

Slurm Commands

Start Jobs

srun

This is the simplest way to run a job on a cluster. Initiate parallel job steps within a job or start an interactive job (with `-pty`).

salloc

Request interactive jobs/allocations. When the job is started a shell (or other program specified on the command line) it is started on the submission host (Frontend). From this shell you should use `srun` to interactively start a parallel applications. The allocation is released when the user exits the shell.

sbatch

Submit a batch script. The script will be executed on the first node of the allocation. The working directory coincides with the working directory of the `sbatch` directory. Within the script one or multiple `srun` commands can be used to create job steps and execute parallel applications.

Examples

```
# General:
sbatch --job-name=<name of job shown in queue> -N <num nodes> --ntasks-per-
node=<spawned processes per node> /path/to/sbatch.script.sh

# A start date/time can be set via the --begin parameter:
--begin=16:00
--begin=now+1hour
--begin=now+60 (seconds by default)
--begin=2010-01-20T12:34:00
```

A `sbatch` script of the command above would look like

```
#!/bin/bash
#SBATCH --job-name=<name of job shown in queue> -N <num nodes>
#SBATCH -N <num nodes>
#SBATCH --ntasks-per-node=<spawned processes per node>
#SBATCH --begin=2010-01-20T12:34:00

/path/to/sbatch.script.sh
```

For more information see `man sbatch`. All parameters used there can also be specified in the job script itself using `#SBATCH`.

Check the status of your job submissions

```
squeue --me
```

Check the status of nodes

```
sinfo
```

Canceling jobs

On allocation, you will be notified of the job ID. Also, within your scripts and shells (if allocated via salloc) you can get the ID via the \$SLURM_JOBID environment variable. You can use this ID to cancel your submission:

```
scancel <jobid>
```

Slurm Cheat Sheet

A summary of the most common commands can be found [here](#).

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