

# **HYDRA: Using Windows Desktop Systems in Distributed Parallel Computing**

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# Problem Description

- Turn Windows desktop systems at IUB student labs into a scientific resource.
  - 2300 systems, 3 year replacement cycle
  - 1.5 Teraflops
  - Fast ethernet or better
- Harvest idle cycles.

# Constraints

- Systems dedicated to students using desktop office applications — not parallel scientific computing
- Microsoft Windows environment
- Daily software rebuild

# What could these systems be used for?

- Many small computations and a few small messages
  - Master-worker
  - Parameter studies
  - Monte Carlo

# Assembling small ephemeral resources

- Different parallel libraries have constraints of some form or the other
  - MPI not designed to handle ephemeral resources

# Solution

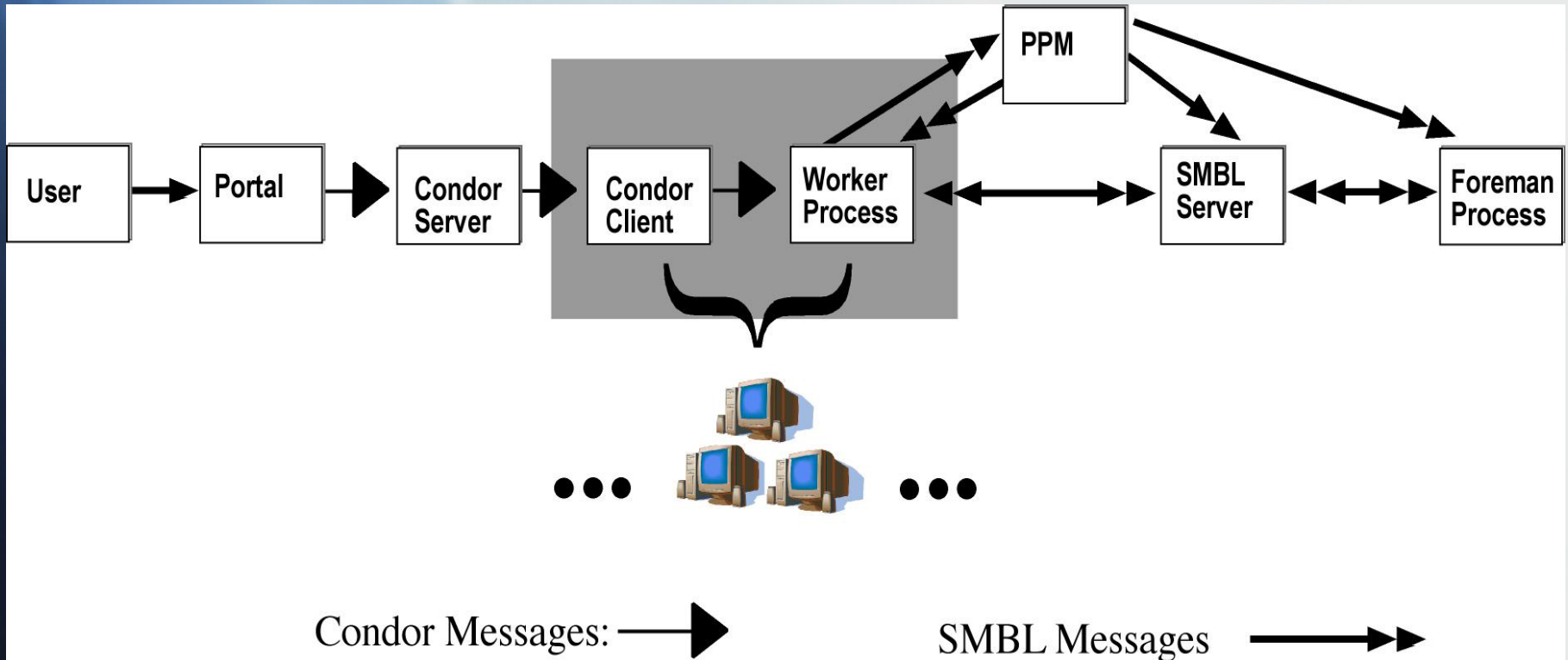
- Simple Message Brokering Library (SMBL)
  - Limited replacement for MPI
- Process and Port Manager (PPM)

... Plus ...

- Condor NT
  - Job management
- Web portal
  - Job submission

# The Big Picture

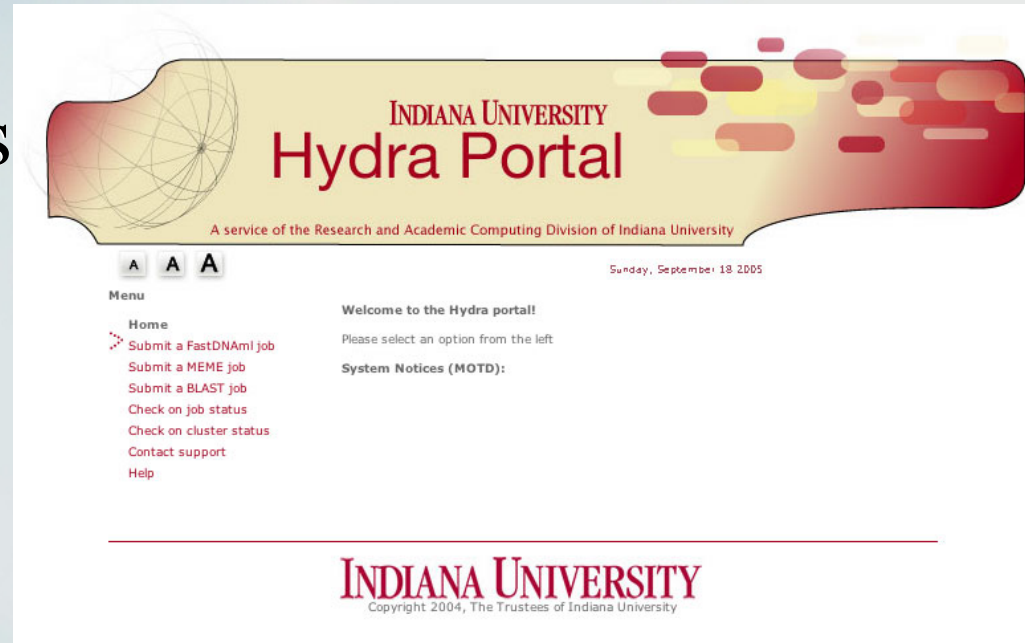
We'll discuss each part in more detail next...



The shaded box indicates components hosted on multiple desktop computers

# Portal

- Creates and submits Condor files, handles data files
- Apache based
- PHP web interface



- <http://hydra.indiana.edu>

# Condor

- Condor for Windows NT/2000/XP
  - “Vanilla universe” -- no support for check-pointing or parallelism
  - Provides:
    - Security
    - Match-making
    - Fair sharing
    - File transfer
    - Job submission, suspension, preemption, restart

# SMBL

- In charge of message delivery for each parallel session
- Client library implements selected MPI-like calls
- Both server and client library based on TCP socket abstraction

## SMBL (Contd ... )

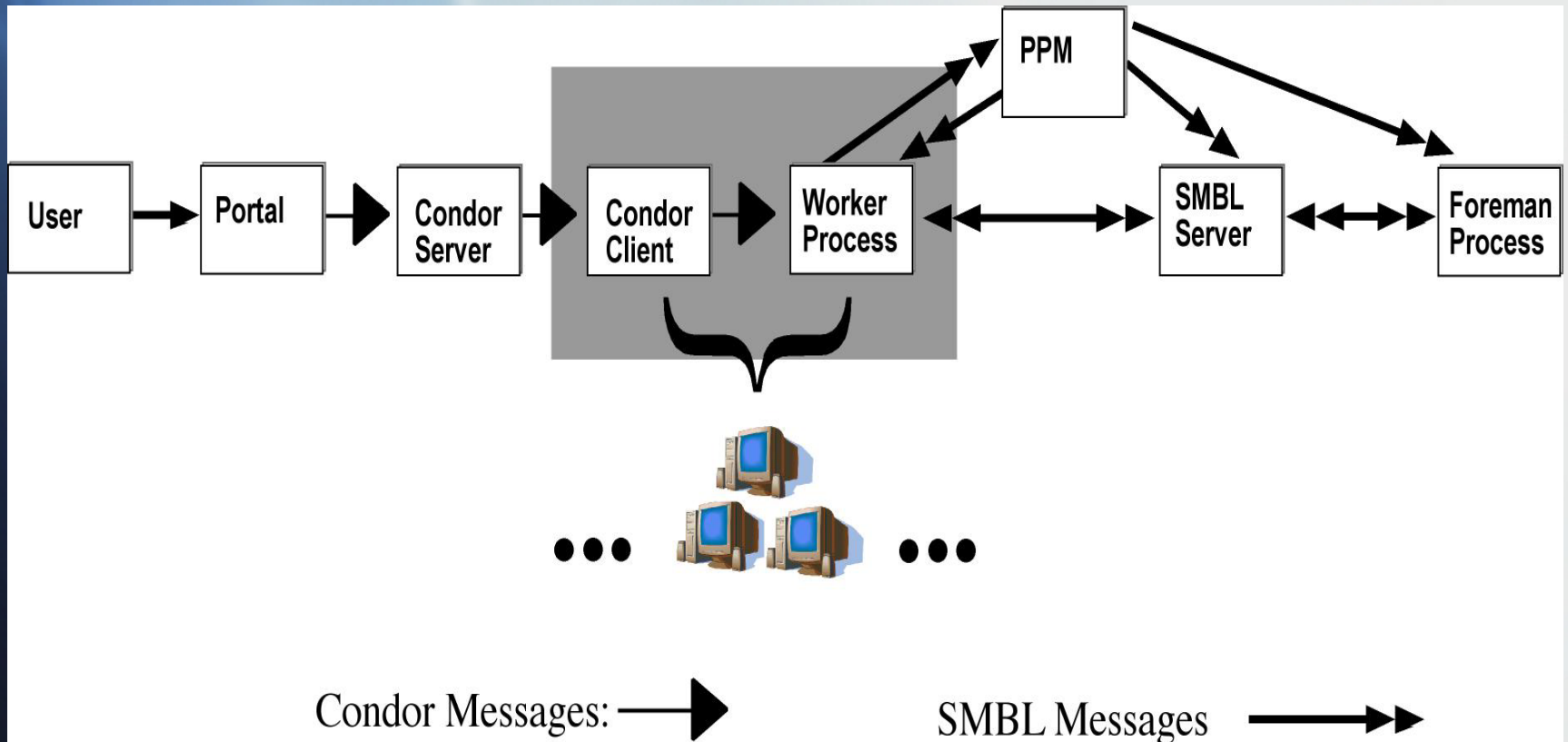
### Managing Temporary Workers

- SMBL server maintains a dynamic pool of client process connections
- Worker job manager hides details of ephemeral workers at the application level
- Porting from MPI is fairly straight forward

# Process and Port Manager (PPM)

- Assigns port/host to each parallel session
- Starts the SMBL server and application processes on demand
- Directs workers to their servers

# Once again ... the big picture



The shaded box indicates components hosted on multiple desktop computers

# System Layout

- PPM, SMBL server and web portal running on Linux server -- Dual Intel Xeon 1.7 GHz, 2 GB memory and GigE inter-connect
- STC Windows worker machines -- Combination of different OS (Windows 2000/XP) and network inter-connect speeds (GigE/100 Mbps/10 Mbps)

# Applications

- FastDNAm1-p
  - Parallel application, master-worker model, small granularity of work
  - Provides generic interface for parallel communication library (MPI, PVM, SMBL)
  - Reliability built in: Foreman process copes with delayed or lost workers
- Blast
- Meme

# Portal

The screenshot shows a web browser window with the URL `https://hydra.indiana.edu/portal.php?module=cluster_status`. The page features a header banner with the text "INDIANA UNIVERSITY Hydra Portal" and a sub-header "A service of the Research and Academic Computing Division of Indiana University". The date "Thursday, September 29 2005" is displayed. A navigation menu on the left includes links for Home, Submit a FastDNAMl job, Submit a MEME job, Submit a BLAST job, Check on job status, Check on cluster status (highlighted), Contact support, and Help. The main content area is divided into several sections: "Condor Queue Status" with a warning message, "Jobs running on the cluster" showing 0 jobs, "Machine statistics" with a table of system counts, a progress bar for available systems, and "Current Gigaflops" showing usage and availability statistics.

https://hydra.indiana.edu/portal.php?module=cluster\_status

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**Hydra Portal**  
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Thursday, September 29 2005

**Menu**

- Home
- Submit a FastDNAMl job
- Submit a MEME job
- Submit a BLAST job
- Check on job status
- Check on cluster status**
- Contact support
- Help

**Condor Queue Status**

This may take a while to process, especially if there is a heavy load..

**Jobs running on the cluster**

0 jobs; 0 idle, 0 running, 0 held

**Machine statistics**

2270	Total systems in the cluster
0	Systems currently running jobs
1445	Systems unavailable, being used by students
825	Systems available

The bar below represents the percentage of the cluster currently available to run jobs.

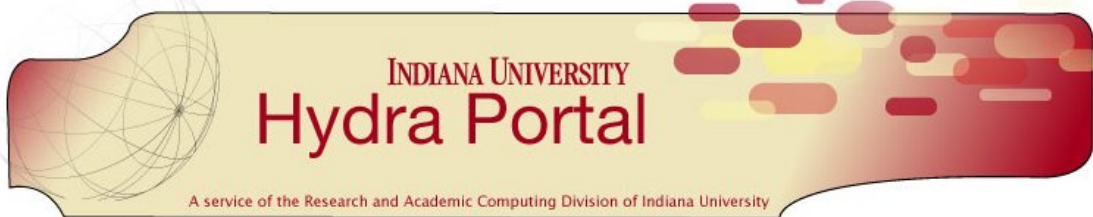
**Current Gigaflops**

In Use: 0.00 Gflops, Unavailable: 961.90 Gflops, Available: 539.69 Gflops, Total: 1501.59 GFlops.

In Use: 0.00 Gflops, Unavailable: 961.90 Gflops, Available: 539.69 Gflops, Total: 1501.59 GFlops.

# Applications – FastDNAm1

https://hydra.indiana.edu/portal.php?module=fastdnaml\_submit



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Menu

- Home
- Submit a FastDNAm1 job
- Submit a MEME job
- Submit a BLAST job
- Check on job status
- Check on cluster status
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- Help

Your E-mail address:

File to upload: (max 100000 bytes)

Number of bootstrap replicates (optional, limit 300):

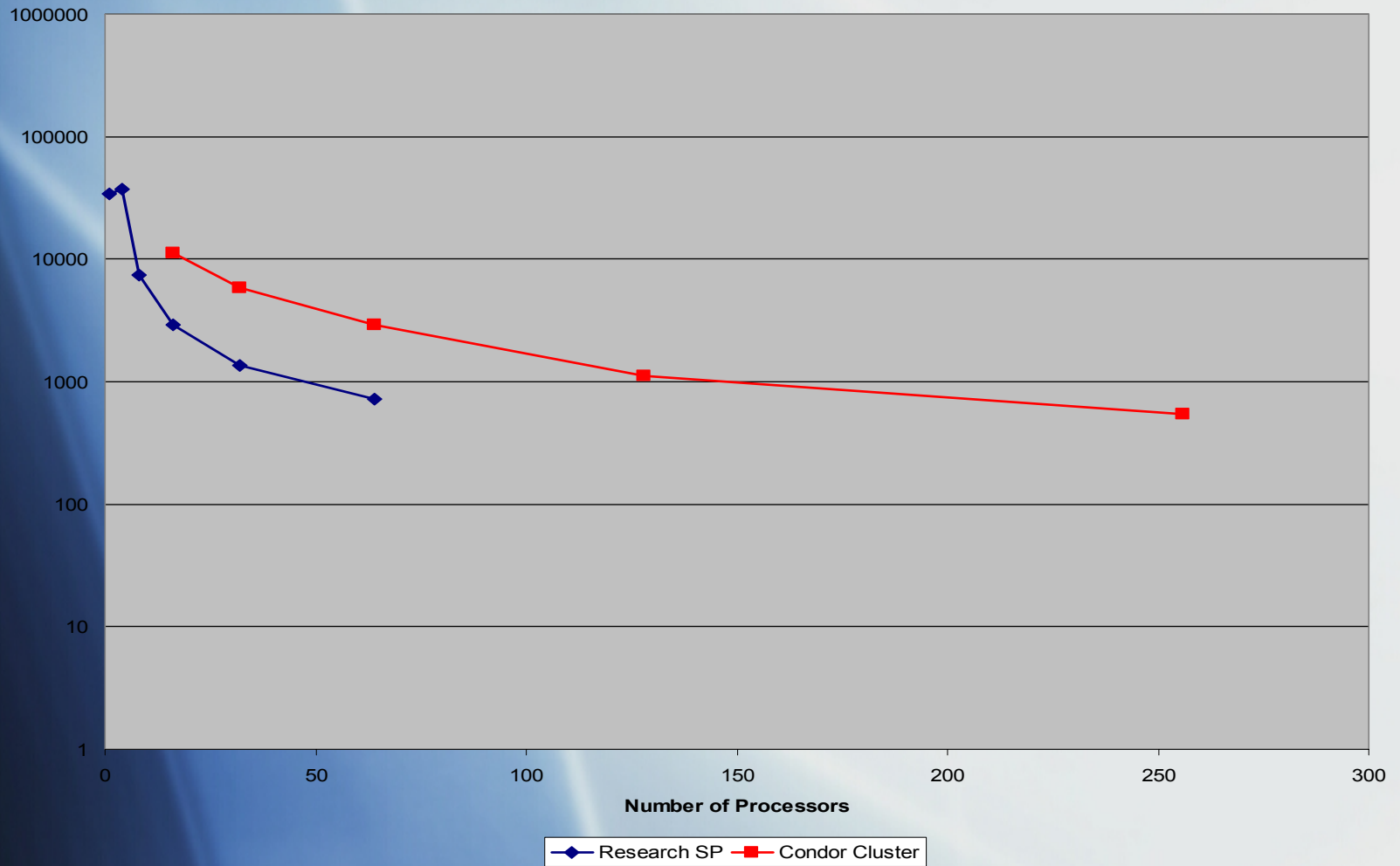
Number of jumbles per repetition (optional, limit 3):

Number of CPUs to run on:  
You are currently limited to using 512 CPUs per job. (total jobs is equal to the number of replicates multiplied by the number of jumbles)

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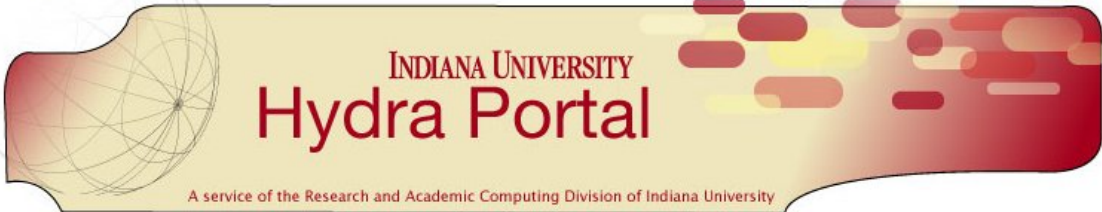
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# FastDNAm1-p Performance



# Other Applications – Parallel MEME

https://hydra.indiana.edu/portal.php?module=meme\_submit



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Menu

- Home
- Submit a FastDNAMl job
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- Submit a BLAST job
- Check on job status
- Check on cluster status
- Contact support
- Help

Your E-mail address:

File to upload: (max 400KB)

Background Markov model file (optional): (max 40MB)

Distribution of motifs:

- one per sequence(oops)
- zero or one per sequence(zoops)
- any number per sequence(tcm -2 component model)

Select sequence alphabet:

- protein
- dna

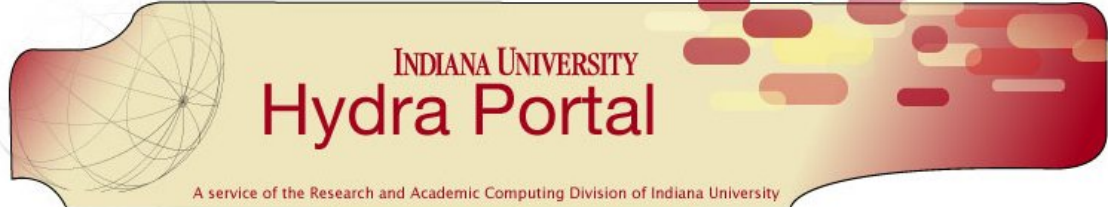
Maximum number of motifs to find:

Additional arguments (optional) :

Number of CPUs to run on:  
You are currently limited to using 512 CPUs for this job.

# Other Applications – BLAST

https://hydra.indiana.edu/portal.php?module=blast\_submit



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Menu

- Home
- Submit a FastDNAmI job
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- Submit a BLAST job
- Check on job status
- Check on cluster status
- Contact support
- Help

Your E-mail address:

File to upload: (max 20MB)

Database name:

Expectation Value (E):

Scoring matrix:

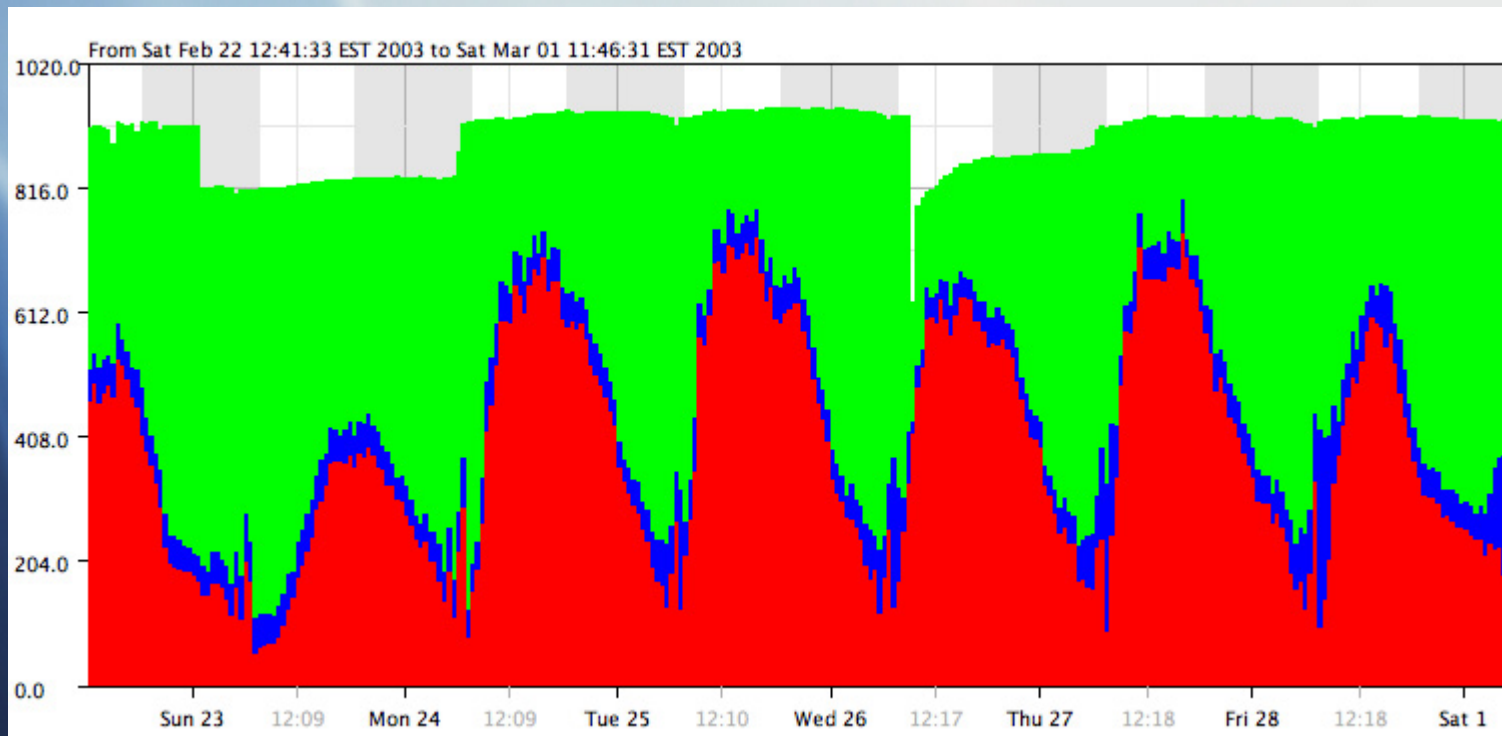
Word size (use 0 for default):

Program type:

Optional blastall arguments:

Number of CPUs (max 512):

# Utilization of Idle Cycles



Red: total owner Blue: total idle Green: total Condor

# Work in Progress/Future Direction

- Teragrid'ize Hydra cluster – allow TG users to access resource
- New Portal – JSR 168 compliant, certificate based authentication capability
- Range of applications – Virtual machines, so forth

# Summary

- Large parallel computing facility created at *very* low cost
  - SMBL parallel message passing library that can deal with ephemeral resources
  - PPM port broker that can handle multiple parallel sessions
- SMBL (Open Source) Home –  
<http://smbl.sourceforge.net>

# Links and References

- Hydra Portal – <http://hydra.indiana.edu>
- SMBL home page – <http://smbl.sourceforge.net>
- Condor home page -- <http://www.cs.wisc.edu/condor/>
- IU Teragrid home page – <http://iu.teragrid.org>
  
- Parallel FastDNAMl –  
<http://www.indiana.edu/~rac/hpc/fastDNAMl>
- Blast -- <http://www.ncbi.nlm.nih.gov/BLAST>
- Meme -- <http://meme.sdsc.edu/meme/intro.html>