Queuing system and batch jobs

Shyam Gopalakrishnan 18th February 2021

What have you learnt so far?

Computerome architecture

- Logging in
 - Finding and loading modules

Running interactive jobs

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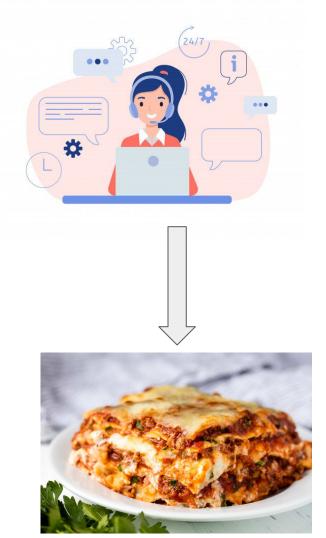
Batch jobs

Batch jobs are resource provisions that run applications on nodes away from the user and do not require supervision or interaction. Batch jobs are commonly used for applications that run for long periods of time or require little to no user input.

Batch jobs are created from a job script which provide resource requirements and commands for the job.

Batch jobs





Batch jobs





Batch system + Compute nodes



Interactive jobs vs. batch jobs

Interactive job

- One at a time *
- Need to keep track of the job
- Cannot do other things *



Batch job

- Many at a time
- Scheduler can keep track of jobs
- Continue with other things



How do I run batch jobs? - the qsub command

... a job script which provide resource requirements and commands for the job ...

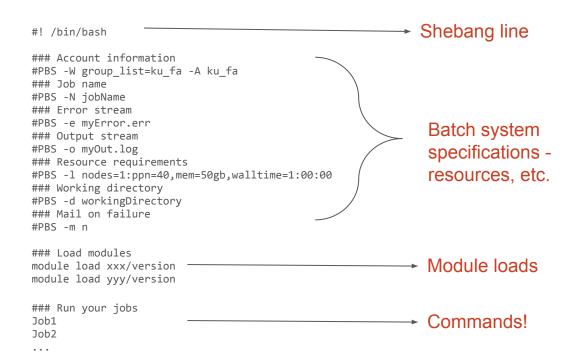
Running a batch job is easy:

qsub myScript.sh

A template script file

```
#! /bin/bash
### Account information
#PBS -W group_list=ku_fa -A ku_fa
### Job name
#PBS -N jobName
### Error stream
#PBS -e myError.err
### Output stream
#PBS -o myOut.log
### Resource requirements
#PBS -l nodes=1:ppn=40,mem=50gb,walltime=1:00:00
### Working directory
#PBS -d workingDirectory
### Mail on failure
#PBS -m n
### Load modules
module load xxx/version
module load yyy/version
### Run your jobs
Job1
Job2
```

A template script file



```
Which account should be
### Account information
                                             charged for the job?
#PBS -W group list=ku fa -A ku fa
                                             Required!
```

```
Name of the job.
### Job name
                                                  Optional - by default the
#PBS -N jobName
                                                  name of the script
```

```
Error and output files:
### Error stream
                                                Optional- if not specified,
#PBS -e myError.err
                                                derived from job name.
### Output stream
                                                Error: jobname.ejob id
#PBS -o myOut.log
                                                Output: jobname.ojob id
```

```
### Resource requirements
#PBS -l nodes=1:ppn=40,mem=50gb,walltime=1:00:00
```

Resource requirement -Multiple different resources specified on the same line. Required!

```
### Resource requirements
#PBS -l nodes=1:ppn=40,mem=50gb,walltime=1:00:00
```

Three resources have to be specified for a job to run on C2:

- Number of nodes and cores per node:
 nodes=1:ppn=40
 node and 40 cores.
- 2. Amount of memory: mem=50gb
 50 GB of RAM
- 3. Time allotment for the job: walltime=1:00:001 hour (dd:hh:mm:ss)

```
### Working directory
#PBS -d workingDirectory
```

Working directory where the job should be run.
Optional - by default your home directory.

```
### Mail on failure
#PBS -m n
```

Get email on failure to complete job.
Optional.

More batch system options

#PBS -j oe

Merge the output and error stream into one stream - the output stream

#PBS -k oe

Merge the output and error stream into one stream - the output stream - with continuously updated streams in your home directory.

#PBS -V

Transfer environmental variables to compute node - not recommended for non-experts

Example script - we will do this in the exercise

```
#! /bin/bash
#PBS -W group list=ku fa -A ku fa
#PBS -N canid1Map
#PBS -e canid1.err
#PBS -o canid1.log
#PBS -l nodes=1:ppn=40,mem=50gb,walltime=1:00:00
#PBS -d /home/projects/C2 test
### Load modules
module load bwa/0.7.15
module load samtools/1.9
module load htslib/1.9
### Run your jobs
bwa mem -t 40 refgenome/canFam31.fasta Canid1.R1.fastq.gz > Canid1.sam
samtools view -b Canid1.sam > Canid1.bam
samtools index Canid1.ham
```

slido

What order do the jobs get launched in?

(i) Start presenting to display the poll results on this slide.

How do I monitor my jobs?

Checkjob job_id

```
shygop@g-12-10002 ~/projects/C2_test
$ checkjob 30518436
job 30518436
AName: canid1Map
State: Completed
Completion Code: 0 Time: Wed Feb 17 15:19:23
Creds: user:shygop group:ku-cbd account:ku-cbd class:batch
WallTime: 00:01:10 of 1:00:00
SubmitTime: Wed Feb 17 15:18:05
  (Time Queued Total: 00:00:08 Eligible: 00:00:08)
TemplateSets: DEFAULT
NodeMatchPolicy: EXACTNODE
Total Requested Tasks: 40
Req[0] TaskCount: 40 Partition: pbs
Dedicated Resources Per Task: PROCS: 1 MEM: 1280M
<u>GMetric[energy_used]</u>    Current: 0.00    Min: 0.00    Max: 0.00    Avg: 0.00    Total: 0.00
NodeSet=FIRSTOF:FEATURE:[NONE]
Allocated Nodes:
[q-01-c0019:40]
Applied Nodeset: g-01-swil01
SystemID: Moab
SystemJID: 30518436
                /home/projects/ku-cbd/people/shygop/C2_test
StartCount:
Execution Partition: pbs
Flags:
                RESTARTABLE
StartPriority: 124999
IterationJobRank: 0
shygop@g-12-10002 ~/projects/C2_test
```

How do I monitor my jobs?

qstat

```
shygop@g-12-10002 ~/projects/C2_test
$ qstat
moab.eth.cla:
                                                                                Req'd
                                                                                           Req'd
                                                                                                       Elap
Job ID
                                                                               Memory
                                                                                           Time
                       Username
                                   Queue
                                            Jobname
                                                            SessID NDS
                                                                          TSK
                                                                                                       Time
30518436
                       shygop
                                   batch
                                            canid1Map
                                                             34062
                                                                                     50qb 01:00:00 C
30518447
                                            canid1Map
                                                                                     50gb 01:00:00 C
                       shygop
                                   batch
shygop@g-12-10002 ~/projects/C2_test
```

Exercise time: Let us try and run a job

Other ways to launch jobs: In line PBS options

```
#! /bin/bash
### Load modules
module load bwa/0.7.15
module load samtools/1.9
module load htslib/1.9

### Run your jobs
bwa mem -t 40 refgenome/canFam31.fasta Canid1.R1.fastq.gz > Canid1.sam
samtools view -b Canid1.sam > Canid1.bam
```

```
qsub -W group_list=ku_fa -A ku_fa -N canid1Map -e canid1.err -o canid1.log -l
nodes=1:ppn=40,mem=50gb,walltime=1:00:00 -d /home/projects/C2_test
mapCanid2.sh
```

Other ways to launch jobs: In line script and PBS options

```
echo "#! /bin/bash
### Load modules
module load bwa/0.7.15
module load samtools/1.9
module load htslib/1.9
### Run your jobs
bwa mem -t 40 refgenome/canFam31.fasta Canid1.R1.fastq.gz > Canid1.sam
samtools view -b Canid1.sam > Canid1.bam
samtools index Canid1.bam
" | qsub -W group_list=ku_fa -A ku_fa -N canid1Map -e canid1.err -o
canid1.log -l nodes=1:ppn=40,mem=50gb,walltime=1:00:00 -d
/home/projects/C2 test mapCanid2.sh
```