

# Running Jobs with SLURM

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## Overview

All three clusters, Puma, Ocelote, and EIGato, use SLURM for resource management and job scheduling.

## Additional SLURM Resources and Examples

Link	Description
<a href="#">Official SchedMD User Documentation</a>	Official SchedMD user documentation. Includes detailed information on SLURM directives and commands.
<a href="#">PBS SLURM Rosetta Stone</a>	Table for converting some common PBS job directives to SLURM syntax.
<a href="#">Puma Quick Start</a>	HPC Quick Start guide. If you have never submitted a batch job before, this is a great place to start.
<a href="#">Job Examples</a>	Basic SLURM example scripts. Includes PBS scripts for comparison.
<a href="#">Even More Job Examples!</a>	Growing repository of example SLURM submission scripts
<a href="#">Intro to HPC</a>	A recorded video presentation of our Intro to HPC workshop. Keep your eyes peeled for periodic announcements in the HPC listserv on upcoming live sessions!=-

## SLURM and System Commands

Command	Purpose	Example(s)
<b>Native Slurm Commands</b>		
sbatch	Submits a batch script for execution	sbatch script.slurm
srun	Run parallel jobs. Can be in place of mpirun/mpixec. Can be used interactively as well as in batch scripts	srun -n 1 --mpi=pmi2 a.out
salloc	Requests a session to work on a compute node interactively	see: <a href="#">Interactive Sessions</a> section below
squeue	Checks the status of pending and running jobs	squeue --job \$JOBID squeue --user \$NETID
scancel	Cancel a running or pending job	scancel \$JOBID scancel -u \$NETID
scontrol hold	Place a hold on a job to prevent it from being executed	scontrol hold \$JOBID
scontrol release	Releases a hold placed on a job allowing it to be executed	scontrol release \$JOBID
<b>System Commands</b>		
va	Displays your group membership, your account usage, and CPU allocation. Short for "view allocation"	va
interactive	Shortcut for quickly requesting an <a href="#">interactive job</a> . Use "interactive --help" to get full usage.	interactive -a \$GROUP_NAME
job-history	Retrieves a running or completed job's history in a user-friendly format	job-history \$JOBID
seff	Retrieves a completed job's memory and CPU efficiency	seff \$JOBID
past-jobs	Retrieves past jobs run by user. Can be used with option "-d N" to search for jobs run in the past N days.	past-jobs -d 5
job-limits	View your group's job resource limits and current usage.	job-limits \$GROUP
nodes-busy	Display a visualization of nodes on a cluster and their usage	nodes-busy --help
system-busy	Display a text-based summary of a cluster's usage	system-busy
cluster-busy	Display a visualization of all three cluster's overall usage	cluster-busy --help

## Batch Job Directives

Command	Purpose
#SBATCH --account=group_name	Specify the account where hours are charged. Don't know your group name? Run the command "va" to see which groups you belong to
#SBATCH --partition=partition_name	Set the job partition. This determines your job's priority and the hours charged. See <a href="#">Job Partition Requests</a> below for additional information
#SBATCH --time=DD-HH:MM:SS	Set the job's runtime limit in days, hours, minutes, and seconds
#SBATCH --nodes=N	Allocate N nodes to your job.  For non-MPI enabled jobs, this should be set to "--nodes=1" to ensure access to all requested resources and prevent memory errors.
#SBATCH --ntasks=N	ntasks specifies the number of tasks (or processes) the job will run. For MPI jobs, this is the number of MPI processes. Most of the time, you can use ntasks to specify the number of CPUs your job needs. However, in some odd cases you might run into issues. For example, see: <a href="#">Using Matlab</a>
#SBATCH --cpus-per-task=M	By default, you will be allocated one CPU/task. This can be increased by including the additional directive --cpus-per-task.  The number of CPUs a job is allocated is cpus/task * ntasks, or M*N
#SBATCH --mem=Ngb	Select N gb of memory <b>per node</b> . If "gb" is not included, this value defaults to MB. Directives --mem and --mem-per-cpu are mutually exclusive.
#SBATCH --mem-per-cpu=Ngb	Select N GB of memory per CPU. Valid values can be found in the <a href="#">Node Types/Example Resource Requests</a> section below. If "gb" is not included, this value defaults to MB.
#SBATCH --gres=gpu:N	Optional: Request N GPUs.
#SBATCH --constraint=hi_mem	Optional: Request a high memory node (Ocelote and Puma only).
#SBATCH --array=N-M	Submits an array job from indices N to M
#SBATCH --job-name=JobName	Optional: Specify a name for your job. This will not automatically affect the output filename.
#SBATCH -e output_filename.e.err #SBATCH -o output_filename.e.out	Optional: Specify output filename(s). If -e is missing, stdout and stderr will be combined.
#SBATCH --open-mode=append	Optional: Append your job's output to the specified output filename(s).
#SBATCH --mail-type=BEGIN END FAIL ALL	Optional: Request email notifications. <b>Beware of mail bombing yourself.</b>
#SBATCH --mail-user=email@address.xyz	Optional: Specify email address. If this is missing, notifications will go to your UArizona email address by default.
#SBATCH --exclusive	Optional: Request exclusive access to node.
#SBATCH --export=VAR	Optional: Export a comma-delimited list of environment variables to a job.
#SBATCH --export=all (default)	Optional: Export your working environment to your job.
#SBATCH --export=none	Optional: Do not export working environment to your job.

## SLURM Environment Variables

Variable	Purpose	Example Value
\$SLURM_ARRAY_JOB_ID	Job array's parent ID	399124
\$SLURM_ARRAY_TASK_COUNT	Total number of subjobs in the array	4
\$SLURM_ARRAY_TASK_ID	Job index number (unique for each job in the array)	1
\$SLURM_ARRAY_TASK_MAX	Maximum index for the job array	7
\$SLURM_ARRAY_TASK_MIN	Minimum index for the job array	1
\$SLURM_ARRAY_TASK_STEP	Job array's index step size	2
\$SLURM_CLUSTER_NAME	Which cluster your job is running on	elgato
\$SLURM_CONF	Points to the <a href="#">SLURM configuration file</a>	/var/spool/slurm/d/conf-cache/slurm.conf
\$SLURM_CPUS_ON_NODE	Number of CPUs allocated to target node	3
\$SLURM_GPUS_ON_NODE	Number of GPUs allocated to the target node	1
\$SLURM_GPUS_PER_NODE	Number of GPUs per node. Only set if --gpus-per-node is specified	1
\$SLURM_JOB_ACCOUNT	Account being charged	groupname
\$SLURM_JOB_GPUS	The global GPU IDs of the GPUs allocated to the job. Only set in batch and interactive jobs.	0
\$SLURM_JOB_ID	Your SLURM Job ID	399072
\$SLURM_JOB_CPUS_PER_NODE	Number of CPUs per node. This can be a list if there is more than one node allocated to the job. The list has the same order as SLURM_JOB_NODELIST	3,1
\$SLURM_JOB_NAME	The job's name	interactive
\$SLURM_JOB_NODELIST	The nodes that have been assigned to your job	gpu[73-74]
\$SLURM_JOB_NUM_NODES	The number of nodes allocated to the job	2
\$SLURM_JOB_PARTITION	The job's partition	standard
\$SLURM_JOB_QOS	The job's QOS/Partition	qos_standard_part
\$SLURM_JOB_USER	The username of the person who submitted the job	netid
\$SLURM_JOBID	Same as SLURM_JOB_ID, your SLURM Job ID	399072
\$SLURM_MEM_PER_CPU	The memory/CPU ratio allocated to the job	4096
\$SLURM_NNODES	Same as SLURM_JOB_NUM_NODES – the number of nodes allocated to the job	2
\$SLURM_NODELIST	Same as SLURM_JOB_NODELIST, The nodes that have been assigned to your job	gpu[73-74]

\$SLURM_NPROCS	The number of tasks allocated to your job	4
\$SLURM_NTASKS	Same as SLURM_NPROCS, the number of tasks allocated to your job	4
\$SLURM_SUBMIT_DIR	The directory where sbatch was used to submit the job	/home/u00/netid
\$SLURM_SUBMIT_HOST	The hostname where sbatch was used to submit the job	<a href="http://wentletrap.hpc.arizona.edu">wentletrap.hpc.arizona.edu</a>
\$SLURM_TASKS_PER_NODE	The number of tasks to be initiated on each node. This can be a list if there is more than one node allocated to the job. The list has the same order as SLURM_JOB_NODELIST	3,1
\$SLURM_WORKING_CLUSTER	<a href="#">Valid for interactive jobs</a> , will be set with remote sibling cluster's IP address, port and RPC version so that any srns will know which cluster to communicate with.	elgato:foo:0000:0000:000

## SLURM Reason Codes

Sometimes, if you check a pending job using `squeue`, there are some messages that show up under Reason indicating why your job may not be running. Some of these codes are non-intuitive so a human-readable translation is provided below:

Reason	Explanation
AssocGrpCpuLimit	This is a per-group limitation on the number of CPUs that can be used simultaneously by all group members. Your job is not running because this limit has been reached. Check your group's limits using "job-limits <group_name>".
AssocGrpMemLimit	This is a per-group limitation on the amount of memory that can be used simultaneously by all group members. Your job is not running because this limit has been reached. Check your group's limits using "job-limits <group_name>".
AssocGrpCPUMinutesLimit	Either your group is out of CPU hours or your job will exhaust your group's CPU hours.
AssocGrpGRES	This is a per-group limitation on the number of GPUs that can be used simultaneously by all group members. Your job is not running because this limit has been reached. Check your group's limits using "job-limits <group_name>".
Dependency	Your job depends on the completion of another job. It will wait in queue until the target job completes.
QOSMaxWallDurationPerJobLimit	Your job's time limit exceeds the max allowable and will never run. To see an individual job's limits, run "job-limits <group_name>".
Nodes_required_for_job_are_DOWN,_DRAINED_or_reserved_or_jobs_in_higher_priority_partitions	This very long message simply means your job is waiting in queue until there is enough space for it to run
Priority	Your job is waiting in queue until there is enough space for it to run.
QOSMaxCpuPerUserLimit	This is a per-user limitation on the number of CPUs that you can use simultaneously among all of your jobs. Your job is not running because this limit has been reached. Check your user limits using "job_limits <group_name>".
ReqNodeNotAvail, Reserved for maintenance	Your job's time limit overlaps with an upcoming maintenance window. Run "uptime_remaining" to see when the system will go offline. If you remove and resubmit your job with a shorter walltime that does not overlap with maintenance, it will likely run. Otherwise, it will remain pending until after the maintenance window.
Resources	Your job is waiting in queue until the required resources are available.

## Job Partition Requests

Partition	SLURM	Details
standard	<pre>#SBATCH -- account=&lt;PI GROUP&gt; #SBATCH -- partition=standard</pre>	Consumes your group's standard allocation. These jobs cannot be interrupted.
windfall	<pre>#SBATCH -- partition=windfall</pre>	Does not consume your group's standard allocation. Jobs may be interrupted and restarted by higher-priority jobs. The <code>--account</code> flag needs to be omitted or an error will occur.
high_priority	<pre>#SBATCH -- account=&lt;PI GROUP&gt; #SBATCH -- partition=high_pri ority #SBATCH -- qos=user_qos_&lt;PI GROUP&gt;</pre>	Available for groups who have purchased compute resources.
qualified	<pre>#SBATCH -- account=&lt;PI GROUP&gt; #SBATCH -- partition=standard #SBATCH -- qos=qual_qos_&lt;PI GROUP&gt;</pre>	Available for groups that have submitted a special project request.

## SLURM Output Filename Patterns

SLURM offers ways to make your job's output filenames customizable through the use of character replacements. A table is provided below as a guide with some examples. Variables may be used or combined as desired. Note: character replacements may also be used with other SBATCH directives such as error filename, input filename, and job name.

Variable	Meaning	Example Slurm Directive(s)	Output
%A	A job array's main job ID	<pre>#SBATCH --array=1-2 #SBATCH -o %A.out #SBATCH --open-mode=append</pre>	12345.out
%a	A job array's index number	<pre>#SBATCH --array=1-2 #SBATCH -o %A_%a.out</pre>	12345_1.out 12345_2.out
%J	Job ID plus <a href="#">stepid</a>	<pre>#SBATCH -o %J.out</pre>	12345.out
%j	Job ID	<pre>#SBATCH -o %j.out</pre>	12345.out
%N	Hostname of the first compute node allocated to the job	<pre>#SBATCH -o %N.out</pre>	r1u11n1.out
%u	Username	<pre>#SBATCH -o %u.out</pre>	netid.out
%x	Jobname	<pre>#SBATCH --job-name=JobName #SBATCH -o %x.out</pre>	JobName.out

# Node Types/Example Resource Requests

## Standard Nodes

Cluster	Max CPUs	Mem/CPU	Max Mem	Sample Request Statement
EIGato	16	4gb	62gb	#SBATCH --nodes=1 #SBATCH --ntasks=16 #SBATCH --mem-per-cpu=4gb
Ocelote	28	6gb	168gb	#SBATCH --nodes=1 #SBATCH --ntasks=28 #SBATCH --mem-per-cpu=6gb
Puma	94	5gb	470gb	#SBATCH --nodes=1 #SBATCH --ntasks=94 #SBATCH --mem-per-cpu=5gb

## GPU Nodes



During the quarterly maintenance cycle on April 27, 2022 the EIGato K20s and Ocelote K80s were removed because they are no longer supported by Nvidia.

GPU jobs are requested using the generic resource, or `--gres`, SLURM directive. In general, the directive to request N GPUs will be of the form: `--gres=gpu:N`

Cluster	Max CPUs	Mem/CPU	Max Mem	Sample Request Statement
Ocelote	28	8gb	224gb	#SBATCH --nodes=1 #SBATCH --ntasks=28 #SBATCH --mem-per-cpu=8gb #SBATCH --gres=gpu:1
Puma <sup>1</sup>	94	5gb	470gb	#SBATCH --nodes=1 #SBATCH --ntasks=94 #SBATCH --mem-per-cpu=5gb #SBATCH --gres=gpu:1

<sup>1</sup> Up to four GPUs may be requested on Puma on a single GPU node with `--gres=gpu:1, 2, 3, or 4`

## High Memory Nodes

When requesting a high memory node, include **both** the memory/CPU and constraint directives

Cluster	Max CPUs	Mem/CPU	Max Mem	Sample Request Statement
Ocelote	48	41gb	2015gb	#SBATCH --nodes=1 #SBATCH --ntasks=48 #SBATCH --mem-per-cpu=41gb #SBATCH --constraint=hi_mem
Puma	94	32gb	3000gb	#SBATCH --nodes=1 #SBATCH --ntasks=94 #SBATCH --mem-per-cpu=32gb #SBATCH --constraint=hi_mem

## Interactive Jobs

When you are on a login node, you can request an interactive session on a compute node. This is useful for checking available modules, testing submission scripts, compiling software, and running programs directly from the command line. We have a built-in shortcut command that will allow you to quickly and easily request a session by simply entering: `interactive`

When you request a session, the full `salloc` command being executed will be displayed for verification/copying/editing/pasting purposes. For example:

```
(ocelote) [netid@junonia ~]$ interactive
Run "interactive -h for help customizing interactive use"
Submitting with /usr/local/bin/salloc --job-name=interactive --mem-per-cpu=4GB --nodes=1 --ntasks=1 --
time=01:00:00 --account=windfall --partition=windfall
salloc: Pending job allocation 531843
salloc: job 531843 queued and waiting for resources
salloc: job 531843 has been allocated resources
salloc: Granted job allocation 531843
salloc: Waiting for resource configuration
salloc: Nodes i16n1 are ready for job
[netid@i16n1 ~]$
```

Notice in the example above how the command prompt changes once your session starts. When you're on a login node, your prompt will show "junonia" or "wentletrap". Once you're in an interactive session, you'll see the name of the compute node you're connected to.

If no options are supplied to the command `interactive`, your job will automatically run using the windfall partition for one hour using one CPU. To use the standard partition, include the flag "-a" followed by your group's name. To see all the customization options:

```
(ocelote) [netid@junonia ~]$ interactive -h
Usage: /usr/local/bin/interactive [-x] [-g] [-N nodes] [-m memory per core] [-n ncpus per node] [-Q
optional qos] [-t hh:mm:ss] [-a account to charge]
```

You may also create your own `salloc` commands using any desired [SLURM directives](#) for maximum customization.

## MPI Jobs

### OpenMPI

For **openmpi** the important variables are set by default, so you do not need to include them in your scripts.

#### Default OpenMPI variables

```
export SBATCH_GET_USER_ENV=1
export OMPI_MCA_btl_openib_cpc_include=rdmacm
export OMPI_MCA_btl_openib_if_include=bnxt_rel
export OMPI_MCA_btl_openib_rroce_enable=1
export OMPI_MCA_btl=vader,self,openib
export OMPI_MCA_oob_tcp_if_include=eth1
```

### Intel MPI

For **Intel MPI**, these variables are set for you:

```
module unload openmpi3 gnu8
```

If you're using Intel MPI with `mpirun` and are getting errors, try replacing `mpirun -np $NPROCESSES` with:

```
srun -n $NPROCESSES --mpi=pmi2
```



## Parallel Work

To make proper use of a supercomputer, you will likely want to use the benefit of many cores. Puma has 94 cores in each node available to Slurm. The exception to that is running hundreds or thousands of jobs using High Throughput Computing.

We have a training course which explains the concepts and terminology of parallel computing with some examples. [Introduction to Parallel Computing](#)

This practical course in [Parallel Analysis in R](#) is also useful