Job workflow support via condor DAGs

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NuComp Meeting

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Outline

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- Condor DAGs
- Supporting experiment job workflows
- Example applications
 - MINERvA MC workflows
 - SAM data handling jobs
 - Everything else
- Status

Motivation

- Job dependencies
 - Many grid processing tasks require multiple steps
 - ► For example, MINERvA MC generation requires 4 serial job submissions
 - $\,\triangleright\,\,$ Output from one stage feeds into the next
 - More complex dependencies are on the horizon
 - ▷ Eg., event overlays for "rock muons" could introduce additional jobs with new dependencies
 - Experiment currently runs stages jobs by hand, or writes scripts to watch condor
 - A generic tool that supports job workflows would be helpful in such cases
- Job associations
 - Most grid computation submits same application in many parallel jobs
 - Typically, many submitted at once with a single script
 - ► A different input / output file for each
 - ► By far the most common and ubiquitous pattern of job submission
 - These jobs are logically related in a way that is invisible to the batch system, and therefore to generic batch system / monitoring tools

The Condor DAG

- Condor has features to support job dependencies
 - Uses directed acyclic graphs (DAG) to represent job dependencies
 - By using DAG to run a set of jobs, condor will:
 - Enforce an arbitrary, user-specified set of dependencies between jobs
 - Optionally run a script before or after any individual job
 - Stop a sequence on an error
 - Provides a "rescue" DAG in this case that knows what has already completed successfully
 - Allow additional monitoring options
 - ▷ condor_q -dag
 - ▷ Visualization of the execution state of the DAG
 - Allow a limit on number of jobs in a DAG that are executing at a given time



Example condor DAG (from condor manual)



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Supporting job workflows

- Most typical use case: replicate a single pattern run in parallel
 - Can specify a large job as N x (the pattern template)
 - REX supporting a simple tool to assist in generating DAGs of this type
 - /grid/fermiapp/common/tools/dagNabbit.py
 - Full documentation available from the script
 /grid/fermiapp/common/tools/dagNabbit.py -manual | less
 - ► User specifies easy things
 - ▷ Job dependency template (a file with a few XML-style tags)
 - Scripts for each template node that produce a list of condor command files for that node
 - *IF job submission scripts already do this*
 - dagNabbit.py then generates the full dependency tree and submits the DAG

Example application (1)

- MINERvA MC workflow
 - Original experiment submission script submits N jobs for one of four stages
 - Modified script to:
 - ► Allow creation of condor command files without submitting them
 - ► Write a template file for multiple steps
 - ▷ For each node, specifies the no-submit script for a single stage
 - Call dagNabbit.py with template as input
 - dagNabbit.py assembles and submits the DAG command file

Command line did not change, except that multiple stage flags are now allowed.

Example application (1)

- MINERvA MC workflow
 - Example template file created by the new script:
 - # This DAG description was created by process_MC_series.pl

```
<serial>
./process_MC_series.pl minerva 130 -genie -no_submit -f 1 -l 5 -n 5 -g -geo Full
</serial>
./process_MC_series.pl minerva 130 -cal -no_submit -f 1 -l 5 -n 5 -g -geo Full
</serial>
./process_MC_series.pl minerva 130 -minos -no_submit -f 1 -l 5 -n 5 -g -geo Full
</serial>
./process_MC_series.pl minerva 130 -reco -no_submit -f 1 -l 5 -n 5 -g -geo Full
</serial>
```

Example application (1)

• MINERvA MC workflow

Resulting DAG command file (the part we want to avoid writing by hand):

JOB Jb 1 /minerva/app/users/condor-tmp/rs/genie wrapper SIM minerva 00000130 0001 v8r3.sh 20110913 235659 1.cmd JOB Jb 2 /minerva/app/users/condor-tmp/rs/genie_wrapper_SIM_minerva_00000130_0002_v8r3.sh_20110913_235700_1.cmd JOB Jb 3 /minerva/app/users/condor-tmp/rs/genie wrapper SIM minerva 00000130 0003 v8r3.sh 20110913 235701 1.cmd JOB Jb 4 /minerva/app/users/condor-tmp/rs/genie wrapper SIM minerva 00000130 0004 v8r3.sh 20110913 235703 1.cmd JOB Jb 5 /minerva/app/users/condor-tmp/rs/genie_wrapper_SIM_minerva_00000130_0005_v8r3.sh_20110913_235704_1.cmd JOB Jb 6 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235705 1.cmd JOB Jb 7 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235706 1.cmd JOB Jb 8 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235708 1.cmd JOB Jb 9 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235709 1.cmd IOB Jb 10 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235710 1.cmd JOB Jb 11 /minerva/app/users/condor-tmp/rs/MinosSim-SIM minerva 00000130 0001 v8r3.sh 20110913 235711 1.cmd JOB Jb 12 /minerva/app/users/condor-tmp/rs/MinosSim-SIM minerva 00000130 0002 v8r3.sh 20110913 235712 1.cmd JOB Jb 13 /minerva/app/users/condor-tmp/rs/MinosSim-SIM minerva 00000130 0003 v8r3.sh 20110913 235714 1.cmd IOB Ib 14 /minerva/app/users/condor-tmp/rs/MinosSim-SIM minerva 00000130 0004 v8r3.sh 20110913 235715 1.cmd JOB Jb 15 /minerva/app/users/condor-tmp/rs/MinosSim-SIM minerva 00000130 0005 v8r3.sh 20110913 235716 1.cmd JOB Jb 16 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235717 1.cmd JOB Jb 17 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235718 1.cmd IOB Jb 18 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235720 1.cmd JOB Jb 19 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235721 1.cmd IOB Ib 20 /minerva/app/users/condor-tmp/rs/SystemTestsApp.exe 20110913 235722 1.cmd parent Jb 1 child Jb 6 parent Jb² child Jb⁷ parent Jb 3 child Jb 8 parent Jb 4 child Jb 9 parent Jb 5 child Jb 10 parent Jb 6 child Jb 11 parent Ib 7 child Ib 12 parent Jb 8 child Jb 13 parent Jb 9 child Jb 14 parent Jb 10 child Jb 15 parent Jb 11 child Jb 16 parent Jb 12 child Jb 17 parent Jb 13 child Jb 18 parent Jb 14 child Jb 19

parent Jb_15 child Jb_20

Example application (2)

- Job that uses a SAM project to deliver files
 - Run all jobs associated with a given SAM dataset within a single DAG
 - A pre-script before all application nodes starts the SAM project
 - A post-script after all application nodes terminates the project



Example application (2)

- Job that uses a SAM project to deliver files
 - Run all jobs associated with a given SAM dataset within a single DAG
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Example application (3)

- Any job that runs parallel instances of a single application
 - i.e, everything we run... Really.
- Why?
 - To manifest the logical connection between jobs that are submitted together
 - ► e.g., jobs processing a single run or set of runs, MC for a given configuration, etc.
 - Allows the monitoring to aggregate jobs that are logically connected
 - Can simplify the long list of jobs otherwise returned by condor_q
 - New monitoring depends upon this (see figures on next 3 pages)
 - Allows management of associated jobs as a unit
 - Set a limit on the number of jobs in a DAG executing at a given time
 - ▷ Can be an important handle for managing resource utilization (eg, disk or DB I/O)
 - Can remove the single DAG process to remove all underlying jobs
 - Can create a single email summary for the entire DAG
 - ▷ Eliminates the deluge of email from the many individual jobs within a single submission

Sample system status page

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Sample user summary page

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Status

- Existing dagNabbit script
 - Supports basic serial and parallel sub-sequences
 - Serial steps or branching parallel steps not yet supported, but will be
 - ► MINERvA MC submission scripts currently using this
 - Supports startup and termination scripts for the entire DAG (almost ready)
 - ► Needed for SAM jobs and a terminal job mailer
- To be added
 - Support for pre and post scripts on individual nodes
 - Integrating SAM project startup, completion
 - Job summary mailer
- Can already start integrating into experiment submission scripts

The end