# Cluster Computing

Dan Barker danbarke@umich.edu Cluster System Administrator

## **Batch Computing Clusters**

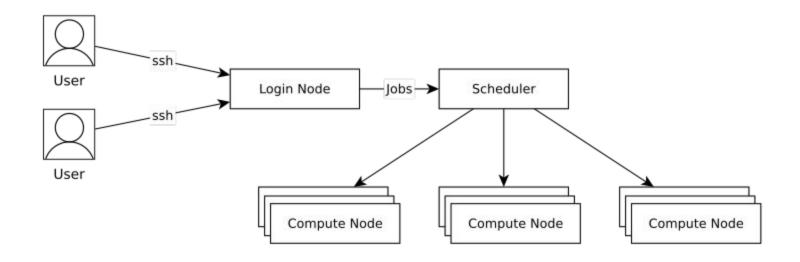


image credit: <a href="https://docs.hpc.qmul.ac.uk/intro/">https://docs.hpc.qmul.ac.uk/intro/</a>

## **Biostatistics Computing Cluster**

55 Compute Nodes

2 Login Nodes

948 Processors

~5.5TB RAM

Red Hat Enterprise Linux

Statistical Software R, SAS, Matlab

## Login with SSH

login host: biostat-login.sph.umich.edu

Enter kerberos <u>password</u> (same as email)

Authenticate with **Duo** 

MacOS: <u>Terminal</u>

Windows: PuTTY

All OSes: Biostatistics Web Portal

### Anatomy of a Batch Job

```
#!/bin/bash

#SBATCH --job-name=hello_world

#SBATCH --time=10:00

#SBATCH --mail-user=danbarke@umich.edu

#SBATCH --mail-type=BEGIN,END,FAIL

#SBATCH --mem=4000mb

#SBATCH --cpus-per-task=1
```

R CMD BATCH script.R

#### Slurm Commands

sbatch <batch\_script\_file> - submits a job

squeue -u <uniqname> - show all jobs for user on cluster

scancel <jobid> - cancel a job

sacct - show data about recently completed or running jobs

All slurm commands have additional options available in their manual pages

Type "man <command>" to bring up the man page

Type "q" to exit the man page

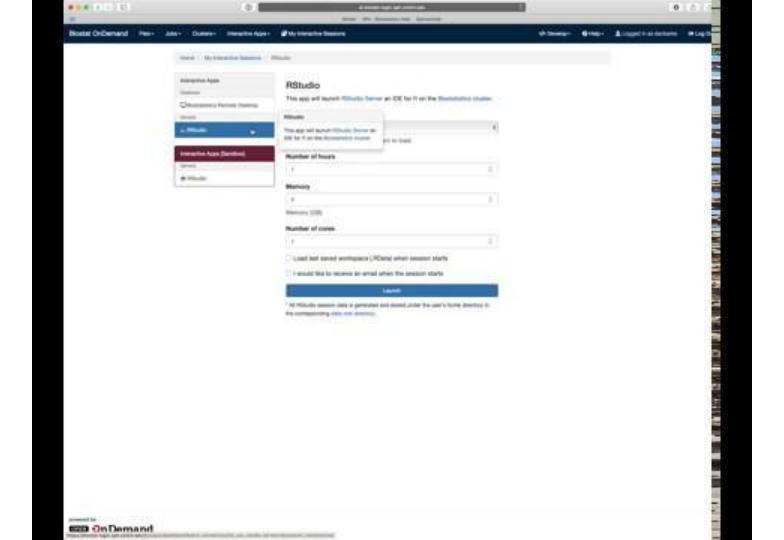
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#### **Basic Linux Commands**

Is - list files or directories

cd - change directory

pwd - print working directory

cat - concatenate

cp - copy

mv - move

rm - remove

mkdir - make a directory

#### Submit Jobs

Should always submit a job to use the cluster. Do not do too much computation on the login nodes. Your session will be killed off.

If you need to do interactive work, submit an interactive job

srun --pty /bin/bash