

High-Performance Computing 101

Health Data Working Group

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Learning objectives

- 1 Introduce scope, utility and capabilities of HPC systems
- 2 Present relevant topics on HPC:
 - job scheduling and monitoring
 - software and libraries usage
 - efficient data creation and management
- 3 Provide some resources for HPC learning at UofT (and beyond)

Audience interests

If you are here for this workshop you may fall into one of these categories

- ① Completely new to HPC
- ② Modest experience in HPC and looking to get useful pointers
- ③ Seem like an interesting thing to do today

What is HPC? - Expectation

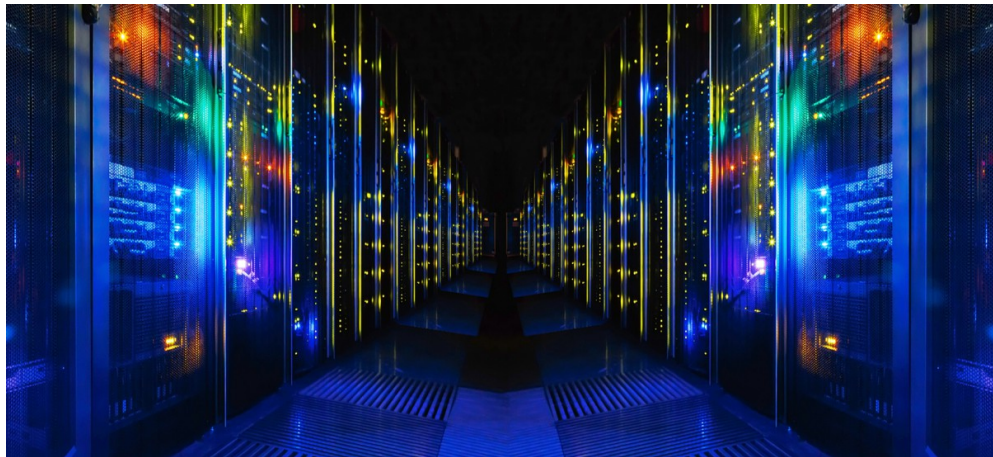


Figure 1: Advertising a supercomputer facility

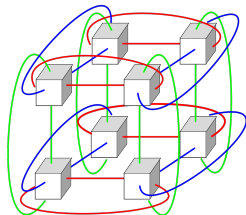
What is HPC? - Reality



Figure 2: Niagara supercomputer at UofT

HPC - in short

- Practice of aggregating computing power (measured in FLOPS)
- Achieved by 'clustering' many smaller computers and processors
 - Each of these computers is called a 'node'
 - Nodes communicate using a dedicated network
- Deliver higher performance than a typical workstation
- Aims to solve large problems in science, engineering, or business



HPC - some applications

- Quantum mechanics
- Weather forecasting
- Molecular modelling
- Astrophysics

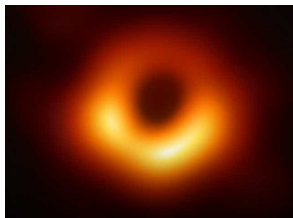
Why using HPC?

Pros:

- Reduce computational time
- Increase CPU capacity
 - Model resolution
 - Number of scenarios
- Increase memory and/or storage
 - Aggregate larger data
 - Solve bigger problems
- Can tackle otherwise unfeasible projects

Cons:

- A relatively steep learning curve
- Largely DIY
- Shared systems → Planning needed



Getting started - SSH

Secure SHell Protocol

- cryptographic network protocol for operating network services securely over an unsecured network

Windows:

- MobaXterm
- PuTTY

MacOS/Linux

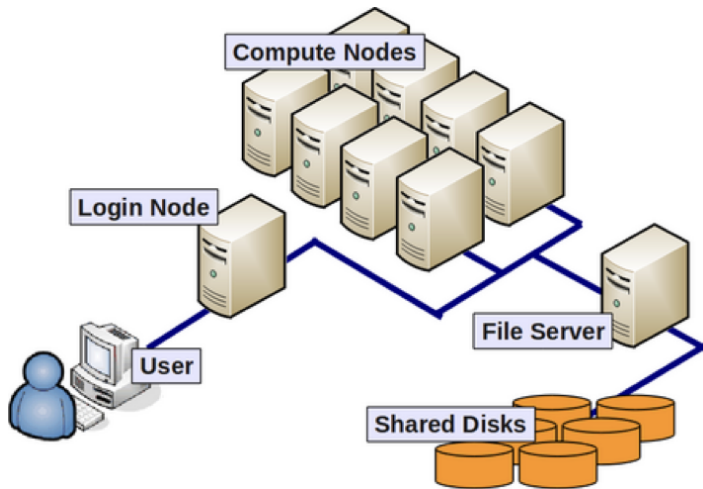
- Terminal



Getting started - login

- Clusters can be accessed over the internet / local network
- `ssh username@hostname`
- Other commonly used syntax: `ssh -Y ...` or `ssh -X ...`
- `man ssh` (MacOS/Linux) for many more options

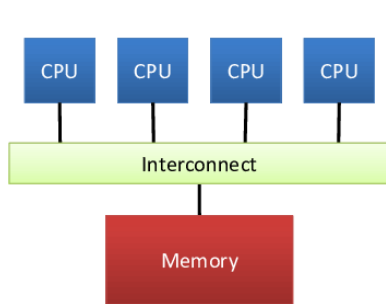
Getting started - basic environment



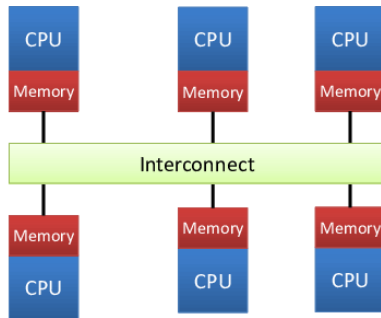
Shell scripting

- This is the most widely used interface in HPC
- For the most part one gets by with basic commands
 - `ls`, `cd`, `mv`, `cp`, `pwd`
- Shell scripting intros/tutorials
 - [shellscrip.sh](#)
 - [The Unix shell](#)
 - [Intro to the Linux shell](#) (account needed)

Shared vs. distributed memory



(a)



(b)

Job scheduling

- Login nodes are not designed to carry out large computations
- As a shared resource, fair use is encouraged / enforced
- Multiple scheduling tools available:
 - Slurm
 - PBS/Torque
 - SGE
 - LSF
 - Different syntax similar purpose ([rosetta stone of workload managers](#))

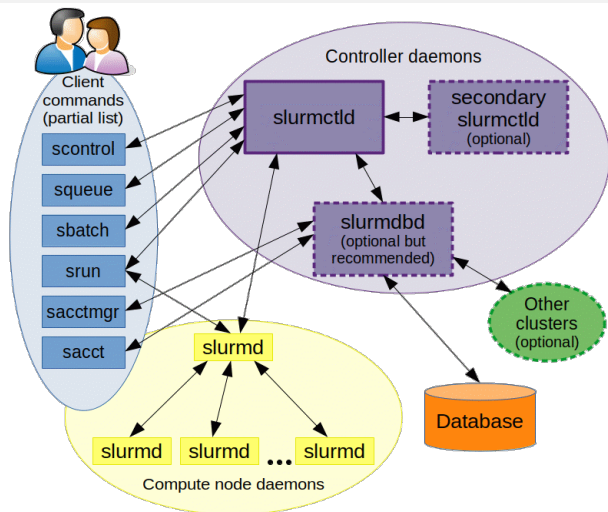
Job scheduling - in a nutshell

- A tool that tells the HPC system what to run, for how long, and how much resources it will need - At all times, for all users
- A job scheduler performs the following tasks
 - Assigns users to compute nodes
 - Provides a framework for initiating, performing, and monitoring work on the assigned nodes
 - Manages the queue of pending work and determines which job will be assigned to the node next

Job scheduling - Slurm

Basic commands:

- sbatch
- squeue
- scancel
- srun
- sacctmgr
- sacct



[Slurm documentation](#)

Job scheduling - a simple example (1)

The following lines are part of a file called `firstjob.sh`

```
#!/bin/bash  
#SBATCH --nodes=2  
#SBATCH --ntasks-per-node=40  
#SBATCH --time=1:00:00  
#SBATCH --job-name=Myfirstjob  
#SBATCH --output=job_output_%j.out  
  
cd $SLURM_SUBMIT_DIR  
  
# ... do something in this job using 80 cores ... #
```

Submit the job as

```
login-node:$ sbatch firstjob.sh
```

Job scheduling - a simple example (2)

Alternatively, we can do the following:

File `secondjob.sh`

```
#!/bin/bash  
  
cd $SLURM_SUBMIT_DIR  
  
# ... do something in this job using 80 cores ... #
```

Submit the job as

```
login-node:$ sbatch -N 2 -ntasks-per-node=40 -t 1:00:00 \  
                -J Mysecondjob -o job_output_%j.out secondjob.sh
```

Job scheduling - a simple example (3)

If successful, the system will show something like:

```
login-node:$ sbatch ... secondjob.sh  
Submitted batch job 34987
```

where 34987 is the job id.

(Or give an error otherwise)

Common errors that may make the job submission fail:

- The bash script is not executable (solution: `chmod 700 firstjob.sh`)
- The script is launched from a read-only path (solution `cd /writable/path`)
- Requesting resources, e.g., wall time, memory, cores

Job scheduling - partitions

Some systems configure different 'queues' or 'partitions'

These are set with option `-p` or `--partition`

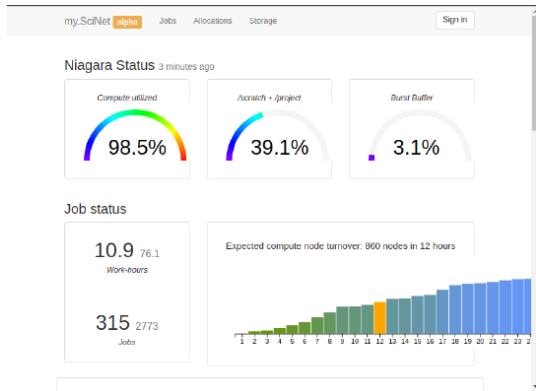
- `walltime`
- `memory available`
- `number of cores per node`

Job monitoring

- `squeue` to show the job queue (`squeue --me` for just your jobs)
- `squeue -j JOBID` information on a specific job (alternatively, `scontrol show job JOBID`, which is more verbose)
- `squeue --start -j JOBID` estimate for when a job will run
- `scancel -i JOBID` cancel the job
- `scancel -u USERID` cancel all your jobs
- `sinfo -p partition` look at available nodes in partition
- `sacct info` on your recent jobs

Job monitoring - my.SciNet

<https://my.scinet.utoronto.ca>



Features

- Niagara cpu and storage utilization
- Status of the login nodes
- Job history
- Per job:
 - jobscript
 - environment
 - wall time
 - *memory usage*
 - *CPU usage*
 - *GFlops/s*
 - *disk I/O*

Job monitoring - my.SciNet

<https://my.scinet.utoronto.ca>

my.SciNet **alpha**

Jobs

Allocations

Storage

Users

TestJobs

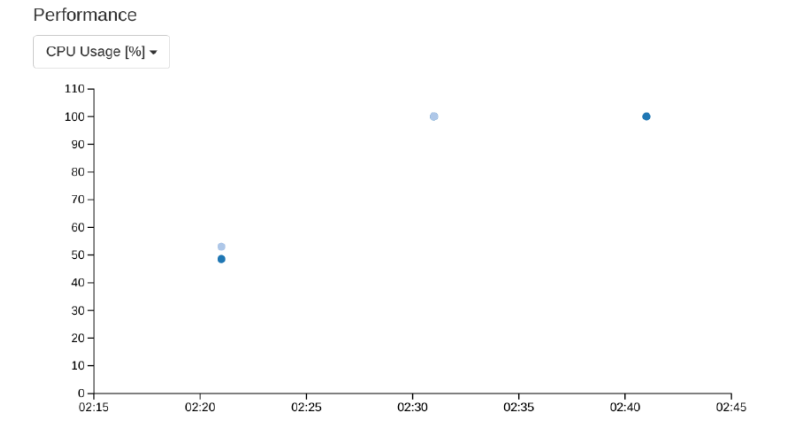
Sign out rzon

Job 824361: mpi_job

State	RUNNING
Partition / QOS	compute / bigprio
Alloctres	cpu=160,node=2,billing=80
Nodelist	nia[0437,1417]
Timelimit	01:00:00
StartTime	2019-01-14 14:16:19.000000
Walltime	00:23:44
Workdir	/gpfs/fs0/scratch/s/scinet/rzon/mpiexample
Maxdiskread	-
Maxdiskwrite	-
MaxRSS	-
MaxVMSize	-
TotalCPU	00:00:00
SystemCPU	-
UserCPU	-
Queue time	0m out of 24m (0.0%)
CPU time	0m out of 31h 39m (0.0%)

Job monitoring - my.SciNet

<https://my.scinet.utoronto.ca>



- Given the wide range of users and applications different software is needed
- Robust software management is necessary
- Tools like `lmod` come to the rescue

Software in HPC - module loading

- Usually, multiple software is installed, all is made available via `module` commands
- `module` sets appropriate environment variables (`PATH`, etc.)
- `module` takes care of conflicting versions of a given software to be available
- relevant for reproducibility purposes

Software in HPC - useful commands

- `module load <module-name>` use particular software
- `module purge` remove currently loaded modules
- `module spider` (or `module spider <module-name>`) list available software packages
- `module avail` list loadable software packages that require no other modules to be loaded first
- `module list` list loaded modules

Software in HPC - available software (SciNet's Niagara)

```
login-node:$ module spider
```

The following is a list of the modules and extensions
currently available:

CCEnv: CCEnv

Compute Canada software modules. Must be loaded to see
Compute Canada modules in 'module spider'.

NiaEnv: NiaEnv/2018a, NiaEnv/2019b

Software modules for Niagara. Must be loaded to see
Niagara modules in 'module spider' (loaded by default).

antlr: antlr/2.7.7

ANTLR, ANother Tool for Language Recognition, ...

...

Software in HPC - software loading details (1)

```
login-node:$ module spider r
```

```
r:
```

Description:

R is a language and environment for statistical computing
and graphics

Versions:

r/3.5.3

...

r/4.1.2

Other possible modules matches:

.singularity antlr arm-forge ...

To find other possible module matches execute:

```
$ module -r spider '.*r.*'
```

For detailed information about a specific "r" package

(including how to load the modules) use the module full name ...

For example:

```
$ module spider r/4.1.2
```

Software in HPC - software loading details (2)

```
login-node:$ module load r/4.1.2
```

Lmod has detected the following error:

These module(s) or extension(s) exist but cannot be loaded as requested: "r/4.1.2"

Try: "module spider r/4.1.2" to see how to load the module(s).

Software in HPC - software loading details (3)

```
login-node:$ module spider r/4.1.2
```

```
-----  
r: r/4.1.2  
-----
```

Description:

R is a language and environment for statistical computing and graphics

You will need to load all module(s) on any one of the lines below before the "r/4.1.2" module is available to load.

```
gcc/8.3.0  
intel/2019u4
```

Help:

R is 'GNU S', a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the R project homepage for further information.

Homepage: <https://www.r-project.org>

Software in HPC - software loading details (4)

```
login-node:$ module load intel/2019u4 r/4.1.2  
login-node:$ R
```

```
R version 4.1.2 (2021-11-01) -- "Bird Hippie"  
Copyright (C) 2021 The R Foundation for Statistical Computing  
Platform: x86_64-pc-linux-gnu (64-bit)
```

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type `'license()'` or `'licence()'` for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type `'contributors()'` for more information and
`'citation()'` on how to cite R or R packages in publications.

Type `'demo()'` for some demos, `'help()'` for on-line help, or
`'help.start()'` for an HTML browser interface to help.
Type `'q()'` to quit R.

>

Installing libraries/packages

- For the most part library/package installation works as in any workstation
 - i.e., `install.packages(...)` in R
- There are some exceptions:
 - cluster has no internet access (usually, only login nodes can reach the www)
 - installation requires special dependencies

Installing libraries/packages - special dependencies

One example: install `data.table` package with OpenMP support

```
login-node:$ ml NiaEnv/2019b ml gcc/8.3.0 openmpi/3.1.3 r/4.1.2
```

```
login-node:$ R
```

```
R version 4.1.2 (2021-11-01) -- "Bird Hippie"
```

```
....
```

```
> install.packages("data.table",  
  configure.args = c(paste0("--with-data.table-include=",  
    Sys.getenv("SCINET_OPENMPI_ROOT"),"/include"),  
    paste0("--with-data.table-libpath=",  
      Sys.getenv("SCINET_OPENMPI_ROOT"),"/lib")))
```

```
...
```

```
* DONE (data.table)
```

```
> library(data.table)
```

```
data.table 1.14.2 using 20 threads (see ?getDTthreads).
```

```
Latest news: r-datatable.com
```

Data creation

We are generating data at unprecedented rates!

General guidelines for (efficient) data creation in HPC:

- File I/O (Input/Output) is slow! Avoid it as much as you can! (CPU operations ≈ 1 ns, disk access times ≈ 5 ms.)
- Do not create lots of little files! They are an inefficient use of space and time (slow to create)
- Instead, save your data in big files which contain all the information you need
- Do not have multiple processes writing to files in the same directory (unless you're using parallel I/O)
- Write data out in binary. Faster and takes less space

Data management

How to organize files on disk?

- Human-interpretable filenames lose their charm after a few dozen files (or after a few months pass)
- Don't use filenames to store run information
- Avoid using a flat directory structure (i.e., no sub-directories). Organize your data in a sensible directory tree
- If you're doing many runs with many varied parameters, consider using a database to store the filenames of your runs, with associated run metadata
- Rigorously maintained meta-data (data about the data) is essential
- Back up your data, especially your metadata or database

Take-home messages

- HPC can greatly accelerate your work
- Understanding how to operate HPC systems is crucial
- Make full and efficient use of available resources

Acknowledgements and additional resources

- Some slides thanks to the SciNet team:
 - [Introduction to SciNet, Niagara & Mist](#) by Mike Nolta (Dec 2021)
 - [Storage and I/O in Large Scale Scientific Projects](#) by Ramses van Zon and Marcelo Ponce (Sep 2016)
- [Introduction to Shell and Cluster computing](#)
- [Niagara Quickstart](#)
- [Education @ SciNet](#) (amply recommended!)

Other clusters

- Compute Canada
- CCM @ Sickkids
- h4h @ UHN
- Galen @ Mount Sinai
- HPC4Health

Related topics of interest (R)

- [Intro to parallel computing in R](#)
- [A guide to parallelism in R](#)
- [Scalable data analysis in R](#)
- [foreach package vignette](#)

Thanks for listening!