Job Queueing and Submission

Introduction

Habana uses Slurm for job submission and queueing. Below are some of the important commands for using Slurm. For more information refer to Slurm Documentation.

Note: Run the python scripts using srun or sbatch, to ensure that concurrent jobs do not interfere with each other.

srun

The Slurm command srun can be used to run individual python scripts in parallel with other scripts on a cluster managed by Slurm. Examples of srun usage are shown below.

```
srun python demo_mnist.py --hpu
```

sbatch

Alternatively, jobs can be submitted to the Slurm workload manager through a batch script by using sbatch command. To do this, create a bash script (submit-demo-mnist-job.sh here as an example) with the commands that you want to execute.

```
#!/bin/sh

srun python demo_mnist.py --hpu
```

Then pass the bash script as an input to the sbatch command as shown below.

```
sbatch submit-demo-mnist-job.sh
```

In case of the need to use multiple HPU's (2 in the example shown below), the sbatch command would be altered as:

```
sbatch --gres=hpu:2 <your_script.sh>
```

squeue

Squeue command provides information about jobs located in the Slurm scheduling queue.

```
squeue
```

scancel

Scancel is used to signal or cancel jobs, job arrays or job steps.

```
scancel job_id
```