

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

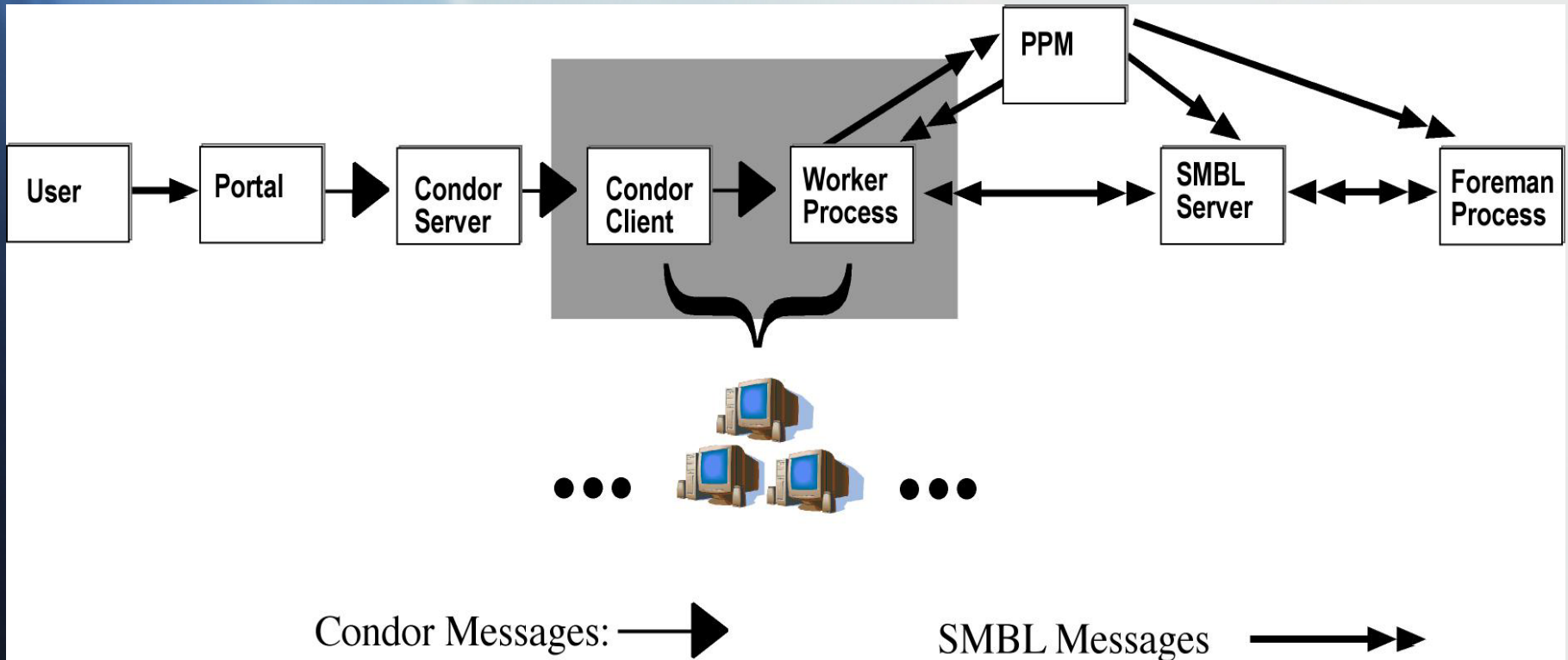
- Simple Message Brokering Library (SMBL)
 - Limited replacement for MPI
- Process and Port Manager (PPM)

... Plus ...

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

The Big Picture

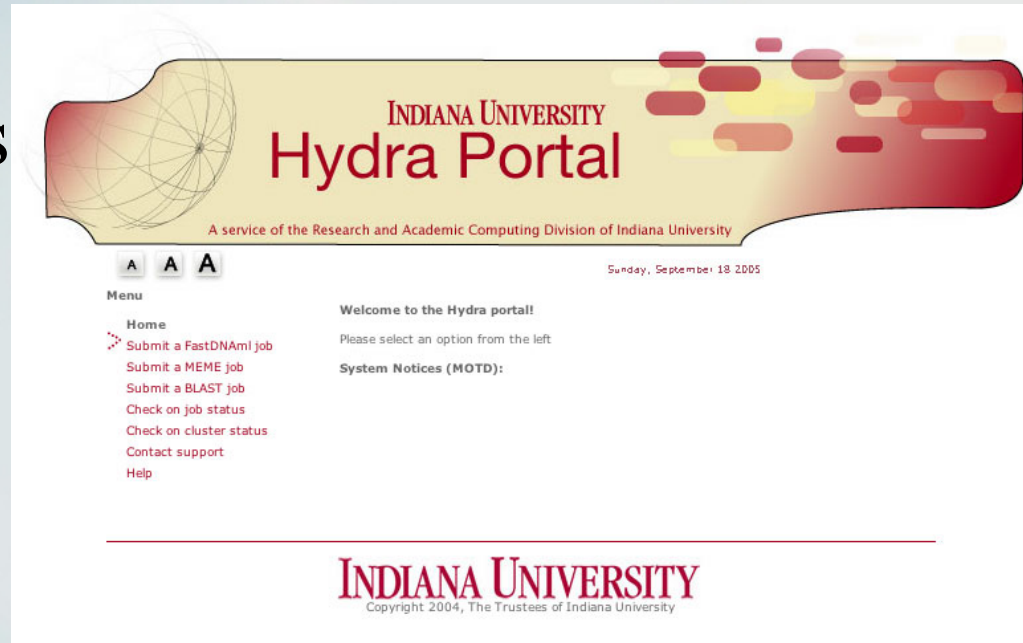
We'll discuss each part in more detail next...



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 ...)

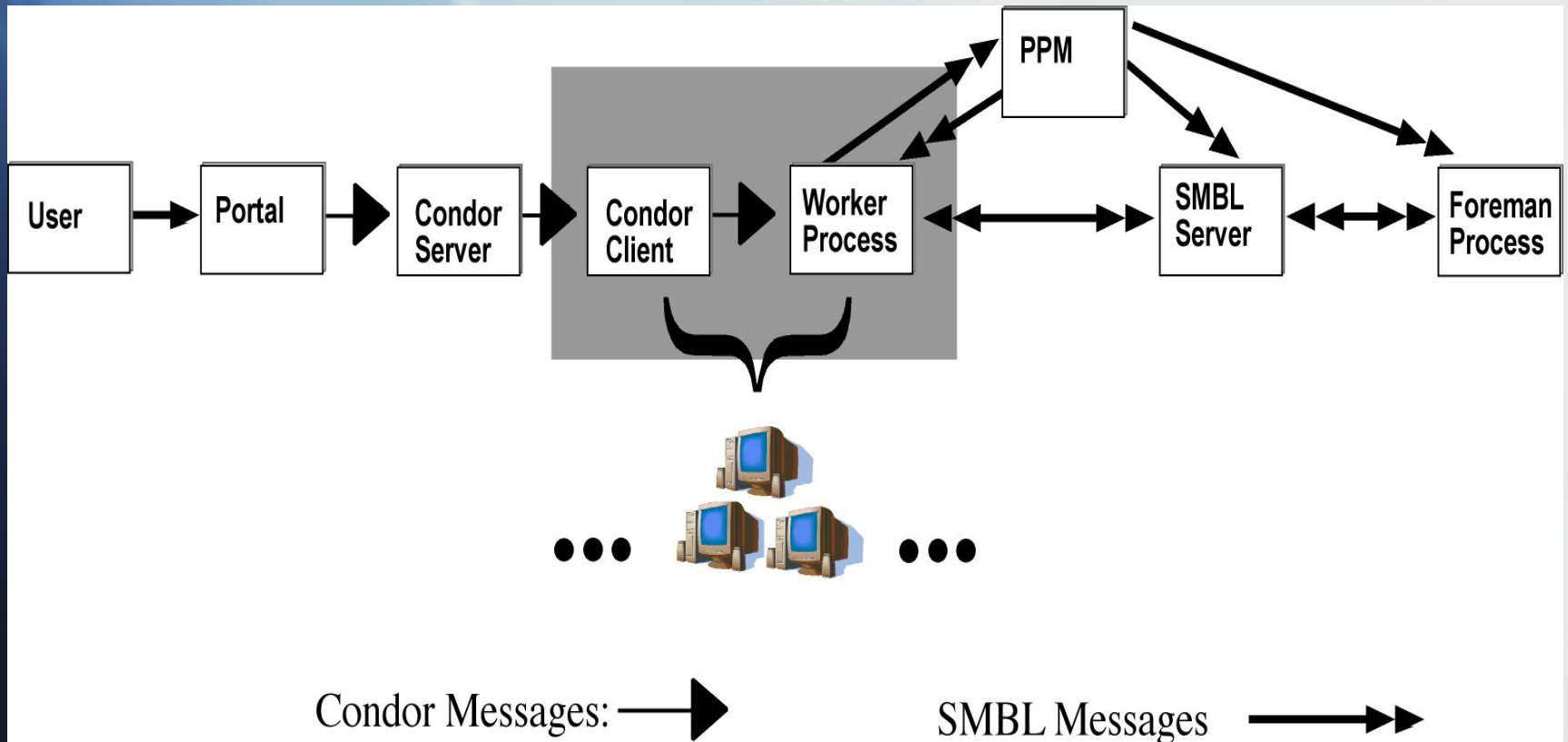
Managing Temporary Workers

- 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

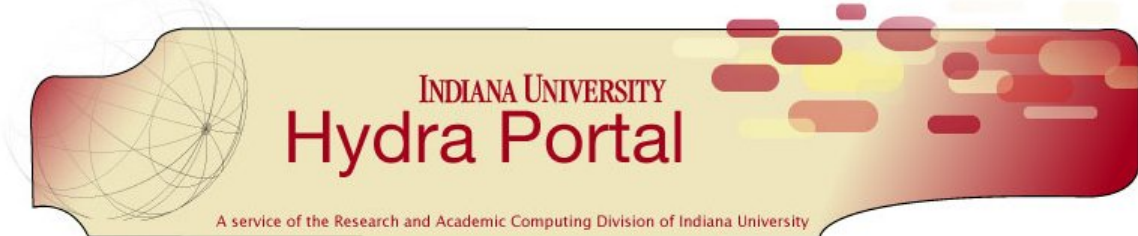
- PPM, SMBL server and web portal running on Linux server -- Dual Intel Xeon 1.7 GHz, 2 GB memory and GigE inter-connect
- STC Windows worker machines -- Combination of different OS (Windows 2000/XP) and network inter-connect speeds (GigE/100 Mbps/10 Mbps)

Applications

- FastDNAml-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

https://hydra.indiana.edu/portal.php?module=cluster_status



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Hydra Portal
A service of the Research and Academic Computing Division of Indiana University

Thursday, September 29 2005

Menu

- Home
- Submit a FastDNAmI 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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Your E-mail address:

File to upload: (max 100000 bytes)

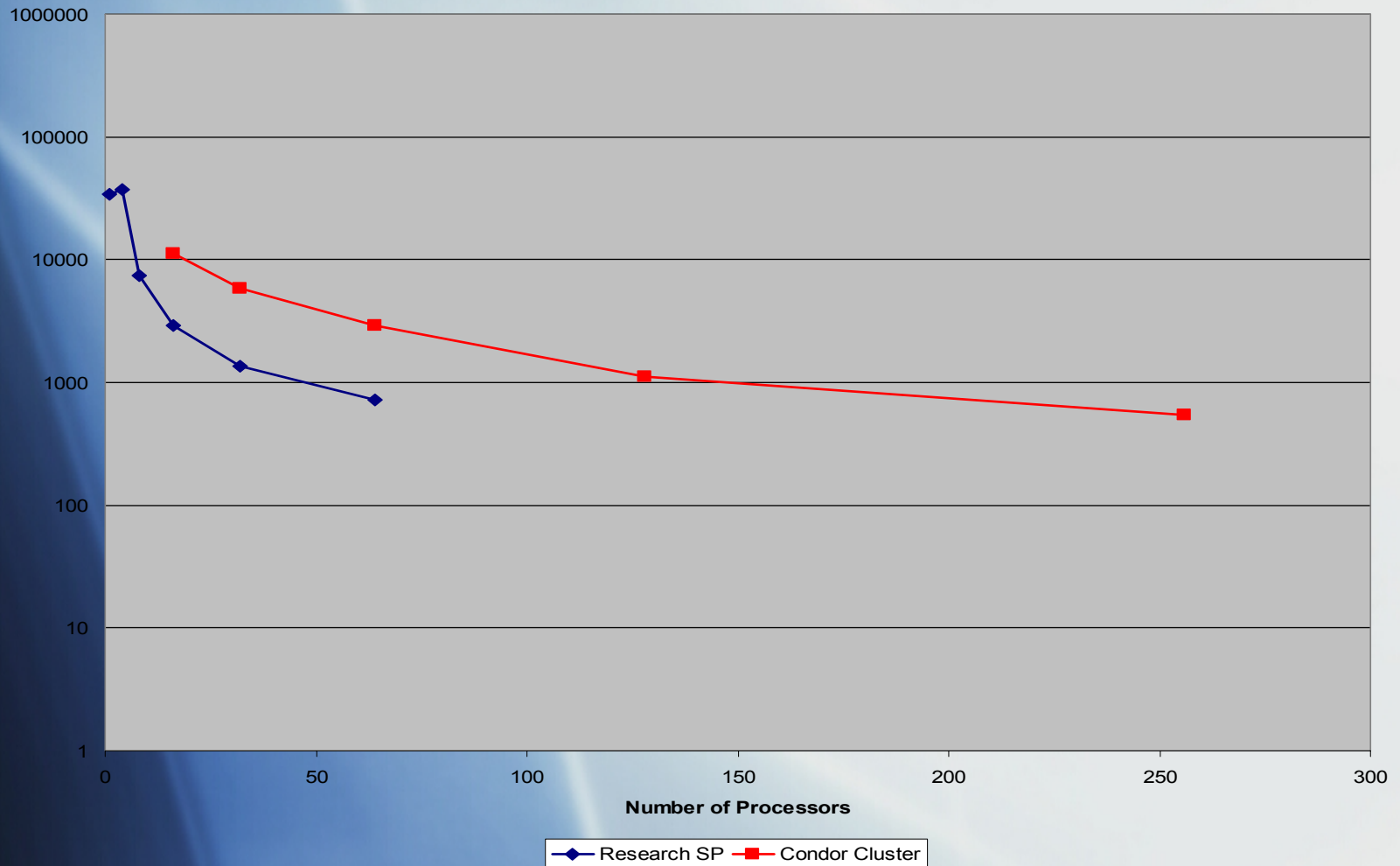
Number of bootstrap replicates (optional, limit 300):

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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FastDNAm1-p Performance



Other Applications – Parallel MEME

https://hydra.indiana.edu/portal.php?module=meme_submit

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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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Your E-mail address:

File to upload: (max 20MB)

Database name:

Expectation Value (E):

Scoring matrix:

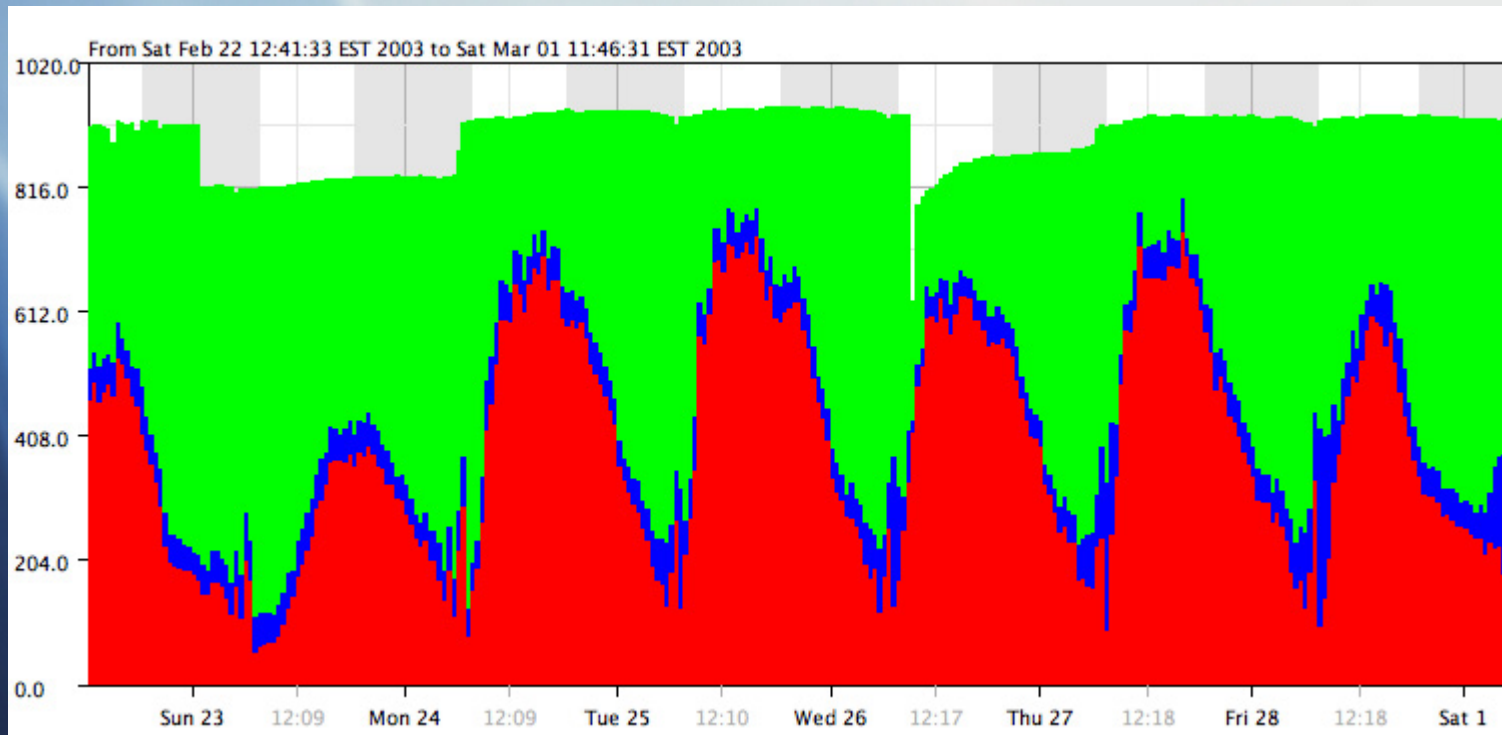
Word size (use 0 for default):

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://smb1.sourceforge.net>

Links and References

- Hydra Portal – <http://hydra.indiana.edu>
- SMBL home page – <http://smb1.sourceforge.net>
- Condor home page -- <http://www.cs.wisc.edu/condor/>
- IU Teragrid home page – <http://iu.teragrid.org>

- Parallel FastDNAm1 – <http://www.indiana.edu/~rac/hpc/fastDNAm1>
- Blast -- <http://www.ncbi.nlm.nih.gov/BLAST>
- Meme -- <http://meme.sdsc.edu/meme/intro.html>