Batch Scheduling and Resource Management

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- The earliest computers could run only one program at a time.
- Programs and data were written on punched cards.
- Decks of cards were submitted in batches.
- These batches were placed in a queue and run one at a time.
- Later, time-sharing allowed multiple simultaneous interactive users.
- Batch processing, or batch queueing, is still useful:
 - Two programs running simultaneously can slow each other down.
 - On a single core the slowdown will be at least a factor of two.
 - $\bullet\,$ It can be ${\it much}$ more with heavy memory or I/O use.
 - Programs may fail due to insufficient memory.

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- Basic batch systems provide:
 - A means of placing jobs on a queue.
 - Some means of examining the queue.
 - A way to remove jobs.
 - Jobs are run when resources are available.
- Additional features provided by some systems:
 - Load balancing across multiple processors
 - Management of resource usage (memory in particular).
 - Protection against runaway jobs.
 - A priority system.
 - Ways of managing parallel jobs.
- More sophisticated features:
 - Checkpointing, suspending, resuming, moving running programs.
 - Integration with grid computing frameworks.



- Need to be able to request a certain number of processors.
- Job can only run once the required number of processors is available.
- The system has to enforce processor limit.
- System, program/framework need to agree on machines to use.
 - For Lam, could have system write a host file, run lamboot.
 - For PVM, could do something similar.
 - $\bullet\,$ System could also provide its own LAM/PVM daemon.
- Open MPI (successor to LAM?) has support built in for
 - SLURM
 - Xgrid
 - SGE (N1)

Support for others, such as OpenPBS is available but optional.

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- PBS and OpenPBS. Originally developed for NASA.
- SLURM. Developed at Lawrence Livermore National Laboratory.
- Sun Grid Engine. Originally from Sun; commercial version is N1.
- Xgrid. From Apple.
- Maui Cluster Scheduler. Commercial version is Moab.
- Condor. From Computer Science at Wisconsin.

Condor



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- Currently Condor is the batch system available on beowulf.
- Some features:
 - Originally developed for scavenging free cycles from workstations.
 - Can support checkpointing and job migration.
 - Requires compilation against Condor libraries.
 - Can be used as scheduler for vanilla jobs.
 - PVM jobs are also supported but seem to require some adjusting.
 - LAM jobs are now supported (as of yesterday).
 - Integrates with the Globus grid computing toolkit.
- Previous current version was from the 6.6 series.
- Has just ben upgraded to 6.8.

Basic Condor Usage

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- Basic use:
 - prepare a submission script
 - submit the script
 - check the queue periodically
 - or check your email to see if the job is done
- Some commands:
 - condor_submit for submitting a job
 - condor_q for examining the queue
 - condor_rm for removing a job
 - condor_status for examining available pool
- Condor universes:
 - standard supports checkpointing, requires special compilation
 - vanilla no restrictions
 - PVM
 - MPI only MPICH 1.2; no longer available in 6.8
 - parallel available in 6.8; use this for LAM

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Submitting a Condor Job

- It is a good idea to create a new directory for your job.
- Place in that directory any files for the job along with a submit file.
- Run the condor_submit command from that directory.
- Some submit file commands:
 - executable: name of the script or binary file to run. One per file. Path name can be absolute or relative to the current directory.
 - arguments: command line arguments for the executable
 - environment: name=value pairs separated by semicolons.
 - universe: most likely vanilla, PVM, or parallel
 - input: file(s) for standard input
 - output: file(s) for standard output
 - error: file(s) for standard error
 - log: file for log messages from Condor
 - queue: place one or more jobs on the queue
 - notification = Never to turn off email notification
- There are many others but these are the most important ones.

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Submit file sub-sleep for a single job that sleeps for 5 seconds:

```
executable = /bin/sleep
arguments = 5
universe = vanilla
output = out
error = err
\log = \log
notification = Never
queue
```

Submit the job with

condor_submit sub-sleep

and check it with

condor_q

Examples are available on line.



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Submit file sub-hostname for two jobs computing the hostname of the executing machine:

```
executable = /bin/hostname
universe = vanilla
output = out.$(Process)
error = err.$(Process)
log = log
notification = Never
queue 2
```

This produces two separate output files and two error files.

Some Simple Examples



```
Submit file sub-R for running two R jobs:
  environment= R LIBS=/cluster/statsoft/Rlibs
  executable = /usr/bin/R
  arguments = --slave
  universe = vanilla
  input = in.$(Process)
  output = out.$(Process)
  error = err.$(Process)
  \log = \log
  notification = Never
  queue 2
This uses two separate input files, in.0 and in.1. File in.0 looks like
  Sys.info()["nodename"]
  .libPaths()
  print(0)
and in.1 looking like
  Sys.info()["nodename"]
  .libPaths()
  print(1)
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```

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Another approach is to use the submit file sub-R2 given by

```
environment= R_LIBS=/cluster/statsoft/Rlibs
executable = /usr/bin/R
arguments = --slave --args $(Process)
universe = vanilla
input = in
output = out.$(Process)
error = err.$(Process)
log = log
notification = Never
queue 2
```

and the common input file in given by

```
Sys.info()["nodename"]
.libPaths()
print(commandArgs(TRUE))
```

Some Simple Examples



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A snow/LAM job using submit file sub-snow-lam

```
environment= R_LIBS=/cluster/statsoft/Rlibs
executable = /cluster/condor/condor/etc/examples/lamscript
arguments = RMPISNOW
machine_count = 3
universe = parallel
input = in-snow-lam
output = out
error = err
log = log
notification = Never
queue
ad the input file in group log given by
```

and the input file in-snow-lam given by

```
cl <- makeCluster()
clusterCall(cl, function() Sys.info()["nodename"])
stopCluster(cl)</pre>
```