

# The Landscape of Academic Research Computing

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



# Who Am I?

- Associate Director Science Gateway Research Center
- PI – Robust PID Project
- Co-chair CODATA School of Research Data Science Task Group
- Chair of the ACM SIGHPC RCE
- Member of the Organizational Advisory Board for RDA
- Co-chair of several CODATA and RDA Task/Working/Interest Groups
- 12 Years - Chief Operations Officer of the Open Science Grid and the Software Assurance Marketplace

# Protein Docking Project at the IU School of Medicine

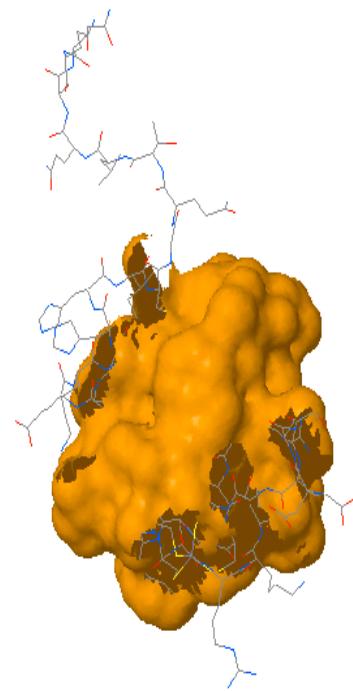
- SPLINTER - Structural Protein-Ligand Interactome
- Used autodock-vina – “...open-source program for drug discovery, molecular docking and virtual screening...”
- First run in 2013 - docked ~3900 Proteins with 5000 Ligands for a total of ~19M docked pairs.
- Submitted via command line to Condor using Pegasus on the OSG-XSEDE submission node
- Infrastructure is set and new runs can be easily started
- To date more than 6.3B dockings completed



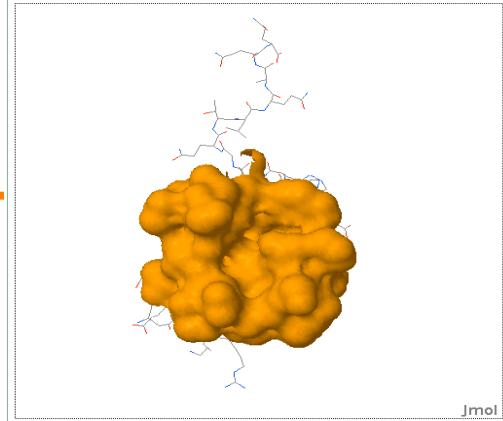
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- Various rotations of Protein CBFA2T1 (Cyclin-D-related protein) (Eight twenty one protein) (Protein ETO) (Protein MTG8) (Zinc finger MYND domain-containing protein 2)

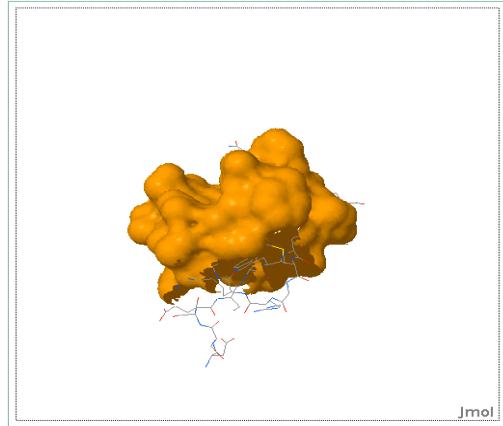
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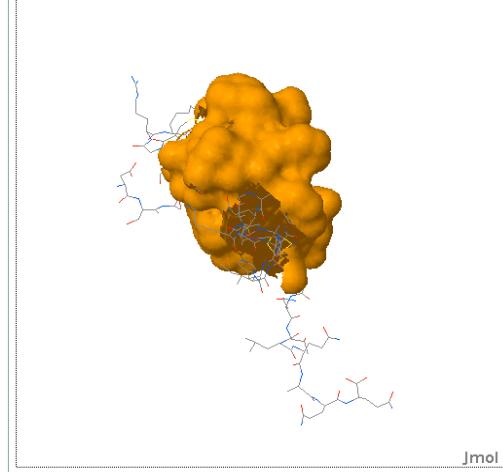
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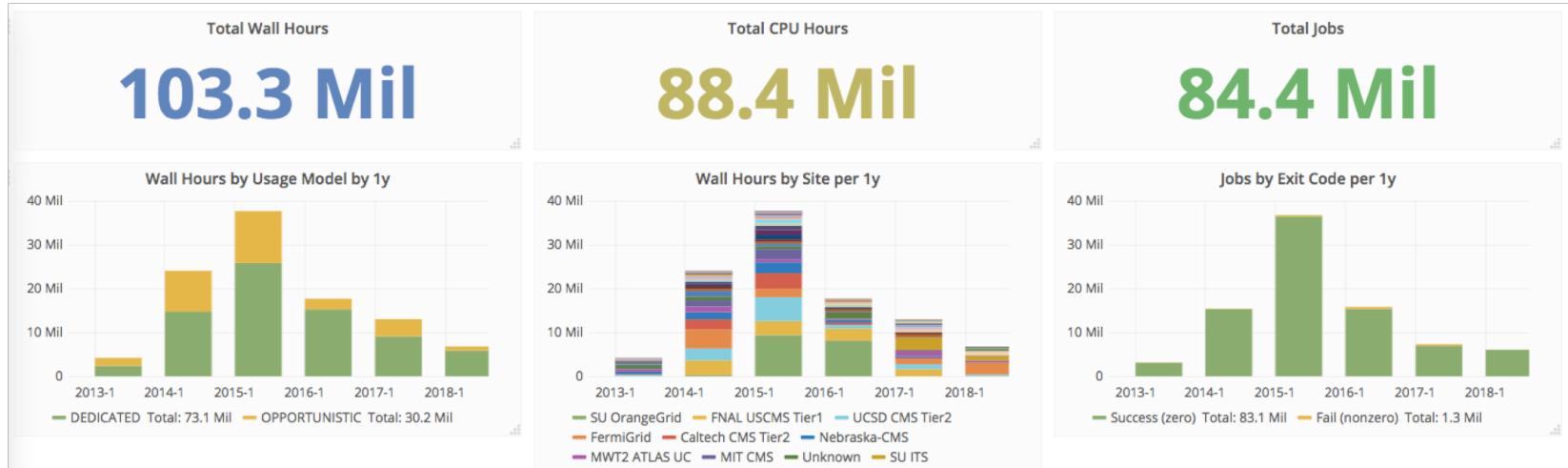


Jmol



Jmol

# Some Numbers



- Amazon EC2 Computing \$0.046/hour
- \$4.066M Compute Only
- Data Transfer and Storage Not Included



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# Follow Along at:



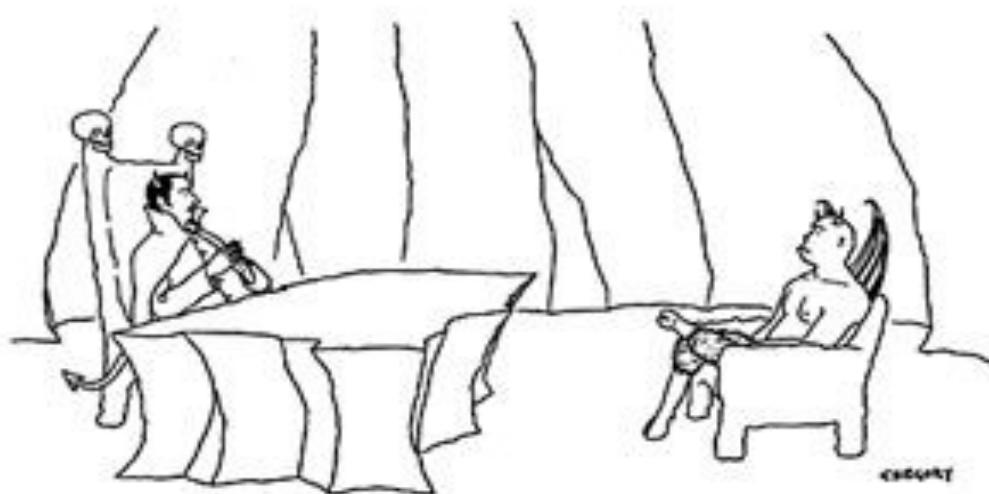
<https://opensciencegrid.org/dosar/DataSaoPaulo2018/Materials/>



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# 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 exercises

- 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](mailto: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), Cloud Computing (XaaS), and Containers
- Shared, Allocated, and Purchased
- What is HTCondor? And why are we learning it?

# The setup: You have a problem

- Your science computing is complex!
  - Monte carlo, image analysis, genetic algorithm, simulation...
- It will take a year (CPU time) to get the results on your laptop, but your paper is due 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” aka High Performance Computing(HPC)

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- “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?

# 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 can access 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**



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# Option 5: Buy (or Borrow) some 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



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# 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 you're 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 academic clouds are becoming more available.

# 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 and optimized 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

# New Technologies

*Only that shall happen*

*Which has happened,*

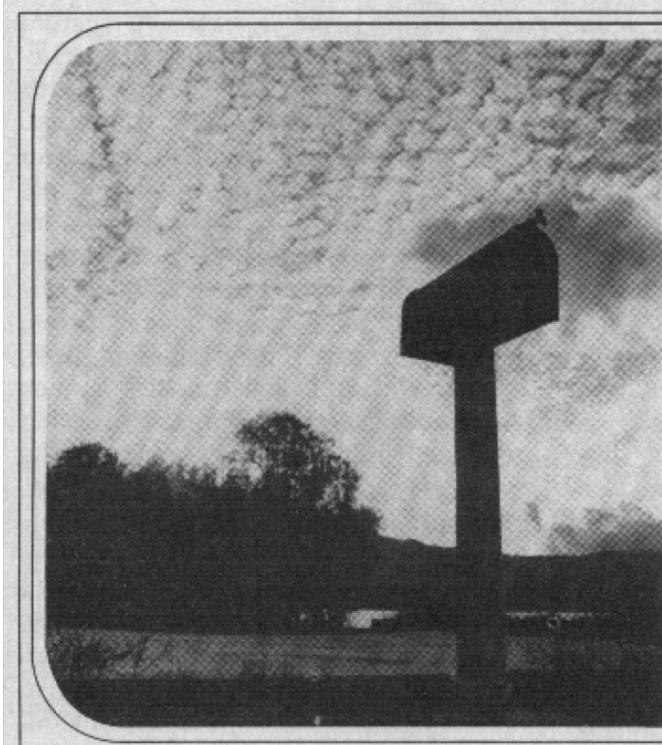
*Only that occur*

*Which has occurred;*

*There is nothing new*

*Beneath the sun!*

Ecclesiastes Chapter 1 verse 9



## What is a "Distributed" Data Processing System?

Philip H. Enslow, Jr.  
Georgia Institute of Technology

- HTC is about many jobs, many users, many servers, many sites and many workflows.
- What's in a buzzword?
  - “I was doing cloud computing since before it was called grid computing.”

# 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

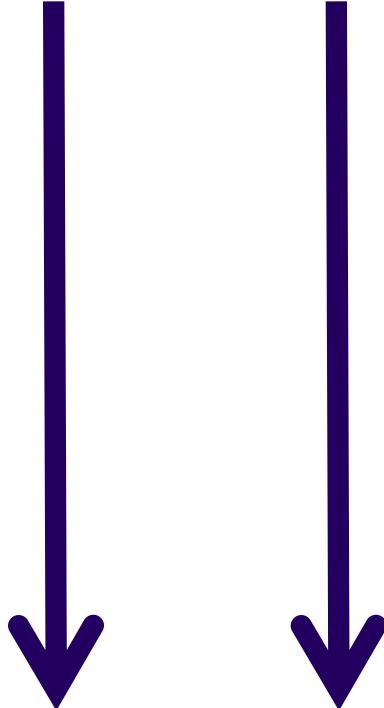
- A scientist has:
  - Question: Does a protein sequence occur in other organisms?
  - Data: lots of protein sequences from various organisms
  - Parameters: how to search the database.
- More throughput means
  - More protein sequences queried
  - Larger/more protein data bases examined
  - More parameter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

Small      Local



- 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

Large      Distributed

# 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 username@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 [rquick@iu.edu](mailto:rquick@iu.edu)

Exercises start here:

<https://opensciencegrid.org/dosar/DataSaoPaulo2018/Materials/>

Slides are also available from this URL.