CANCER RESEARCH UK | CAMBRIDGE INSTITUTE

CRUK CI HPC cluster introduction (II of III)

Using the scheduler for job submission

UNIVERSITY OF CAMBRIDGE

SLURM will allow you to:

- Submit jobs to the cluster.
- Specify which queue/account to submit your jobs to.
- Request memory resources for your jobs.
- Set memory limits for your jobs.
- Set time limits for your jobs
- Check the status of the jobs you have submitted.
- Check the status of the hosts within the cluster.
- Kill jobs that you have submitted to the cluster.

The most useful SLURM commands

These are:

- **sinfo**
- **squeue**
- **sbatch**
- **scancel**
- **salloc**
- **srun**
- **scontrol**
- **sstat**
- **sacct**
- **sacctmgr**

Type command followed by -h for usage details.

man <COMMAND>
<COMMAND> --usage, lists options
<COMMAND> --help, explain options

Usage: srun [OPTIONS...] executable [args...]

Parallel run options:
  -A, --account=name charge job to specified account
      --acctg-freq=<datatype>=<interval> accounting and
profiling sampling
       intervals. Supported datatypes:
       task=<interval> energy=<interval>
       network=<interval> filesystem=<interval>
…
Help options:
  -h, --help   show this help message
      --usage   display brief usage message

Other options:
  -V, --version   output version information and exit

SLURM documentation: https://slurm.schedmd.com/
SLURM summary: https://slurm.schedmd.com/pdfs/summary.pdf

A Job

Job = SLURM instructions + your program

srun [OPTIONS...] executable [args...]

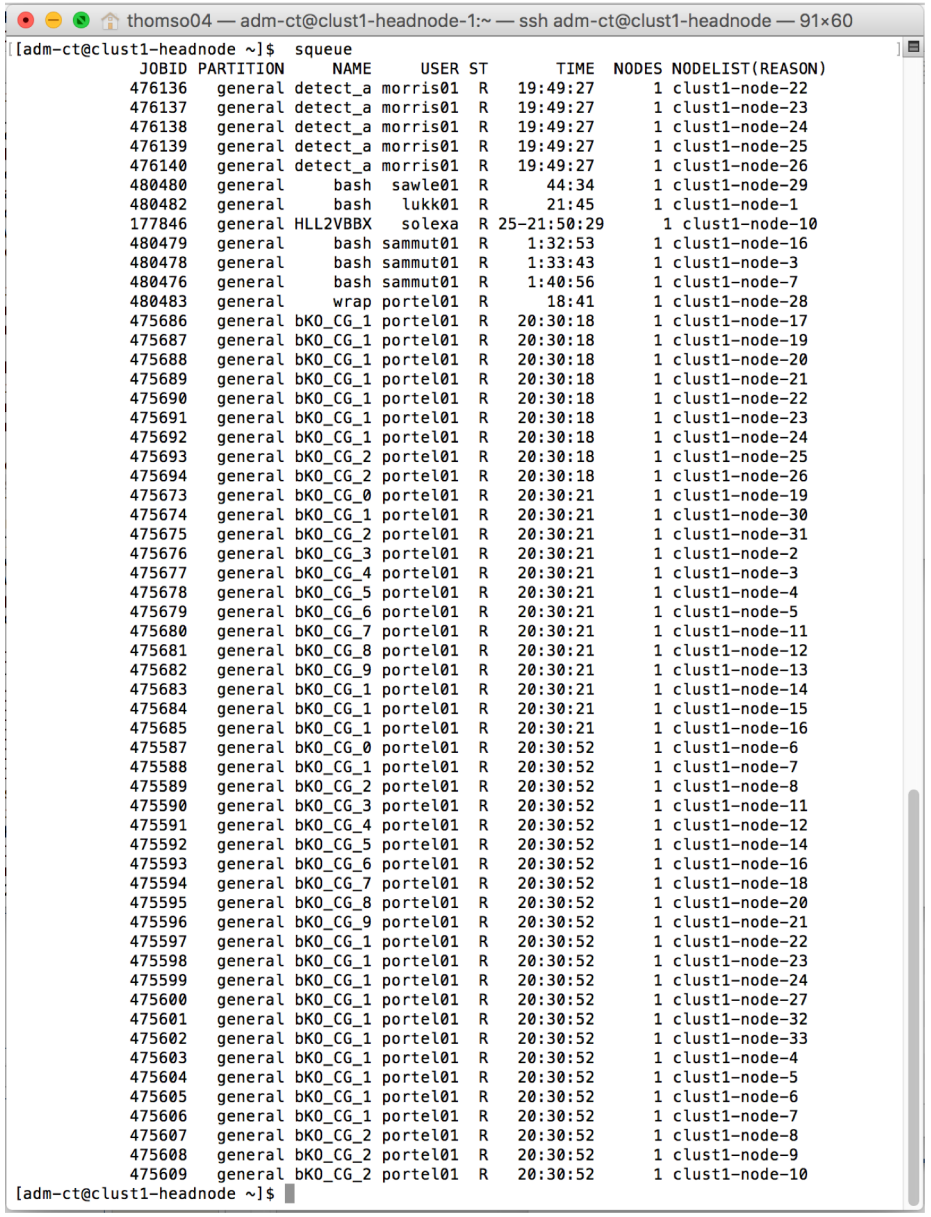
Can be a single command or a complex piece of BASH programming

In CI, many jobs are done in parallel

A command or series of commands submitted to the cluster with associated resource requirements and limits.

Status of jobs running on the cluster can be seen with the command

clust1-headnode $ **squeue**
clust1-headnode $ **squeue –u <USERNAME>**



Output from SLURM

clust1-headnode > squeue

```
[obrien04@clust1-headnode ~]$ squeue
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REASON)
            427309   general RK307bam   lukk01 PD       0:00      1 (Dependency)
            427311   general RK309bam   lukk01 PD       0:00      1 (Dependency)
…
            436869   general mutect2.    wan01  R    4:25:25      1 clust1-node-16
```

A Queue:

A queue for job submissions associated with specified users and cluster hosts, and providing specified default resources.

SLURM calls queues ‘partitions.’

We have a single general ‘partition’, with few restrictions (currently).

Checking the status of hosts within the cluster

SLURM

Clust1-headnode > sinfo
Clust1-headnode > squeue
Clust1-headnode > sacct

```
[obrien04@clust1-headnode ~]$ sinfo
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
general*     up   infinite     15    mix clust1-node-[1-7,9,12-16,18,21]
general*     up   infinite     18   idle clust1-node-[8,10-11,17,19-20,22-33]
```

Checking the status of hosts within the cluster

SLURM

Clust1-headnode > sinfo
Clust1-headnode > squeue
Clust1-headnode > sacct

```
[obrien04@clust1-headnode ~]$ sinfo
PARTITION AVAIL  TIMELIMIT  NODES  STATE NODELIST
general*     up   infinite     15    mix clust1-node-[1-7,9,12-16,18,21]
general*     up   infinite     18   idle clust1-node-[8,10-11,17,19-20,22-33]
```

Submitting a simple command job

SLURM

<COMMAND> [OPTIONS...] executable [args...]

Clust1-headnode > srun –n2 -l hostname

Allocate Resources
The more specific your jobs are, the more likely they are to be run soon

sbatch option

--mem-per-cpu

--time=<walltime>
-t <walltime>

--nodes=<number>
-N <number>

--ntasks=<number> -n <number>
-n <number>

--output=<path>/<file pattern>
-o <path>/<file pattern>

--error=<path>/<file pattern>
-e <path>/<file pattern>

--mail-user=<email>
--job-name=<jobname>

-J <jobname>
--account=<project account>

-A <project_account>

--requeue or --no-requeue

Submitting a batch script job

SLURM

Clust1-headnode > sbatch myscript.sh

```
#!/bin/bash#
#SBATCH -p general # partition (queue)
#SBATCH -N 1 # number of nodes
#SBATCH -n 1 # number of cores
#SBATCH --mem 100 # memory pool for all cores
#SBATCH -t 0-2:00 # time (D-HH:MM)
#SBATCH -o slurm.%N.%j.out # STDOUT
#SBATCH -e slurm.%N.%j.err # STDERR
for i in {1..100}; do
echo $RANDOM >> SomeRandomNumbers.txt
Done
sort SomeRandomNumbers.txt
```

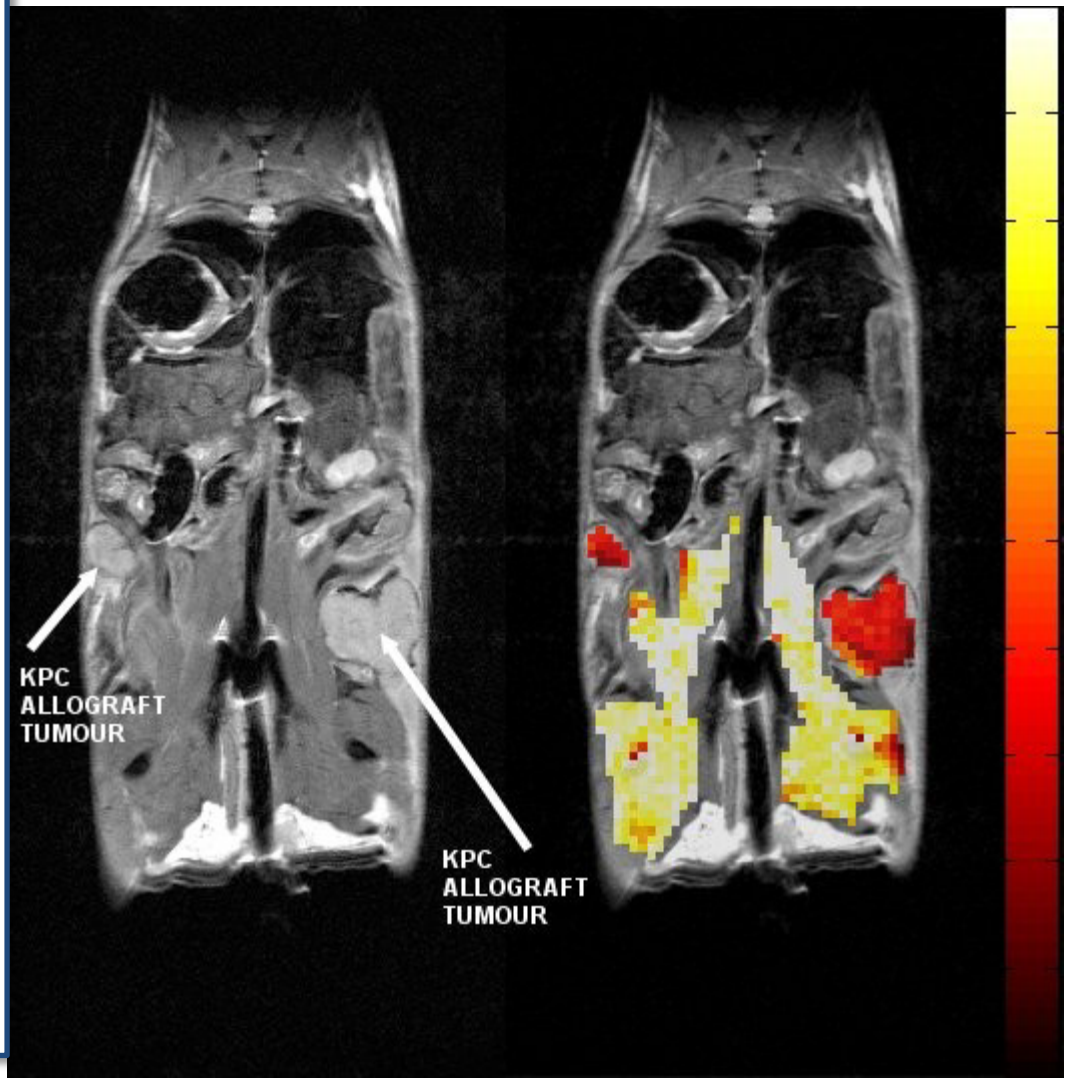
Killing jobs with scancel (jing)

clust1-headnode $ **scancel** **<job-id>**

Simple Parallel Computing

(marc)
Most HPC at CRI consists of breaking up your dataset into chunks and firing off a separate job for each chunk.

> *‘ Magnetisation Transfer Map Example*
>
> *Here small groups of pixels from T2 weighted image slices are processed to calculate the elements of the MT map.’*
>
> (Example courtesy of Dominick McIntyre, Griffiths Group)



Simple Parallel Computing

Example

Job dependency

SLURM allows many different ways to express dependencies, using the `--dependency` switch

Some SLURM dependencies:

`after:job_id[:jobid...]`
This job can begin execution after the specified jobs have begun execution.

`afterany:job_id[:jobid...]`
This job can begin execution after the specified jobs have terminated.

`afterok:job_id[:jobid...]`
This job can begin execution after the specified jobs have successfully executed (ran to completion with an exit code of zero).

```
[clust1-headnode ~] $ sbatch job1.sh
11254323
[clust1-headnode ~] $ sbatch --dependency=afterok:11254323 job2.sh
```

CANCER RESEARCH UK | CAMBRIDGE INSTITUTE

Practical session II

UNIVERSITY OF CAMBRIDGE