Slurm: A quick start tutorial

Slurm is a resource manager and job scheduler. Users can submit jobs (i.e. scripts containing execution instructions) to slurm so that it can schedule their execution and allocate the appropriate resources (CPU, RAM, etc..) on the basis of a user's preferences or the limits imposed by the system administrators. The advantages of using slurm on a computational cluster are multiple. For an overview of them please read these pages.

Slurm is **free** software distributed under the GNU General Public License.

What is parallel computing?

A parallel job consists of tasks that run simultaneously. Parallelization can be achieved in different ways. Please read the relevant wiki page here to know more.

Slurm's architecture

Slurm is made of a slurmd daemon running on each compute node and a central slurmctld daemon running on a management node (with the possibility of setting up a fail-over twin). If `accounting' is enabled, then there is a third daemon called slurmdbd managing the communications between an accounting database and the management node.

Common slurm user commands include *sacct, salloc, sattach, sbatch, sbcast, scancel, scontrol, sinfo, smap, squeue, srun, strigger and sview* and they are available on each compute node. Manual pages for each of these commands are accessible in the usual manner, that is `man sbatch` for example (see below).

Node

A node in slurm is a compute resource. This is usually defined by particular consumable resources, i.e. memory, CPU, etc…

Partitions

A partition (or queue) is a set of nodes with usually common characteristics and/or limits.

Partitions group nodes into logical (even overlapping if necessary) sets.

Jobs

Jobs are allocations of consumable resources assigned to a user under specified conditions.

Job Steps

A job step is a single task within a job. Each job can have multiple tasks (steps) even parallel ones.

Common user commands

- **sacct**: used to report job or job step accounting information about active or completed jobs.
- **salloc**: used to allocate resources for a job in real time. Typically this is used to allocate resources and spawn a shell. The shell is then used to execute srun commands to launch parallel tasks.
- **sbatch**: used to submit a job script for later execution. The script typically contains an srun command to launch parallel tasks plus any other environment definitions needed.
- **scancel**: used to cancel a pending or running job or job step.
- **sinfo**: used to report the state of partitions and nodes managed by Slurm.
- **squeue**: used to report the state of running and pending jobs or job steps.
- **srun**: used to submit a job for execution or initiate job steps in real time. srun allows users to requests arbitrary consumable resources.

Examples

Determine what partitions exist on the system, what nodes they include, and the general system state.

```
$ sinfo
```

A * near a partition name indicates the default partition. See `man sinfo`

Display all active jobs by user bongo?

```
$squeue -u <username>
```

See `man squeue`.

Report more detailed information about partitions, nodes, jobs, job steps, and configuration

```
$ scontrol show partition notebook
```

```
$scontrol show node maris004
```

```
novamaris [1087] $ scontrol show jobs 1052
```

See `man scontrol`.

Create three tasks running on different nodes

```
novamaris [1088] $ srun -N3 -l /bin/hostname
2: maris007
```

```
0: maris005
1: maris006
```

Create three tasks running on the same node

```
novamaris [1090] $ srun -n3 -l /bin/hostname
2: maris005
1: maris005
0: maris005
```

Create three tasks running on different nodes specifying which nodes should at least be used

```
 srun -N3 -w "maris00[5-6]" -l /bin/hostname
1: maris006
0: maris005
2: maris007
```

Allocate resources and spawn job steps within that allocation

```
novamaris [1094] $ salloc -n2
salloc: Granted job allocation 1061
novamaris [997] $ srun /bin/hostname
maris005
maris005
novamaris [998] $ exit
exit
salloc: Relinquishing job allocation 1061
novamaris [1095] $
```

Create a job script and submit it to slurm for execution

Suppose `batch.sh` has the following contents

```
#!/bin/env bash
#SBATCH -n 2
#SBATCH -w maris00[5-6]
srun hostname
```

then submit it using `sbatch script.sh`.

See `man sbatch`.

Less-common user commands

- **sacctmgr**
- **sstat**
- **sshare**
- **sprio**
- **sacct**

sacctmgr

Display info on configured qos

```
$ sacctmgr show qos format=Name,MaxCpusPerUser,MaxJobsPerUser,Flags
      Name MaxCPUsPU MaxJobsPU                Flags
---------- --------- --------- --------------------
    normal
playground        32                    DenyOnLimit
  notebook         4         1          DenyOnLimit
```

sstat

Displays information pertaining to CPU, Task, Node, Resident Set Size (RSS) and Virtual Memory (VM) of a running job

```
$sstat -o JobID,MaxRSS,AveRSS,MaxPages,AvePages,AveCPU,MaxDiskRead
8749.batch

       JobID     MaxRSS     AveRSS MaxPages   AvePages     AveCPU
MaxDiskRead
------------ ---------- ---------- -------- ---------- ---------- ----------
--
8749.batch      196448K    196448K        0          0  01:00.000 7.03M
```


Note that in the example above the job is identified by id `8749.batch` in which the word `batch' is appended to the id displayed using the squeue command. This is a necessary addition whenever a running program is not parallel i.e. not using `srun'.

sshare

Display the shares associated to a particular user

```
$ sshare -U -u xxxxx
             Account       User  RawShares  NormShares    RawUsage
EffectvUsage  FairShare
-------------------- ---------- ---------- ----------- ----------- ---------
---- ----------
xxxxx                    yyyyyy          1    0.024390    37733389
0.076901   0.112428
```

sprio

Display priority information of a pending job id xxx

```
sprio -l -j xxx
```

To find what priority a running job was given type

```
squeue -o %Q -j <jobid>
```

sacct

It displays accounting data for all jobs and job steps in the Slurm job accounting log or Slurm database. For instance

```
sacct -o JobID,JobName,User,AllocNodes,AllocTRES,AveCPUFreq,AveRSS,Start,End
-j 13180,13183
       JobID    JobName      User AllocNodes  AllocTRES AveCPUFreq
AveRSS               Start                 End
------------ ---------- --------- ---------- ---------- ---------- ---------
- ------------------- -------------------
13180             test2   xxxxxxx          1 cpu=8,mem+
2017-04-10T13:34:33 2017-04-10T14:08:24
13180.batch       batch                    1 cpu=8,mem+    116.13M
354140K 2017-04-10T13:34:33 2017-04-10T14:08:24
13183             test3   xxxxxxx          1 cpu=8,mem+
2017-04-10T13:54:52 2017-04-10T14:26:34
13183.batch       batch                    1 cpu=8,mem+         2G
10652K 2017-04-10T13:54:52 2017-04-10T14:26:34
13183.0         xpyxmci                    1 cpu=8,mem+      1.96G
30892K 2017-04-10T13:54:53 2017-04-10T14:26:34
```

Tips

To minimize the time your job spends in the queue you could specify multiple partitions so that the job could start as soon as possible. Use `–partition=notebook,playground,computation` for instance.

To have a rough estimate of when your queued job will start type `squeue –start`

To translate a job script written for a scheduler different than slurm to slurm's own syntax consider using http://www.schedmd.com/slurmdocs/rosetta.pdf

top-like node usage

Should you want to monitor the usage of the cluster nodes in a top-like fashion type

```
sinfo -i 5 -S"-O" -o "%.9n %.6t %.10e/%m %.10O %.15C"
```

top-like job stats

To monitor the resources consumed by your running job type

```
watch -n1 sstat --format
JobID,NTasks,nodelist,MaxRSS,MaxVMSize,AveRSS,AveVMSize,AveCpuFreq
<jobid>[.batch]
```

Make local file available to all nodes allocated to a slurm job

To transmit a file to all nodes allocated to the currently active Slurm job use `sbcast`. For instance

```
> cat my.job
  #!/bin/env bash
  sbcast my.prog /tmp/my.prog
  srun /tmp/my.prog

> sbatch --nodes=8 my.job
  srun: jobid 145 submitted
```

Specify nodes for a job

For instance `#SBATCH –nodelist=maris0xx`

Environment variables available to slurm jobs

Type `printenv | grep -i slurm` to display them.