



# Job submission using Slurm

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## Topics

Head node vs Compute nodes

Slurm Workload Manager

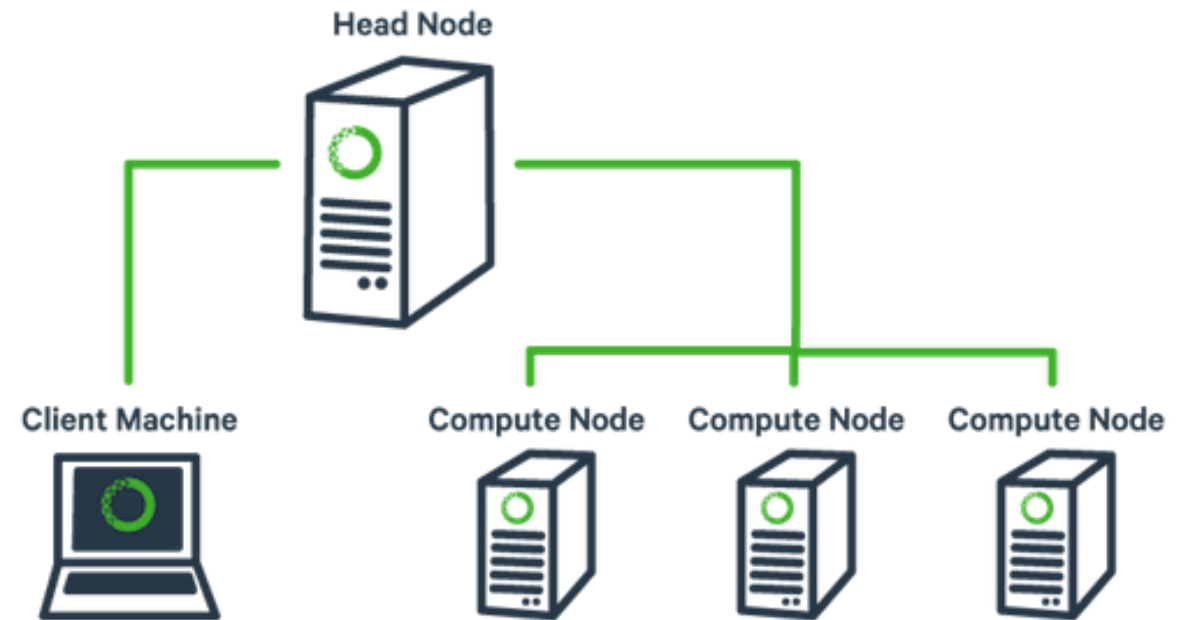
Job submission on Teton

Other Slurm commands

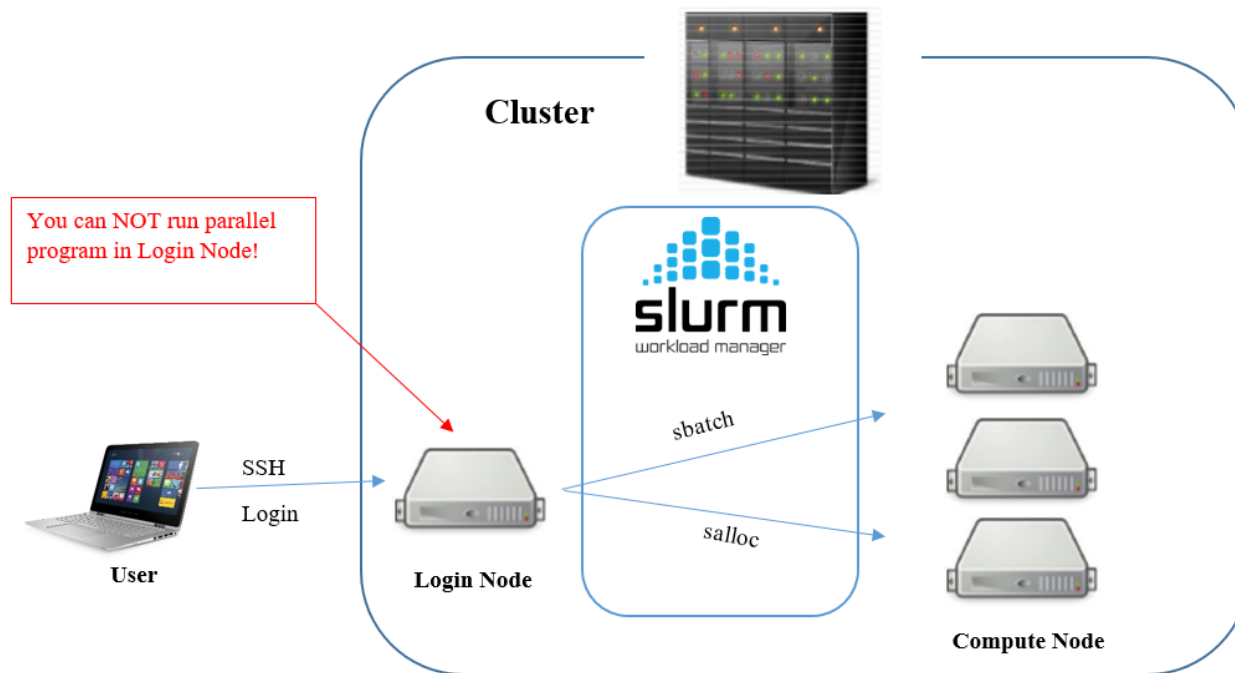


# Head node vs Compute nodes

- Typically when you access a cluster system you are accessing a **head node**.
- **Compute nodes** are the **nodes** on which work runs. It performs the computational work in a cluster.
- Since there may be many users simultaneously logged into cluster headnode, it's important not to run intensive tasks on the headnode. Such tasks should be performed on compute nodes.
- **Note: Never run a job directly on the head node!**



# Slurm Workload Manager

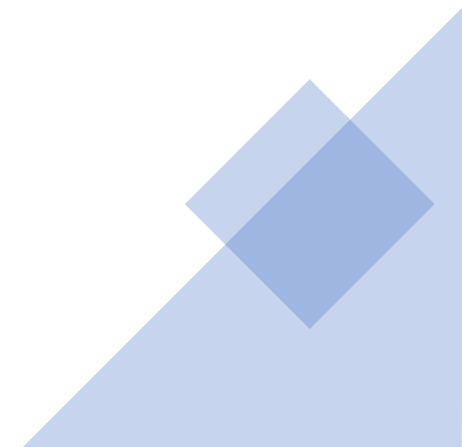


<https://pdc-support.github.io/hpc-intro/09-scheduling/>

- Scheduler on ARCC: SLURM
- Slurm is highly scalable cluster management and job scheduling system for large and small Linux clusters.
- Slurm is a flexible and scalable scheduler that implements job scheduling, allocate desirable resources, and time to specific job.
- Compute nodes



# Job Script

- A job script is a text file containing job setup information for the batch system followed by commands to be executed.
  - It can be created using any text editor and may be given any name.
  - A job script is simply a shell script. It consists of SLURM directives, comments, and executable statements.
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# Slurm Job Script

```
#!/bin/bash
#SBATCH --chdir="/project/wystack-poptml/hkashgar/3-
Slurm-materials/solver-and-instances"
#SBATCH --account=wystack-poptml
#SBATCH --time=0-01:00:00
#SBATCH --partition=teton
#SBATCH --job-name=instance1-%J
#SBATCH --output=./instance1-%J.out
#SBATCH --error=./instance1-%J.error

./abcsat_r18 instances/instance-3.cnf
```

# Slurm Commands

- sinfo: reports the state of partitions and nodes managed by Slurm
- sbatch: is used to submit a job script for later execution  
sbatch submit\_job
- srun: is used to submit a job for execution or initiate job steps in real time
- srun
- squeue: reports the state of jobs or job steps.
- sacct: is used to report job or job step accounting information about active or completed jobs.

# Git repo

- <https://github.com/haniyeka/WyStack-materials>



# Additional Sources

- <https://slurm.schedmd.com/quickstart.html>
- <https://slurm.schedmd.com/tutorials.html>
- <https://hpc.iastate.edu/guides/introduction-to-hpc-clusters/slurm>
- [https://ucdavis-bioinformatics-training.github.io/2017\\_2018-single-cell-RNA-sequencing-Workshop-UCD\\_UCB\\_UCSF/day1/cluster.html](https://ucdavis-bioinformatics-training.github.io/2017_2018-single-cell-RNA-sequencing-Workshop-UCD_UCB_UCSF/day1/cluster.html)
- <https://www.osc.edu/supercomputing/batch-processing-at-osc/job-scripts>
- <https://pdc-support.github.io/hpc-intro/09-scheduling/>