

Common Slurm Commands

Quick reference for the most common Slurm commands on the TAU HPC cluster.

Submitting Jobs

Command	Description
<code>sbatch job.sh</code>	Submit a batch job script
<code>srun --pty bash</code>	Start an interactive session
<code>sbatch --depend=afterok:JOBID job.sh</code>	Submit job after another completes

Monitoring Jobs

Command	Description
<code>squeue -u username</code>	Your running and pending jobs
<code>squeue</code>	All jobs on the cluster
<code>scontrol show job JOBID</code>	Full details of a job
<code>sacct -j JOBID --format=JobID,JobName,State,MaxRSS,Elapsed</code>	Job accounting and memory usage
<code>sattach JOBID</code>	Attach to a running job's output

Managing Jobs

Command	Description
<code>scancel JOBID</code>	Cancel a specific job
<code>scancel -u username</code>	Cancel all your jobs

Cluster Information

Command	Description
<code>sinfo</code>	Partition and node status
<code>scontrol show partition PARTITION</code>	Partition details and limits
<code>check_my_partitions</code>	Your available partitions and accounts
<code>features</code>	Available node constraints/features

Environment Modules

Command	Description
<code>module avail</code>	List all available modules
<code>module avail NAME</code>	Search for a specific module
<code>module spider NAME</code>	Detailed module info including dependencies
<code>module load NAME</code>	Load a module
<code>module list</code>	List loaded modules
<code>module unload NAME</code>	Unload a module
<code>module purge</code>	Unload all modules

Common SBATCH Directives

Directive	Description
<code>#SBATCH --job-name=NAME</code>	Job name
<code>#SBATCH --account=ACCOUNT</code>	Account name
<code>#SBATCH --partition=PARTITION</code>	Partition/queue
<code>#SBATCH --qos=QOS</code>	Quality of Service
<code>#SBATCH --time=HH:MM:SS</code>	Max run time
<code>#SBATCH --ntasks=N</code>	Number of tasks
<code>#SBATCH --nodes=N</code>	Number of nodes
<code>#SBATCH --cpus-per-task=N</code>	CPU cores per task
<code>#SBATCH --mem-per-cpu=NG</code>	Memory per CPU
<code>#SBATCH --mem=NG</code>	Total memory
<code>#SBATCH --gres=gpu:N</code>	Number of GPUs
<code>#SBATCH --constraint=FEATURE</code>	Node constraint/feature

Directive	Description
#SBATCH --array=1-N	Job array
#SBATCH --output=FILE_%j.out	Output file (%j = job ID)
#SBATCH --error=FILE_%j.err	Error file
#SBATCH --mail-user=EMAIL	Notification email
#SBATCH --mail-type=END,FAIL	When to notify

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