
- Ensures that no one user or core monopolizes Orchestra
- Users are assigned dynamic priorities
- Queues also have priorities
- Submitting lots of jobs reduces your fairshare priority
- Even if many jobs are pending, your jobs will start quickly provided you have not submitted many jobs

Logging Into Orchestra: Mac



Open a terminal (search "terminal") ssh username@orchestra.med.harvard.edu

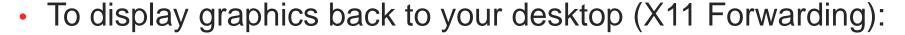
To display graphics back to your desktop (X11 forwarding) Install XQuartz (google it) and have it running

ssh -X username@orchestra.med.harvard.edu

Logging Into Orchestra: Windows

- Install PuTTY (google it)
- In box under "Host Name (or IP address)"

orchestra.med.harvard.edu



- Install Xming (google it) and have it running
- In PuTTY, under Connection -> SSH -> X11:
- Check "Enable X11 Forwarding" first and THEN log in 3.



Logging Into Orchestra: Linux



Open a terminal (search: "terminal")

ssh username@orchestra.med.harvard.edu

For graphics (X11 Forwarding)

ssh -X username@orchestra.med.harvard.edu

Welcome to Orchestra!

Where are you in Orchestra? See your terminal!

mfk8@mezzanine: ~\$

- You are logged into a "shell login server." Usually "mezzanine" or "loge." These are not meant for heavy lifting!
- You are in your home directory. This is symbolized by the "tilde " (~). This is shorthand for: /home/username
- You are in a bash environment. "\$" means "ready to accept your commands!"

Interactive Sessions

The login servers are not designed to handle intensive processes. Using 40% of a CPU results in a process being terminated. It is sometimes better to use an "interactive session." These last up to 12 hours. Start by entering your first job! This will (usually) log you into a "clarinet!"

mfk8@mezzanine:~\$ bsub -Is -q interactive bash

"bsub" is how jobs are submitted to Orchestra LSF

-Is (capital eye, s) tells Orchestra you want an interactive shell

-q is the "queue" to enter (interactive)

"bash" opens the bash session

mfk8@clarinet001:~/\$



Listing a Folder's Contents

 To see the contents of the current folder you are in (~ means "/home/username/"), type list (ls):

mfk8@clarinet001:~\$ Is

- To get the details of a folder's contents, add "-I" mfk8@clarinet001:~\$ Is -I
- You don't have to be in a directory to see its contents

mfk8@clarinet001:~\$ ls /groups/rc-training/introtohpc

Viewing File Contents

- "less" to view file contents
- Navigate up/down, search
- "q" to quit

mfk8@clarinet001:~\$ less /groups/rc-training/introtohpc/testfile.txt

Making a Folder (Directory)

- "mkdir" stands for "make directory."
- Create a new directory for this exercise
- Spaces are discouraged. (Underscores are fine!) Case counts in Linux.

mfk8@clarinet001:~\$ mkdir MyTestDir

Moving Around: Change Directory

- "cd" stands for "change directory"
- 1 period "."means "current directory"
- 2 periods ".." means "the directory above"

mfk8@clarinet001:~\$ cd MyTestDir

Notice how the prompt tells you where you are!

mfk8@clarinet001:~/MyTestDir\$ cd ...

mfk8@clarinet001:~\$

Creating a Simple Text File

- "Nano," "vi", "emacs" are simple command-line editors available.
- To create a new file, type the editor you want, then the name of the new file. To edit an existing file, do the same.

```
mfk8@clarinet001:~$ nano myfile.txt
   This is my new file text.
   (Control-X to save (yes) and exit.)
mfk8@clarinet001:~$
mfk8@clarinet001:~$ Is
   myfile.txt
```



Copying Files

"cp" to copy a file from a destination to a new destination. "cp" "from"
 "to"

mfk8@clarinet001:~\$ cp myfile.txt MyTestDir/

 You can copy a file to the current folder or to a new folder with a different name by specifying a different name (rename)

```
mfk8@clarinet001:~$ cp myfile.txt MyTestDir/myfilecopy.txt
```

```
mfk8@clarinet001:~$ cp myfile.txt mycopy2.txt
```

mfk8@clarinet001:~\$ cp /groups/rc-training/introtohpc/testfile.txt ~/MyTestDir/



Copying Directories

- "cp" "options" "source" "destination"
- Options:
 - -r: recursively (copies all)

mfk8@clarinet001:~\$ cp -r MyTestDir MyTest2

Moving Data

"move" "from" "to"

mfk8@clarinet001~:\$ mv MyTestDir/myfilecopy.txt ~

mfk8@clarinet001~:\$ mv MyTestDir/ MyTestDir2/

Removing Files/Folders

• "rm" to remove a file

mfk8@clarinet001:~\$ rm myfile.txt

"rm –r" to remove a folder recursively

mfk8@clarinet001:~\$ rm -r MyTest2

Wildcard * Pattern Matching

- Useful for copying/removing/etc all files matching a certain pattern
- Example Case:

To copy "all" files ending in ".fastq":

\$ cp *.fastq NewFastqFolder

Getting Data Onto Orchestra

- Use an FTP client of your choice
- Mac/Windows/Linux: Filezilla (google it)
- Connect to:

transfer.orchestra.med.harvard.edu your username and password port 22



Using Software: Environment Modules

- Most "software" on Orchestra is installed as an environment module. Allows for clean, easy loading, including most dependencies, and switching versions.
 - \$ module avail
 - \$ module avail seq/
 - \$ module avail stats/
 - \$ module avail seq/bowtie/

Loading/Unloading Modules

- Loading modules
 - \$ module load seq/bowtie/2.0.6
- Which module version is loaded (if at all)?
 - \$ which bowtie
- See all modules loaded
 - \$ module list
- Unloading modules
 - \$ module unload seq/bowtie/2.0.6
- Dump all modules
 - \$ module purge



Compiling your own software

- Users can compile software in their /home or /groups directories, where they have permission
- Binaries just require "unzipping" (ie tar –zxvf .tgz)
- Common compiling libraries are found as modules:

dev/compiler/gcc-4.8.5

dev/boost/1.57.0

dev/openblas/0.2.14

dev/lapack

Common libraries are found in "utils"

Installing Software: Binary Example

- mfk8@loge:~\$ bsub -ls -q interactive bash
- mfk8@clarinet001:~\$ wget http://path/to/binary/mysoftware.tar.gz
- mfk8@clarinet001:~\$ tar -zxvf mysoftware.tar.gz
- mfk8@clarinet001:~\$ Is mysoftware/bin

Installing Software: Source

- mfk8@loge:~\$ bsub —ls —q interactive bash
- mfk8@clarinet001:~\$ module load dev/compiler/gcc-4.8.5
- mfk8@clarinet001:~\$ wget http://path/to/source/mysoftware.tar.gz
- mfk8@clarinet001:~\$ tar -zxvf mysoftware.tar.gz
- mfk8@clarinet001:~\$ cd mysoftware
- mfk8@clarinet001:~\$ less README
- mfk8@clarinet001:~\$./configure --prefix=/home/mfk8/software
- mfk8@clarinet001:~\$ make
- mfk8@clarinet001:~\$ make install









Python, R, Perl

- Users manage their own package libraries: get the version you want, when you want it!
- Python: virtual environment allows pip/easy installs https://wiki.med.harvard.edu/Orchestra/PersonalPythonPackages
- R: set up personal R library for cran, Bioconductor https://wiki.med.harvard.edu/Orchestra/PersonalRPackages
- Perl: local::lib allows cpan, cpanm https://wiki.med.harvard.edu/Orchestra/PersonalPerlPackages
- Shebangs: #!/usr/bin/env python/Rscript/perl



MATLAB on Orchestra



- Free to use, with 2000 licenses
- Graphical interface (GUI) available, but lag over X11
- Compiling code does not improve performance
- Parallel Computing Toolbox: look for future seminars!
- MathWorks specialists will hold Office Hours this semester



Submitting Jobs

- In an "interactive session", programs can be called directly.
 - mfk8@clarinet001:~\$ bowtie -p 4 hg19 file1_1.fq file1_2.fq
- From the login shell (and also interactive or any compute nodes), a program is submitted to Orchestra via a job (bsub).
 - mfk8@clarinet001:~\$ bsub < mybowtiejob.sh
- Orchestra will notify you when the job is done, or if there is an error.

https://rc.hms.harvard.edu/

The "bsub"

mfk8@clarinet001:~\$ bsub -q queue -W hr:min job

- Necessary:
 - -q (queue)
 - -W (runtime in hr:min)

Shared Queues

- mpi queue if you have an MPI parallel job
- priority queue if you have just one or two jobs to run
- mcore queue if you have multi-core jobs to run.
- short queue if your jobs will take less than 12 hours to run.
- Else: long queue.

Shared Queues Breakdown

Queue Name	Priority	Max Cores	Max Runtime
interactive	12	12	12 hours
priority	14	12	1 month
mcore	12	20	1 month
mpi	12	400	1 month
parallel	10	400	1 month
short	8	12	12 hours
long	6	12	1 month
mini	5	1	10 minutes

Runtime Limit

- -W in hours:minutes
- Runtimes are subject to the maximum time permitted per queue (see table)
- If your job exceeds your runtime, your job will be killed ⊗
- Running many jobs that finish quickly (less than a few minutes) is suboptimal and may result in job suspension, contact RC to learn how to batch jobs

CPU Limit

- Amount of seconds the cluster works on your job (calculated by LSF)
- Ncores * Runlimit (-n * -W)
- Common error:

bsub –q short –W 8:00 tophat –p 8

tophat asks for 8 cores but only 1 requested (no -n), job killed in 1 hour

Multithreading

- A single CPU can execute multiple processes (threads) concurrently
- n indicates how many cores are requested
- Jobs that are overefficient (use more cores than reserved) jeopardize the health of a node
- Reserve the same amount of cores in your job and your bsub!

Reserving Memory

- Most nodes have 90GB memory available over all cores, some have more
- Make a resource request with
 - -R "rusage[mem=16000]" (memory requested in MB)
- Memory multiplies by cores requested, so
 - -n 4 –R "rusage[mem=16000]" reserves 64GB memory
- Asking for more memory may cause jobs to pend longer
- TERM_MEMLIMIT errors indicate that not enough memory was reserved



MPI

- Efficient way to run parallel jobs
- Dedicated queue with same-type compute nodes for optimal performance (400 cores)
- Matlab, Python, Java, R, C++, Fortran have MPI options
- Orchestra implementation: openMPI-1.8.6
- Talk to us first!



GPU

- **Graphical Processing Unit**
- Image processing, deep learning, and more!
- Experimental, limited queue to gauge the interest and needs of the research community
- K20, K80, M40 currently available
- Send us feedback on workflows and requirements!

Other bsub options

- -n 4 (number of cores requested)
- -R "rusage[mem=16000]" (memory requested in MB)
- -J jobname
- -a openmpi (type of mpi run)
- -Is (interactive shell)
- -e errfile (send errors to file)
- -o outfile (send screen output to file)
- -N (notify when job completes)



Monitoring Jobs

List info about jobs/their status:

```
mfk8$loge:~$ bjobs
```

- -r (running jobs)
- -p (pending jobs)
- -I (command entered, long form)
- List historical job information

```
mfk8$loge:~$ bhist jobid
```

Job Suspensions

- Jobs in the "long" queue can be suspended by LSF temporarily to allow jobs from the "short" queue (less than 12h) to run.
- If a job is suspended for >50% of the –W runlimit cumulatively, it will be automatically moved to the "no_suspend" queue where it can't be suspended anymore.

https://rc.hms.harvard.edu/

Terminating Jobs

Terminate a job (jobid given at submission)

mfk8\$loge:~\$ bkill jobid

Terminate multiple jobs

mfk8\$loge:~\$ bkill jobid1 jobid2 jobid3

Terminate all of your jobs (be careful!)

mfk8\$loge:~\$ bkill 0

Shell Scripts: The Basics

#! /bin/sh #always at the top

#program with options

module load seq/tophat/2.1.0 seq/bowtie/2.2.4 seq/samtools/1.2

tophat -p 4 -o ./mytophatdir1 hg19 file1_1.fastq file1_2.fastq

tophat -p 4 -o ./mytophatdir2 hg19 file2_1.fastq file2_2.fastq

#save as myshellscript.lsf



Calling a Shell Script

mfk8@balcony:~\$ bsub -q mcore -W 12:00 -n 4 -e %J.err -o %J.out –N sh myshellscript.lsf

Creating a Complete Shell Script

```
#! /bin/sh
#BSUB -q mcore
#BSUB -W 12:00
#BSUB -o %J.out
#BSUB -e %J.err
#BSUB -N
#BSUB -n 4
#BSUB -R "rusage[mem=12000]"
module load seq/tophat/2.1.0 seq/bowtie/2.2.4 seq/samtools/1.2
tophat -p 4 -o ./mytophatdir1 hg19 file1_1.fastq file1_2.fastq
#save as myshellscript2.lsf
```

Calling a Complete Shell Script

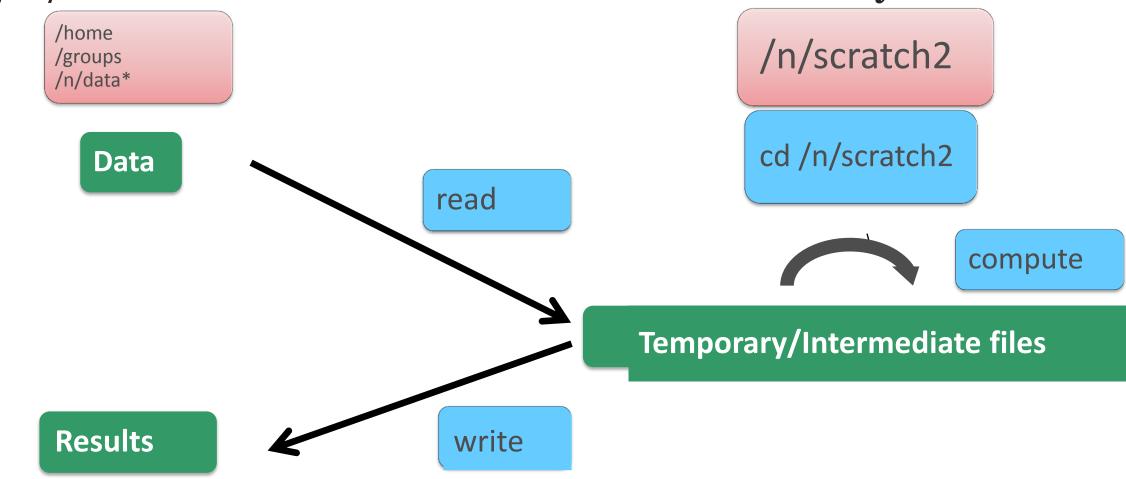
mfk8@balcony:~\$ bsub < myshellscript2.lsf

Using /n/scratch2

- Designed for writing large, temporary files
- Use cases:
- Keep original files in /groups (/n/data*) or /home, write intermediate files to /n/scratch2, write final files to /groups (/n/data*) or /home
- Change working directory to /n/scratch2, read files from /groups (/n/data*) or /home, write temp files to working directory, write or copy output back to /groups (/n/data*) or /home
- Copy input files to /n/scratch2, compute against, copy output files to /groups (/n/data*) or /home

/n/scratch2 Workflow: Redundancy /n/scratch2 /home /groups /n/data* cp/rsync cd /n/scratch2 Data Data compute **Temporary/Intermediate files** cp/rsync compute **Results Results**

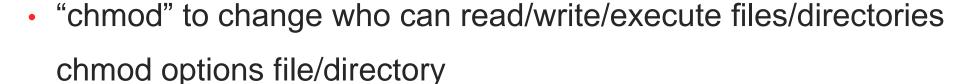
/n/scratch2 Workflow: Medium Flexibility



/n/scratch2 Workflow: Best Practice

/home /groups /n/data* /n/scratch2 **Data** read read/write Temporary/Intermediate files compute read/write write Results

File Properties



Who? user group others all (u/g/o/a)

What? **r**ead **w**rite execute (r/w/x)

Do? +/-

- chmod u+x myfile #makes a file executable to owner
- chmod o-rwx myfile #takes away permission from others to read/write execute



Data lifecycle for biomedical research



Creation

- •raw data
- associated protocols, reagents, etc.



Analysis

- •analytical methods
- •analysis results



Access,

Re-use,

Re-purpose

Storage & Maintenance

- •store on appropriate tier, with proper security
- •store locally on servers, or
- •in the cloud

Distribution & Use

- share data with collaborators
- annotate datasets & upload to public repositories
- include in relevant publications and reports



Long-term storage & Archiving

- •in compliance with HMS & federal
- •as requested by investigators



Evaluate for Retention

- retain essential research records only
- organize and annotate appropriately



Data Management Working Group



Scripting: Version Tracking

- Record changes (additions/deletions/replacements) to scripts
- Collaboration: many people can work on a file at once
- Helps with reverting to previous (working) versions
- Public or private repository options
- GitHub
- Bitbucket
- SVN





Class Exercises

- In your "home" directory, create a file called ".forward" using nano with this piece of information: your preferred email address for Orchestra notifications. Save.
- Copy the .bam file from /groups/rc-training/introtohpc to your "home" directory, load "samtools" module, and submit a job to the "short" queue for "1 hr" that has this command:
 - samtools sort control.bam sorted.bam
- Monitor this job, then kill it
- Delete all class files (except .forward)



For more direction:

- https://wiki.med.harvard.edu/Orchestra/NewUserGuide
- http://rc.hms.harvard.edu
- rchelp@hms.harvard.edu
- Office Hours: Wednesdays 1-3p Gordon Hall 500
- Class survey:

http://hmsrc.me/introhpc2016-survey5