

Slurm

This is the front page for information to our compute resource sharing system. We use software called Slurm to fairly share compute resources.

For job submission we will be using a piece of software called [Slurm](#). Simply put, Slurm is a queue management system; it was developed at the Lawrence Livermore National Lab. It currently supports some of the largest compute clusters in the world. The best description of Slurm can be found on its homepage:

"Slurm is an open-source workload manager designed for Linux clusters of all sizes. It provides three key functions. First it allocates exclusive and/or non-exclusive access to resources (computer nodes) to users for some duration of time so they can perform work. Second, it provides a framework for starting, executing, and monitoring work (typically a parallel job) on a set of allocated nodes. Finally, it arbitrates contention for resources by managing a queue of pending work."¹

Slurm is similar to most other queue systems in that you write a batch script, then submit it to the queue manager. The queue manager schedules your job to run on the queue (or partition in Slurm parlance) that you designate. Below is an outline of how to submit jobs to Slurm, how Slurm decides when to schedule your job, and how to monitor progress.

Communication

Mailing List

If you are going to be a user of any of the CS Slurm clusters please sign up for the mailing list. Downtime and other relevant information will be announced here.

[Mailing List](#)

Discord

There is a dedicated text channel `#slurm` on the UChicago CS Discord server. Please note that this Discord server is *only* for UChicago-affiliated users. You can find a link to our Discord server on the [front page](#) of this wiki.

Clusters

We have a couple different clusters. If you don't know where to start please use the Peanut cluster. The AI Cluster is for GPU jobs and more advanced users.

- [Peanut Cluster](#)
- [AI Cluster](#)

Peanut Cluster

Think of these machines as a dumping ground for discrete computing tasks that might be rude or disruptive to execute on the main (shared) shell servers (i.e., `focal0`, `focal1`, ..., `focal7`).

Additionally, this cluster is used for courses that require it.

AI Cluster

This cluster is mainly made up of GPU machines and is used primary for research.

To use this cluster there are specific nodes you need to log into. Please visit the dedicated AI cluster page for more information.

Where to begin

Slurm is a set of command line utilities that can be accessed via the command line from **most** any computer science system you can login to. Using our main shell servers (`linux.cs.uchicago.edu`) is expected to be our most common use case, so you should start there.

```
ssh user@linux.cs.uchicago.edu
```

If you want to use the AI Cluster you will need to have previously requested access by sending in a ticket. Afterwards, you may login into:

```
ssh user@fe.ai.cs.uchicago.edu
```

Please read up on the specifics on the cluster you are interested in.

Documentation

The [Slurm website](#) should be your primary source for documentation.

A great way to get details on Slurm commands are the manuals that are already on the cluster. For example, if you type the following command:

```
man sbatch
```

you will get the manual page for the `sbatch` command.

Resources

- [Common Slurm commands](#)
- [Official Slurm website](#)

- [Official Slurm documentation](#)
- [Slurm tutorial videos](#)
- [LLNL quick start user guide](#)
- [Yale's User Guide](#)

Job Submission

Jobs submitted to the cluster are run from the command line. Almost anything that you can run via the command line on any of our machines in our labs can be run on our job submission server agents.

The job submission servers run the same software as you will find on our lab computers, but without the X environment.

You can submit jobs from the departmental computers that you have access to. You will not be able to access the job server agent directly.

Command Summary

Cheat Sheet

	Slurm	Example
Submit a batch serial job	sbatch	sbatch runscript.sh
Run a script interactively	srun	srun -pty -p interact -t 10 -mem 1000 /bin/bash /bin/hostname
Kill a job	scancel	scancel 4585
View status of queues	squeue	squeue -u cnetid
Check current job by id	sacct	sacct -j 999999

Usage

Below are some common examples. You should consult the [documentation](#) of Slurm if you need further assistance.

Default Quotas

By default we set a job to be run on one CPU and allocate 100MB of RAM. If you require more than that you should specify what you need. Using the following options will do: `--mem-per-cpu`, `--nodes`, `--ntasks`.

MPI Usage

The AI cluster supports the use of MPI. The following example illustrates its basic use.

```
amcguire@fe01:~$ cat mpi-hello.c
#include <mpi.h>
#include <unistd.h>
#include <stdio.h>

int main(int argc, char **argv) {
    // Initialize MPI
    MPI_Init(&argc, &argv);

    // Get the number of processes in the global communicator
    int count;
    MPI_Comm_size(MPI_COMM_WORLD, &count);

    // Get the rank of the current process
    int rank;
    MPI_Comm_rank(MPI_COMM_WORLD, &rank);

    // Get the current hostname
    char hostname[1024];
    gethostname(hostname, sizeof(hostname));

    // Print a hello world message for this rank
    printf("Hello from process %d of %d on host %s\n", rank, count,
hostname);

    // Finalize the MPI environment before exiting
    MPI_Finalize();
}

amcguire@fe01:~$ cat hello-job.sh
#!/bin/bash
#SBATCH -J mpi-hello          # Job name
#SBATCH -n 2                  # Number of processes
#SBATCH -t 0:10:00             # Max wall time
#SBATCH -o hello-job.out       # Output file name

# Disable the Infiniband transport for OpenMPI (not present on all clusters)
#export OMPI_MCA_btl="^openib"

# Run the job (assumes the batch script is submitted from the same
#directory)
mpirun -np 2 ./mpi-hello

amcguire@fe01:~$ mpicc -o mpi-hello mpi-hello.c
amcguire@fe01:~$ ls -l mpi-hello
-rwxrwx--- 1 amcguire amcguire 16992 Jun 30 10:49 mpi-hello
amcguire@fe01:~$ sbatch -w p001,p002 -p peanut-cpu hello-job.sh
Submitted batch job 1196702
amcguire@fe01:~$ cat hello-job.out
Hello from process 0 of 2 on host p001
Hello from process 1 of 2 on host p002
```

Exclusive access to a node

You will need to add the `--exclusive` options to your script or command line options. This option will ensure that when your job runs it is the only job running on that particular node.

sbatch

The `sbatch` command is used for submitting jobs to the cluster. `sbatch` accepts a number of options either from the command line, or (more typically) from a batch script. An example of a Slurm batch script is shown below:

Sample script

Make sure you create a directory in which to deposit the `STDIN`, `STDOUT`, `STDERR` files.

```
mkdir -p $HOME/slurm/out

#!/bin/bash
#
#SBATCH --mail-user=cnetid@cs.uchicago.edu
#SBATCH --mail-type=ALL
#SBATCH --output=/home/cnetid/slurm/out/%j.%N.stdout
#SBATCH --error=/home/cnetid/slurm/out/%j.%N.stderr
#SBATCH --chdir=/home/cnetid/slurm
#SBATCH --partition=debug
#SBATCH --job-name=check_hostname_of_node
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --mem-per-cpu=500
#SBATCH --time=15:00

hostname
```

If any of the above options are unclear as to what they do please check the man page for `sbatch`

```
man sbatch
```

Make sure to replace all instances of the word `cnetid` with your CNETID.

Submitting job script

Using the above example you will want to place your tested code into a file. '`hostname.job`' is the file name in this example.

```
sbatch hostname.job
```

You can then check the status via squeue or see the output in the output directory '\$HOME/slurm/slurm_out'.

srun

Used to submit a job to the cluster that doesn't necessarily need a script.

```
user@host:~$ srun -n2 hostname
slurm2
slurm2
```

srun will remain in the foreground until the job has finished.

```
user@host:~$ srun -n1 sleep 400
```

squeue

This command will show jobs in the queue.

```
user@host:~$ squeue
JOBID PARTITION      NAME      USER ST      TIME   NODES NODELIST(REASON)
 29      debug      sleep      user  R      0:11      1 research2
```

scancel

Cancel one of your own jobs. Please read the `scancel` manual page (`man scancel`) as there are many ways of canceling your jobs if they are of any complexity.

```
scancel 29
```

sinfo

View information about Slurm nodes and partitions.

The following code block shows the what happens when you run the `sinfo` command. You get a list of 'partitions' on which you can run your code. Each partition is comprised of certain types of nodes. In the case below the default (denoted by a *) is 'debug'. The job time limit is short and is meant only to debug your code. The other partitions will usually have a particular purpose in mind. 'hardware', for example, is to be used if you require direct access to the hardware instead of the KVM layer between the hardware and the OS.

```
user@host:~$ sinfo
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug*      up 1-00:00:00      1      mix slurm1
fast        up 1-00:00:00      6      idle slurm[9-14]
```

general	up	21-00:00:0	6	idle	slurm[2-6,8]
pascal	up	3-00:00:00	1	idle	gpu2
quadro	up	3-00:00:00	1	idle	gpu1
titan	up	3-00:00:00	1	mix	gpu3

Monitoring Jobs

squeue and sacct are two different commands that allow you to monitor job activity in Slurm. squeue is the primary and most accurate monitoring tool since it queries the Slurm controller directly. sacct gives you similar information for running jobs, and can also report on previously finished jobs, but because it accesses the Slurm database, there are some circumstances when the information is not in sync with squeue.

Running squeue without arguments will list all currently running jobs. It is more common, though to list jobs for a particular user (like yourself) using the -u option...

```
squeue -u cnetid
```

or for a particular job id.

```
squeue -j 7894
```

Interactive Jobs

Though batch submission is the best way to take full advantage of the compute power in the job submission cluster, foreground, interactive jobs can also be run.

An interactive job differs from a batch job in two important aspects:

1. The partition to be used is the interact partition
2. Jobs should be initiated with the srun command instead of sbatch.

This command:

```
srun -p general --pty --cpus-per-task 1 --mem 500 -t 0-06:00 /bin/bash
```

will start a command line shell (/bin/bash) on the 'general' queue with 500 MB of RAM for 6 hours; 1 core on 1 node is assumed as these parameters (-n 1 -N 1) were left out. When the interactive session starts, you will notice that you are no longer on a login node, but rather one of the compute nodes dedicated to this queue. The --pty option allows the session to act like a standard terminal.

Job Scheduling

We use a [multifactor](#) method of job scheduling. Job priority is assigned by a combination of fair-share, partition priority, and length of time a job has been sitting in the queue. The priority of the queue is the highest factor in the job priority calculation. For certain queues this will cause jobs on lower priority queues which overlap with that queue to be requeued. The second most important factor is fair-share score. You can find a description of how Slurm calculates Fair-share [here](#). The third most important is how long you have been sitting in the queue. The longer your job sits in the queue the higher its priority grows. If everyone's priority is equal then FIFO is the scheduling method. If you want to see what your current priority is just do `sprio -j JOBID` which will show you the calculation it does to figure out your job priority. If you do `sshare -u USERNAME` you can see your current fair-share and usage.²⁾

We also have backfill turned on. This allows for jobs which are smaller to sneak in while a larger higher priority job is waiting for nodes to free up. If your job can run in the amount of time it takes for the other job to get all the nodes it needs, Slurm will schedule you to run during that period. **This means knowing how long your code will run for is very important and must be declared if you wish to leverage this feature. Otherwise the scheduler will just assume you will use the maximum allowed time for the partition when you run.**³⁾

Array Jobs

Instead of submitting multiple jobs to repeat the same process for different data (e.g. getting results for different datasets for a paper) you can use a job arrays.

```
#SBATCH start-finish[:step][%maximum concurrent]
```

Examples:

```
#SBATCH --array 0-15          0, 1, ..., 15
#SBATCH --array 1-3            0, 1, 2, 3
#SBATCH --array 1,3,4,6        1, 3, 4, 6
#SBATCH --array 1-8:2          1, 3, 5, 7
#SBATCH --array 1-10:3%2       1, 5, 9, but the only two of these will ever
run concurrently.
```

You can differentiate the various tasks using the variable `SLURM_ARRAY_TASK_ID`.

```
#!/bin/bash
#
#SBATCH --mail-user=cnetid@cs.uchicago.edu
#SBATCH --mail-type=ALL
#SBATCH --output=/home/cnetid/slurm/out/%j.%N.stdout
#SBATCH --error=/home/cnetid/slurm/out/%j.%N.stderr
#SBATCH --chdir=/home/cnetid/slurm
#SBATCH --partition=debug
```

```
#SBATCH --job-name=check_hostname_of_node
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --mem-per-cpu=500
#SBATCH --time=15:00
#SBATCH --array 1-4

input=("small_dataset" "medium_dataset" "large_dataset" "huge_dataset")
./process ${input[$SLURM_ARRAY_TASK_ID]}
```

Additionally, tasks can be used to add job dependencies and other fancy features. For more information consult the [manual](#)

Common Issues

Error	What does it mean?
JOB <jobid> CANCELLED AT <time> DUE TO TIME LIMIT	You did not specify enough time for your job to run. The -t flag will allow you to set the time limit.
Job <jobid> exceeded <mem> memory limit, being killed	Your job is attempting to use more memory than you have requested for it. Either increase the amount of memory you have requested or reduce the amount of memory usage your application is trying to use.
JOB <jobid> CANCELLED AT <time> DUE TO NODE FAILURE	There can be many reasons for this message, but most often it means that the node your job was set to run on can no longer be contacted by the Slurm controller.
error: Unable to allocate resources: More processors requested than permitted	It usually has nothing to do with privileges you may or may not have. Rather, it usually means that you have allocated more processors than one compute node actually has.

Using the GPU

GRES Multiple GPU's on one system

GRES: Generic Resource. As of 2018-05-04 these only include GPU's.

Jobs will not be allocated any generic resources unless specifically requested at job submit time using the --gres option supported by the salloc, sbatch and srun commands. The option requires an argument specifying which generic resources are required and how many resources. The resource specification is of the form name[:type:count]. The name is the same name as specified by the GresTypes and Gres configuration parameters. type identifies a specific type of that generic resource (e.g. a specific model of GPU). count specifies how many resources are required and has a default value of 1. For example:

```
sbatch --gres=gpu:titan:2 ....
```

Jobs will be allocated specific generic resources as needed to satisfy the request. If the job is

suspended, those resources do not become available for use by other jobs.

Job steps can be allocated generic resources from those allocated to the job using the `--gres` option with the `srun` command as described above. By default, a job step will be allocated all of the generic resources allocated to the job. If desired, the job step may explicitly specify a different generic resource count than the job. This design choice was based upon a scenario where each job executes many job steps. If job steps were granted access to all generic resources by default, some job steps would need to explicitly specify zero generic resource counts, which we considered more confusing. The job step can be allocated specific generic resources and those resources will not be available to other job steps. A simple example is shown below.

Ok, but I don't want to read the wall of text above

Fine.

The `--gres` (man `srun`) is required if you want to make use of a gpu.

```
--gpu=gpu:N      # where 'N' is the number of GPUs requested.  
                  # Please try to limit yourself to one GPU per person.
```

Example when using tensorflow:

Given the file `f`:

```
#!/usr/bin/env python3  
from tensorflow.python.client import device_lib  
print(device_lib.list_local_devices())
```

Here we can see that no GPU was allocated to us because we did not specify the `--gres` option

```
user@bulldozer:~$ srun -p titan --pty /bin/bash  
user@gpu3:~$ ./f 2>&1 | grep physical_device_desc  
user@gpu3:~$
```

If we request only 1 GPU.

```
user@bulldozer:~$ srun -p titan --pty --gres=gpu:1 /bin/bash  
user@gpu3:~$ ./f 2>&1 | grep physical_device_desc  
physical_device_desc: "device: 0, name: GeForce GTX 1080 Ti, pci bus id:  
0000:19:00.0, compute capability: 6.1"
```

If we request 2 GPUs.

```
user@bulldozer:~$ srun -p titan --pty --gres=gpu:2 /bin/bash  
user@gpu3:~$ ./f 2>&1 | grep physical_device_desc  
physical_device_desc: "device: 0, name: GeForce GTX 1080 Ti, pci bus id:  
0000:19:00.0, compute capability: 6.1"  
physical_device_desc: "device: 1, name: GeForce GTX 1080 Ti, pci bus id:  
0000:1a:00.0, compute capability: 6.1"
```

If we request more GPUs then are available.

```
kauffman3@bulldozer:~$ srun -p titan --pty --gres=gpu:5 /bin/bash
srun: error: Unable to allocate resources: Requested node configuration is
not available
```

Cool, but how do I know where and what resources are available

Turns out the `sinfo` command is super useful.

```
$ sinfo -O partition,nodelist,gres,features,available
PARTITION      NODELIST      GRES      FEATURES
AVAIL
debug*          slurm1      (null)    (null)
up
fast            slurm[9-14]  (null)    (null)
up
general        slurm[2-6,8]  (null)    (null)
up
pascal          gpu2        gpu:gtx1080:1  'pascal,gtx1080'
up
quadro          gpu1        gpu:p4000:2   'quadro,p4000'
up
titan            gpu3        gpu:gtx1080ti:4 'pascal,gtx1080ti'
```

FEATURES: Is actually just an arbitrary string in the configuration file that defines a node. However, techstaff hopes it actually provides some useful info.

GRES: Don't depend on this being accurate, however it will definitely give you a clue as to how many generic resources are in a partition.

Checking how many Generic RESources are being consumed

Simple use the `-O` option for `squeue` and you can see how many generic resources any particular job is consuming.

```
$ squeue -O username,nodelist,gres
USER      NODELIST      GRES
someusername  gpu3        gpu:1
otherusername  gpu3        gpu:3
...
```

Environment Variables

CUDA_HOME, LD_LIBRARY_PATH

Please make sure you specify \$CUDA_HOME and if you want to take advantage of CUDNN libraries you will need to append /usr/local/cuda-x.x/lib64 to the \$LD_LIBRARY_PATH environment variable.

```
cuda_version=11.1
export CUDA_HOME=/usr/local/cuda-${cuda_version}
export LD_LIBRARY_PATH=$LD_LIBRARY_PATH:$CUDA_HOME/lib64
```

Currently we support the same versions of CUDA that the latest version of CUDNN supports. This is not written in stone and we can accommodate most other versions if required; just let techstaff know what your needs are.

PATH

You may also need to add the following to your \$PATH

```
export PATH=$PATH:/usr/local/cuda/bin
```

CUDA_VISIBLE_DEVICES

Do not set this variable. It will be set for you by Slurm.

The variable name is actually misleading; since it does NOT mean the amount of devices, but rather the physical device number assigned by the kernel (e.g. /dev/nvidia2).

For example: If you requested multiple gpu's from Slurm (-gres=gpu:2), the CUDA_VISIBLE_DEVICES variable should contain two numbers(0-3 in this case) separated by a comma (e.g. 0,1).

The numbering is relative and specific to you. For example: two users with one job which require two gpus each could be assigned non-sequential gpu numbers. However CUDA_VISIBLE_DEVICES will look like this for both users: 0,1

Example

This sbatch script will get device information from the installed Tesla gpu.

```
#!/bin/bash
#
#SBATCH --mail-user=cnetid@cs.uchicago.edu
#SBATCH --mail-type=ALL
#SBATCH --output=/home/cnetid/slurm/slurm_out/%j.%N.stdout
#SBATCH --error=/home/cnetid/slurm/slurm_out/%j.%N.stderr
#SBATCH --workdir=/home/cnetid/slurm
#SBATCH --partition=gpu
#SBATCH --job-name=get_tesla_info
```

```
export PATH=$PATH:/usr/local/cuda/bin
export LD_LIBRARY_PATH=$LD_LIBRARY_PATH=/usr/local/cuda/lib

cat << EOF > /tmp/getinfo.cu
#include <stdio.h>

int main() {
    int nDevices;

    cudaGetDeviceCount(&nDevices);
    for (int i = 0; i < nDevices; i++) {
        cudaDeviceProp prop;
        cudaGetDeviceProperties(&prop, i);
        printf("Device Number: %d\n", i);
        printf(" Device name: %s\n", prop.name);
        printf(" Memory Clock Rate (KHz): %d\n",
               prop.memoryClockRate);
        printf(" Memory Bus Width (bits): %d\n",
               prop.memoryBusWidth);
        printf(" Peak Memory Bandwidth (GB/s): %f\n\n",
               2.0*prop.memoryClockRate*(prop.memoryBusWidth/8)/1.0e6);
    }
}
EOF

/usr/local/cuda/bin/nvcc /tmp/getinfo.cu -o /tmp/a.out
/tmp/a.out
rm /tmp/a.out
rm /tmp/getinfo.cu
```

Output

STDOUT will look something like this:

```
cnetid@focal0:~$ cat $HOME/slurm/slurm_out/12567.gpu1.stdout
Device Number: 0
Device name: Tesla M2090
Memory Clock Rate (KHz): 1848000
Memory Bus Width (bits): 384
Peak Memory Bandwidth (GB/s): 177.408000
```

STDERR should be blank.

Feedback

If you feel this documentation is lacking in some way please let techstaff know. Email techstaff@cs.uchicago.edu, call (773-702-1031), or stop by our office (Crerar 357).

More

Sometimes other universities have documentation that is better in some areas.

1. [USC Slurm Docs](#)
2. [NESI Slurm Docs](#)

1)

<http://slurm.schedmd.com/>

2) ,

<https://rc.fas.harvard.edu/resources/running-jobs>

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