# Scheduling Basic Jobs

January 9, 2025

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#### **Slides & Exercises**

https://github.com/ResearchComp uting/hpc\_fundamentals\_micro\_cre dential

In "scheduling\_jobs" directory





### Learning Objectives

- Obtain a clear overview of job submission on an HPC system
- Learn about submitting both a batch and an interactive job to Alpine using the terminal



#### **Session Overview**

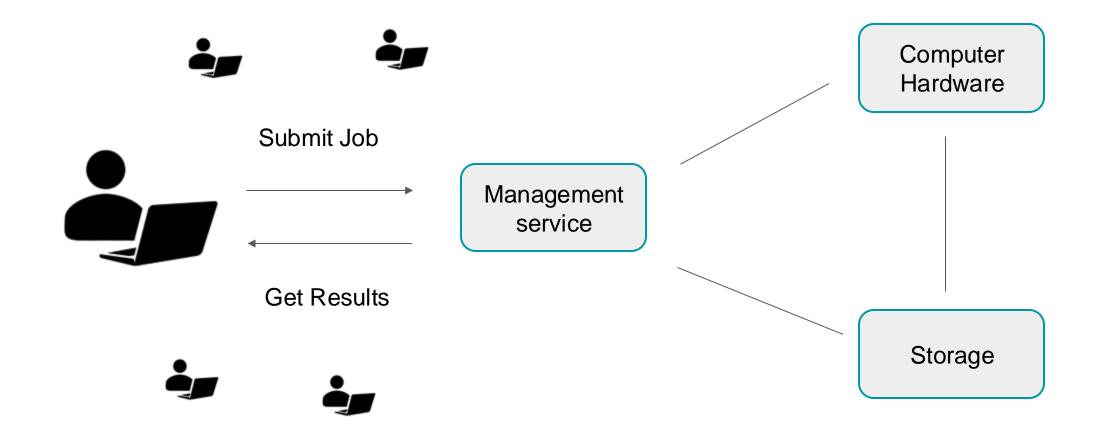
- General overview of Job submission
- Introduction to batch jobs
  - Submission of a batch job
- Checking/monitoring jobs
- Utilizing software in a job
- Introduction to interactive jobs



Remember, when you login to the HPC system you are put on a login node. You need to then gain access to a compute node to run software.



#### General Overview of Job Submission



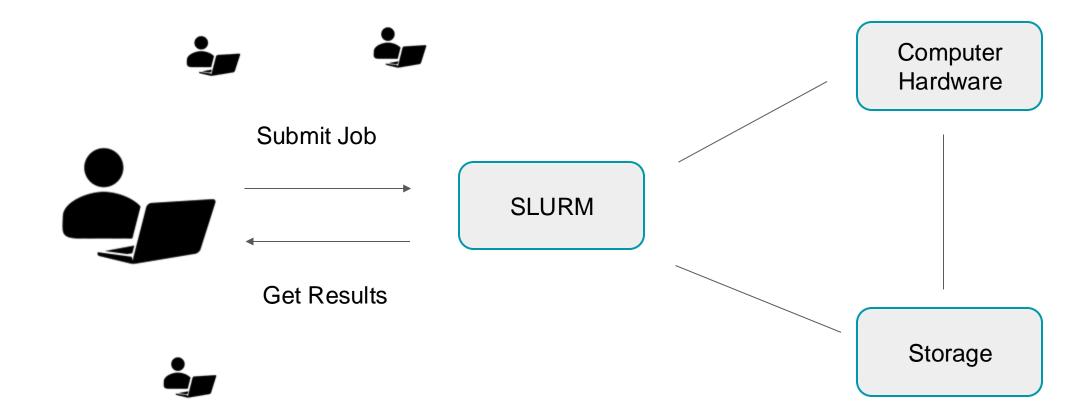


#### Introduction to Jobs

- Because our clusters are shared resources with many users trying to utilize available compute with their applications, we need a system to divide compute in a simple and fair system
- SLURM
  - Simple Linux Utility for Resource Management
- Through SLURM, users can grab allotments of compute resources called Jobs
- 2 Types of Jobs
  - Batch Jobs
  - Interactive Jobs



#### General Overview of Job Submission





#### Job directives

- Directives are special flags that specify what type of HPC resources you would like to use
  - "I want to run on 1 CPU for 1 hour"
- Used for both interactive and batch jobs
- Can be specified via the command line or in a job script
- All directives shown are specific to SLURM



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#### Common directives

- Partition A collection of compute nodes
  - --partition=<partition\_name>
- Quality of service (QoS) System defined constraints for a job (more on this later!)

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- --qos=<qos>
- Allocation Account to "charge to"
  - --account=<account\_name>
- Number of nodes to run on
  - --nodes=<nodes>
- Number of cores to run on
  - --ntasks=<number-of-tasks>



#### Common directives

- Wall time How long you want to run on these resources
  - --time=<wall time>
- Job name
  - --job-name=<jobname>
- Output Where all output that would be written to the terminal should go
  - --output=<name>
- Send an email when events happen in the job
  - --mail-type=<type>
- Email address to send updates to
  - --mail-user=<user>



### Alpine Partitions

 Partitions are a collection of compute nodes e.g. computers with common characteristics

Partition	Description	# of nodes	RAM/core (GB)	cores/node	GPUs/node
amilan	General Compute Node: AMD Milan	376	3.75	32,48,64	0
ami100	GPU Node: 3x AMD MI100	8	3.75	64	3
aa100	GPU Node: 3x Nvidia A100	12	3.75	64	3
amem	High-memory node	24	21.5	48,64	0



### Alpine Testing Partitions

 For many of the partitions we have testing partitions that provide quicker access to resources.

**Note:** there are restrictions on the amount of resources you can request. These restrictions can be found in our documentation.

Partition	Description	# of nodes	RAM/core (GB)	cores/node	GPUs/node
atesting	General Compute Node: AMD Milan	2	3.75	64	0
acompile	General Compute Node: AMD Milan	4	3.75	64	0
atesting_mi100	GPU Node: 3x AMD MI100	1	3.75	64	3
atesting_a100	GPU Node: 3x Nvidia A100	1	3.75	64	6 MIG instances



### Quality of Service (QoS)

- Quality of Service specifies additional constraints for a job
  - On Alpine, QoS can be used to run long jobs, specify testing partitions, and select high-memory nodes

QoS	Description	Max wall time	Max jobs/user	Max nodes/user
normal	Default QoS	24 H	1000	128
long	For jobs needing longer wall times	7 D	200	20
mem	High-memory jobs	7 D	n/a	12
testing	For jobs submitted to testing partitions	1 H	1	n/a
compile	For jobs submitted to compile partition	12 H	1	n/a



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#### Batch Jobs

- Batch Jobs are jobs you submit to the scheduler that are run later without supervision
  - By far the most common job on Alpine
  - Requires a job script
- A job script is simply a script that includes **SLURM directives** (resource specifics) ahead of any commands.



### Anatomy of a job script

It's just a bash script with SLURM specific directives!

```
#!/bin/bash

## Directives
#SBATCH --<option>=<value>

## Software
module load <software>

## User scripting
<command>
```



### Directives in a job script



### Example job script

```
#!/bin/bash
## Directives
#SBATCH --ntasks=1
                                       # Number of requested tasks/cores
#SBATCH --time=0:01:00
                                       # Max run time
#SBATCH --partition=amilan
                                       # Specify Alpine CPU node
#SBATCH --output=test_%j.out
                                       # Rename standard output file
## Software
module purge
                                       # Purge all existing modules
## User commands
echo "This is a test of user $USER"
```



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### Submitting a Job script

- Once a job script has been constructed you must submit it to the HPC system using SLURM
  - Done using sbatch
- If we created the job script "my\_first\_job.sh" then we would submit it as follows:

sbatch /path/to/my\_first\_job.sh



### Job output

- Once a job completes its execution, the standard output of the script will be redirected to an output file.
  - Great for debugging!
  - Could be different from output generated by your application
  - File is created in directory job was run unless specified in your --output directive.
  - If the directive --output is not provided, then a generic file name will be used (slurm\_xxxxxx.out).



### Checking your jobs

- squeue: Monitor your jobs status in queue and while running:
  - By default, shows all jobs in queue can specify using:

```
$ squeue -u <username>
$ squeue -p <partition>
```

- sacct: Check back on usage statistics of previous Jobs
  - By default, only checks all jobs from the start of the current day can specify using:

```
$ sacct -u <username>
$ sacct --start=MM/DD/YY -u <username>
$ sacct -j <job-id>
```



### Checking your jobs

- Another method of checking details of your job while running is with scontrol
  - Advanced command usually used by system administrators, but you can use it too!

```
$ scontrol show job <job number>
```

 To check the percentage of CPU and memory usage of a job after it completes, use seff

```
$ module load slurmtools
$ seff <job number>
```



#### Software and Jobs

- Okay so running a job is easy, but how do I run a job with my software?
- We can utilize all the software we discussed in the previous talk in the job script!
- Any non-GUI related commands you would run from the command line can be put in your job script!
  - If you would like to use GUI applications, you will need X11 forwarding and an interactive job



#### Software job script example

```
#!/bin/bash
## Directives
#SBATCH --ntasks=1
                                      # Number of requested tasks/cores
                                      # Max run time
#SBATCH --time=0:01:00
#SBATCH --partition=amilan
                                      # Specify Alpine CPU node
#SBATCH --output=test_%j.out
                                      # Rename standard output file
## Software
module purge
                                        # Purge all existing modules
module load anaconda
                                        # Load Anaconda
conda activate <my-conda-environment> # Activate CONDA environment
## Run Python script
python my cool script.py
```



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#### Interactive jobs

- Interactive jobs are used to gain access to a compute node in real time
  - Great for testing and debugging!
- Interactive jobs can be subject to normal wait times!
- We can get access to a compute node interactively with sinteractive
- We also have a specialized command called acompile that provides you with an interactive session
  - Access to quick resources
  - Limit of 4 CPUs for up to 12 hours



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### Running an interactive job

- Here we will run a Python script using an interactive job
- First request resources:

```
$ sinteractive --partition=acompile -qos=compile --time=00:10:00
```

 When the job starts you will be put on a compute node and you can execute your commands:

```
$ module load anaconda
$ python my_very_cool_script.py
```

To quit:

```
$ exit
```



#### Interactive GUI job

- If you have software that has a Graphical User Interface (GUI) it is sometimes possible to display that GUI on your local machine.
  - This is done using X11 forwarding
  - This GUI may be laggy if you are on a compute node or if your connection is unstable
  - See our documentation: https://curc.readthedocs.io/en/latest/runningjobs/interactive-jobs.html#interactive-gui-applications

Note: you can also use our Open OnDemand "Core Desktop" application to display a GUI. This tends to be more stable than X11 forwarding.



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## Thank you!

