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Slurm and job management



When we talk about cpu, we mean core of a cpu since all modern cpu are multi cores.
So, one cpu = one core.

What is Slurm ?

According to [Slurm official website](#) :

Slurm is an open source, fault-tolerant, and highly scalable cluster management and job scheduling system for large and small Linux clusters. Slurm has three key functions.

- *it allocates exclusive and/or non-exclusive access to resources (compute nodes) to users for some duration of time so they can perform work.*
- *it provides a framework for starting, executing, and monitoring work (normally a parallel job) on the set of allocated nodes.*
- *it arbitrates contention for resources by managing a queue of pending work.*

Great, so what does it mean for the users of our HPC clusters ?

It means Slurm is the only way to being granted HPC resources. In order to request the resources you need to submit a *job* to Slurm or to ask it to allocate resources.

It is important to learn a few terms that are specific to Slurm :

- a resource: this may be cpu, gpu, running time (called wall time), memory, license or disk
- a [job](#) once resources are granted to you, your code is running on them and releases them when it finish. When you “submit a job”, you'll ask resources and your job will be put on waiting queue.
- a [partitions](#) determines on which resources your job will run
- a [priority](#) determine when you'll get access to a resource and your job will start

Resources

Before explaining more about Slurm jobs, it is important to understand to concept of **partition** and some other limits.

Partitions

What is a partition ?

A partition is a group of compute nodes accessible with some specific properties (such as maximum execution time, etc.).

- There are two main categories of partitions :
 - **public partitions** are available for everybody on the clusters,
 - **private partitions** are only available to their owners.
- When the HPC team buys compute nodes with UNIGE's funds, those nodes are 100% public which means they will be inside **public partitions** (public-*).
 - Public partitions allow a maximum execution time of **4 days**

- Public-short-* allows a maximum execution time of **1 hour**, with a maximum of **6 cpu** per jobs and **1 job running** per user (multiple submit is allowed).
- When a research group buys compute nodes with their funds (private, FNS, etc.), those nodes will be inside both **shared and private partitions**.
 - Private partitions give a higher **priority** to jobs (shorter waiting time) ;
 - Private partitions also allow a maximum execution time of **7 days**
- When the owner of the **private partition** is not using it, the nodes can be used by anyone else in the cluster since the nodes are *shared* in the **shared partitions** (shared-*).
 - Hence, the (shared-*) partitions contain all the cluster's nodes (public and private nodes)
 - Shared partitions allow a maximum execution time of **12 hours**

Our clusters Baobab and Yggdrasil are heterogeneous, which means the nodes in a partition are not necessarily identical.

You can get a complete list of the nodes and their specifications in [For advanced users - Compute nodes](#)

Which partition for my job ?

This is a very important question, and choosing the right partition can save you (and others) a lot of time.

- Shared partitions :
 - shared-cpu - for CPU jobs that need to run up to 12h
 - shared-gpu - for GPU jobs that need to run up to 12h
 - shared-bigmem - same as shared-cpu, but when you need a crazy amount of RAM (max. 12h)
 - N.B. shared-* partition contain more nodes than public-* (the sum of public and private nodes), but the maximum wall time is 12h.
- Public partitions:
 - public-cpu - for CPU jobs that need to run between 12h and 4 days (max. 4 days)
 - public-gpu - for GPU jobs that need to run between 12h and 4 days (max. 4 days)
 - public-bigmem - same as public-cpu, but when you need a crazy amount of RAM (max. 4 days)
 - N.B. public-* partition contain less nodes than shared-*, but the maximum wall time is 4 days.
- Special public partitions:
 - debug-cpu - to test your CPU jobs and make sure everything works fine (max. 15 min)
 - debug-gpu - to test your GPU jobs and make sure everything works fine (max. 15 min)
 - public-interactive-cpu - for interactive CPU jobs (max. of 6 cores for 8h)
 - public-longrun-cpu - for CPU jobs that don't need much resources, but need a longer runtime time (max. of 2 cores for 14 days)
 - public-short-cpu for CPU jobs that need to run 1h max and 6 CPU max (limited to 1 job running per user but multiple submits allowed)
- Private partitions:
 - The number of CPU/GPU nodes in a private partition depends on the partition
 - If none of your colleagues are using the private partition, max. waiting time is 12h
 - For jobs that need to run for more than 4 days (max. 7 days)

You can read more about job priorities and waiting time in the [Slurm Job priority](#) section.

Partitions lists

The command `sinfo` shows you more details about the partitions you have access to (default time, etc.)

```
[root@admin1 ~]# sinfo
PARTITION      AVAIL  TIMELIMIT  NODES  STATE NODELIST
debug-cpu*      up      15:00        2   idle cpu[001-002]
debug-gpu       up      15:00        1   idle gpu001
public-cpu      up 4-00:00:00   77  alloc cpu[006-082]
public-bigmem   up 4-00:00:00    4   idle cpu[112-115]
public-gpu      up 2-00:00:00    6   idle gpu[002-006,008]
shared-cpu      up    12:00:00   33   mix
cpu[005,084-111,116-119]
shared-cpu      up    12:00:00   77  alloc cpu[006-082]
[...]
```



The default partition is `debug-cpu` (see, there is as `*` in its name). If you want to use another one, you must explicitly specify it.

In the list of partitions (see below), the “Max mem per core” is the suggested value, but it is not enforced. Please refer to the [Memory and CPU usage](#) section for details about how to request a specific amount of memory. If you need more than 10GB RAM per core, you might want to use one of the `*-bigmem` partition.

Clusters partitions



As of 2020-11, the new partition naming is available on Baobab.

Partition	Time Limit	Max mem per core
debug-cpu	15 Minutes	full node memory
debug-gpu	15 Minutes	full node memory
public-interactive-cpu	8 hours	10GB
public-longrun-cpu	14 Days	10GB
public-cpu	4 Days	10GB
public-gpu	4 Days	10GB
public-bigmem	4 Days	half node memory
shared-cpu	12 Hours	10GB
shared-gpu	12 Hours	10GB
shared-bigmem	12 Hours	500GB

All the compute nodes have 3GB of memory per core by default. Minimum resource is one core.

N.B. : no debug-gpu, nor public-gpu partitions on Baobab, as there are only private GPU nodes.

Private partitions

To avoid confusion, private partitions aren't detailed here.

Partition	Time Limit	Max mem per core	default Mem Per core
private-<privatename>	7 Days	full node memory	3GB

To see details about a given partition, go to the web page <https://baobab.unige.ch> and click on the "status" tab. If you belong in one of these groups, please contact us to request to have access to the correct partition as we have to manually add you.

Wall time

When you submit a job, you need to specify the estimated duration of your job.

The time formats accepted by Slurm are as follows:

```
minutes
minutes:seconds
hours:minutes:seconds
days-hours
days-hours:minutes
days-hours:minutes:seconds
```

Example:

```
1-12:30:25
```

Means: 1 day, 12 hour, 30 min and 25 seconds



Make sure you estimate the amount of time you correctly for your job and make sure the partition you use **allows** to run your code for this duration. Your job has more chance to start quickly if you ask less resources.

Memory

When you submit a job, the usable memory you have is **3GB per core**. If you are running a job which requires more or less memory per core, you can specify it like this:

```
--mem-per-cpu=1000 # in MB
```

Even if you have requested a full node, you still need to specify how much memory you need:

```
--mem=60000 # 60'000 MB => 60 GB
```

This is even the case if you request a partition such as `*-bigmem!`



The value of 0 will request all the node's memory. You can use `--mem=0` to ensure you use the entire memory of a node.

GPU

Currently on Baobab and Yggdrasil there are several nodes equipped with GPUs. To request a GPU, it's not enough to specify a partition with nodes having GPUs, you must as well specify how many GPUs and optionally the needed GPU type.

To specify how many GPU to request, use the option `--gpus=n` with `n` having a value between 1 and the maximum according to the table below.

You should also specify the type of GPU you want:

- ampere, high end architecture for multipurpose use
- titan, for single precision computation, like machine learning
- pascal, for double precision computation like physical simulations
- rtx, to accelerate machine learning, data science workflows and ray tracing

Example to request three titan cards: `--gpus=titan:3`.

You can find a detailed list of GPUs available on our clusters here :

https://doc.ererech.unige.ch/hpc/hpc_clusters#for_advanced_users

Resources :

- [P100 specifications](#)
- [Titan x \(pascal\) specifications](#)
- [RTX 2080 Ti \(turing\) specifications](#)
- [Generic Resource \(GRES\) Scheduling in SLURM](#)

CPU



You can request all the CPUs of a compute node minus two that are reserved for the OS. See [slurm core spec](#)

CPU types

It's normally not important on which type of node your job is running. But there are some cases where it is important to be able to stick to a given kind of CPU or a certain generation of CPUs.

You can request for example to have only nodes with CPU E5-2660V0 :

```
srun --constraint=E5-2660V0
or
#SBATCH --constraint=E5-2660V0
```

Or you can specify that you want a node of generation V3 :

```
srun --constraint=V3
or
#SBATCH --constraint=V3
```

You can specify as well multiple constraints using logical *or* with the symbol `|`. For example if you don't want to use nodes of generation V1:

```
srun --constraint="V2|V3|V4|V5|V6"
or
#SBATCH --constraint="V2|V3|V4|V5|V6"
```

If you want a list of those specifications, please check : [For advanced users - Compute nodes](#)

Single thread vs multi thread vs distributed jobs

There are three job categories each with different needs:

Job type	Number of cpu used	Examples	Keywords	Slurm
single threaded	one CPU	Python, plain R	-	
multi threaded	all the CPUs of a compute node (best case scenario)	Matlab, Stata-MP	OpenMP, SMP	--cpus-per-tasks
distributed	can spread tasks on multiple compute nodes	Palabos OpenFOAM	OpenMPI, workers	--ntasks

There are also **hybrid** jobs, where each tasks of such a job behave like a multi-threaded job. This is not very common and we won't cover this case.

In slurm, you have two options for asking CPU resources:

- `--cpus-per-tasks`: this will specify that you want more than one CPU per task.
- `--ntasks`: this will launch n time your job. **ONLY** specify a value bigger than one if your job knows how to handle multitasking properly. For example OpenMPI job can benefit of this option. If your job doesn't handle this option correctly, it will be launched n time doing strictly the same things, this is not what you want and will wait resources and create corrupted output files.

Submitting jobs

After connecting to the login node, you need to submit a *job* to Slurm to request computing resources. You can request it in 3 ways :

method	execute job	blocking command	support job array	batch script needed
salloc	no	yes	no	no
srun	yes, single one	yes	no	no
sbatch	yes	no	yes	yes (or -w option)

By blocking command, we mean that you need to keep your terminal open during the whole process. If you close it, your job will finish.

An “sbatch” script is a Bash script with special instructions for Slurm.

Do not execute directly the sbatch script as bash script, but submit it using sbatch (otherwise your script will be launched on the login node and [this is forbidden](#)):



```
[sagon@login2 slurm] $ sbatch example.sh
Submitted batch job 40721231
```

The number 40721231 is the jobid that is a uniq number. You can use it later for reporting, see logs or cancel for example.

Whatever method you use, you need to pass some arguments (such as how many CPU you need, which Slurm partition to use, how long your script will run, how to execute your code). Slurm will then add your job in a **queue** with other users' jobs, and find the fastest way to provide the resources you asked for. When the resources are available, your job will start.

There are various possibilities to submit a job on the cluster. We have detailed the most common usage below.



If you belong to more than one account, you should specify which account should be used with the option `--account=<account>`

Batch mode (sbatch)

To use the batch mode, you need a sbatch script. Here is an Example of an sbatch script `my_sbatch.s` with `#SBATCH` directives :

```
#!/bin/sh
#SBATCH --job-name jobname          # this is a parameter to help you sort
your job when listing it
```

```
#SBATCH --error jobname-error.e%j      # optional. By default a file slurm-
{jobid}.out will be created
#SBATCH --output jobname-out.o%j        # optional. By default the error and
output files are merged
#SBATCH --ntasks 1                      # number of tasks in your job. One by
default
#SBATCH --cpus-per-task 1                # number of cpus for each task. One by
default
#SBATCH --partition debug-cpu            # the partition to use. By default
debug-cpu
#SBATCH --time 15:00                    # maximum run time.

module load my_software                  # load a specific software using
module, for example Python

srun my_software                        # run your software
```

To submit your job proceed as follows:

```
[sagon@login1 ~]$ sbatch example.sh
Submitted batch job 53697
```

The job number can be useful if you want to see the status of the job on the queue or kill it for example.

To have a list of all options, please check [Slurm documentation - sbatch](#)

You can submit a batch job either with the help of a **script** or directly by specifying the options on the command line. The recommended way to use options for sbatch is to add them directly in the script as in the previous example.

Here are some examples to illustrate the second possibilities.

A simple example to launch a batch job `my_sbatch.sh` using 16 cpus on the default partition:

```
sbatch --ntasks=16 my_sbatch.sh
```



If not specified, the default partition is `debug-cpu` and the default number of cpus per task is **1**

Launch a job specifying the partition “`shared-cpu`” (see [Partitions and limits](#) section) and max execution time:

```
sbatch --ntasks=8 --partition=shared-cpu --time=0-00:05:00 my_sbatch.sh
```



You will have more chance to have your job quickly scheduled if you specify an accurate max execution time (i.e. not the permitted maximum).

Monothreaded jobs

[Click here for job type comparison.](#)

When you submit a job on the clusters, the minimum resources that are allocated to you is a one cpu. As the node may be shared with other users, it is wise to specify the amount of memory you need per core. If you don't, the default memory allocated is 3GB per core.

Let's say you want to launch one job that needs 1GB per core. Your sbatch script is named `example.sh`

```
#!/bin/bash

#SBATCH --partition=public-cpu
#SBATCH --time=05:00
#SBATCH --ntasks=1
#SBATCH --mem-per-cpu=1000 # in MB

srun ./yourprog
```

To submit your job do as follows:

```
[sagon@login1 ~]$ sbatch example.sh
Submitted batch job 53697
```

The number you get is the `jobid`.

Adapt this example to fit your needs. If you need to scale this solution to a bigger number of similar tasks, see the [Job array](#) section.

Multithreaded jobs

[Click here for job type comparison.](#)

When you have a program that needs more than one core per task (openMP, STATA etc), you can adapt the [Monothreaded jobs](#) example by adding one line:

```
#SBATCH --cpus-per-task=x
```

where `x` is between 1 and 128. We have only a couple of AMD nodes with 128 cores. If you request a high number of cpus per task, be sure that you need it as you may have to wait many days for them to be available.

If you want to use all the cores of a node, but you don't know in advance the characteristic of the node, you can use this sbatch script:

```
#!/bin/sh
#SBATCH --job-name=test
```

```
#SBATCH --time=00:15:00
#SBATCH --partition=public-cpu
#SBATCH --output=slurm-%J.out
#SBATCH --exclusive
#SBATCH --ntasks=1

# We want to have a node with minimum
# 2 sockets, 4 cores per socket and 1 thread per core
# nb_cores = 2 * 4 * 1 = 8 cores
# if you want more cores, you can increase the number of cores per socket to
# 6 or 8 to have 12 or 16 cores.
#SBATCH --extra-node-info=2:4:1

We want to have at least 12GB RAM on this node
#SBATCH --mem=12000

# run one task which use all the cpus of the node
srun --cpu_bind=mask_cpu:0xffffffff ./mySoft
```

Distributed jobs

When you want to distribute your jobs across nodes, your software will probably use an MPI implementation such as [OpenMPI](#) or [Intel](#).

To specify the number of MPI workers, you need to specify the number of tasks in slurm.

`--ntasks-per-node`: maximum number of tasks per node. Can be used in conjunction with `--ntasks`.

`-n, --ntasks=<number>`: number of workers in total

`-N, --nodes=<minnodes [-maxnodes]>`: number of nodes allocated to this job

You can have as well a hybrid job requiring tasks and cpus (for OpenMPI + OpenMP for example).

If you request for example 20 tasks and 1 CPU per task, your job may be executed by one compute node having 20 cpus if available or may be spread across any number of compute nodes. The issue may be that the compute nodes are shared with other jobs and not from the same generation.

To circumvent this, you can specify the cpu type you want, but you'll have more wait time. You may as well want to specify the `--exclusive` flag to be sure that your compute node won't be shared with other jobs. In this case, please do not specify the number of compute node or you may waste resources.

You may as well be interested by the distribution parameter.

`--distribution`: Specify alternate distribution methods for remote processes.

If you need more details, please consult the [sbatch man](#) page.

If you want to compile your software against MPI, it is very important not to compile using directly

gcc, icc or similar commands, but rather rely on the wrappers mpicc, mpic++, mpicxx or similar ones provided by [module](#).

Remember that you need to load the same module at runtime as well.

See [here](#) for more information about the toolchains

GPGPU jobs

When we talk about [GPGPU](#) we mean using a GPU to perform calculation, not for visualization.

You can see on this table [How our clusters work](#) all the GPUs models we have on the cluster. You may notice that we have a very wide range of GPU models, from low end to high end. It is important to select the correct GPU model to avoid to waste resources. The important characteristics of a GPU are:

- on board memory in GB
- simple precision vs double precision for float calculation
- compute capability

Specify the memory needed. For example, request one GPU that has 10G at least.

```
srun --gres=gpu:1,VramPerGpu:10G
```

If you just need a GPU and you don't care of the type, don't specify it. You'll get the lower model available.

```
#SBATCH --gpus=1
```

Example to request two double precision GPU model:

```
#!/bin/sh
#SBATCH --partition=shared-gpu
#SBATCH --gpus=2
#SBATCH --constraint=DOUBLE_PRECISION_GPU

srun nvidia-smi
```

It's not possible to put two types in the GRES request, but you can ask for specific compute capability, for example you want to request any GPU model with compute capability bigger or equal to 7.5:

Example

```
#!/bin/sh
#SBATCH --partition=shared-gpu
#SBATCH --gpus=1
#SBATCH --
constraint="COMPUTE_CAPABILITY_7_5|COMPUTE_CAPABILITY_8_0|COMPUTE_CAPABILITY_8_6|"
```

Example of script (see also <https://gitlab.unige.ch/hpc/softs/tree/master/c/cuda>):

```
#!/bin/env bash

#SBATCH --partition=shared-gpu
#SBATCH --time=01:00:00
#SBATCH --gpus=titan:1

module load CUDA

# see here for more samples:
# /opt/cudasample/NVIDIA_CUDA-8.0_Samples/bin/x86_64/linux/release/

# if you need to know the allocated CUDA device, you can obtain it here:
echo $CUDA_VISIBLE_DEVICES

srun deviceQuery
```

If you want to see what GPUs are in use in a given node:

```
scontrol -d show node gpu002
[...]
Gres=gpu:titan:3
GresUsed=mic:0,gpu:titan:3(IDX:0-2)
[...]
```

In this case, this means that node gpu002 has three Titan cards, and all of them are allocated.

Interactive jobs

If you need to perform some debug/tests or if your software requires a graphical interface, you can start an interactive session on a compute node. For example, let's say you want to start a session on the debug-cpu partition for a duration of 15 minutes, using 2 CPUs:

```
[sagon@login2 ~]$ salloc -n1 -c2 --partition=debug-cpu --time=15:00 --x11
```

When the resources are allocated to you, you can see the login prompt change to reflect that you are using a compute node and not the login node:

```
[sagon@nodexxx ~]$
```

When done, you can stop the session like this:

```
[sagon@nodexxx ~]$ exit
```



Adding the option `--x11` will allow you to submit graphical job



For interactive programs, you might want to use the `public-interactive-cpu` partition ([Which partition for my job](#))

Job array

Slurm supports natively the notion of job arrays. A job array is useful when you have a lot of the same jobs to launch and you just want to give a different parameter to every job.

Here is an example for launching n time a monothreaded job.

The following sbatch script `my_job_array.sh` is used and the variable `${SLURM_ARRAY_TASK_ID}` shows the task ID in the job array:

```
#!/bin/bash

#SBATCH --partition=shared-cpu
#SBATCH --time=00:10:00
#SBATCH --cpus-per-task=1
#SBATCH --ntasks=1
#SBATCH --mem-per-cpu=1000 # in MB
#SBATCH -o myjob-%A_%a.out

srun echo "I'm task_id " ${SLURM_ARRAY_TASK_ID} " on node " $(hostname)
```

When you want to execute a job array, use the `--array` option. You may specify how many cores ONE instance of your array needs with `--ntasks` if you are using MPI or with `--cpus-per-task` otherwise. You must specify the array size and offset by specifying the start and stop of the array index.

N.B. The maximum size of an array is currently set to **10 000**.

We encourage you to limit the maximum number of simultaneously running tasks from the job array may be specified using a “%” separator.

For example “`--array=0-15%4`” will limit the number of simultaneously running tasks from this job array to 4

Example to launch an array of 100 jobs, each one using one core:

```
sbatch --array=1-100%4 my_job_array.sh
```

The max number %100 seems to be a good limit :)

Advanced usage

Job dependency

Slurm can handle job dependencies in various way.

Some of the dependency features available in Slurm (cf. man sbatch)

- `after:job_id[[+time][:jobid[+time]...]]`
- `afterany:job_id[:jobid...]`
- `afternotok:job_id[:jobid...]`
- `afterok:job_id[:jobid...]`
- `expand:job_id`
- `singleton`

Example to submit multiple batch jobs that are dependent from each other. The dependent job will only start when the previous one terminated with success:

```
[sagon@login2 ~]$ sbatch pre_process.bash
Submitted batch job nnnnn
[sagon@login2 ~]$ sbatch --dependency=afterok:nnnnn do_work.bash
Submitted batch job 12346
```

N.B. in this example, the first submitted job is given the job ID “nnnnn” (in real life, it will be a number), and the second one depends on it thanks to the option `--dependency=afterok:nnnnn`. You obviously need to replace `nnnnn` with the job ID returned by Slurm.

You can see [here](#) an example with `singleton` used to restart a job when time limit is reached.

Master/Slave

You can run different job step in an allocation. This may be useful in case of a master/slave program for example.

For example, if you want to launch a master program on core 0 and 4 slaves jobs on cores 1-4:

```
[sagon@login2 ~]$ cat master.conf
#TaskID Program Arguments
0 masterprogramm
1-4 slaveprogramm --rank=%0

[sagon@login2 ~]$ srun --ntasks=5 --multi-prog master.conf
```

Use `%t` and `%o` to obtain respectively the task **id** and **offset**.

Checkpoint

A *checkpoint* allows you to pause/stop a program and to restart it from the “saved” point. This is usually done by saving your *progress* to a file, and your program can be restarted from that file.

Not all programs implement checkpointing, so you have to check if this is an option for you.

If you can use checkpoints, this can be interesting :

- to save your progress and avoid starting all over again if your job fails.
- to run a time-consuming task in multiple short jobs to obtain resources faster
 - instead of requesting a job for 4 days, you could execute it by running multiple 12h jobs consecutively. This could decrease your waiting time to obtain the resources (as it's usually faster to get a slot of 12h than it is for 4 days).

Please check this post :

- [\[tutorial\] How to automatically restart a slurm job after time limit](#)

Reservation

to request for reservation; contact the HPC team following the instruction <https://doc.ererech.unige.ch/hpc/start> > contact the hpc team by email

list reservation:

```
(baobab)-[alberta@login2 ~]#scontrol show res
```

Use reservation via srun:

```
(baobab)-[alberta@login2 ~]# srun --reservation <reservation_name> hostname
```

Use reservation via script sbatch:

```
#SBATCH --reservation <reservation_name>
```

```
#!/bin/bash
```

```
#SBATCH --job-name=test_unitaire
```

```
#SBATCH --reservation test
```

```
srun hostname
```

Job monitoring

If you want to get an estimated start time for your job, you can use `--test-only` :

```
srun --test-only -n100 -p public-cpu -t 10 hostname
```

To see the queue :

```
squeue
```

Add the `-u <username>` to see a list of all your job together with the node they are scheduled on and the reason why they might not be starting.

Add the `-start` flag to obtain the scheduled time of when your job should start. ¹⁾

```
squeue -u $USER --start
```

To get an estimation of when your job is scheduled to start :

```
scontrol show jobid 5543
```



Those commands give an estimation. Sometimes the waiting time will be longer, sometimes it will be shorter

Email notification of job events

When a determined event occurs in your job's life, it is possible to receive an email to the address used during your [Account](#) registration :

```
--mail-type=<type> BEGIN, END, FAIL, REQUEUE, and ALL (any state change).
```

Those options can be used with `sbatch` and `srun`.

If your job get killed, one of the reason could be that you have used too much memory. To check if it's the case, you can have a look at `dmesg`.

For instance :

```
dmesg
Memory cgroup out of memory: Kill process 62310 (cavity3d) score 69 or
sacrifice child
```

The email you receive contains important information about why your job failed for instance, but it's not always easy to read it. For example in this excerpt, you need to look inside the big block at the beginning to find the **Reason** *PartitionTimeLimit* (meaning the requested time is too long for the requested partition) :

```
[...]
$ scontrol show Job=123456
JobId=123456 JobName=/home/users/b/brero/testFailed.sh
[...]
JobState=PENDING Reason=PartitionTimeLimit Dependency=(null)
Requeue=1 Restarts=0 BatchFlag=1 Reboot=0 ExitCode=0:0
RunTime=00:00:00 TimeLimit=5-13:20:00 TimeMin=N/A
[...]
```

Memory and CPU usage

You can see how much memory/cpu your job is using if it is still running using sstat. :

```
sstat --format=AveCPU,MaxRSS,JobID,NodeList -j <yourjobid>
```

If your job is no longer running, you can use sacct to see stats about. :

```
sacct --format=Start,AveCPU,State,MaxRSS,JobID,NodeList,ReqMem --units=G -j
<yourjobid>
```

If you want other information please see the sacct manpage.

Energy usage

CPUs

You can see the energy consumption of your jobs on Yggdrasil (Baobab soon). The energy is shown in Joules using sacct.

```
(yggdrasil)-[root@admin1 state] (master *)$ sacct --
format=Start,State,JobID,ConsumedEnergy,ConsumedEnergyRaw --units=k -j
28478878
```

Start	State	JobID	ConsumedEnergy	ConsumedEnergyRaw
2023-10-12T09:48:28	COMPLETED	28478878	43.13K	43127
2023-10-12T09:48:28	COMPLETED	28478878.ex+	43.13K	43127
2023-10-12T09:48:28	COMPLETED	28478878.0	43.11K	43109



It is working only for Intel nodes (at least for the moment). Only in the case of an exclusive job allocation does this value reflect the job's real energy consumption.

GPUs

If you are interested by the power usage of a GPU card your job is using, you can issue the following command while your job is running on a GPU node:

```
(baobab)-[root@gpu002 ~]$ nvidia-smi dmon --select p --id 0
```

# gpu	pwr	gtemp	mtmp
# Idx	W	C	C
0	63	55	-
0	59	55	-

0	62	55	-
---	----	----	---

Other tools

spart

spart ²⁾ is a tool to check the overall partition usage/description.

More info in [this post](#).

```
[brero@login2 ~]$ spart
      QUEUE STA   FREE  TOTAL RESORC  OTHER   FREE  TOTAL ||   MAX
DEFAULT  MAXIMUM CORES   NODE
      PARTITION TUS   CORES  CORES PENDNG PENDNG  NODES  NODES ||  NODES
JOB-TIME  JOB-TIME /NODE MEM-GB
      debug-EL7  *    32    64  50114    1    2    4 ||    2
15 mins   15 mins    16    64
      mono-EL7    120   784  4197    43    0   49 ||    -
1 mins    4 days    16    64
      parallel-EL7  120   784  2108    18    0   49 ||    -
1 mins    4 days    16    64
      shared-EL7   326  3572   734   489    1  224 ||    -
1 mins   12 hour    12    40
      mono-shared-EL7  326  3572 144348   615    1  224 ||    -
1 mins   12 hour    12    40
      bigmem-EL7    14    16    66    0    0    1 ||    1
1 mins    4 days    16   256
      shared-bigmem-EL7  63   212   820    0    1   10 ||    -
1 mins   12 hour    8    256
      shared-gpu-EL7  415   484    16   36    3   12 ||    -
1 mins   12 hour    12   128
      admin-EL7    16    16    0    0    1    1 ||    -
1 mins    7 days    16    64

      YOUR YOUR YOUR YOUR
      RUN PEND OTHR TOTL
COMMON VALUES:    0    0    0    0
```

pestat

pestat ³⁾ is another tool to check cluster usage, this time focusing on single nodes

More info in [this post](#).

```
[brero@login2 ~]$ pestat
Hostname      Partition      Node Num_CPU  CPUload  Memsize  Freemem
Joblist
```

			State Use/Tot			(MB)	(MB)	JobId
User ...								
gpu002	shared-gpu-EL7+	mix	6	12	8.29*	257820	231499	
39803837	krivachy 39806932	salamda0	39795512	blonde0	39795511	blonde0		
39795510	blonde0 39795480	blonde0						
gpu004	shared-gpu-EL7	mix	6	20	7.27*	128820	102173	
39795515	blonde0 39795516	blonde0	39795485	blonde0	39795481	blonde0	39795482	
blonde0	39795499	blonde0						
gpu005	shared-gpu-EL7	mix	5	20	6.05*	128820	97620	
39795513	blonde0 39795463	blonde0	39795464	blonde0				
[...]								
node001	debug-EL7*	idle	0	16	8.64*	64000	47239	
node002	debug-EL7*	alloc	16	16	7.63*	64000	16393	
39772071	gonzalcr							
node003	debug-EL7*	alloc	16	16	11.16*	64000	18610	
39772072	gonzalcr							
node004	debug-EL7*	drain*	0	16	0.01	64000	62061	
node005	mono-EL7	drng*	8	16	2.52*	64000	38015	
39802885	vie							
node007	parallel-EL7	alloc	16	16	16.03	64000	53761	
39524658	robinsh8							
node008	mono-EL7	mix	8	16	2.13*	64000	53388	
39802883	vie							
node009	parallel-EL7	alloc	16	16	0.01*	64000	54509	
39524658	robinsh8							
node010	parallel-EL7	alloc	16	16	0.01*	64000	49796	
39524658	robinsh8							
node011	mono-EL7	mix	8	16	1.53*	64000	48417	
39802889	vie							

seff

seff is tool get a Slurm job efficiency report

```
[sagon@login2 ~] $ seff 30455298
Job ID: 30455298
Cluster: baobab
User/Group: savchenk/hpc_users
State: COMPLETED (exit code 0)
Cores: 1
CPU Utilized: 00:00:01
CPU Efficiency: 0.77% of 00:02:10 core-walltime
Job Wall-clock time: 00:02:10
Memory Utilized: 34.16 MB
Memory Efficiency: 1.14% of 2.93 GB
```

HDF5 profiling plugin

The HDF5 plugin can help profile your jobs ⁴⁾.

Official documentation :

- https://slurm.schedmd.com/hdf5_profile_user_guide.html#Profiling

The HDF5 files will be saved as `/opt/cluster/slurm/hdf5/${USERNAME}/${JOBID}.h5`.

You can analyse the HDF5 files directly on the login node via HDFView ⁵⁾.

Cancel jobs

If you realise you made a mistake in your code or in your sbatch script, you can cancel your pending jobs or your running job (only yours).

If you want to cancel a particular job, you need to know its **job id** (you can see it on the web interface or using `squeue`).

Cancelling a job using its job id:

```
scancel <jobid>
```

Cancel a job and send a custom signal (for example to force the binary to generate a checkpoint):

```
scancel --signal=signal_name
```

You can read this topic [Gracefully quit when job is cancelled](#)

Cancel all the jobs belonging to one user that are in a pending state:

```
scancel --user=meyerx --state=pending
```

Job priorities

How is the priority of a job determined ?

HPC users often wonder how is the job priority calculated by Slurm.

On our clusters, the priority is obtained in general by four criteria, and each criterion has a different weight.

```
partition : 15000  
age: 300  
jobsize: 1000  
fairshare: 30000
```

- The partition criterion is always the same for a given user on a given partition. It is higher if you use a private partition.
 - For example, if you submit a job to the partition shared-cpu you'll get a priority of **3750** for the partition criterion.
 - However, this partition criterion may have a multiplier, ie : if you use a private partitions.
 - For example, if a user submit a job on a private partition, the multiplication factor is 4 and he will have a priority of **15000** for the partition criterion.
 - The reason for this is because private nodes are simultaneously part of multiple partitions : a private partition and shared-cpu partition. The multiplier ensures that the people with access to private partitions have a faster access to their private node.
- The age criterion starts to increase as soon as the job is submitted. Hence, the priority will slowly increase with time. This is used to prevent a job with a low priority to stay in the queue for ages.
- The jobsizes criterion is here to favour big jobs, but the weight is very low unless you submit a very big job.
- The fairshare criterion is based on the past usage of the user. If you use the cluster a lot, your fairshare criterion will decrease. Every 2 weeks, half of your past usage is "forgotten" by Slurm.

You can see how the priority of a job and see how it is calculated with the `sprio` command. Example

- for a public partition (partition weight 3750)

```
[root@master ~]# sprio -j xxx
```

	JOBID	PARTITION	PRIORITY	SITE	AGE	FAIRSHARE
JOBSIZE	PARTITION	QOS				
	xxx	mono-shar	3810	0	6	53
2	3750	0				

- for a private partition (partition weight 15000)

```
[root@master ~]# sprio -j xxx
```

	JOBID	PARTITION	PRIORITY	SITE	AGE	FAIRSHARE
JOBSIZE	PARTITION	QOS				
	yyy	wesolowsk	19590	0	1	4586
4	15000	0				
	zzz	dpnc-EL7	21288	0	0	6297
2	15000	0				

The priority is calculated by summing the values of all four criteria (it's actually a little more complex than that, as the priority returned by `sprio` isn't an exact sum, but you get the general idea). The bigger the priority, the higher is your chance to be scheduled compared to a job with a lower priority. The partition and fairshare criteria have then the strongest impact on the total priority calculation.

If you want to learn more about it, you can check this presentation :

- [Slurm Priority, Fairshare and Fair Tree](#) (might differ from how we do things on UNIGE clusters)

Priority vs. waiting time

Please also remember that the *priority* of a job is one thing, but the actual *waiting time* is another.

- Your priority is calculated regardless of the amount of resources you request for a job.
- If you request a large amount of resources, it might take more time for Slurm to provide those resources (the time to wait until they are free).
- Hence, asking for more or less memory won't change the *priority*, but asking for more resources might affect the *waiting time*.
- So it is better to request as little resources as possible if you want increase your chances to be scheduled quickly.

The waiting time is a pessimistic estimation and is based on the maximum time a job is announced to take. If you don't use the `#SBATCH -time` directive in your sbatch script, the default time for a job is given by the maximum time limit of the partition (12h, 4 day or 7 days depending on the partition). This implies that a job with a maximum run time of 4 days will be scheduled to take the whole 4 days and other jobs will be scheduled to run after it has finish. However if the job only take 10 hours the other jobs can start sooner. ⁶⁾

However, if you are using a shared-* partition, bear in mind that a new job on a private partition might “cut in line” as they have a higher priority.

If you are requesting for example 12h00 of wall-time and 16 cores, and another user is asking for a wall-time of 1 minute and 1 core, this job will most likely be scheduled before your job thanks to the **backfill mechanism** even if you job has a higher priority.

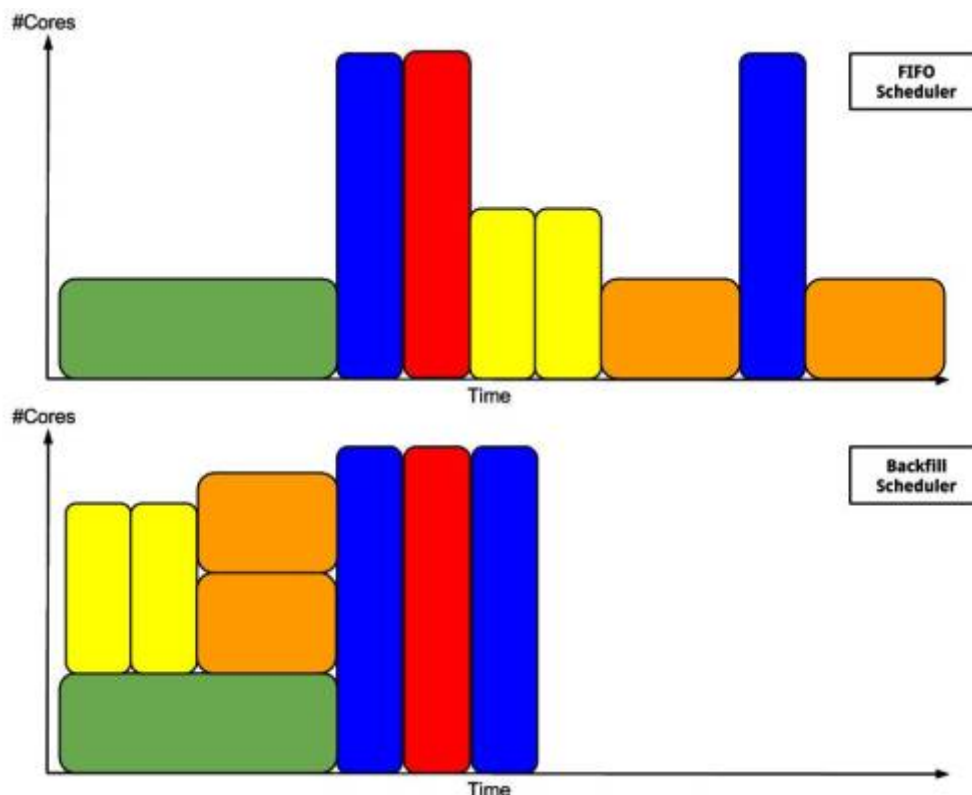
The total number of running jobs of a given user doesn't change the priority of a job. But if the user uses the cluster a lot (especially a lot in a short time), then his/her `fairshare` criterion will decrease.

Please also check this post : [HPC Community - Job priority explanation](#)

Backfill mechanism

The priority is determined by various factors like the usage history, job age and its size.

The scheduler use a backfill to maximize the cluster usage.



To benefit of the backfill allocation, you can specify a minimum and a maximum execution time when you submit a job. If the resources for the max execution time are not available, the scheduler will try to decrease the execution time until it reaches the minimum execution time. In the following example, we submit a job specifying that we want ideally a two days execution time with a one day minimum:

```
srun --tasks=128 --time-min=1-00:00:00 --time=2-00:00:00 --partition shared-cpu myjob
```

Attention

Warning : Be sure that you have some kind of checkpointing activated as your job will be terminated between the min and max execution time.

1)

<https://hpc-community.unige.ch/t/question-about-mono-el7-and-shared-el7-partitions-usage/1006/2>

2)

<https://github.com/mercanca/spart>

3)

https://github.com/OleHolmNielsen/Slurm_tools

4)

<https://hpc-community.unige.ch/t/slurm-monitor-resources-during-job/505/3>

5)

<https://hpc-community.unige.ch/t/new-software-installed-hdfview-2-14-system-java-centos7/1020>

6)

<https://hpc-community.unige.ch/t/estimated-wait-time/1088>

From:

<https://doc.ererech.unige.ch/> - **eResearch Doc**

Permanent link:

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Last update: **2025/06/11 12:27**

