

An introduction to compute resources in Biostatistics

Chris Scheller
schelcj@umich.edu

1. Resources
 1. Hardware
 2. Account Allocation
 3. Storage
 4. Software
2. Usage
 1. Environment Modules
 2. Tools
 3. Compiles
3. SLURM
 1. Scheduler
 2. Submitting Jobs
 3. Queue management
4. Summary
 1. Other Compute Resources
 2. More information

Hardware

- 19 nodes, 264 cores
- 32 GB of memory per node
- gigabit networking
- Nodes running Ubuntu-server (a debian based distribution)
- uses the SLURM Resource manager and job scheduler
- login node: biostat-login.sph.umich.edu

Account Allocation

Cluster accounts are available at cost to all biostat faculty, students and researchers. Account requests have to come from your faculty advisor. Your login name is your umich username and the password is your SPH AFS password.

Storage

- /home
 - 50GB quota per user
 - Only for current jobs
 - Backed up nightly
- /tmp
 - not shared across nodes
 - can server as scratch space for jobs
 - not backed up
- /afs
 - SPH AFS cell only
 - only available on login nodes

Software

- Defaults
 - OpenMPI
 - R
 - gcc/g++
- Available
 - SAS
- Coming soon
 - MATLAB
 - OpenMP
- Standard tools are also available
 - make, awk, sed
 - perl, python
 - vim, nano

Usage

Software modules

- module list
 - list loaded modules
- module load <modulename> ☐
 - load <modulename> for use
- module avail ☐
 - show all available modules
- module avail <modulename>
 - show all versions of <modulename> available
- module rm <modulename>
 - unload a currently loaded module

Introduction to SLURM

- SLURM is the Simple Linux Utility for Resource Management
- Slurm manages the resources of the cluster ie; cores, nodes
- Slurm also is the job scheduler
- Access to all compute nodes goes through the slurm job scheduler

The Scheduler

- Current scheduler limitations
 - Limited number of jobs in the queue in a running or pending state
 - Maximum number of running jobs
 - Max walltime of any running job
- Upcoming changes
 - The longer a job is in the queue the higher its priority
 - Recent usage: Accounts with less usage over the past week will have a higher priority than those with a lot of usage.

Job Queue

- Jobs are ran on a First In First Out basis
- Any holes in resource usage will be backfilled by the scheduler with smaller jobs that would have sat waiting.
- Reservations can be placed on nodes for users and or groups

Submitting jobs

There are two primary means of submitting jobs to the cluster.

- **srun**

- submit a single job via the command line

- `srun --time= <command_to_run>`

- time is a required option

- `srun --time=02:00 R CMD BATCH script.R`

- `srun --time=00:05 --nodes=2 hostname`

- `srun --time=1-0 --license=SAS script.SAS`

- `srun --time=28-0 --cpus_per_task=4 a.out`

- **sbatch**

- submit batch jobs from a batch file. A batch file is a short text file with the commands to run your job along with commands for the scheduler.

- `sbatch <batch_file>`

```
$ cat job.txt
#!/bin/sh
#SBATCH --mail-type=ALL
#SBATCH --mail-user=uniquename@umich.edu
#SBATCH --time=1-12:00
#SBATCH --nodes=2
#SBATCH --job-name=test_job
```

R CMD BATCH script.R

```
$sbatch ./job.txt
Submitted batch job 123456
```

```
$ cat slurm-123456.out
# STDOUT/STDERR are written to this file
```

Queue Management

- **queue**
 - view the contents of the job queue
- **scancel**
 - kill a queued job regardless of state
- **sinfo**
 - view information about cluster nodes and partitions

Summary

- Other compute resources
 - unfunded student compute servers.
 - Not part of the cluster, jobs are run locally.
 - compute0.sph.umich.edu
 - compute4.sph.umich.edu
 - <http://www.sph.umich.edu/computing/unix/machines.html>
 - FLUX
 - University wide cluster ran by the Center for Advanced Computing.
 - Currently has 2000 cores available
 - Allocations have a cost billed per core per month
 - <http://cac.engin.umich.edu/>

More Information

- To request an account have your advisor email sph-biostat-help@umich.edu with your username.
- Primary cluster documentation
 - <https://webservices.itcs.umich.edu/mediawiki/Biostatistics/index.php>
- New user introduction page
 - <https://webservices.itcs.umich.edu/mediawiki/Biostatistics/index.php/Cluster/NewUserIntro>