# Biostatistics Linux Cluster

Chris Scheller

schelcj@umich.edu

http://www.sph.umich.edu/biostat/computing/cluster/

# Hardware

- 20 nodes for total 276 cores

- 32 GB of memory per node

- 3 nodes with 128GB+ memory available

- Gigabit networking

- Nodes running ubuntu-server(debian based)

- SLURM Resource Manager / Job Scheduler

- Login node: biostat-login.sph.umich.edu

# Account Allocation

- Accounts available to all biostat faculty, students and researchers

- Currently no cost associated with allocations

- Account requests should come from faculty advisor or PI

- Send requests to sph-biostat-help@umich.edu

# Storage

- /home
  - 50GB quota per user
  - Only for current jobs, not permanent storage
  - Backed up nightly
- /tmp
  - Unique per node
  - Servers as scratch space for jobs
  - Not backed up
  - Purged after 30 days of inactivity

# Storage

- /afs
  - Umich IFS Cell
  - Available only on login nodes
  - Can not be referenced from running jobs

# Software

- The *modules* package is used to control software

- Full list of available modules
  http://www.sph.umich.edu/biostat/computing/cluster/software.html#availablemodules

- To request new software contact sph-biostat-help@umich.edu

# Modules

- The Environment Modules package provides for the dynamic modification of a user's environment via modulefiles.

- Typically modulefiles instruct the module command to alter or set shell environment variables such as PATH, MANPATH, etc

# Module Examples

*$ module load R*

*$ which R*

*$ module unload R*

*$ module show R*

*$ module load openbugs*

# Module Subcommands

| Subcommand | Description |
| --- | --- |
| list | List currently loaded modules |
| load | Load module for use |
| unload | Remove a currently loaded module |
| avail | Show all available moduels |
| show | Display detailed module information |

# Slurm

- SLURM is the Simple Linux Utility for Resource Management

- Manages the cluster resources ie; cores, nodes, memory

- Also serves as the job scheduler

# Job Scheduler

- Current scheduler limitations

  - Max of 500 jobs in queue regardless of state

  - Max wall time of 28 days for all jobs

  - A time estimate is required for all jobs

  - Default 1GB of memory per job with more memory available at job request time

# Job Queue

- All jobs are scheduled on a FIFO with backfill.

- The backfill scheduler will initiate a lower-priority job if doing so does not delay the expected initiation time of higher priority jobs

- Smaller jobs are used to fill holes in the resource allocation plan

# Submitting Jobs

- Using the batch system

  - Create a batch file – a short text file with batch commands and your code

  - Submit the batch file to the cluster

  - Check the status of your job

  - Delete your job if you want to cancel it

# Creating a batch file

```
#!/bin/sh
#
#SBATCH --mail-type=ALL
#SBATCH --mail-user=uniqname@umich.edu
#SBATCH --time=1-12:00
#SBATCH –job-name=test_job
#SBATCH –mem_per_cpu=2000
#SBATCH –output=results.txt
#SBATCH –error=errors.txt
#SBATCH –workdir=/home/uniqname/proj1

srun  R CMD BATCH script.R
```

# Job Control

- Submit your batch script with the `sbatch` command

    *$ sbatch ./job.txt*

- Check the status of your job with the `squeue` command

    *$ squeue -u $USER*

- Delete your job with the `scancel` command

    *$ scancel <jobid>*

# More Information

- For account requests contact

  sph-biostat-help@umich.edu

- Primary cluster documentation
  http://www.sph.umich.edu/biostat/computing/cluster/

- Slurm documentation

  https://computing.llnl.gov/linux/slurm/

- Batch file examples
  http://www.sph.umich.edu/biostat/computing/cluster/examples/