

Turning science problems into HTC jobs Tuesday, Dec 7 2pm

Zach Miller Condor Team University of Wisconsin-Madison





You now know how to run jobs using Condor, create basic workflows using DAGMan, and how to run a simple BLAST query. Let's put these pieces together to tackle larger problems.

This session will focus on how to break down and process large problems.



Review of Blast Example

• First, run blast locally

Login to a treinamentoXX machine

source /opt/workshop/zkm_exercises/blast/blast.sh

blastp -db /opt/workshop/zkm_exercises/blastdb/yeast.aa -query query1

(You did this in the morning... This is intended as a sanity check to make sure your setup is still working)

Open Science Grid Think about running your application remotely

- What are the dependencies?
 - Architecture
 - OS // Linux Distro
 - Shared libraries
 - Input files
 - Environment variables
 - Scratch space
 - Availble cpu ...



- Did we get all dependencies?
- Are we sized correctly?
- How long will the job run?
- How much data will it produce?
- What kind of load are we putting on various system resources?



- If the job is too small, there's too much overhead
- If the job is too big, there's potentially for "badput"
- Badput is when a job runs for a while but is preempted and the output thrown away
- Rule of thumb: between 1 and 8 hours



Other Considerations

- Besides how long a job will run, consider:
 - Memory requirements
 - Disk requirements
 - Network I/O
 - Consumable Licenses
- Try to identify all types of resources needed.



- Processing multiple sequences
- You get all queries in one file
- Blast will accept input files with multiple queries
- Try running BLAST with the input file:
- /opt/workshop/zkm_exercises/examples/five_inputs
 How long does it take?



- Now, let's try running a much larger input /opt/workshop/zkm_exercises/examples/larger_input
- Note: it contains 6298 input files and will take 20 minutes or more! (Go ahead and submit it while I talk!)
 - blastp -db yeast.aa -query large_input | grep '^Query=' | nl
- Let's think about how we can do this more quickly...



- BLAST Input can be split at sequence boundaries
- Make a temporary directory in your home dir, and copy the file

/opt/workshop/zkm_exercises/examples/five_inputs into the temporary directory

- Edit five_inputs, and look at the structure
- With only 5, it could be split manually, but...



- But with 6298 sequences, doing this manually is out of the question.
- We need some sort of automation!
- Write a script to split apart the input file, or copy /opt/workshop/zkm_exercises/scripts/split_file.pl
- Use your script first on five_inputs to create five input files:

- split_file.pl SMALL_TEST 1 < five_inputs</pre>



- But how to submit?
- You could create a submit file for each new input file...
- Or you can use some fancy features in Condor to use a template submit file.
- Copy

/opt/workshop/zkm_exercises/examples/blast_template.sub to a temporary directory and examine it



- Now run:
 - condor_submit blast_template.sub
- Watch it run with condor_q
- Examine the output (*.out)
- Count the results:
 - grep '^Query=' *.out | nl



- Now do the same with a very large input:
 - Create a temporary directory and cd to it
 - cp /opt/workshop/zkm_exercises/examples/large_input .
 - /opt/workshop/zkm_exercises/scripts/split_file.pl
 BIG_TEST 315 < large_input
 - cp /opt/workshop/zkm_exercises/examples/blast_template_2.sub .
 - condor_submit blast_template_2.sub
- Again, watch it run:
 - condor_q -dag
 - condor_q -run



- Problems with this approach:
 - Not completely automated
 - Requires editing template files
 - How do you know when the workflow is done?
 - How do you know it was all successful?



- Using DAGMan can help here!
- DAGMan brings the ability to implement several features:
 - Final notification when all pieces are complete
 - Verification that all results are present
 - Filtering or massaging the output into a final form
 - Throttling job submission for busy pools



- Once again, this can be automated
- Write a script that also generates a .dag file and also the submit files. The DAG will list all jobs but no relationships between them. (see

/opt/workshop/zkm_exercises/examples/example.dag)

 Optionally, copy this script which does it for you: /opt/workshop/zkm_exercises/scripts/gen_dag.pl



- Try splitting the input into 20 pieces
- 6298 sequences / 20 == 315 per file
- gen_dag.pl LARGE_RUN 315 < large_input
 Look at what that script produced
- condor_submit_dag LARGE_RUN.dag
- Watch it run... How long is each piece taking?
- How would you change these numbers for an input of one million queries?



- Modify your script to create a new node in the DAG that is a child of all other nodes
- Make a submit file for that node that runs a script. What should that script do?
 - Send email?
 - Verify results?
 - Concatenate results?
 - Compress results?
- How many of those you can implement?



- Different nodes in the DAG can be different types of job: Vanilla, Grid, or Local
- Make the final node LOCAL universe (Check Condor Manual for details). You want it to run locally to verify that all results received are intact.
- Feel free to use and edit my script: /opt/workshop/zkm_exercises/scripts/gen_dag_w_final.pl



- Run the individual pieces on OSG using Condor-G, instead of in the Vanilla universe
- Write another script that does everything using the pieces we just wrote:
 - Splits the input
 - Generates the DAG
 - Submits the workflow
 - Waits for completion (hint: condor_wait)
 - Combines results



- Try running five_inputs and large_input against other databases. You'll need to:
 - Run a single input as a test. How long did it take?
 - Estimate how many compute hours this will take...
 - Decide how to split up the input appropriately
 - Get access to enough available resources to do this in a reasonable amount of time



- Questions about splitting, submitting, automating, etc?
- Break Time, resume after lunch