A Quick Tutorial on Slurm

General commands

PBS Command	Slurm Command	Meaning
qsub <job-file></job-file>	sbatch <job-file></job-file>	Submit <job script=""> to the queue</job>
qsub -I	salloc <options></options>	Request interactive job
showstart	squeuestart	Show estimated start time
qstat <-u username>	squeue <-lu username> -l: long report	Check jobs for a particular user in the scheduling queue
qstat <queue></queue>	squeue -p <partition></partition>	Display queue/partition entries
qstat -f <job_id></job_id>	scontrol show job <job_id></job_id>	Show job details
qdel <job_id></job_id>	scancel <job_id></job_id>	Delete <job_id></job_id>

Frequently used Options

PBS	Slurm	Meaning
qsub	sbatch/salloc	Submit batch/interactive job script to queue*
-1 procs= <number></number>	ntasks= <number></number>	# of processes to run
-l nodes=X:ppn=Y	ntasks= <multiply x*y=""></multiply>	# of processes to run
-l walltime= <hh:mm:ss></hh:mm:ss>	time= <hh:mm:ss></hh:mm:ss>	How long the job will run
-1 mem= <number></number>	mem= <number></number>	Total memory (single node)
-1 pmem= <number></number>	mem-per-cpu= <number></number>	Memory per cpu
-l: <attribute></attribute>	constraint= <attribute></attribute>	Node property to request (avx, IB)
-q <queue_name></queue_name>	 partition= <partition_nam e></partition_nam 	Which set of nodes to run job on

Ref: https://hpcc.usc.edu/support/documentation/pbs-to-slurm/

Examples

Interactive mode: \$ salloc --ntasks-per-node=16 --nodes=2 --time=1:00:00 --constraint=IB

To submit a job: \$ sbatch job.sl where job.sl is:

#!/bin/bash

#SBATCH --ntasks-per-node=8

#SBATCH -N 2

#SBATCH --mem-per-cpu=2GB

#SBATCH -t 01:00:00

#SBATCH -p priya

#SBATCH -A lc_pv

to run with pure MPI

Export OMP_NUM_THREADS=1 srun -n 16 --mpi=pmi2 ./a.out

To get node from a specified partition, need to specify your account as well.

#!/bin/bash

#SBATCH --ntasks-per-node=8

#SBATCH -N 2

#SBATCH --mem-per-cpu=2GB

#SBATCH -t 01:00:00

to run with hybrid MPI & OMP

export OMP_NUM_THREADS=2 srun -n 8 -c 2 --mpi=pmi2 ./a.out

 $\textbf{Ref:} \ \underline{\text{https://www.nersc.gov/users/computational-systems/cori/running-jobs/example-batch-scripts/particles} \\ \text{Ref:} \ \underline{\text{https://www.nersc.gov/users/cori/running-jobs/example-batch-scripts/particles} \\ \text{Ref:} \ \underline{\text{https://www.nersc.gov/users/cori/running-jobs/exa$

The srun "-c" option

- Request that ncpus be allocated per process. This may be useful if the job is multithreaded and requires more than one CPU per task for optimal performance.
- The "-c" value should be set as

 # of logical cores(hyper thread) the node can support

 # of MPI tasks per node

 e.g. To run a program with 16 MPIs/node and 4 OMPs/MPI on KNL:

e.g. To run a program with 16 MPIs/node and 4 OMPs/MPI on KNL: $\frac{64*4 (256 logical cores on KNL)}{64*4 (256 logical cores on KNL)} = 16$

16

\$ export OMP_NUM_THREADS=4

\$ srun -n 16 -c 16/exe

Ref: [1] https://www.nersc.gov/users/computational-systems/cori/running-jobs/example-batch-scripts-for-kni [2] https://www.alcf.anl.gov/files/Knight_Software_JobSubmission_2.pdf

Useful jobscript generator

• https://my.nersc.gov/script_generator.php