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The Landscape of Academic Research Computing

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Chief Operations Officer - Open Science Grid
Manager High Throughput Computing

Some Slides Contributed by the University of Wisconsin HTCondor Team and Scot Kronenfeld



Who Am I?



- Chief Operations Officer of the Open Science Grid
 10+ years
- Manager High Throughput Computing Indiana University (IU)
- IU Institutional OSG PI
- Co-PI Science Node (Formally International Science Grid This Week)
- External Advisor to European Grid Infrastructure
- Member of the Organizational Advisory Board for RDA





Protein Docking Project at the USchool of Medicine

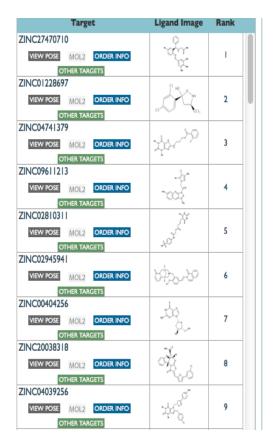
- SPLINTER Structural Protein-Ligand Interactome
- Used autodock-vina "...open-source program for drug discovery, molecular docking and virtual screening..."
- Frist run in 2013 docked ~3900 Proteins with 5000 Ligands for a total of ~19M docked pairs.
- Submitted via command line to Condor using Pegasus on the OSG-XSEDE submission node
- Infrastructure is set and new runs can be easily started

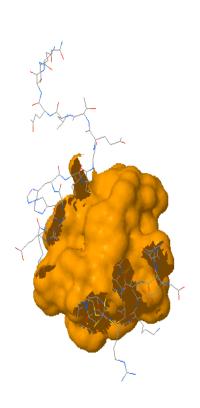


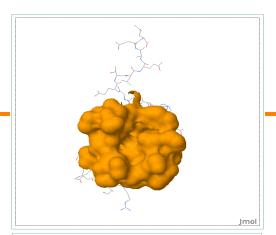
U.S.

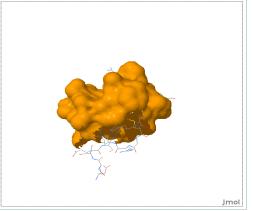


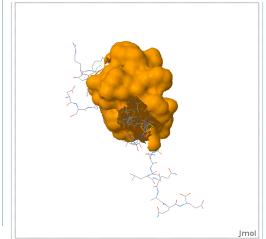
•Various rotations of Protein CBFA2T1 (Cyclin-D-related protein) (Eight twenty one protein) (Protein ETO) (Protein MTG8) (Zinc finger MYND domain-containing protein 2)









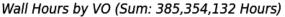


Jmol

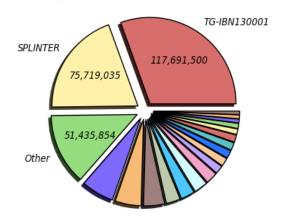


Some Numbers





1309 Days from Week 00 of 2013 to Week 31 of 2016



■ TG-IBN130001 (117,691,501)
■ DUKE-QGP (23,624,207)
■ CPDARKMATTERSIMULATION (10,292,491)
■ ALGDOCK (8,520,865)
■ SOURCECODING (5,684,844)
■ DUKE-4FERMION (3,939,893)

FUTURECOLLIDERS (2,684,213)

- SPLINTER (75,719,035)
 LIGO (18,859,313)
 Z2DQMC (10,049,026)
 RIT (5,966,501)
 SPHENIX (5,589,611)
 BIOGRAPH (3,652,186)
 DETECTORDESIGN (2,511,013)
- Other (51,435,854) ■ AMS (15,191,200) □ SNOWMASS (9,972,493) □ SEQ2FUN (5,961,412) ■ NUMFPI (5,222,110) ■ UPRRP-MR (2,786,365)
- Amazon EC2 Computing \$0.073/hour
- \$5.5M Compute Only
- Data Transfer and Storage Not Included



Follow Along at:



https://twiki.grid.iu.edu/bin/view/Education/RDASummerSchool/

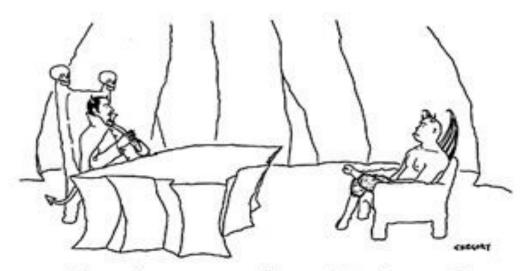




Overview of day



- Lectures alternating with exercises
 - Emphasis on lots of exercises
 - Hopefully overcome PowerPoint fatigue



"I need someone well versed in the art of torture—do you know PowerPoint?"





Some thoughts on the exercise



- It's okay to move ahead on exercises if you have time
- It's okay to take longer on them if you need to
- If you move along quickly, try the "On Your Own" sections and "Challenges"





Most important!



- Please ask questions!
 - ...during the lectures
 - ...during the exercises
 - ...during the breaks
 - ...during the meals
 - ...over dinner
 - ...via email after we depart (rquick@iu.edu)
- If I don't know, I'll find the right person to answer your question.





Goals for this session



- Define Local, Clustered, High Throughput Computing (HTC), High Performance Computing (HPC), and Cloud Computing (XaaS)
- Shared, Allocated, and Purchased
- What is HTCondor? And why are we using it in this Summer School?





The setup: You have a problem



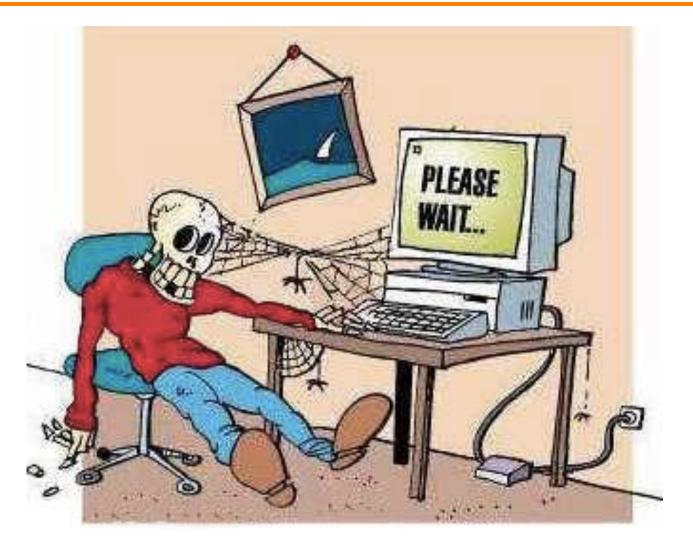
- Your science computing is complex!
 - Monte carlo, image analysis, genetic algorithm, simulation...
- It will take a year to get the results on your laptop, but the conference is in a week.
- What do you do?





Option 1: Wait a year









Option 2: Local Clustered Computing



- Easy access to additional nodes
- Local support for porting to environment (maybe)
- Often a single type of resource
- Often running at capacity





Option 3: Use a "supercomputer" Open Science Grid aka High Performance Computing (HPC)

- "Clearly, I need the best, fastest computer to help me out"
- Maybe you do…
 - Do you have a highly parallel program?
 - i.e. individual modules must communicate
 - Do you require the fastest network/disk/memory?
- Are you willing to:
 - Port your code to a special environment?
 - Request and wait for an allocation?



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Option 4: Use lots of commodity computers



- Instead of the fastest computer, lots of individual computers
- May not be fastest network/disk/memory, but you have a lot of them
- Job can be broken down into separate, independent pieces
 - If I give you more computers, you run more jobs
 - You care more about total quantity of results than instantaneous speed of computation
- This is high-throughput computing



Option 5: Buy (or Borrow) some Open Science Grid computing from a Cloud Provider



- Unlimited resources (if you can afford them)
- Full administrative access to OS of the resources you 'buy'
- Specialized VM images reducing effort in porting
- XaaS Business Model





These are All Valid Options



- Remember the problem you have one month to publish results for your conference
 - Option 1: You will miss your deadline
 - Option 2: You might miss your deadline But if your lucky you'll make it (or if you know the admin)
 - Option 3: If you have parallelized code and can get an allocation you have a good chance
 - Option 4: If you can serialize your workflow you have a good chance
 - Option 5: You can meet your deadline for a price. Though some efforts are underway to enable academic clouds





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Computing Infrastructures



- Local Laptop/Desktop Short jobs with small data
- Local Cluster Larger jobs and larger data but subject to availability
- HPC Prime performance with parallelized code
- HTC Sustained computing over a long period for serialized
- Cloud Need deeper permission on an
 OS and have deeper pockets



Why focus on high-throughput computing? (HTC)



- An approach to distributed computing that focuses on long-term throughput, not instantaneous computing power
 - We don't care about operations per second
 - We care about operations per year
- Implications:
 - Focus on reliability
 - Use all available resources
 - Any Linux based machine can participate





Think about a race



- Assume you can run a four minute mile
- Does that mean you can run a 104 minute marathon?
- The challenges in sustained computation are different than achieving peak in computation speed







An example problem: BLAST



A scientist has:

- Question: Does a protein sequence occur in other organisms?
- Data: lots of protein sequences from various organisms
- Parameters: how to search the database.
- More throughput means
 - More protein sequences queried
 - Larger/more protein data bases examined
 - More parameter variation





Why is HTC hard?



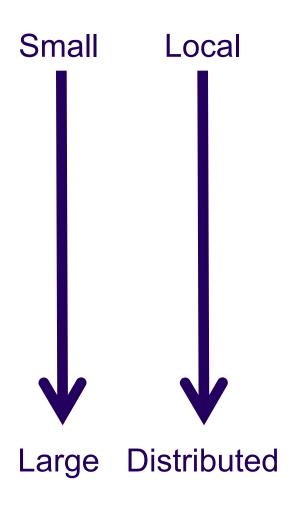
- The HTC system has to keep track of:
 - Individual tasks (a.k.a. jobs) & their inputs
 - Computers that are available
- The system has to recover from failures
 - There will be failures! Distributed computers means more chances for failures.
- You have to share computers
 - Sharing can be within an organization, or between orgs
 - So you have to worry about security
 - And you have to worry about policies on how you share
- If you use a lot of computers, you have to handle variety:
 - Different kinds of computers (arch, OS, speed, etc..)
 - Different kinds of storage (access methodology, size, speed, etc...)
 - Different networks interacting (network problems are hard to debug!)





Let's take one step at a time





- Can you run one job on one computer?
- Can you run one job on another computer?
- Can you run 10 jobs on a set of computers?
- Can you run a multiple job workflow?
- How do we put this all together?

This is the path we'll take





Discussion



- For 5 minutes, talk to a neighbor: If you want to run one job in a local environment:
 - 1) What do you (the user) need to provide so a single job can be run?
 - 2) What does the system need to provide so your single job can be run?
 - Think of this as a set of processes: what needs happen when the job is given? A "process" could be a computer process, or just an abstract task.





What does the user provide?



- A "headless job"
 - Not interactive/no GUI: how could you interact with 1000 simultaneous jobs?
- A set of input files
- A set of output files
- A set of parameters (command-line arguments)
- Requirements:
 - Ex: My job requires at least 2GB of RAM
 - Ex: My job requires Linux
- Control/Policy:
 - Ex: Send me email when the job is done
 - Ex: Job 2 is more important than Job 1
 - Ex: Kill my job if it runs for more than 6 hours





What does the system provide?



Methods to:

- Submit/Cancel job
- Check on state of job
- Check on state of available computers

Processes to:

- Reliably track set of submitted jobs
- Reliably track set of available computers
- Decide which job runs on which computer
- Manage a single computer
- Start up a single job



Quick UNIX Refresher Before We Start



- \$ #This symbolizes the prompt.
- ssh <u>username@</u>training.osgconnect.net
- nano, vi, emacs, cat >, etc.
- which, rpm, ps, mkdir, cd, gcc,ls
- A varitey of condor_* commands





Questions?



- Questions? Comments?
 - Feel free to ask me questions now or later:
 Rob Quick <u>rquick@iu.edu</u>

Exercises start here:

https://twiki.grid.iu.edu/bin/view/Education/RDASummerSchool/RDASchoolMaterials

Presentations are also available from this URL.

