

Biostatistics Linux Cluster

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<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 modules
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=uniquename@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/uniquename/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/>