Habanero - Submitting Jobs

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Jobs can request compute resources on a per-core basis or a per-node basis.

Core-Based Jobs

Jobs wishing to use less than a full node should specify the number of cores required. If you're not sure how many cores to request then 1 is most likely to be the correct number to use. The maximum number of cores available on a node is 24, but if that really is the number of cores you need you should probably request an entire node instead (see the Node-Based Jobs section below).

Cores can be requested using either -c or --cpus-per-task (in this and the following examples, "or" indicates an exactly equivalent alternative syntax).

```bash
#SBATCH -c 1
```

or

```bash
#SBATCH --cpus-per-task=1
```

It is important to also specify your memory requirement when using less than a full node as this will allow the scheduler to ensure that there will be enough memory available on the node where your job runs.

Node-Based Jobs

Jobs can also request entire nodes. This is often the most efficient way to run parallel distributed jobs, such as those using MPI. To request an entire node or nodes, specify the --exclusive flag in your submit file.
To specify the number of nodes, use -N or --nodes.

```bash
#SBATCH --nodes=1
```

You do not need to specify (and should not specify) a memory requirement when requesting exclusive use of a node. However, if your job requires more than the standard 128 GB then you can add a constraint to request one of the cluster's high memory nodes, each of which has 512 GB of memory. The feature to request is “mem512”.

```bash
#SBATCH --constraint=mem512
```

**Interactive Jobs**

Interactive jobs allow user interaction during their execution. They deliver to the user a new shell from which applications can be launched.

The currently known way to submit an interactive job is (we may eventually simplify that):

```bash
#SBATCH --exclusive
```
srun --pty -t 0-01:00 -A <ACCOUNT> /bin/bash

where "<ACCOUNT>" is your group’s account name. The Slurm directives noted below that begin with #SBATCH are available on the command line as well for interactive jobs.

For example, to run an interactive job on a large node, use:

srun --pty -t 0-01:00 -C mem512 -A <ACCOUNT> /bin/bash

If a node is available, it will be picked for you automatically, and you will see a command line prompt on a shell running on it. If no nodes are available, your current shell will wait.

Graphical User Interfaces

Add section

Basic Job Directives

The following table lists the most common (in our estimation) directives used in Slurm submit scripts. Each should be preceded by #SBATCH when used in a submit script. Many directives have a short alternate name and these are listed where available. The examples sometimes use the long version of a given directive and sometimes the short version; in either case no preference is implied.

<table>
<thead>
<tr>
<th>Directive</th>
<th>Short Version</th>
<th>Description</th>
<th>Example</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>--account=&lt;account&gt;</td>
<td>-A &lt;account&gt;</td>
<td>Account.</td>
<td>#SBATCH --account=stats</td>
<td></td>
</tr>
<tr>
<td>--job-name=&lt;job name&gt;</td>
<td>-J &lt;job name&gt;</td>
<td>Job name.</td>
<td>#SBATCH -J DiscoProject</td>
<td></td>
</tr>
<tr>
<td>--time=&lt;time&gt;</td>
<td>-t &lt;time&gt;</td>
<td>Time required.</td>
<td>#SBATCH --time=10:00:00</td>
<td>The maximum time allowed is five days.</td>
</tr>
<tr>
<td>--mem=&lt;memory&gt;</td>
<td>-m &lt;memory&gt;</td>
<td>Memory required per node.</td>
<td>#SBATCH --mem=16gb</td>
<td></td>
</tr>
<tr>
<td>--constraint=mem512</td>
<td>-C mem512</td>
<td>Specifying a large (512 GB RAM) node.</td>
<td>#SBATCH -C mem512</td>
<td></td>
</tr>
<tr>
<td>--cpus-per-task=&lt;cpus&gt;</td>
<td>-c &lt;cpus&gt;</td>
<td>CPU cores per task.</td>
<td>#SBATCH -c 1</td>
<td>Nodes have a maximum of 24 cores.</td>
</tr>
<tr>
<td>--nodes=&lt;nodes&gt;</td>
<td>-N &lt;nodes&gt;</td>
<td>Nodes required for the job.</td>
<td>#SBATCH -N 4</td>
<td></td>
</tr>
<tr>
<td>--array=&lt;indexes&gt;</td>
<td>-a &lt;indexes&gt;</td>
<td>Submit a job array.</td>
<td>#SBATCH -a 1-4</td>
<td>See below for discussion of job arrays.</td>
</tr>
<tr>
<td>--mail-type=&lt;ALL,BEGIN,END,FAIL,NONE&gt;</td>
<td></td>
<td>Send email job notifications</td>
<td>#SBATCH --mail-type=ALL</td>
<td></td>
</tr>
</tbody>
</table>
Array Jobs

Multiple copies of a job can be submitted by using a job array. The --array option can be used to specify the job indexes Slurm should apply.

An existing submit file can be used to submit a job array by adding the flag to the sbatch command line.

```bash
$ sbatch -a 1-5 helloworld.sh
Submitted batch job 629249
```

In this example the job IDs will be the number 629249 followed by _1, _2, etc. so the first job in the array can be accessed using the job ID 629249_1 and the last 629249_5.

```bash
$ scontrol show job 629249_1
```

Job scheduling basics

The walltime limit on the cluster is 5 days (120 hours).

You have priority access to the nodes owned by your group. That implies that the maximum time a job from your group will need to wait for one of those nodes is 12 hours (and that occurs only in one of those rare case when a job by someone from another group starts running on such a node just before you or someone else in your group launch yours).

In order to guarantee that, users are allowed to run on other groups’ nodes only for maximum of 12 hours.

Obviously, public nodes are not subject to such restrictions and everyone competes for those with the walltime limit of 5 days.

Slurm Quick Start Guide

See the Slurm Quick Start Guide for a more in-depth introduction on using the Slurm scheduler.