## Summary of the tutorial

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### Dalmia (NYU Abu Dhabi)

**Transfering data to/from the clusters**

**Transfering data to/from Prince cluster using Globus**

**Submittin g jobs with sbatch**

**Available software**

**Licensed Software Available on the HPC Cluster**

**Building Software**

**Slurm Tutorial**

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**Scratch Area Cleanup**

**Programming for Biologists**
Running jobs on the Prince Cluster

Accessing the Prince Cluster

From Windows workstation

From Mac workstation

Software and Environment Module

Job script and resource request

Introduction to job scheduling

Submitting jobs with sbatch

Requesting resources
Using computing nodes interactively

Monitoring batch jobs
  Monitoring batch jobs - squeue
  What is running and where? slurmtop

Canceling your jobs

Compiling your own software

Putting all pieces together
  An Amber example
  A R example

Summary

- You can compile, edit scripts and view results on the login nodes, but **computational work should be run on the compute nodes**
- You can access compute nodes with `srun`
  - Either via a job script, or interactively
  - Compute nodes are allocated to jobs by the scheduler, so your job might not start immediately
  - Jobs must request resources, but mostly need not specify a queue.
  - Requesting just slightly more than when you expect to need is generally the best practice
- **Short jobs get higher priority, and short or small jobs are easier to schedule quickly**
- You can monitor your job’s progress with `squeue, sstat, sacct, scontrol` or slurmtop
- Software is managed by Environment Modules
  - Use ‘module avail’ to find software packages
  - And ‘module load’ to load them into your environment
    - including within job scripts!
  - Use ‘module purge’ to return to a clean environment before loading a new set of modules
  - Other useful commands are ‘module list’ and ‘module show’