

Example Submit Script

```
#!/bin/bash
#SBATCH --job-name= ' my-job '      Job Name
#SBATCH --ntasks=4                  Number of tasks
#SBATCH -t 2-10:30:00                Maximum job execution time
#SBATCH -p genacc_q                  Partition to submit job to
#SBATCH --mem-per-cpu=7.8G           Memory per CPU
#SBATCH -o job_output.txt            (optional)specify output name
#SBATCH -e job_errors.log            (optional)specify error output
#SBATCH --nodes=2                    # of physical nodes to allocate
#SBATCH -C "YEAR2012,intel"          Specific feature of node for job

module load intel                    Load kernel modules
srun my_program.sh < input.txt       run program (use srun not MPI)

Try our Submit Script Generator for more options: https://rcc.fsu.edu/ssg
```

Submitting Jobs

Submit a Job to the Slurm Scheduler

```
$ sbatch MY_SCRIPT.sh
```

```
Submitted batch job 1234567
```

Check Specific Job Status

```
$ squeue -j 1234567
```

Check All Job Statuses

```
$ squeue --me
```

Cancel Job

```
$ scancel 1234567
```

View Job Status While Running

```
$ sstat -j 1234567
```

Job States

PD	Pending
CF	Configuring
R	Running
CG	Completing
PR	Preempted
S	Suspended
TO	Timeout
F	Failed
NF	Node Failed
CA	Cancelled



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Common Commands

Connect to the HPC

```
ssh <your_FSUID>@hpc-login.rcc.fsu.edu
```

Check Storage Quota

```
$ gpfs_quota
```

Display My Running/Pending Jobs

```
$ squeue -u $(whoami)
```

Display My Partitions (Login Required)

```
$ rcctool my:partitions
```

Display Node Information in a Partition

```
$ sinfo -p <partition_name>
```

Estimated Job Start Time

```
$ squeue -start -j <job_id>
```

Display Available Slurm Node Features

```
$ sinfo -o %f
```

General Access Partitions

Name	Max Job Length	Purpose
genacc_q	2 weeks	General Access
condor	90 days	Long Jobs / No MPI
backfill	4 hours	Short Jobs
backfill2	4 hours	Pre-emption Enabled
quicktest	10 min	For Testing