QuickStart for Slurm/HPC

Connections

ssh	utln@login.cluster.tufts.edu (eg ssh -XC utln@login.cluster.tufts.edu)
sftp,scp	utln@xfer.cluster.tufts.edu (xfer is used for data transfers to the cluster)
	(e.g. scp big_data.dat utln@xfer.cluster.tufts.edu:directory_for_data)

Commands

squeue	show submitted and pending jobs with jobids (e.g. squeue -u utln)
sinfo	show details of partitions (queues)
scancel	terminates a job (need jobid e.g. scancel my_jobid)
salloc	obtains resource allocations, runs commands
sbatch	submits batch jobs with resource allocations
srun	submits a command for execution

Partitions

batch*	batch jobs submission (* default, 72 hour limit)
interactive	interactive jobs (4 hour limit)
largemem	large memory nodes (384 Gb, 120 hour limit)
mpi	parallel job submission (168 hour limit)
gpu	gpu resource partition (72 hour limit)

Examples

Interactive jobs (load modules needed first in general)

srun {options} –p interactive --pty bash # start an interactive session
srun {options} –p interactive --pty --x11=first –c 4 matlab # starts a GUI session

--pty sets up a pseudo terminal
--x11=first is necessary for graphics
-p partition specifies which partition is to be used
-c # specifies how many cores are needed

Batch jobs

sbatch {options} –p {batch|mpi|gpu|largemem} batch.script
sbatch {options} –p { batch|mpi|gpu|largemem} --wrap="python analysis.py d.dat"
(pick one)

```
===generic bash script adjust as needed===
#!/bin/bash          #required
#SBATCH -N 1         # nodes requested
#SBATCH -n 1         # tasks requested
#SBATCH -c 4         # cores requested
#SBATCH --mem=4000   # memory in Mb
#SBATCH -o outfile   # send stdout to outfile
#SBATCH -e errfile   # send stderr to errfile

module load necessary_modules
body of script
```

-wrap="command" allows command to be submitted as a script

{options} follow #SBATCH, e.g. --mem=4000, -c 4. Can be in the script or on the command line.

For more information

cluster wiki	http://go.tufts.edu/cluster under slurm
cluster help	tts-research@tufts.edu