



THE UNIVERSITY OF
CHICAGO



Scientific Workflow Systems for 21st Century

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Collaborators:

Many many people, see the “More Information” slide at the end



MWGS08: MidWest Grid School 2008
September 17th, 2008

Workflow Systems

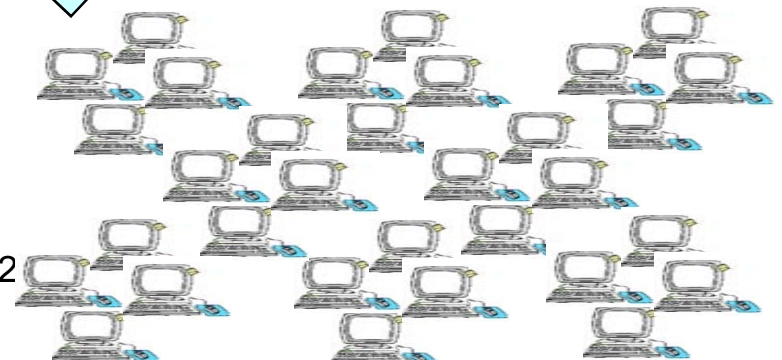
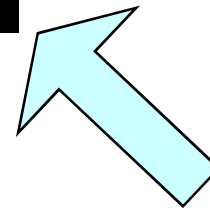
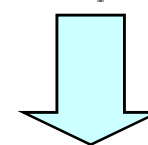
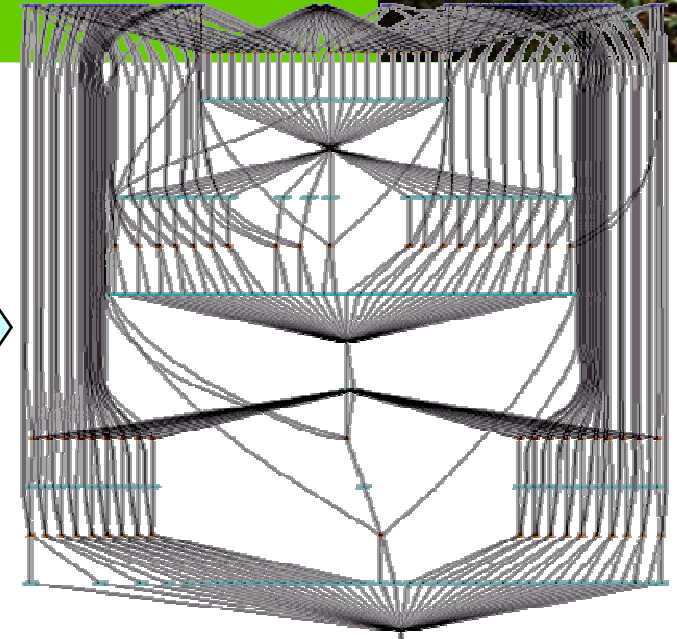
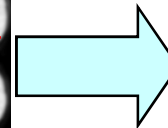
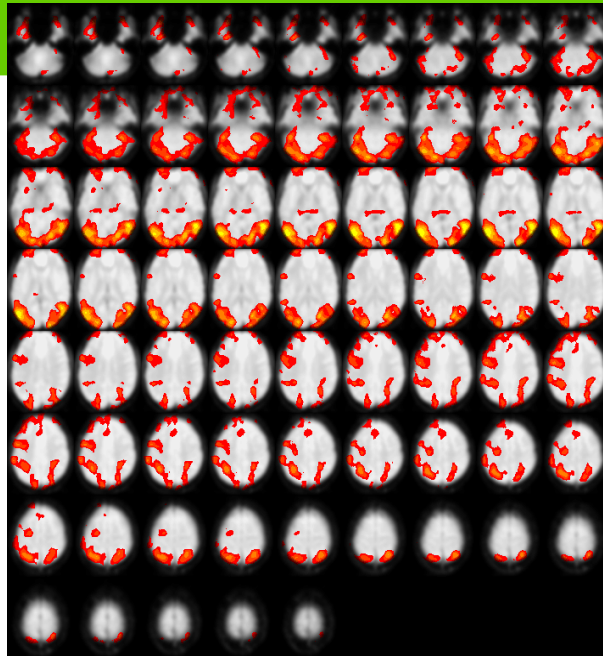
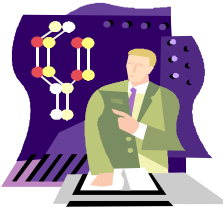


Describes computation components, ports and channels

Describes data and event flow

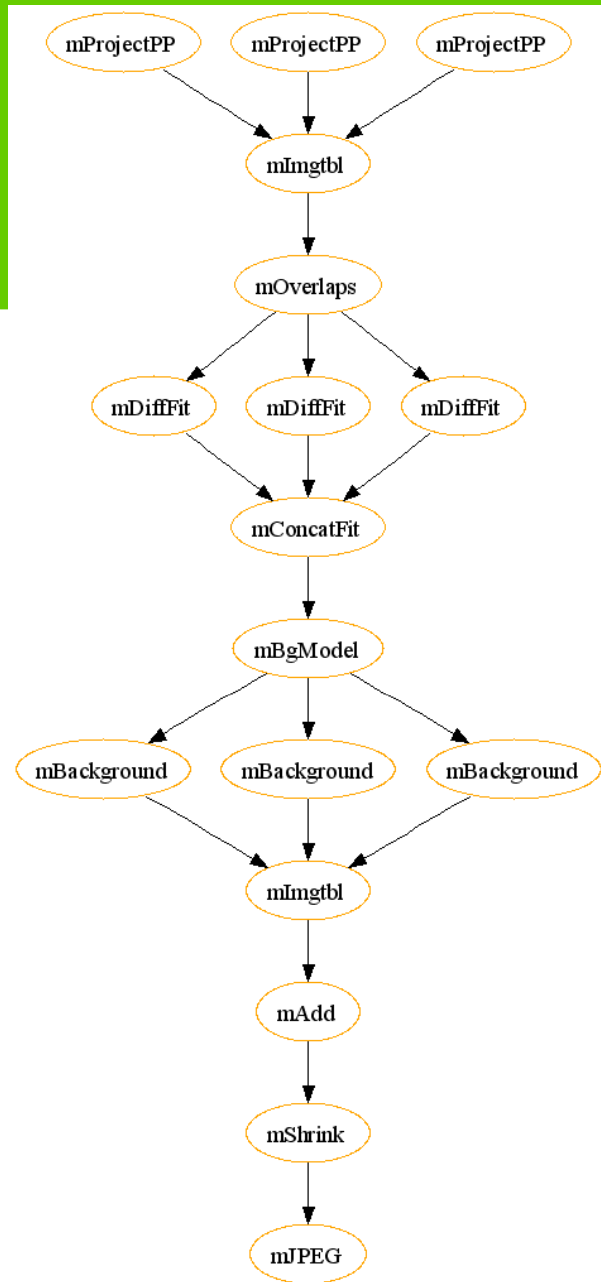
Coordinate the execution of the components

Functional MRI (fMRI)

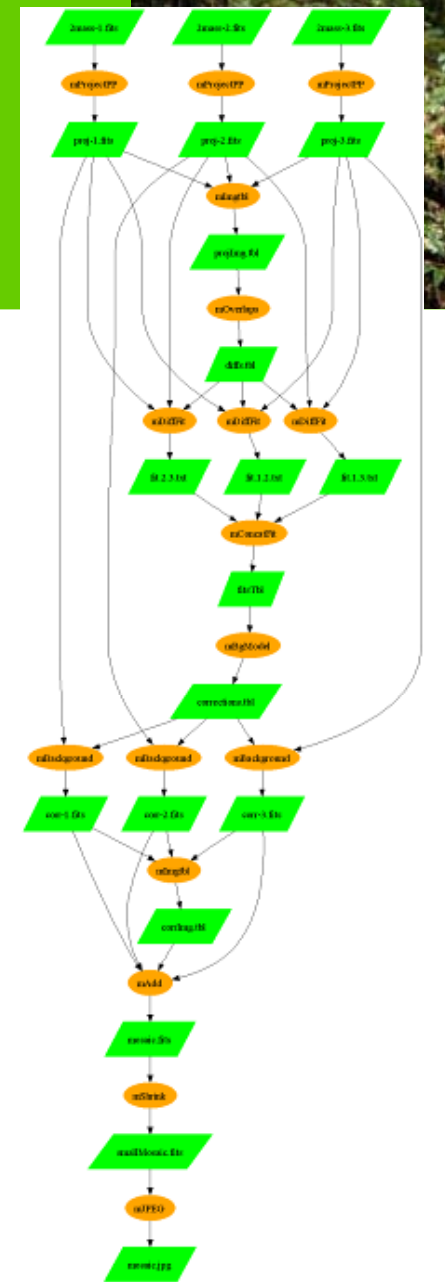


ems for 2

- Wide range of analyses
 - Testing, interactive analysis, production runs
 - Data mining
 - Parameter studies



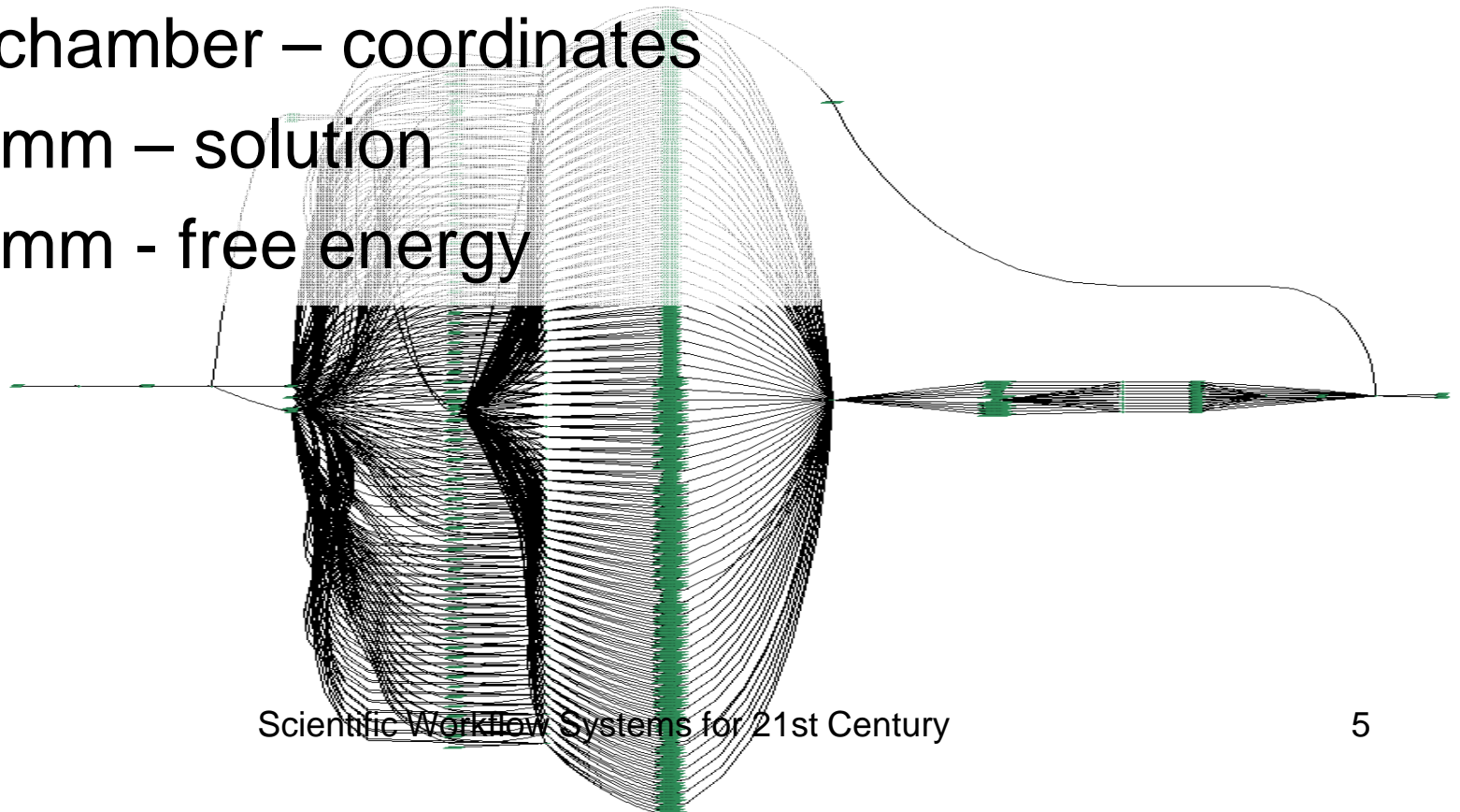
B. Berriman, J. Good (Caltech)
 J. Jacob, D. Katz (JPL)



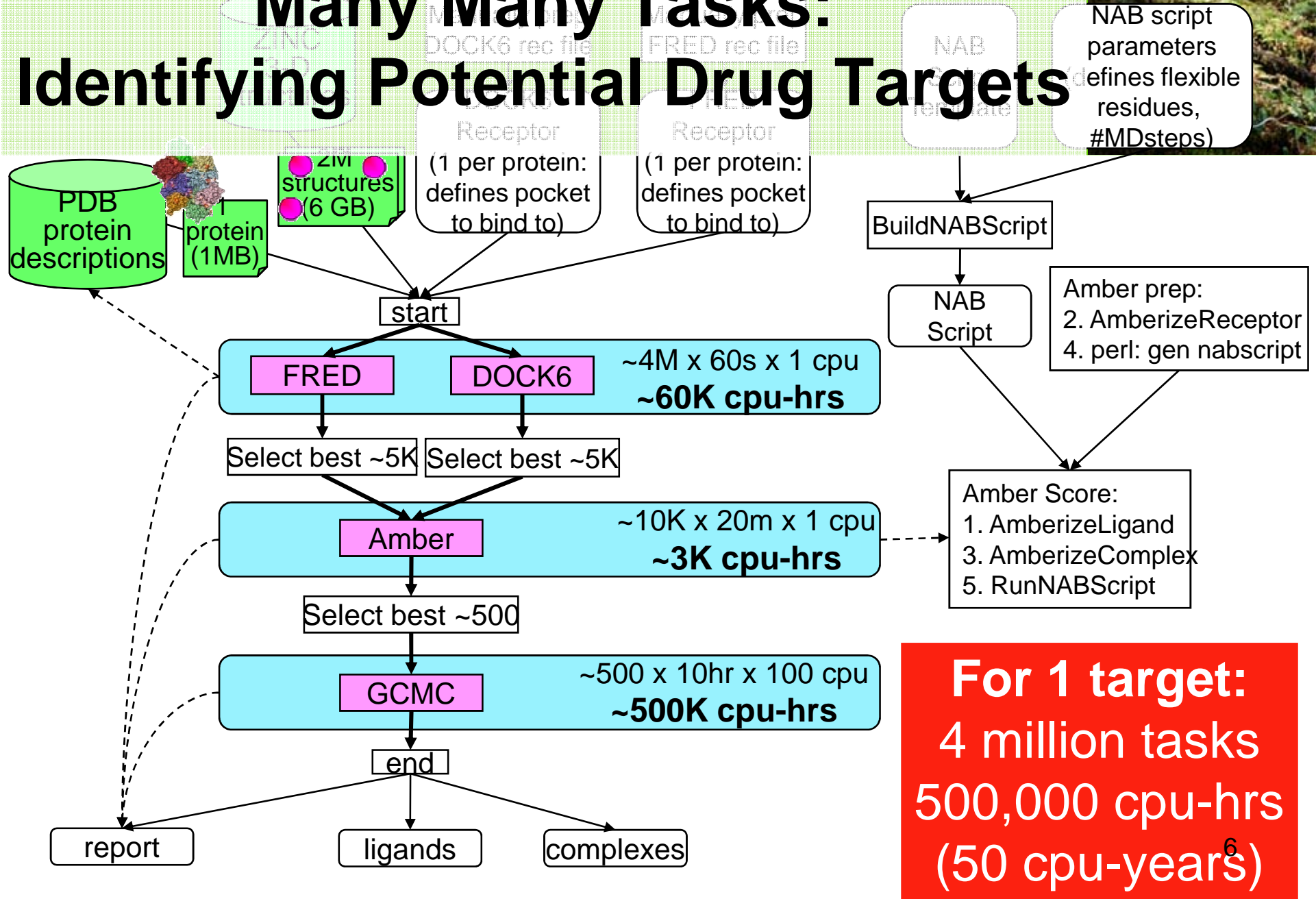
Molecular Dynamics



- Determination of free energies in aqueous solution
 - Antechamber – coordinates
 - Charmm – solution
 - Charmm - free energy



Many Many Tasks: Identifying Potential Drug Targets



**For 1 target:
4 million tasks
500,000 cpu-hrs
(50 cpu-years)⁶**

Characterizing Scientific Workflows



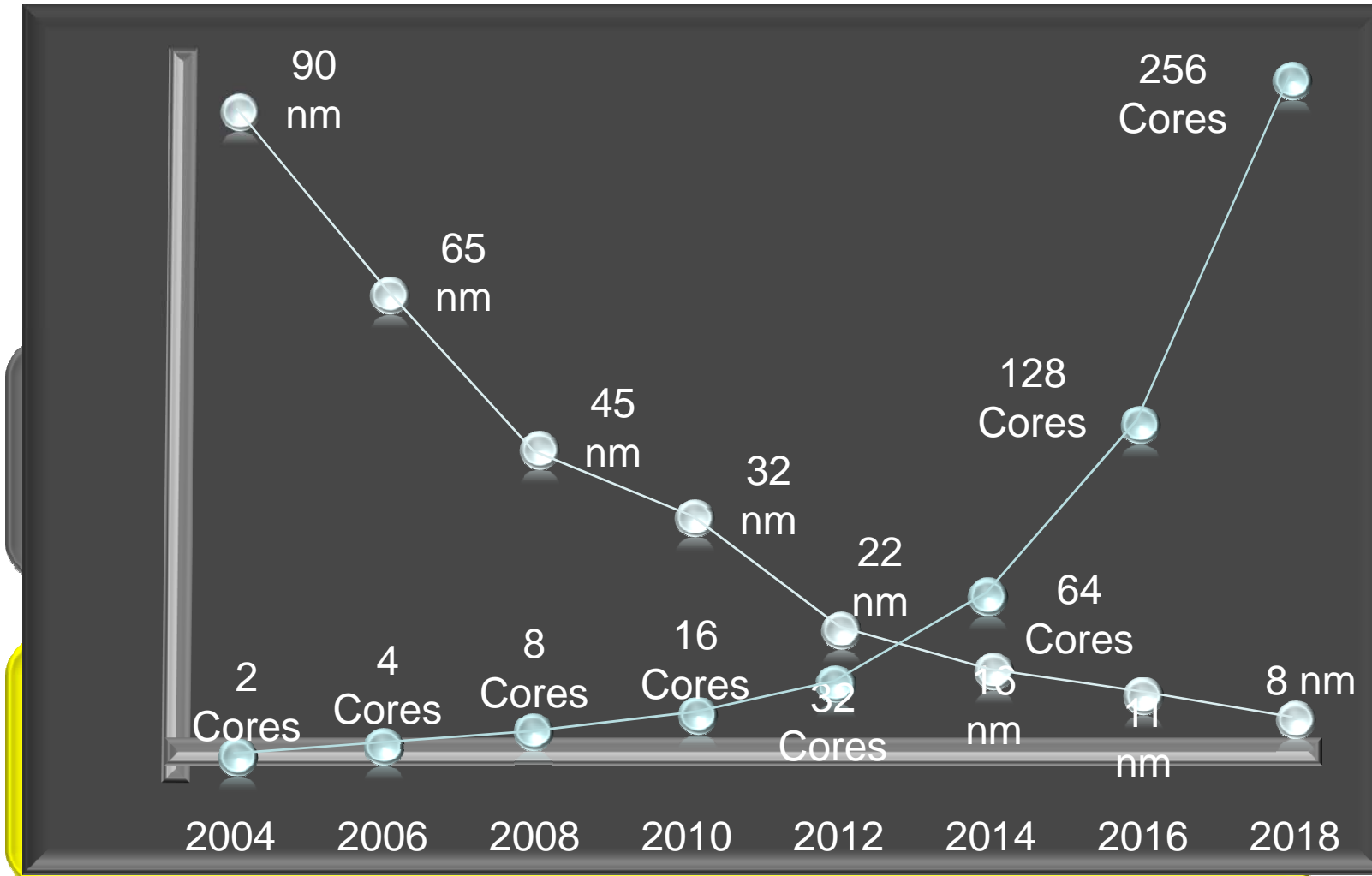
- Inherit *workflow system* definition +...
- Describe complex scientific procedures
- Automate data derivation processes
- High performance computing (HPC) to improve throughput and performance
- Provenance management and query

Characterizing Scientific Applications

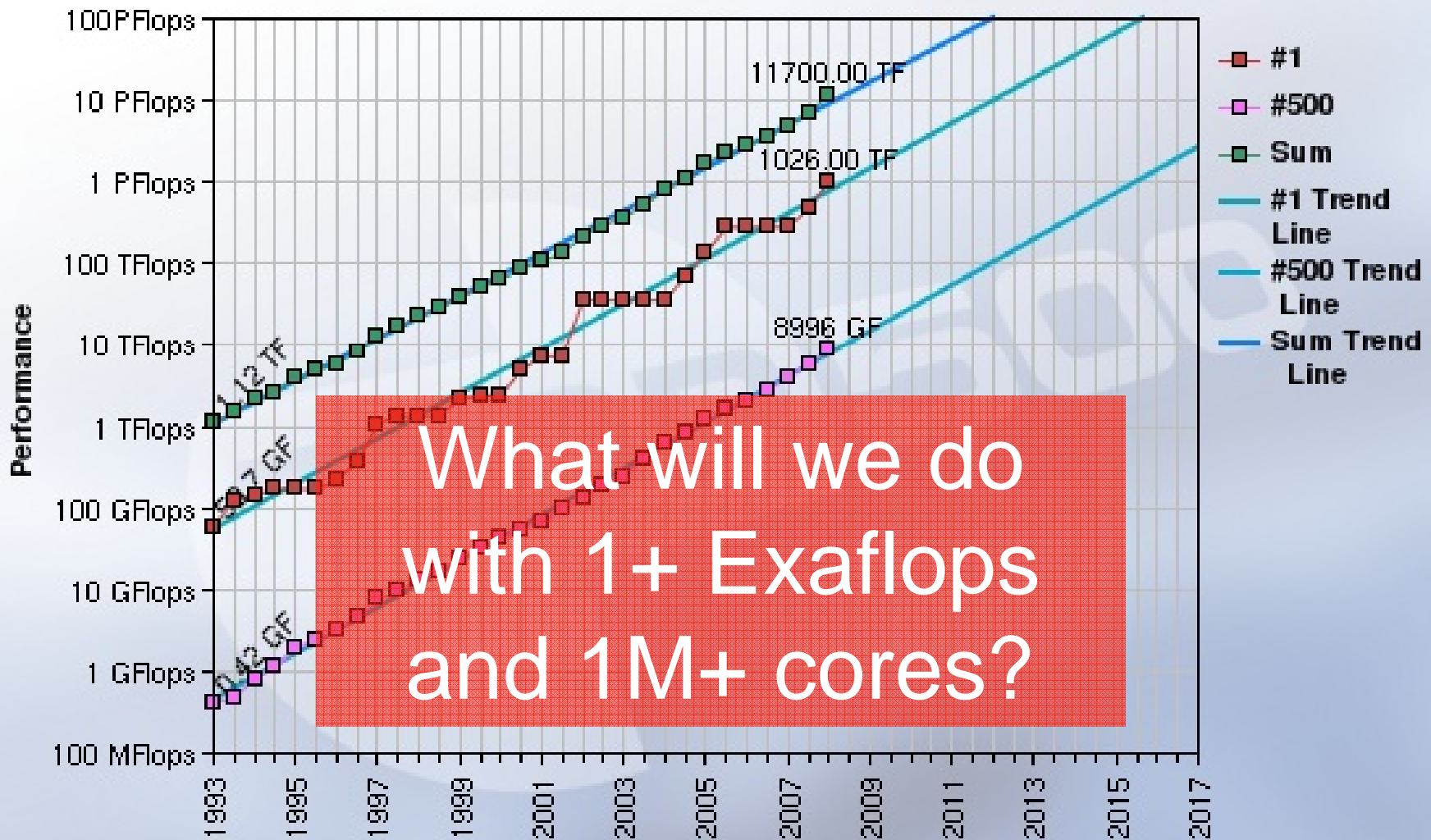


- Increasing in scale and complexity
 - Wide inherent parallelism
 - Multiple successive stages
 - Wide range of number of tasks
 - thousands to billions
- Potentially compute intensive
 - Widely varying task execution times
 - 100s of ms to 10s of hours
- Potentially data intensive
 - I/O operation rates and aggregate I/O rates
 - Meta-data creation and modification
 - Significant data re-use
 - Produced data is consumed by later stages

Many-Core Growth Rates

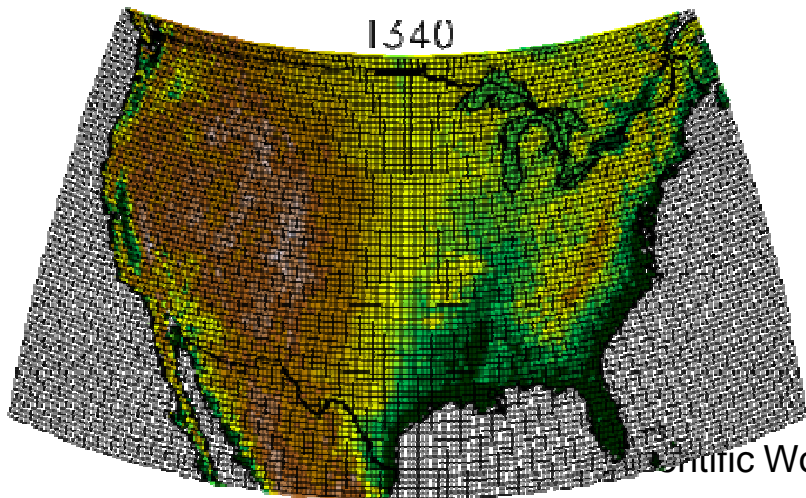
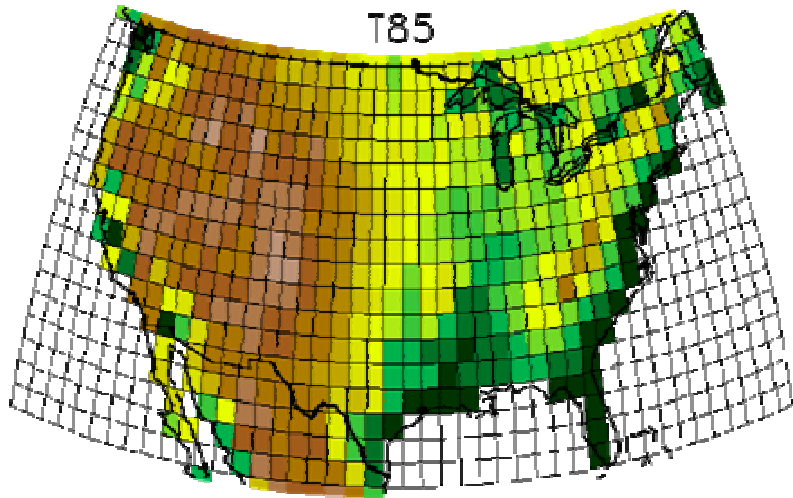


Projected Performance Development



What will we do with 1+ Exaflops and 1M+ cores?

1) Tackle **Bigger and Bigger** Problems

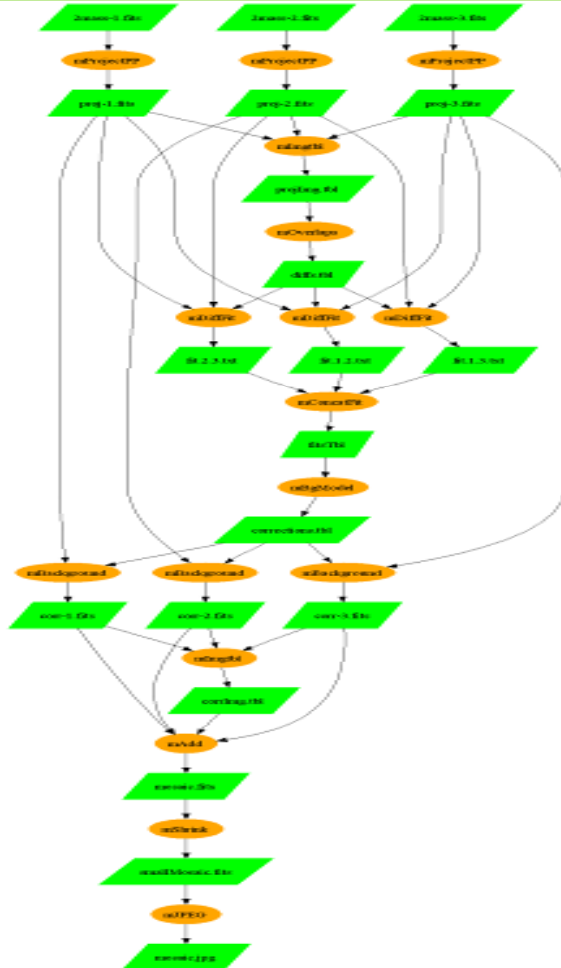


Computational
Scientist
as
Hero

2) Tackle **Increasingly Complex** Problems



Computational
Scientist
as
**Logistics
Officer**



“More Complex Problems”



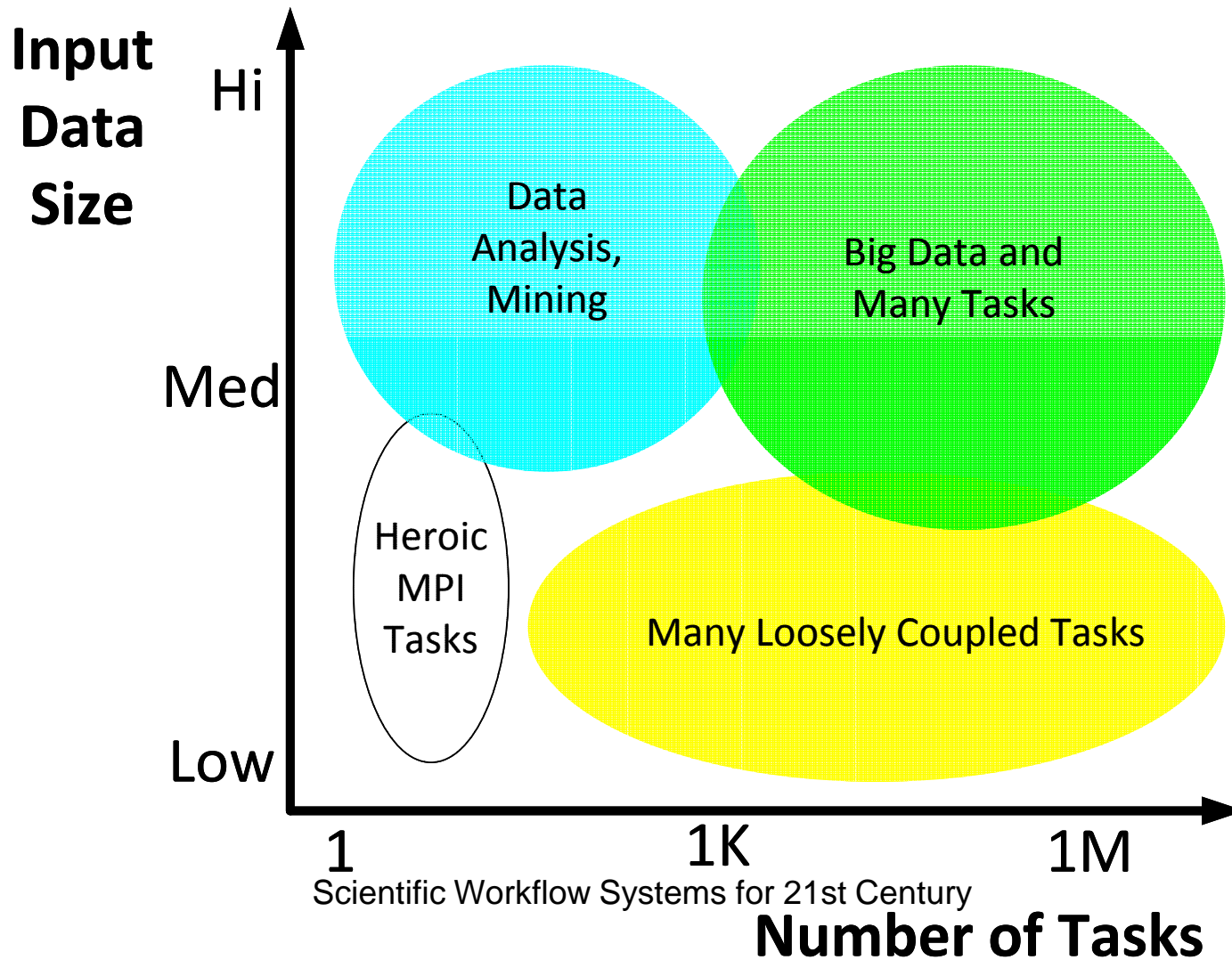
- Ensemble runs to quantify **climate model uncertainty**
- Identify **potential drug targets** by screening a database of ligand structures against target proteins
- Study **economic model sensitivity** to parameters
- Analyze **turbulence dataset** from many perspectives
- Perform **numerical optimization** to determine optimal resource assignment in energy problems
- Mine collection of data from **advanced light sources**
- Construct databases of computed properties of **chemical compounds**
- Analyze data from the **Large Hadron Collider**
- Analyze **log data** from 100,000-node parallel computations

Programming Model Issues

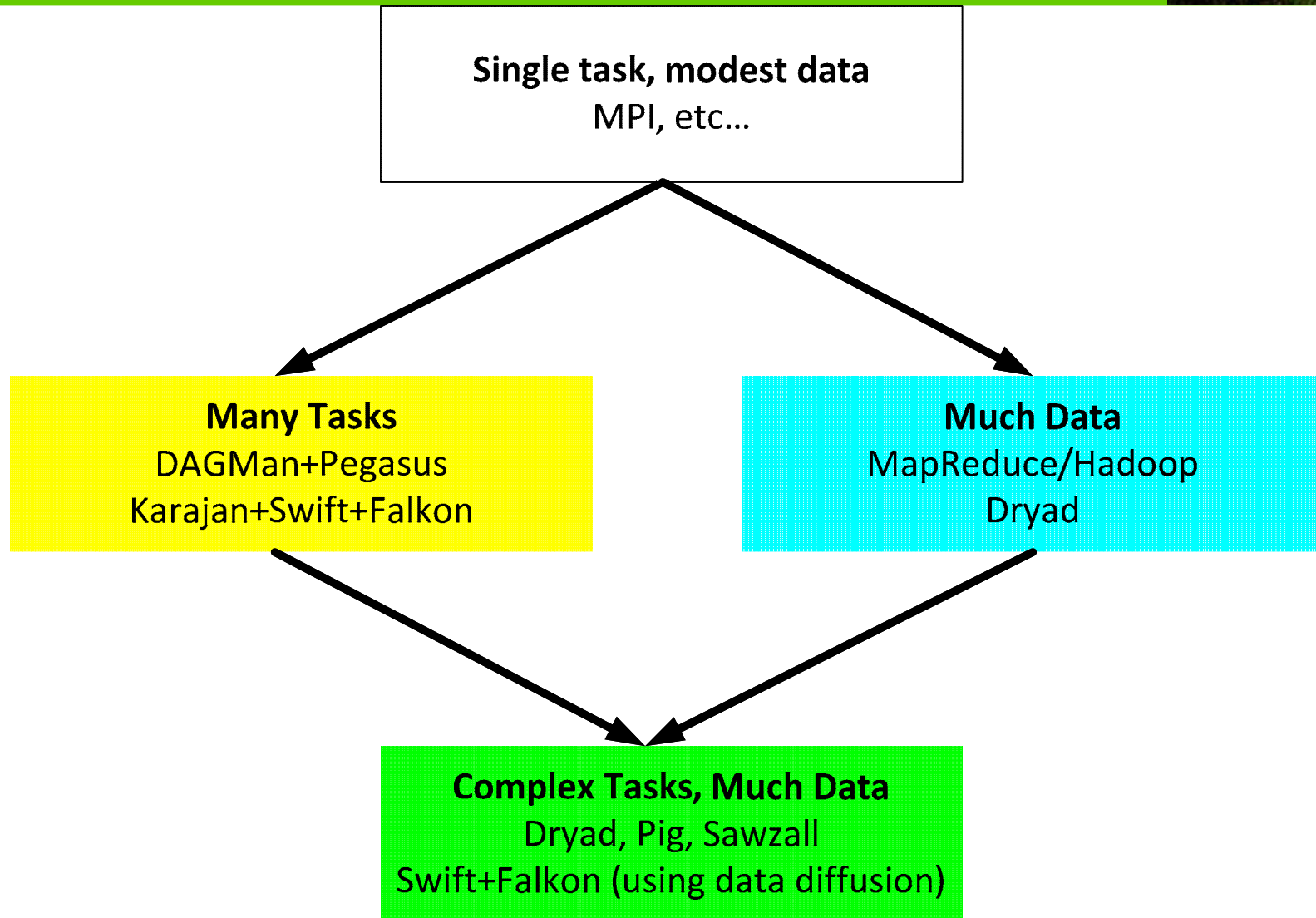


- Massive **task parallelism**
- Massive **data parallelism**
- Integrating **black box applications**
- Complex **task dependencies** (task graphs)
- **Failure**, and other execution management issues
- **Data management**: input, intermediate, output
- **Dynamic computations** (task graphs)
- **Dynamic data access** to large, diverse datasets
- **Long-running** computations
- Documenting **provenance** of data products

Problem Types



An Incomplete and Simplistic View of Programming Models and Tools



Major Challenges to Large Scale Scientific Computation

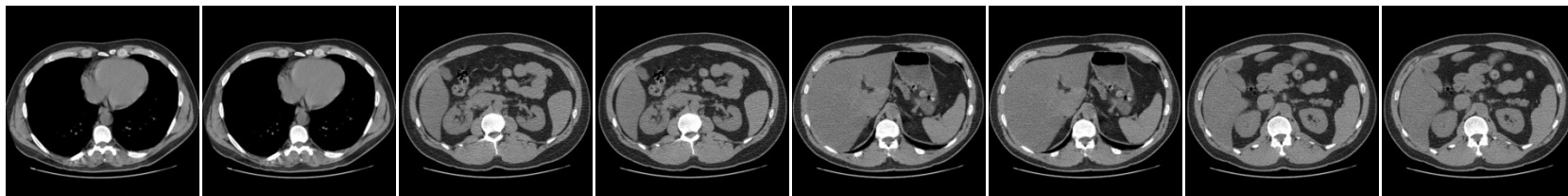


- Managing heterogeneous scientific data
 - Idiosyncratic layouts & formats (file sys, db, spreadsheet, XML, etc...)
- Describing complex science problems
- Coordinating distributed diverse computation procedures
 - Executables, scripts, Web services
- Long wait queue times
- Scheduling & executing numerous tasks reliably and efficiently
 - Large quantity of data (Petabytes/year)
 - Large number of parallel/dependent tasks ($10^3 \sim 10^6$ tasks)
- Organizing, archiving and tracking
 - Datasets, procedures, workflows, provenance
- Supporting data-intensive applications

Grid Opportunities in Medical Imaging A Case Study



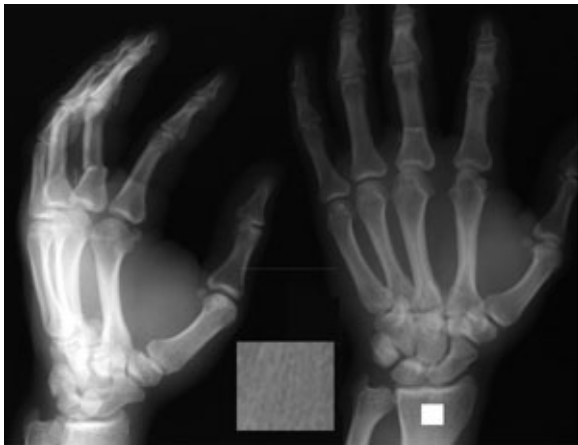
- Daniela S. Raicu, PhD
 - Assistant Professor
 - Email: draicu@cs.depaul.edu
 - Lab URL: <http://facweb.cs.depaul.edu/research/vc/>
 - Original slides:
http://www.ci.uchicago.edu/wiki/bin/viewfile/VDS/DsICS/DSLWorkshop2007?rev=1;filename=draicu_DSL_workshop.pdf



What is Medical Imaging (MI)?



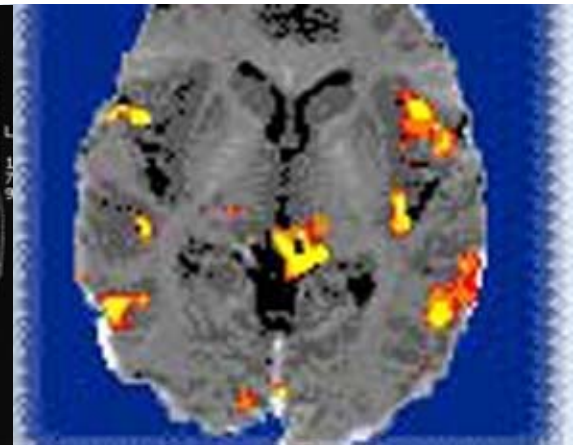
The study of *medical imaging* is concerned with the interaction of all forms of radiation with tissue and the development of appropriate technology to extract clinically useful information from observation of this technology.



X-Ray



CT



fMRI

CT Medical Imaging (MI)@ CTI

INTELLIGENT MULTIMEDIA PROCESSING LABORATORY

Intelligent Multimedia Processing Laboratory

DEPAULCTI

IMP Mission

The Intelligent Multimedia Processing Laboratory's (IMP Lab) mission is focused on medical imaging, image processing, computer vision, content-based multimedia retrieval, and data mining. Our goal is to develop both the theory and the tools for real world applications from various domains, such as medicine, homeland security, intellectual property, and business intelligence domain.

IMP Research Interests

[Medical Imaging](#)

[Intellectual Property](#)

[Bioinformatics](#)

[Graduates \(REU\)](#)



Project 1: Texture-based soft-tissue segmentation

Segmentation

Analysis

Project 2: Content-based medical image retrieval

Visualization

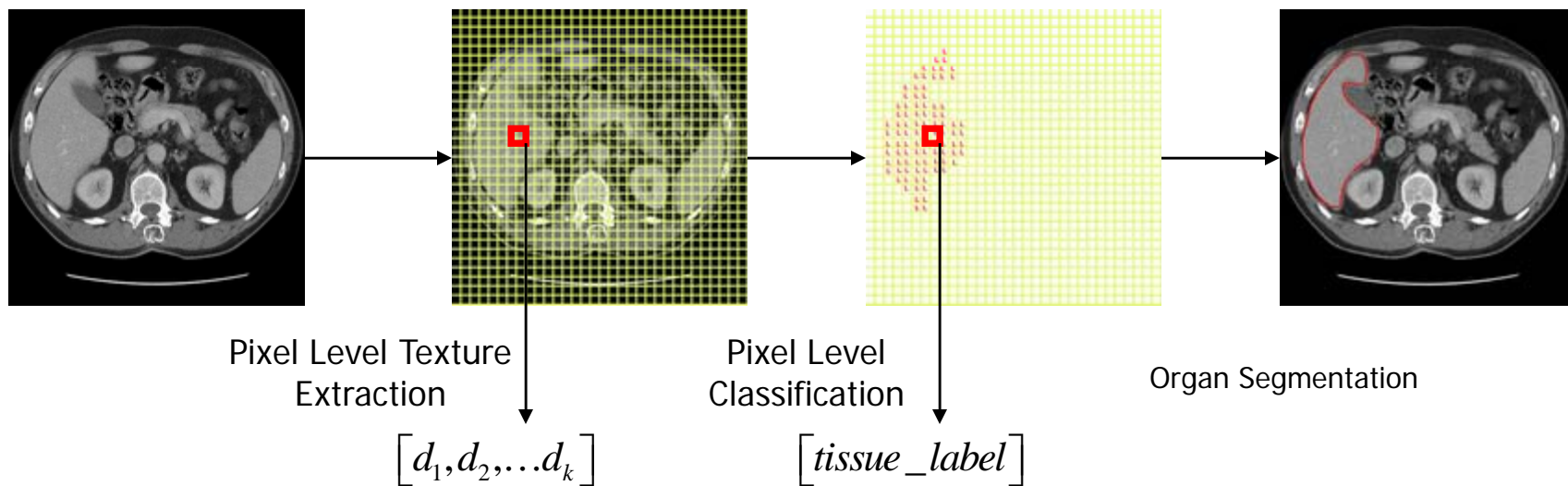
Classification

Retrieval

Soft-tissue Segmentation in Computed Tomography



Goal: context-sensitive tools for radiology reporting
Approach: pixel-based texture classification



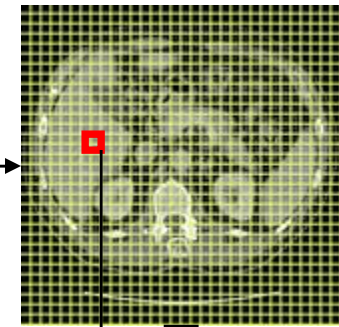
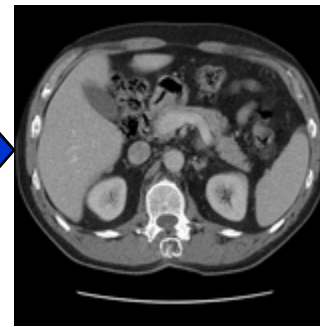
Soft-tissue Segmentation in Computed Tomography



Pixel-based texture extraction:

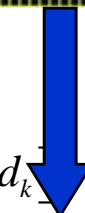
Input Patient Data Characteristics:

- hundreds of images per patient
- image spatial resolution: 512 x512
- image gray-level resolution: 2^{12}



Pixel Level Texture
Extraction

$[d_1, d_2, \dots, d_k]$



Challenges:

- Storage:
 - Input: 0.5+ terabyte of raw data dispersed over about 100K+ images
 - Output: 90+ terabytes of low-level features in a 180 dimensional feature space
- Compute:
 - 24 hours of compute time = 180 features for a single image on a modern 3GHz workstation

Output Data Characteristics:

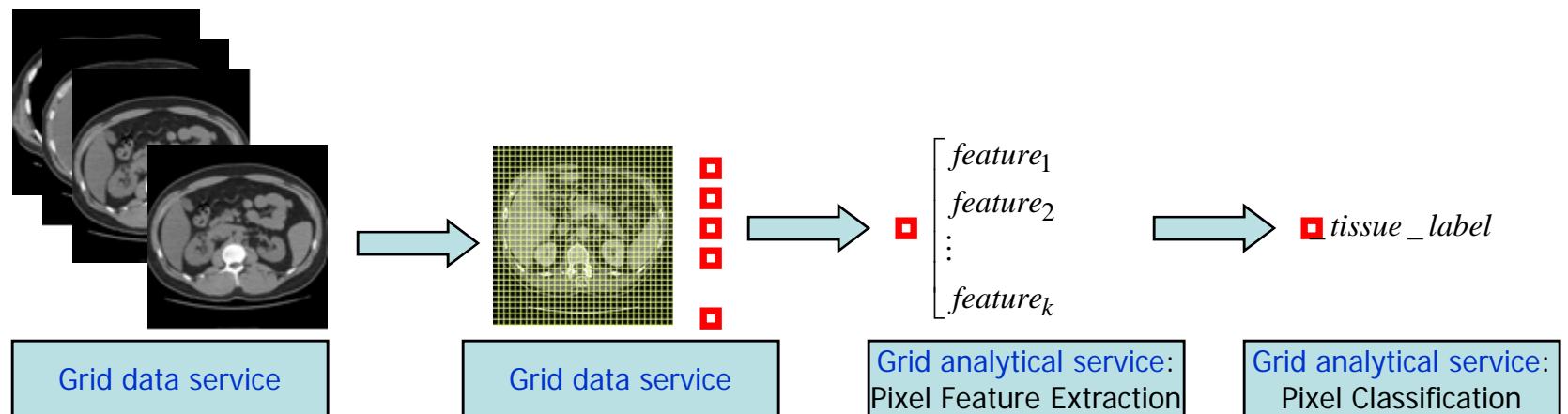
- low-level image features (numerical descriptors)
- $k=180$ Haralick texture features per pixel (9 descriptors x4 directions x5 displacements)

Grid Computing Opportunities



Challenges and Grid Opportunities:

- **Storage**
 - define the logical and physical organization of the medical image datasets along with the relevant information extracted from them
- **Compute time**
 - coordinate the *parallel execution* of the texture feature extraction and classification algorithms such that each *image, pixel and feature* could be processed independently of the other images, pixels and features, respectively.



Content-based medical image retrieval (CBMS) systems



Definition of Content-based Image Retrieval:

Content-based image retrieval is a technique for retrieving images on the basis of automatically derived image features such as texture and shape.

Applications of Content-based Image Retrieval:

- Teaching
- Case-base reasoning
- Evidence-based medicine

Choose a nodule



SeriesID	Slice	Nodule	NoduleID
1.3.6.1.4.1.9328.50.3.272	289	1	4026
1.3.6.1.4.1.9328.50.3.272	290	1	4026
1.3.6.1.4.1.9328.50.3.272	311	2	4009
1.3.6.1.4.1.9328.50.3.272	312	2	4009
1.3.6.1.4.1.9328.50.3.272	289	1	2593
1.3.6.1.4.1.9328.50.3.272	290	1	2593
1.3.6.1.4.1.9328.50.3.272	291	1	2593
1.3.6.1.4.1.9328.50.3.378	438	3	001
1.3.6.1.4.1.9328.50.3.378	437	3	001
1.3.6.1.4.1.9328.50.3.378	436	3	001
1.3.6.1.4.1.9328.50.3.378	434	3	001
1.3.6.1.4.1.9328.50.3.378	436	3	4064
1.3.6.1.4.1.9328.50.3.378	437	3	4064
1.3.6.1.4.1.9328.50.3.378	438	3	4064
1.3.6.1.4.1.9328.50.3.378	436	3	3096

Distance Measure

Haralick: Gabor:
Euclidean Chi-Square (H)
Choose Vector ...

Markov:
Chi-Square (H)

Run Query

0 result(s)

Precision:

Recall:

Analyze

Distance:

Restrict Results

Top 10 items

SeriesID	Slice	Nodule	NoduleID	Distance	Score
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LIDC Nodule Viewer 1.1 [1168 nodule(s) loaded]

1.3.6.1.4.1.9328.50.3.272

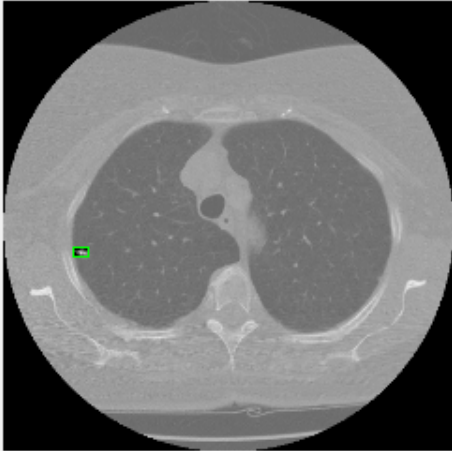
Slice #: 290
Nodule #: 1
NoduleID: 2593

-- HARALICK DESCRIPTORS --

[*] Contrast: 7.571e2
[*] Correlation: -0.2012
[*] Energy: 0.009
[*] Homogeneity: 0.0532
Entropy: 4.1423
3rd Order Moment: -6.640e2
Inverse Variance: 0.0154
Sum Average: 62.112
Variance: 1.085e3
Cluster Tendency: 1.772e3
Maximum Probability: 0.009

-- PHYSICIAN ANNOTATIONS --

Calcification: #####
Internal Structure: #
Lobulation: #####
Malignancy: ###
Margin: ##
Sphericity: ###
Spiculation: #####
Subtlety: ###
Texture: ###



SeriesID	Slice	Nodule	NoduleID
1.3.6.1.4.1.9328.50.3.272	289	1	4026
1.3.6.1.4.1.9328.50.3.272	290	1	4026
1.3.6.1.4.1.9328.50.3.272	311	2	4009
1.3.6.1.4.1.9328.50.3.272	312	2	4009
1.3.6.1.4.1.9328.50.3.272	289	1	2593
1.3.6.1.4.1.9328.50.3.272	290	1	2593
1.3.6.1.4.1.9328.50.3.272	291	1	2593
1.3.6.1.4.1.9328.50.3.378	438	3	001
1.3.6.1.4.1.9328.50.3.378	437	3	001
1.3.6.1.4.1.9328.50.3.378	436	3	001
1.3.6.1.4.1.9328.50.3.378	434	3	001
1.3.6.1.4.1.9328.50.3.378	436	3	4064
1.3.6.1.4.1.9328.50.3.378	437	3	4064
1.3.6.1.4.1.9328.50.3.378	438	3	4064
1.3.6.1.4.1.9328.50.3.378	436	3	3096

Distance Measure

Haralick: Gabor: Markov:

Euclidean

Restrict Results

Top 10 items

0 result(s)

Precision:

Recall:

Distance:

Choose an image feature & a similarity measure

SeriesID	Slice	Nodule	NoduleID	Distance	Score
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M. Lam, T. Disney, M. Pham, D. Raicu, J. Furst, "Content-Based Image Retrieval for Pulmonary Computed Tomography Nodule Images", SPIE Medical Imaging Conference, San Diego, CA, February 2007



1.3.6.1.4.1.9328.50.3.648

Slice #: 837
 Nodule #: 9
 NoduleID: 4116

-- HARALICK DESCRIPTORS --
 Contrast: 6.583e3
 [*] Correlation: 0.0672
 Energy: 0.0026
 Homogeneity: 0.0292
 [*] Entropy: 5.6123
 3rd Order Moment: -1.154e5
 Inverse Variance: 0.0101
 Sum Average: 189.7917
 Variance: 8.731e3
 Cluster Tendency: 1.869e4
 Maximum Probability: 0.0032

-- PHYSICIAN ANNOTATIONS --
 Calcification: #####
 Internal Structure: #
 Lobulation: #
 Malignancy: #####
 Margin: #
 Sphericity: ##
 Spiculation: ##
 Subtlety: #####
 Texture: ####

SeriesID	Slice	Nodule	NoduleID
1.3.6.1.4.1.9328.50.3.648	694	8	4112
1.3.6.1.4.1.9328.50.3.648	705	8	4112
1.3.6.1.4.1.9328.50.3.648	716	8	4112
1.3.6.1.4.1.9328.50.3.648	727	8	4112
1.3.6.1.4.1.9328.50.3.648	738	8	4112
1.3.6.1.4.1.9328.50.3.648	749	8	4112
1.3.6.1.4.1.9328.50.3.648	761	8	4112
1.3.6.1.4.1.9328.50.3.648	783	9	4116
1.3.6.1.4.1.9328.50.3.648	794	9	4116
1.3.6.1.4.1.9328.50.3.648	805	9	4116
1.3.6.1.4.1.9328.50.3.648	816	9	4116
1.3.6.1.4.1.9328.50.3.648	827	9	4116
1.3.6.1.4.1.9328.50.3.648	837	9	4116
1.3.6.1.4.1.9328.50.3.648	838	9	4116
1.3.6.1.4.1.9328.50.3.648	839	9	4116



1.3.6.1.4.1.9328.50.3.648

Slice #: 827
 Nodule #: 9
 NoduleID: 4116

-- HARALICK DESCRIPTORS --
 Contrast: 5.282e3
 [*] Correlation: 0.074
 Energy: 0.003
 Homogeneity: 0.0288
 [*] Entropy: 5.5241
 3rd Order Moment: 7.396e4
 Inverse Variance: 0.0106
 Sum Average: 166.6416
 Variance: 7.426e3
 Cluster Tendency: 1.593e4
 Maximum Probability: 0.003

-- PHYSICIAN ANNOTATIONS --
 Calcification: #####
 Internal Structure: #
 Lobulation: #
 Malignancy: #####
 Margin: #
 Sphericity: ##
 Spiculation: ##
 Subtlety: #####
 Texture: ####

Distance Measure

Haralick: Gabor:
 Euclidean Chi-Square (H)
 Choose Vector ...

Markov:
 Chi-Square (H)

Run Query

10 result(s)

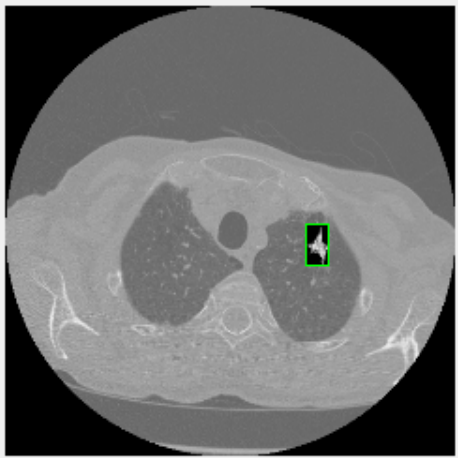
Precision: **0.1000**
 Recall: **0.0556**

Restrict Results

Top 10 items

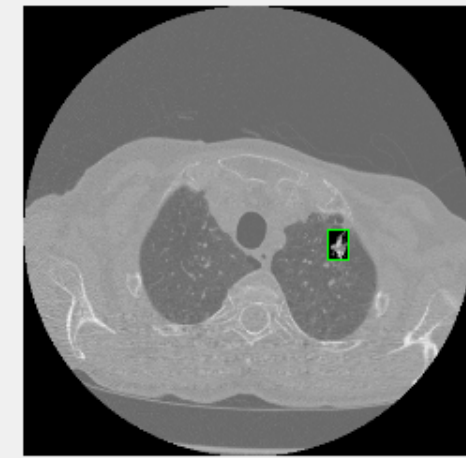
Analyze

Distance: **0.0133**



SeriesID	Slice	Nodule	NoduleID	Distance	Score
1.3.6.1.4.1.9328.50.3.6761	6775	69	2	0.00715...	1
1.3.6.1.4.1.9328.50.3.6761	6826	71	3	0.01270...	1
1.3.6.1.4.1.9328.50.3.648	827	9	4116	0.01326...	0
1.3.6.1.4.1.9328.50.3.6761	6820	71	3	0.02143...	1
1.3.6.1.4.1.9328.50.3.6761	6827	71	3	0.02167...	1
1.3.6.1.4.1.9328.50.3.6761	6821	71	3	0.02359...	1
1.3.6.1.4.1.9328.50.3.648	838	12	2677	0.03127...	2
1.3.6.1.4.1.9328.50.3.6761	6831	71	5175	0.03272...	0
1.3.6.1.4.1.9328.50.3.6761	6823	71	3	0.03279...	1
1.3.6.1.4.1.9328.50.3.6873	6863	74	1074	0.03474...	1

Retrieved Images



Grid Computing Opportunities



Challenges and Grid Opportunities:

- **Compute time:** Given the image retrieval system, four different layers can be identified that offer potential for parallelization:
 - Queries tend to be mutually independent. Thus, several queries can be processed in parallel. This is of interest, if several users access the system at the same time or if several queries are run in batch mode.
 - The distances from the queries to the database images can be calculated in parallel as the database images are independent from each other.
 - Parallelization is possible on the feature level, because the distances for the individual features can be calculated in parallel.
 - Multiple combinations of feature spaces and similarity metrics can be run in parallel to determine the best retrieval results
 - $2047 \text{ vectors} * 3 \text{ similarity measures} * 5 \text{ number of retrieved images} = 30,705$ combinations

Solutions?



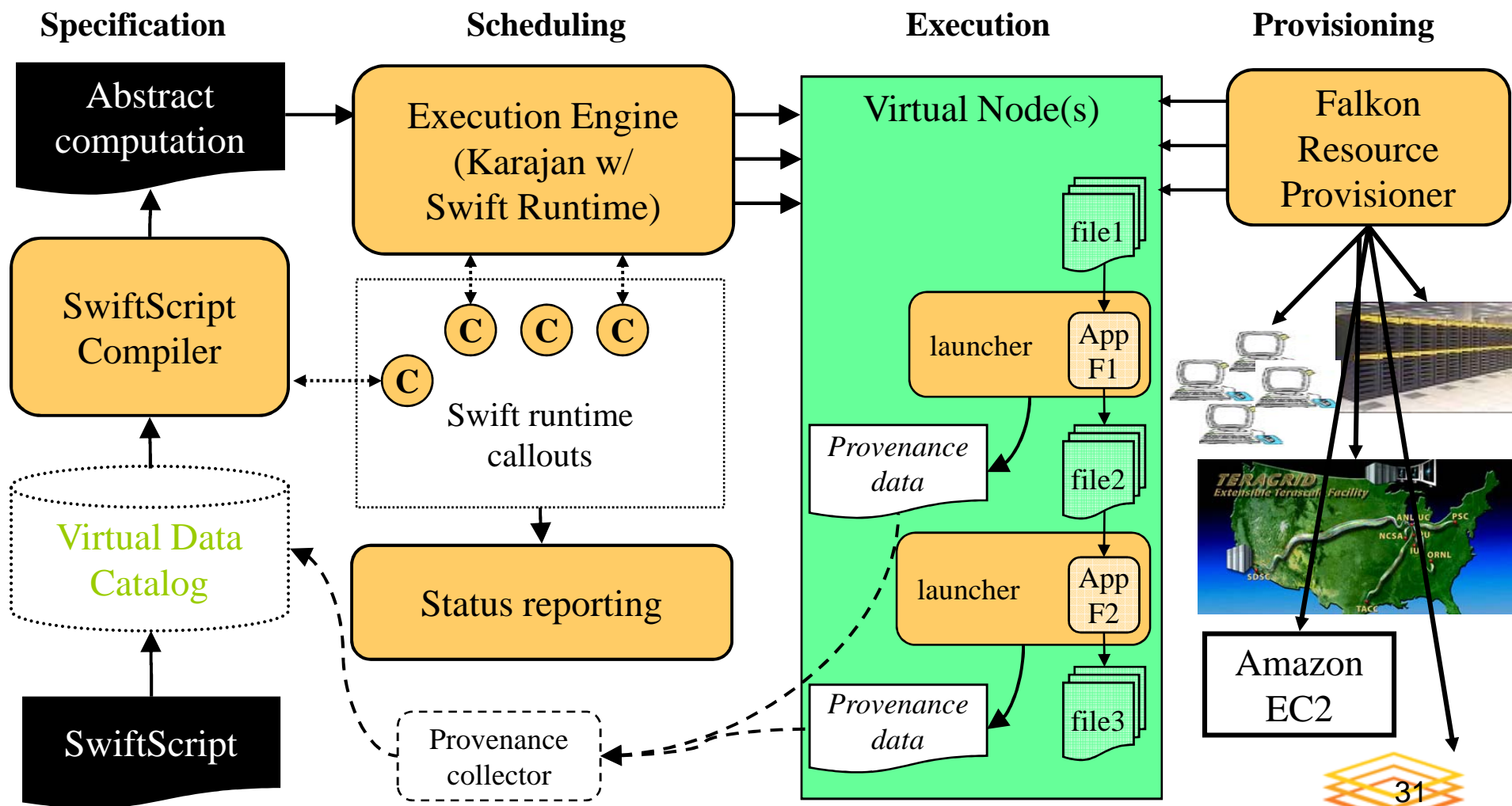
Workflows?

Existing and emerging workflow technologies

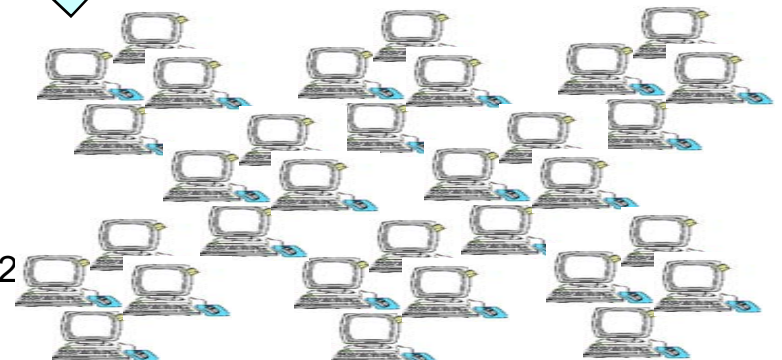
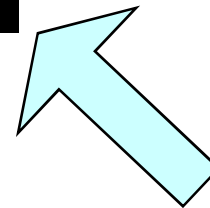
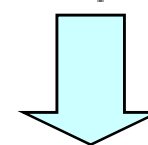
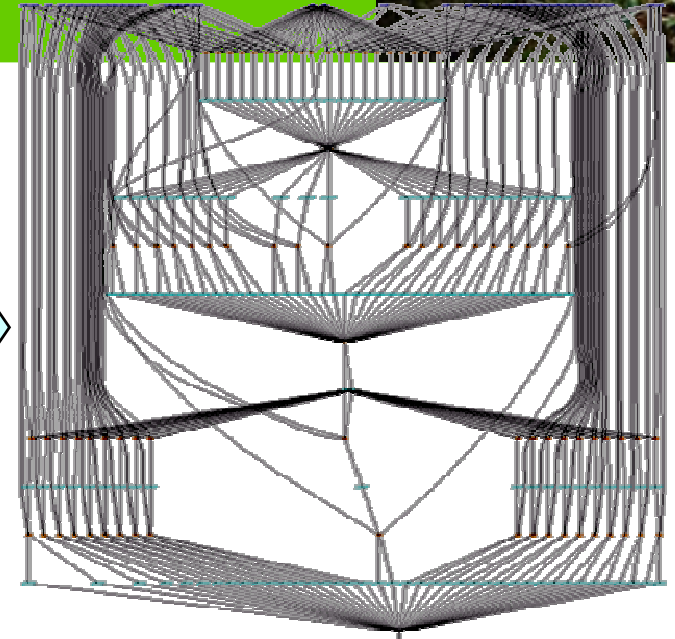
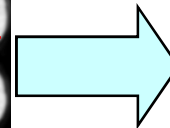
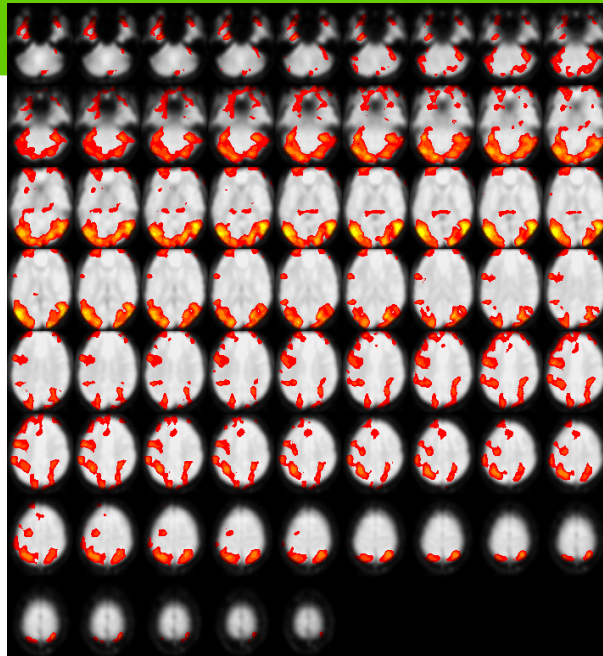
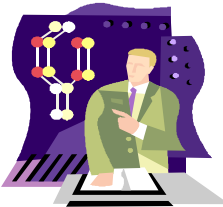


	Star-P	Mapreduce	Kepler	Triana	Tavena	DAGMan	MS Workflow Fundation	XPDL	BPDL	Swift
Scales to Grids	+	+	-	-	-	++	-	-	-	++
Typing	+	-	+	-	-	-	++	++	++	++
Iteration	+	+	+	-	-	-	+	-	-/+	++
Scripting	++	-	-	-	+	+	+	-	-	++
Dataset Mapping	-	-	-	-	-	-	-	-	-	+
Service Interop	-	-	+	-	-	-	-	+	-	+
Subflow/comp.	+	-	+	+	-	-	+	+	-	+
Provenance	-	-	+	-	+	-	+	-	-	+
Open source	-	-	+	+	+	+	-	+	+	+

Swift Architecture



Functional MRI (fMRI)



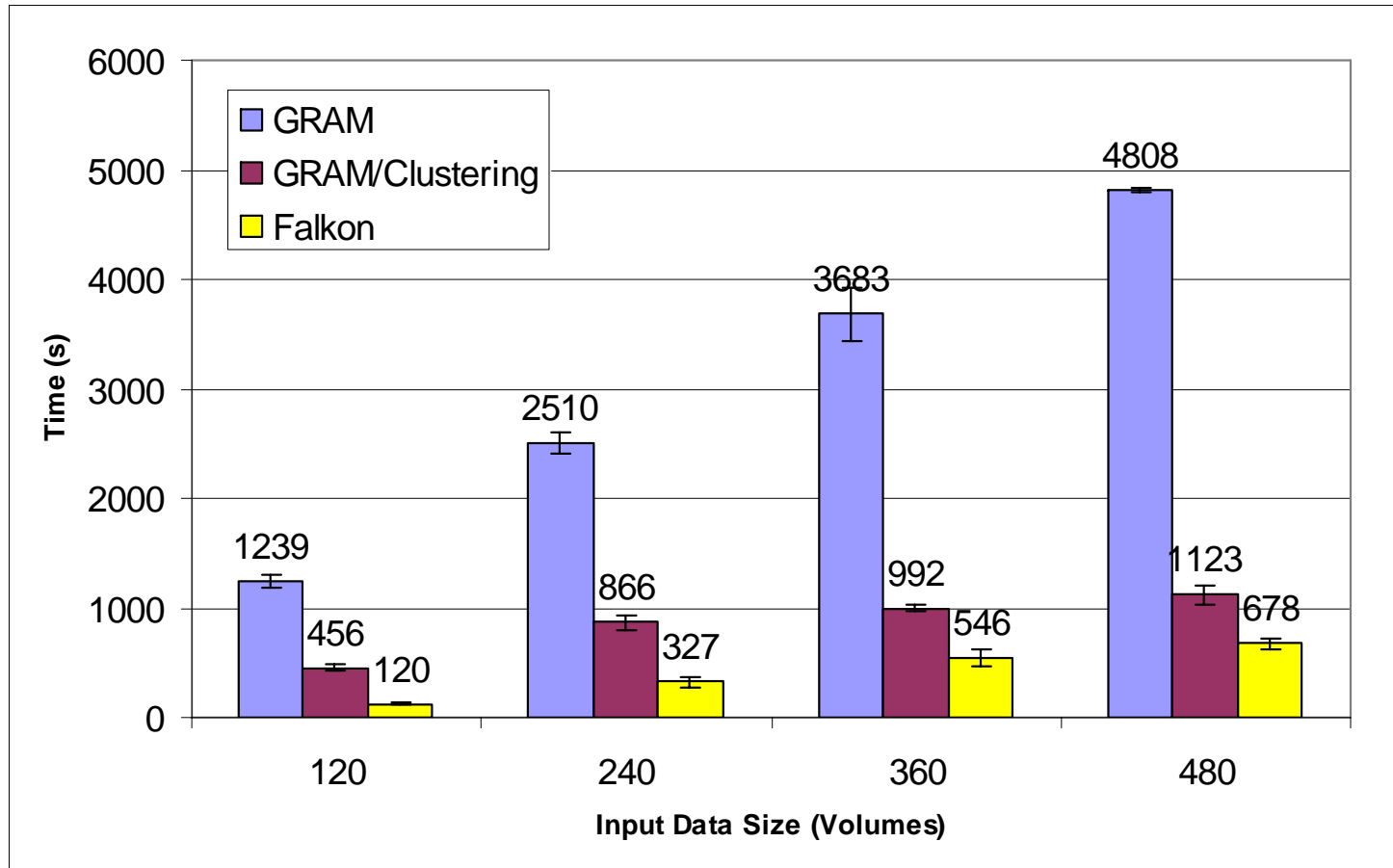
ems for 2

- Wide range of analyses
 - Testing, interactive analysis, production runs
 - Data mining
 - Parameter studies

Completed Milestones: fMRI Application



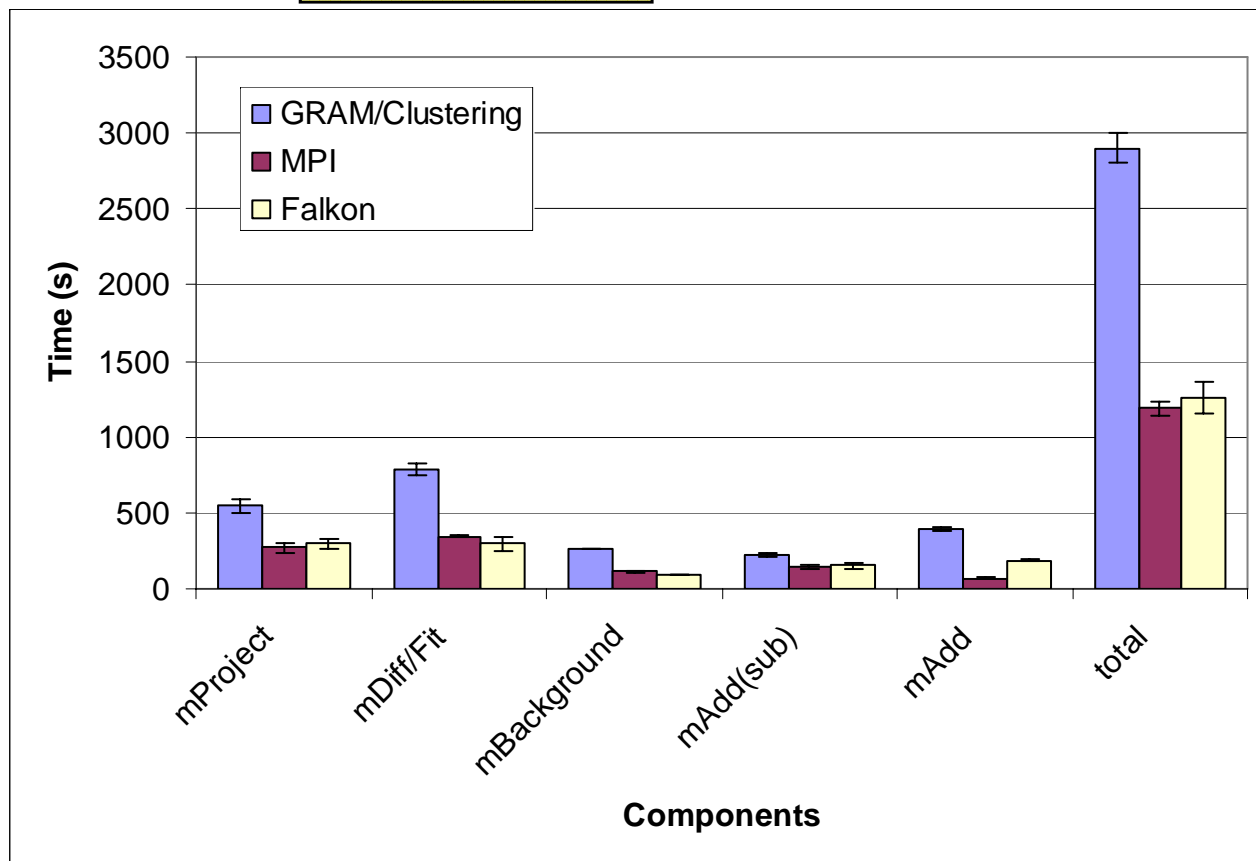
- GRAM vs. Falcon: 85%~90% lower run time
- GRAM/Clustering vs. Falcon: 40%~74% lower run time



Completed Milestones: Montage Application



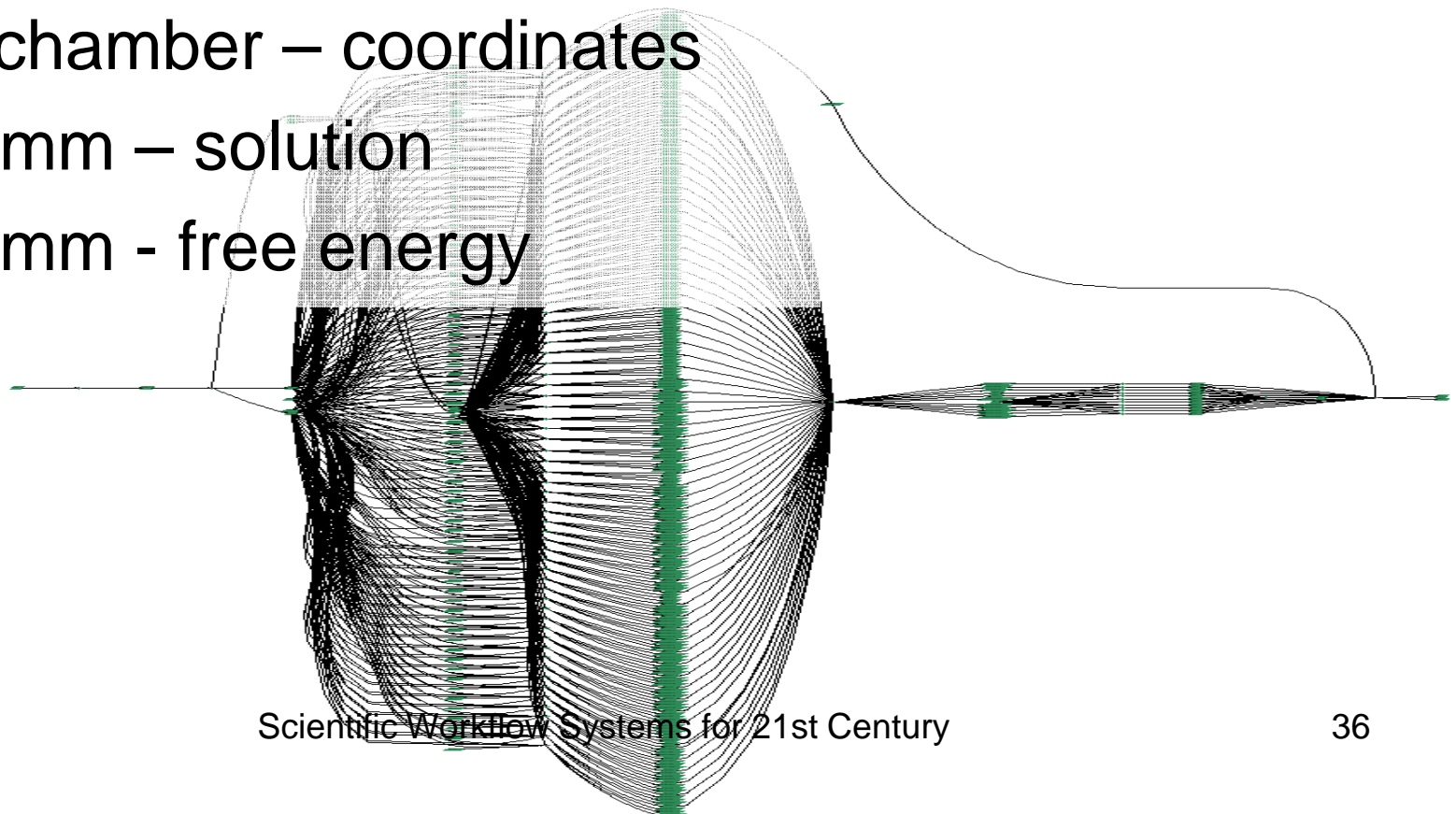
- GRAM/Clustering vs. Falcon: **57%** lower application run time
- MPI* vs. Falcon: **4%** higher application run time
- * MPI should be **lower bound**



Molecular Dynamics

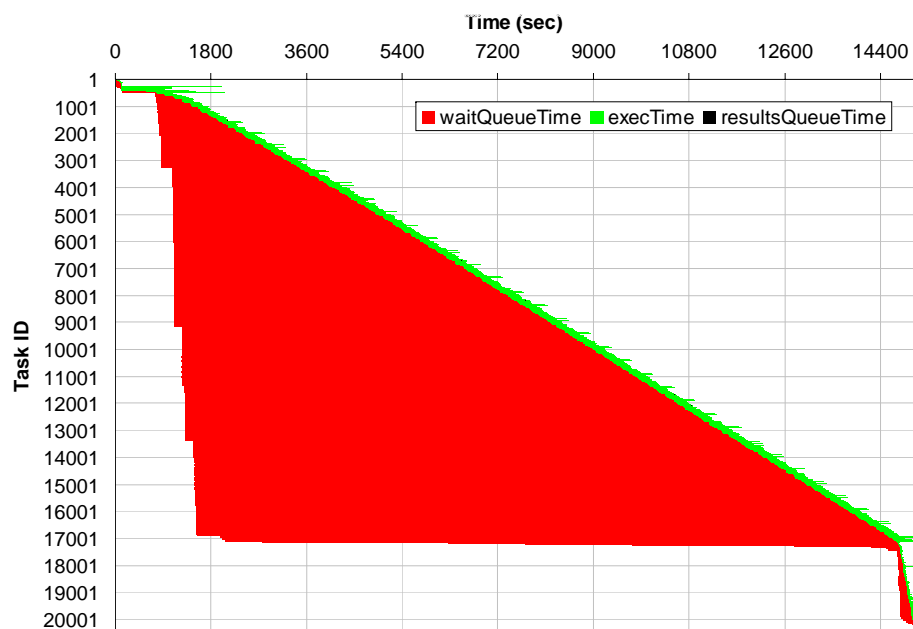


- Determination of free energies in aqueous solution
 - Antechamber – coordinates
 - Charmm – solution
 - Charmm - free energy

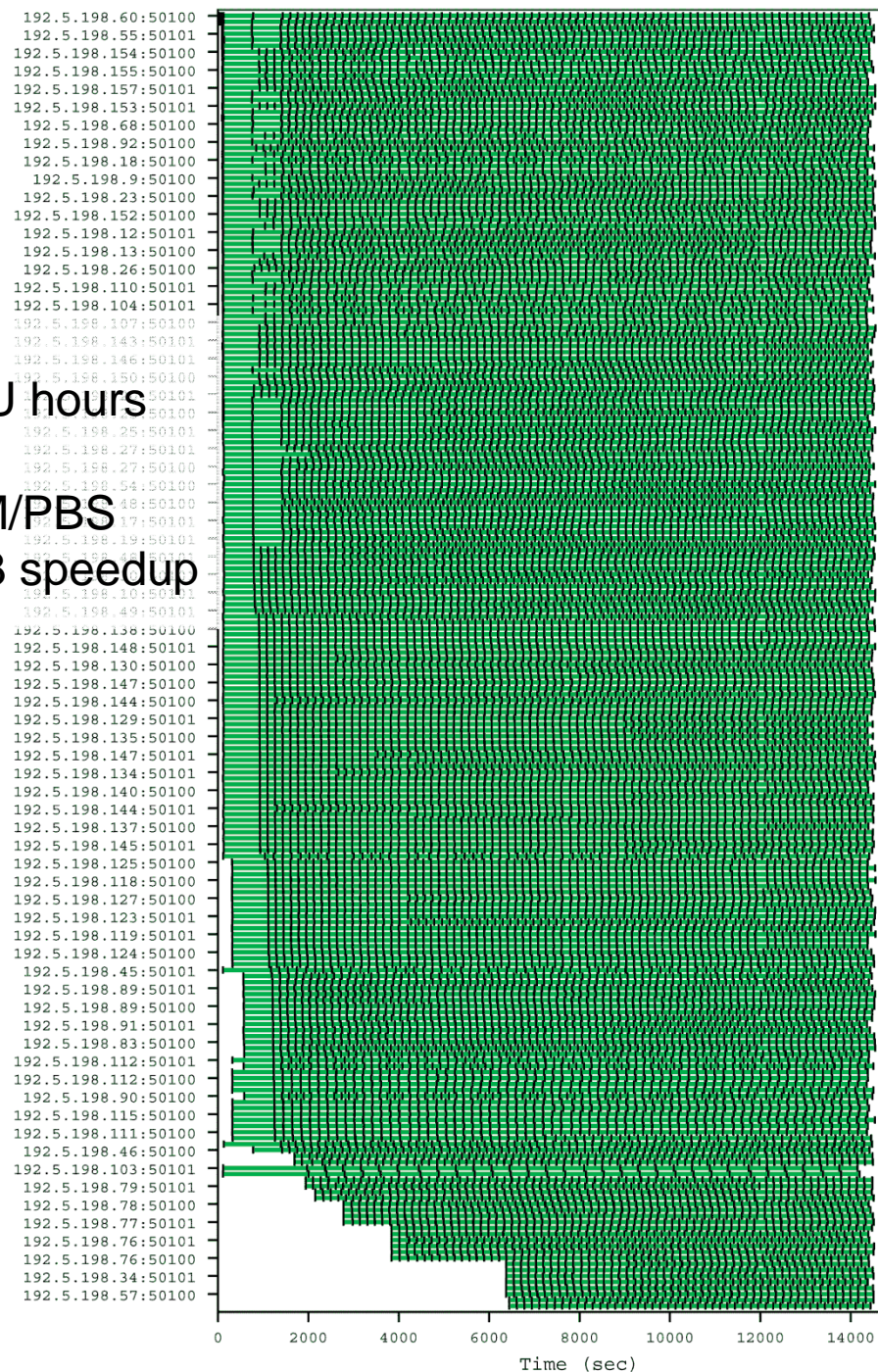


MolDyn Application

- 244 molecules \rightarrow 20497 jobs
- 15091 seconds on 216 CPUs \rightarrow 867.1 CPU hours
- Efficiency: **99.8%**
- Speedup: 206.9x \rightarrow 8.2x faster than GRAM/PBS
- 50 molecules w/ GRAM (4201 jobs) \rightarrow 25.3 speedup



Scientific Workflow Sys

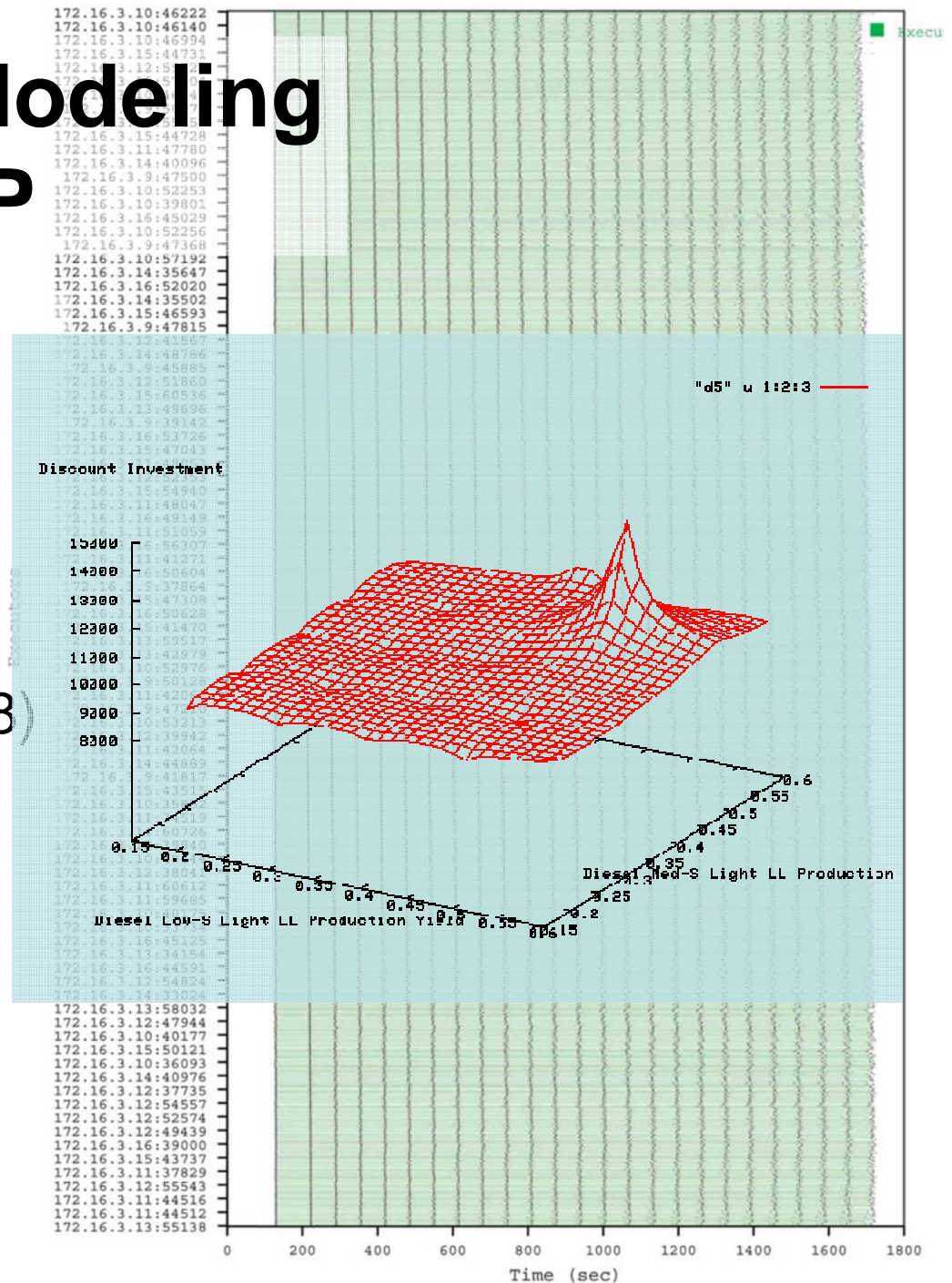


MARS Economic Modeling on IBM BG/P

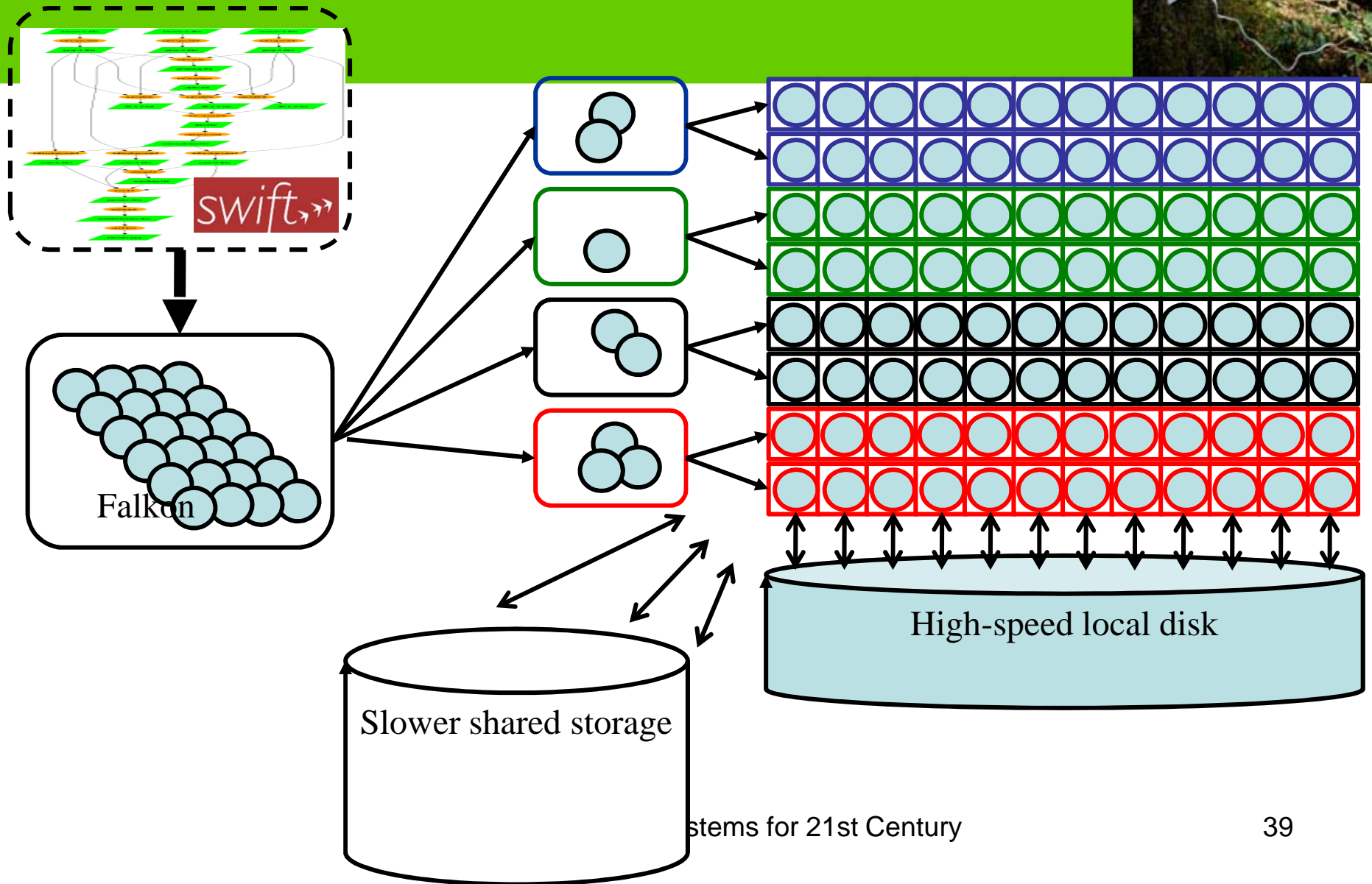
- CPU Cores: 2048
- Tasks: 49152
- Micro-tasks: 7077888
- Elapsed time: 1601 secs
- CPU Hours: 894
- Speedup: 1993X (ideal 2048)
- Efficiency: 97.3%



ic Workf



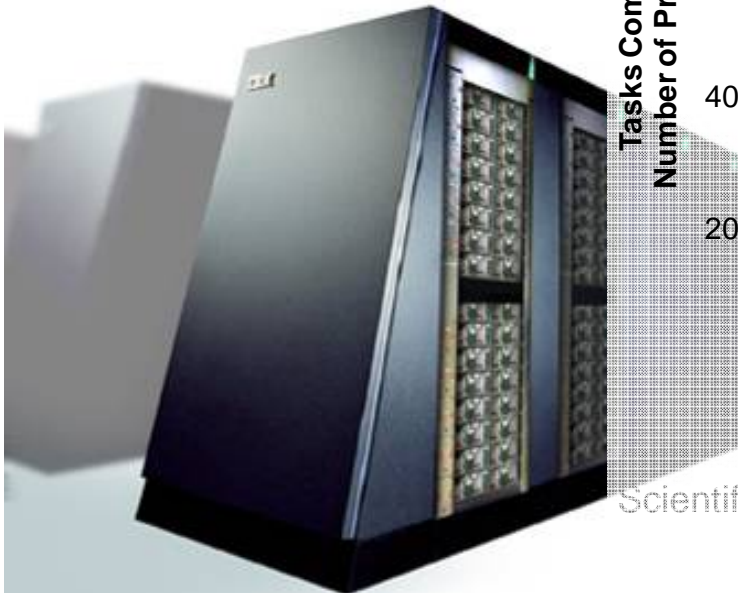
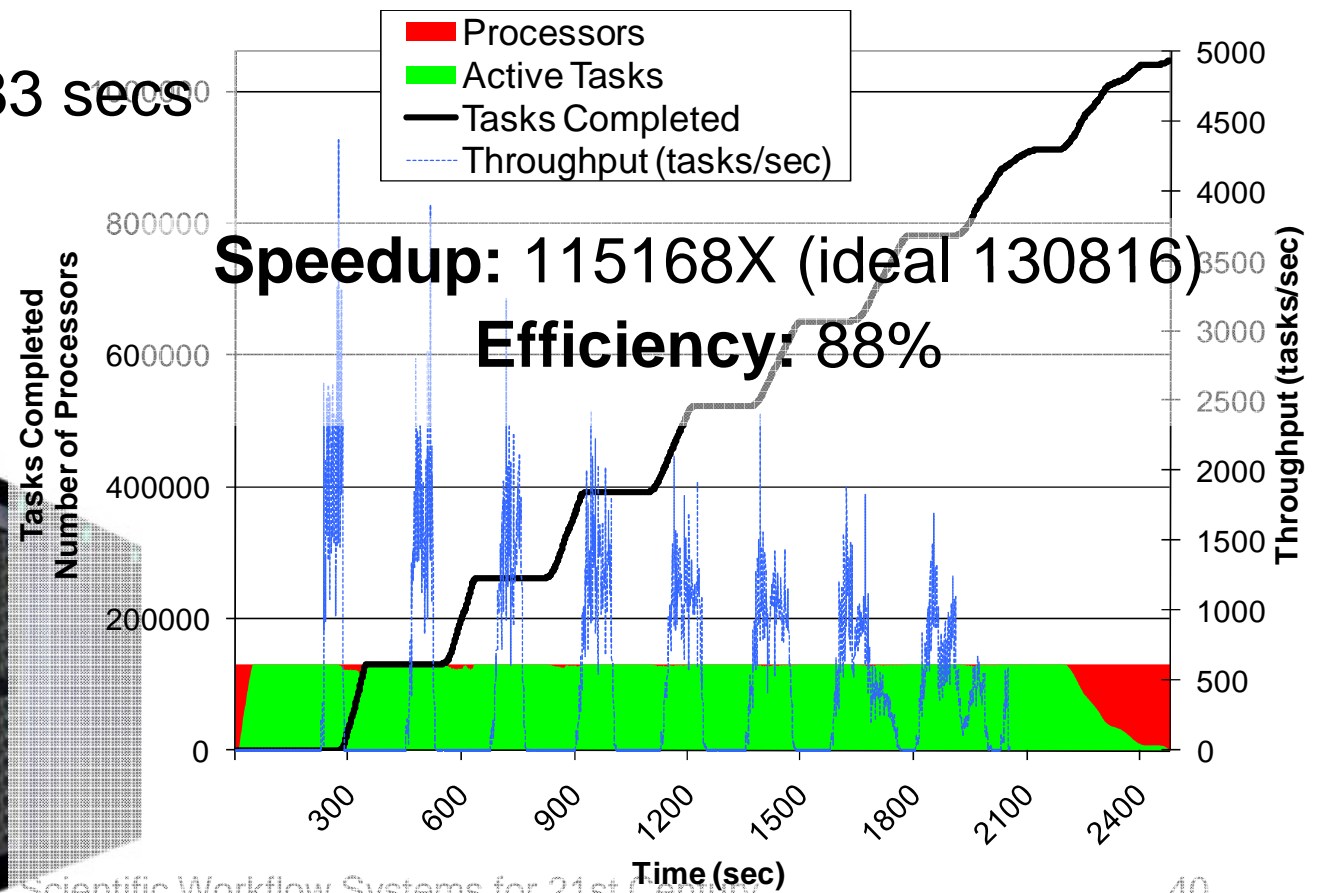
Managing 120K CPUs



MARS Economic Modeling on IBM BG/P (128K CPUs)



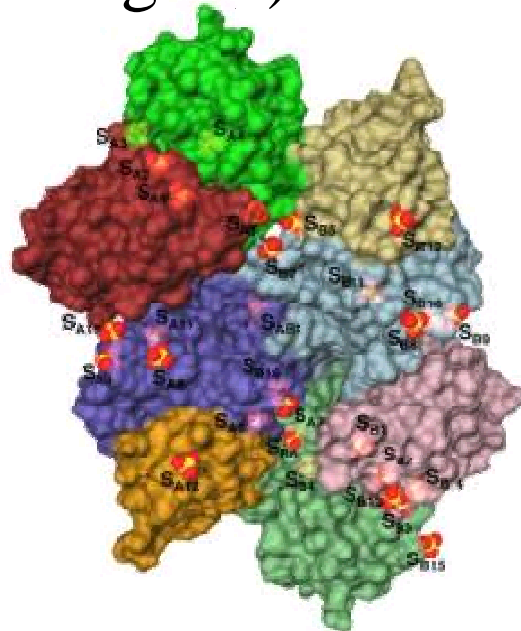
- CPU Cores: 130816
- Tasks: 1048576
- Elapsed time: 2483 secs
- CPU Years: 9.3



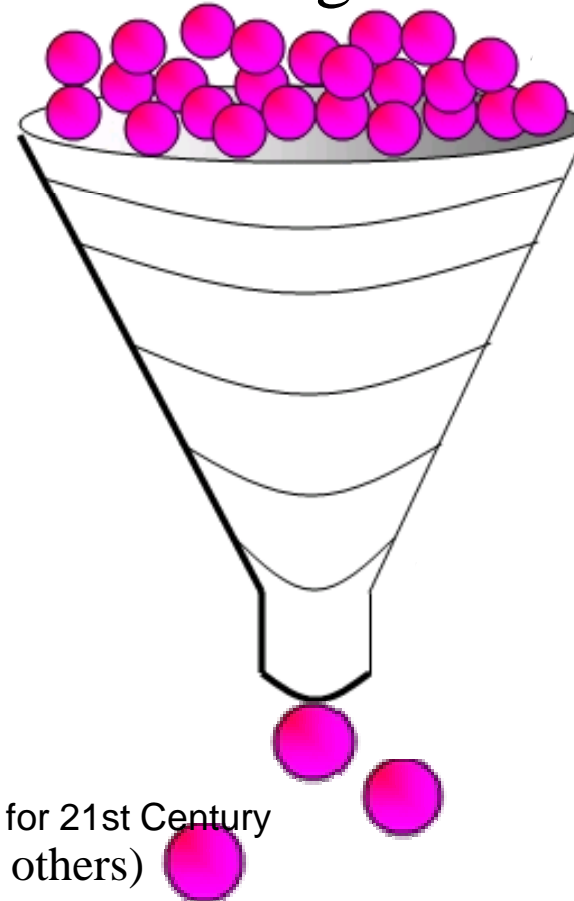
Many Many Tasks: Identifying Potential Drug Targets



Protein
target(s) x

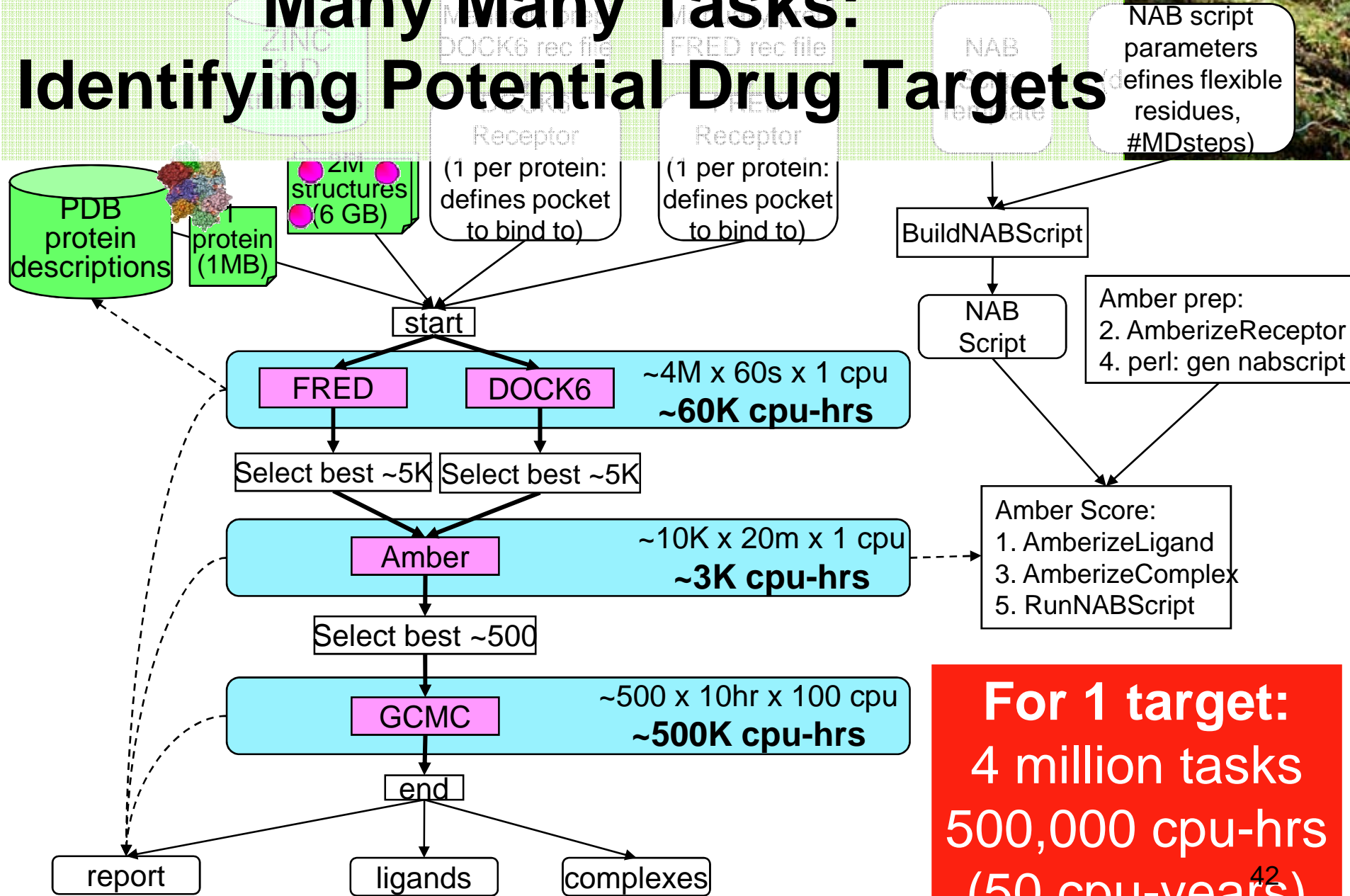


2M+ ligands



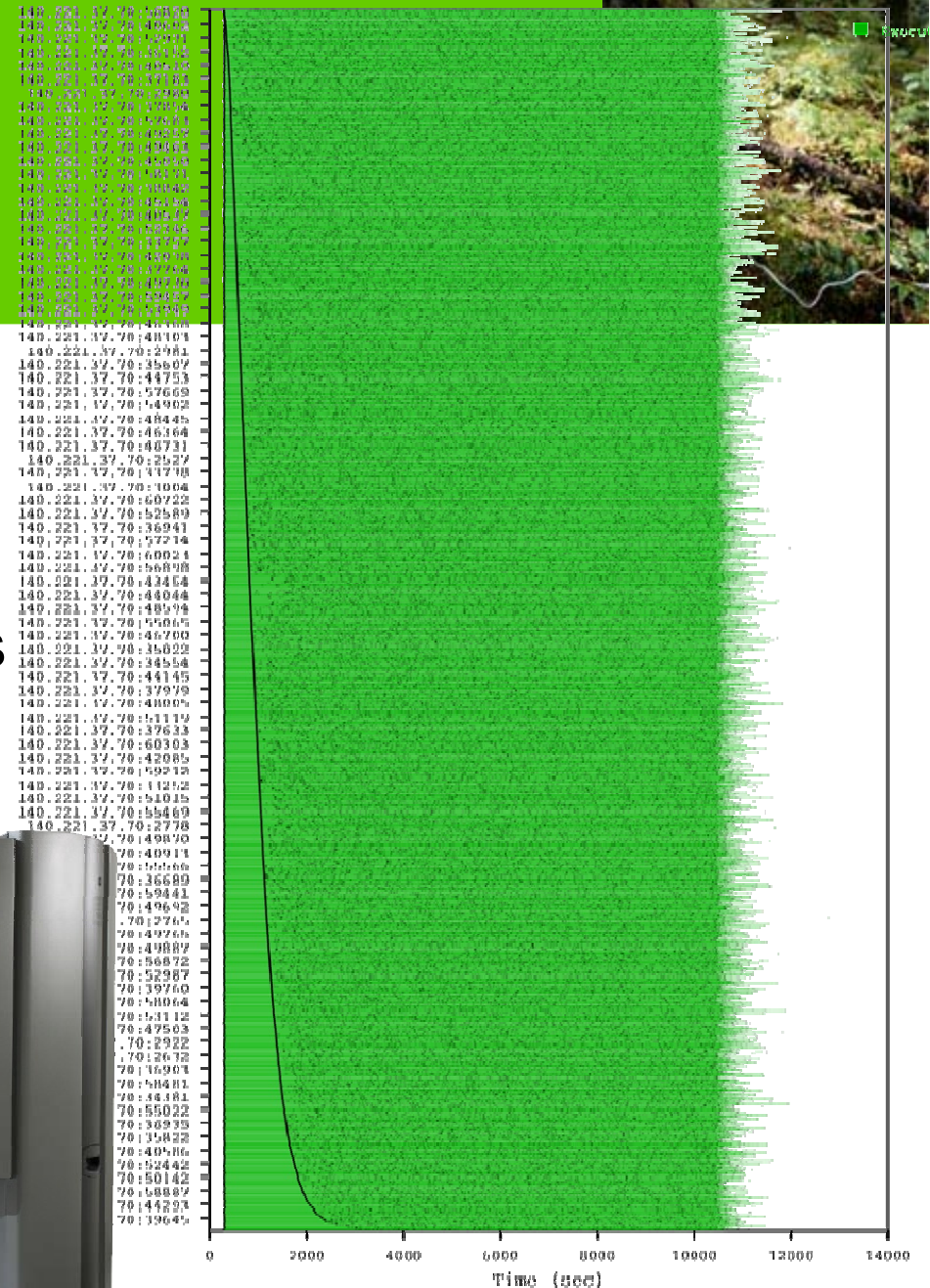
Scientific Workflow Systems for 21st Century
(Mike Kubal, Benoit Roux, and others)

Many Many Tasks: Identifying Potential Drug Targets



DOCK on SiCortex

- CPU cores: 5760
- Tasks: 92160
- Elapsed time: 12821 sec
- Compute time: 1.94 CPU years
- Average task time: 660.3 sec
- Speedup: 5650X (ideal 5760)
- Efficiency: 98.2%



Scalability for 21st Century

DOCK on the BG/P



CPU cores: 118784

Tasks: 934803

Elapsed time: 2.01 hours

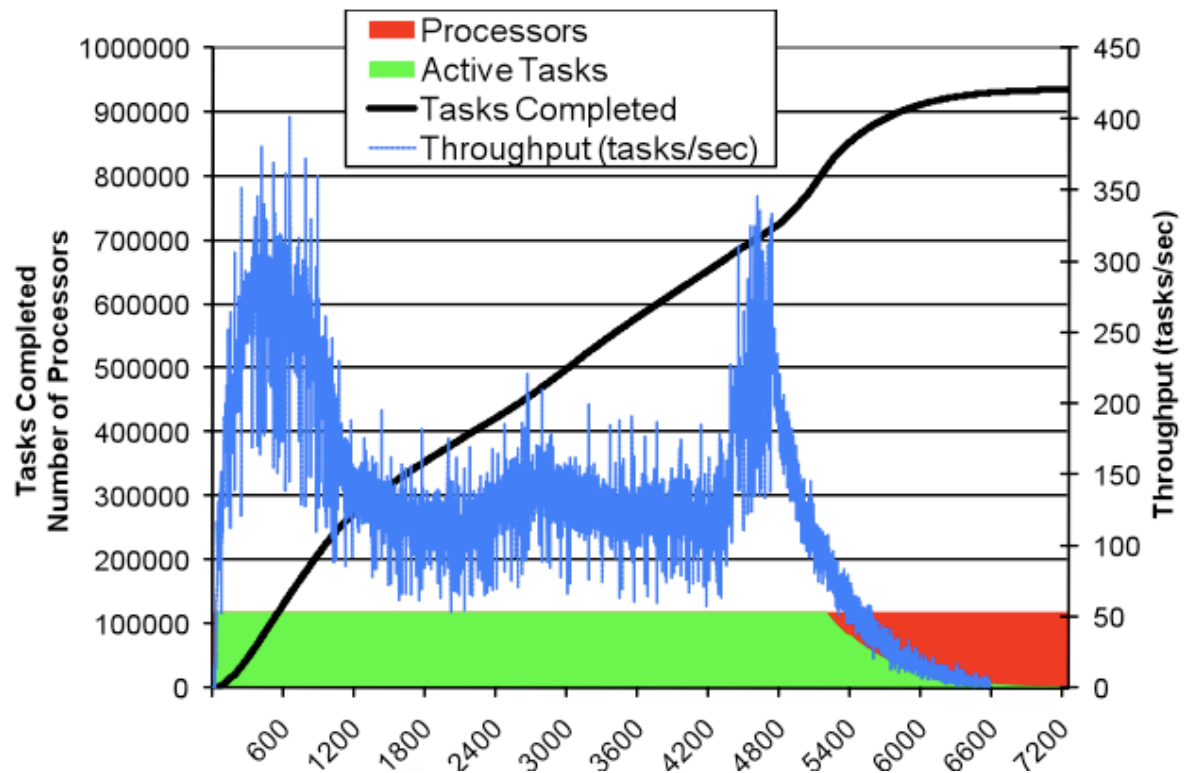
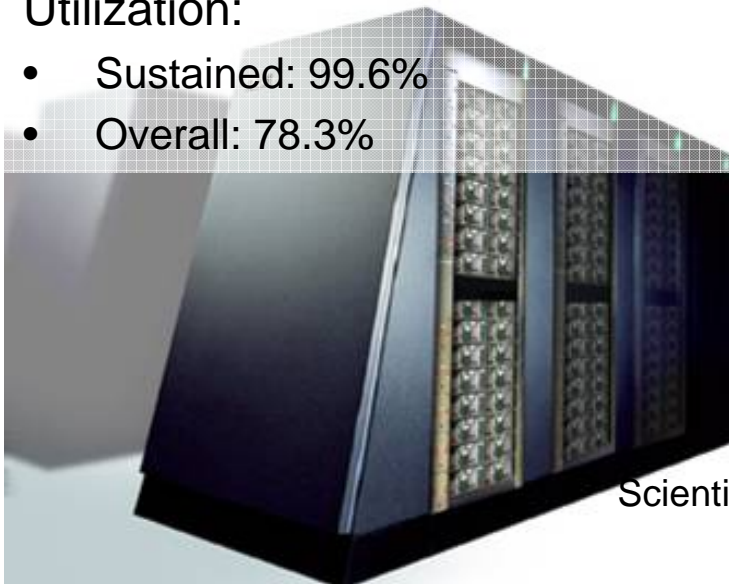
Compute time: 21.43 CPU years

Average task time: 667 sec

Relative Efficiency: 99.7%
(from 16 to 32 racks)

Utilization:

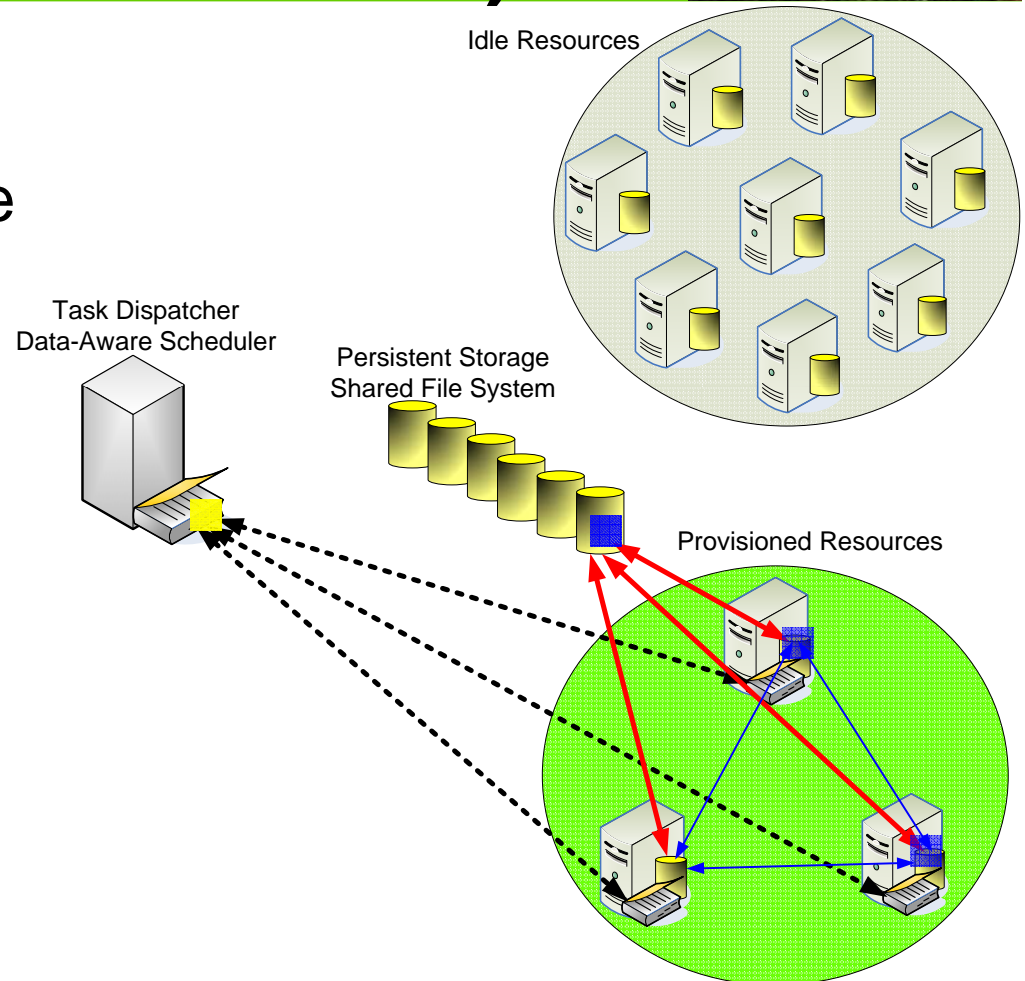
- Sustained: 99.6%
- Overall: 78.3%



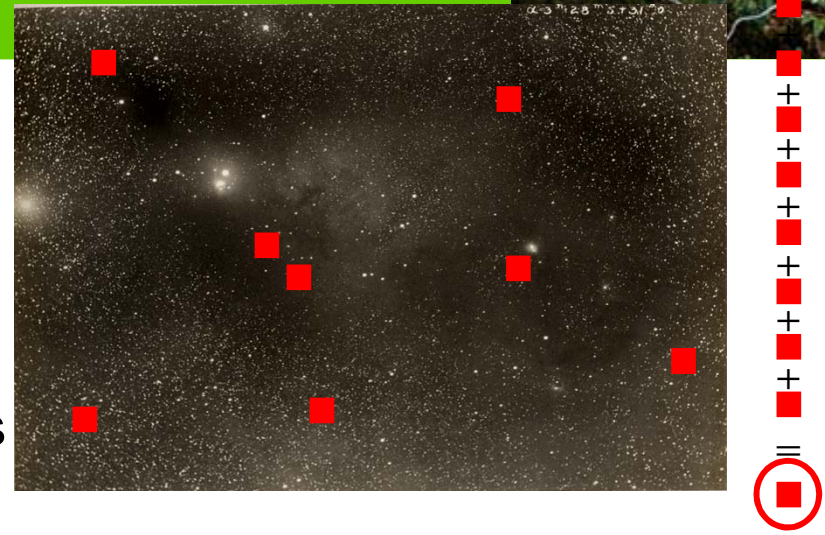
Support for Data Intensive Applications (Falkon and Data Diffusion)



- Resource acquired in response to demand
- Data and applications diffuse from archival storage to newly acquired resources
- Resource “caching” allows faster responses to subsequent requests
 - Cache Eviction Strategies: RANDOM, FIFO, LRU, LFU
- Resources are released when demand drops

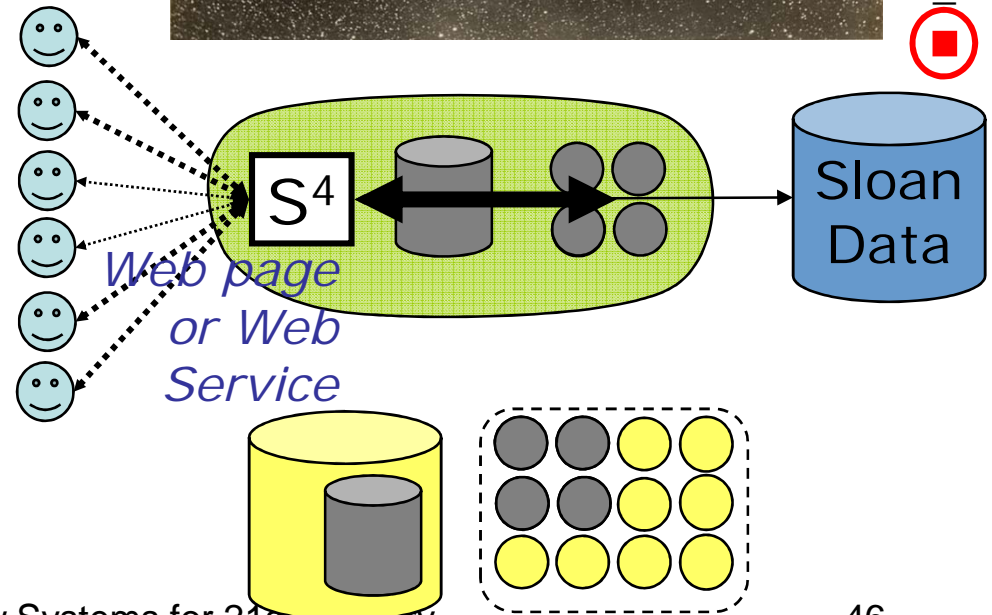


AstroPortal Stacking Service



- Purpose
 - On-demand “stacks” of random locations within ~10TB dataset
- Challenge
 - Rapid access to 10-10K “random” files
 - Time-varying load
- Sample Workloads

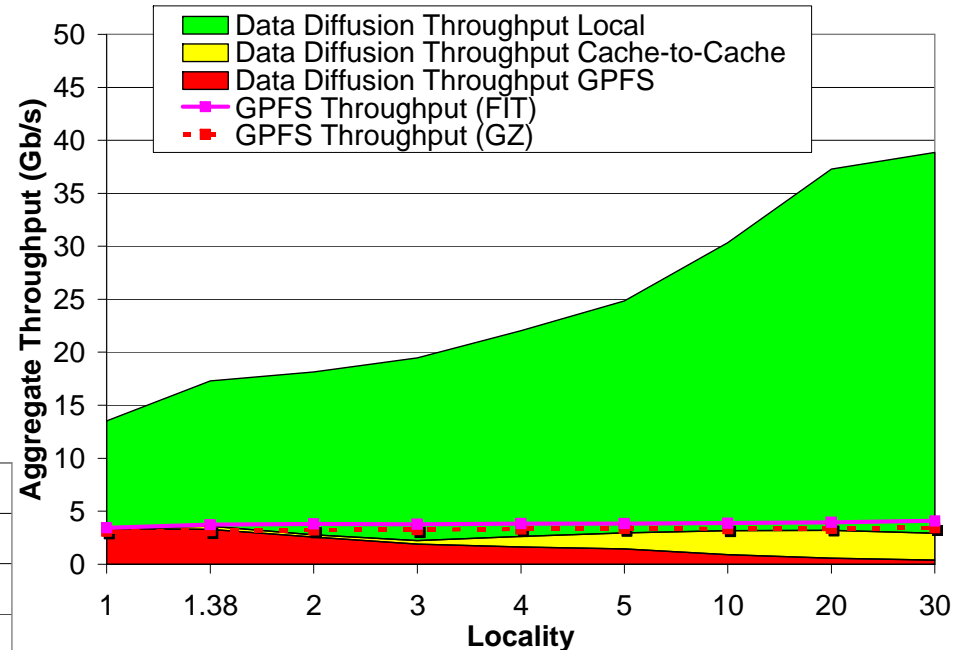
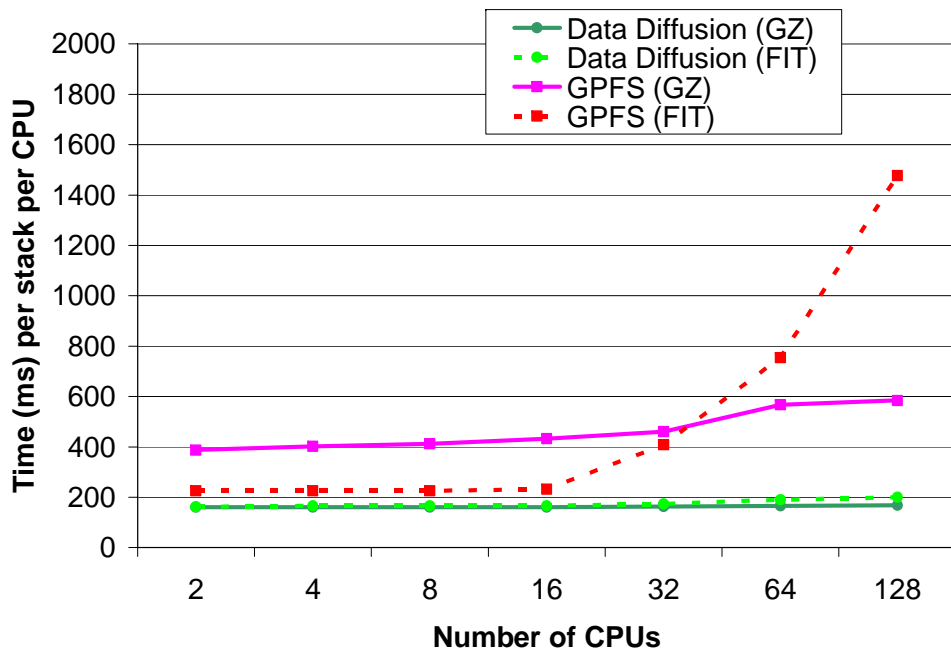
Locality	Number of Objects	Number of Files
1	111700	111700
1.38	154345	111699
2	97999	49000
3	88857	29620
4	76575	19145
5	60590	12120
10	46480	4650
20	40460	2025
30	23695	790



AstroPortal Stacking Service with Data Diffusion



- Aggregate throughput:
 - 39Gb/s
 - 10X higher than GPFS
- Reduced load on GPFS
 - 0.49Gb/s
 - 1/10 of the original load

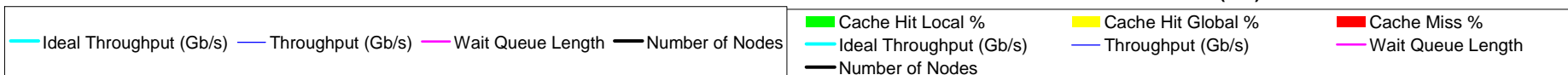
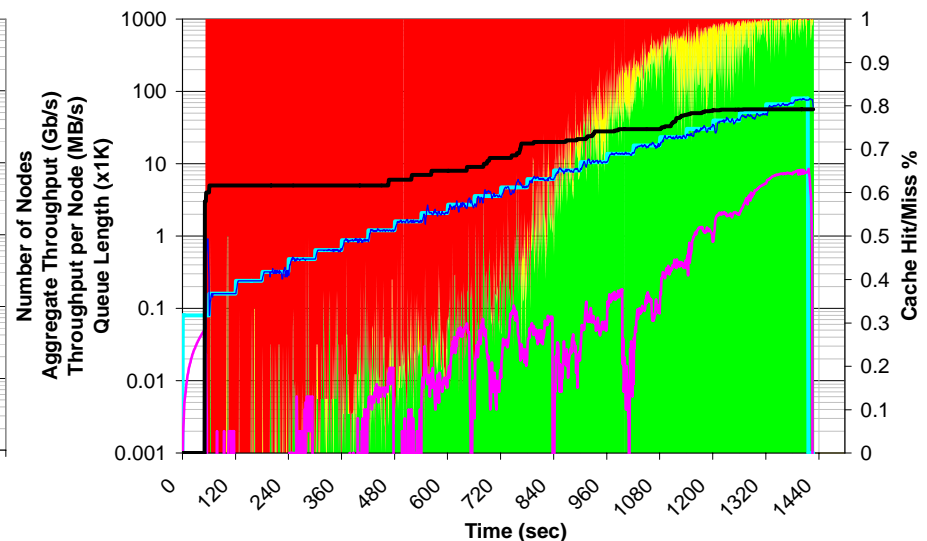
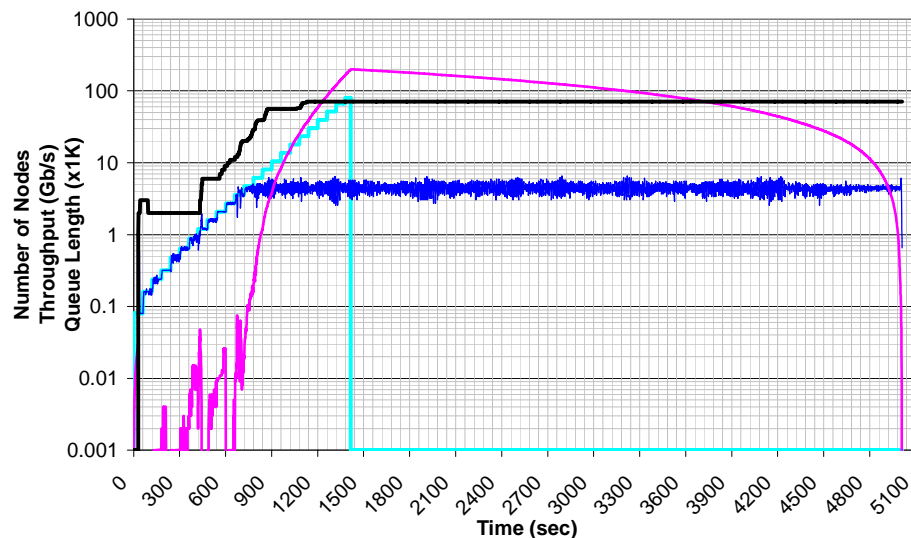


← High data locality
– Near perfect scalability

Data Diffusion: Data-Intensive Workload



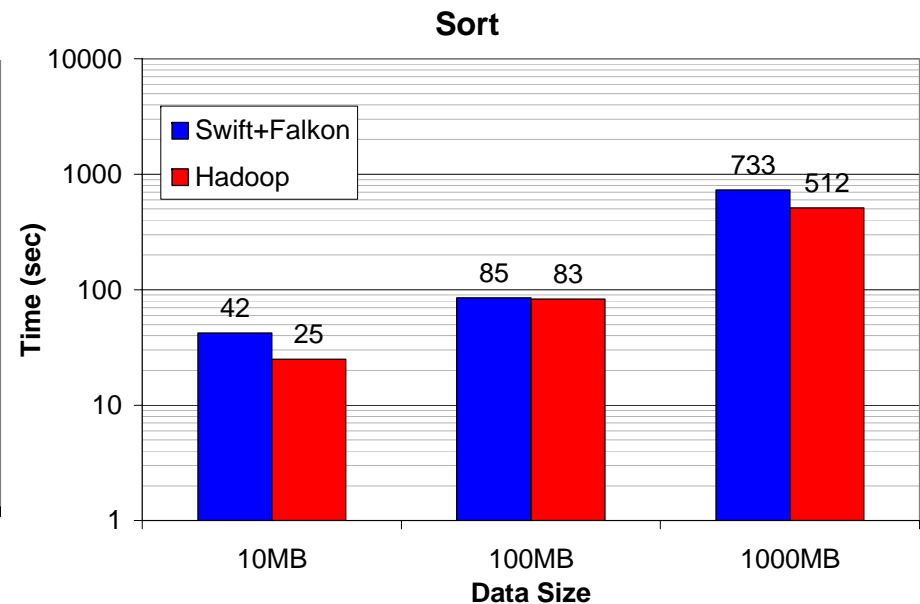
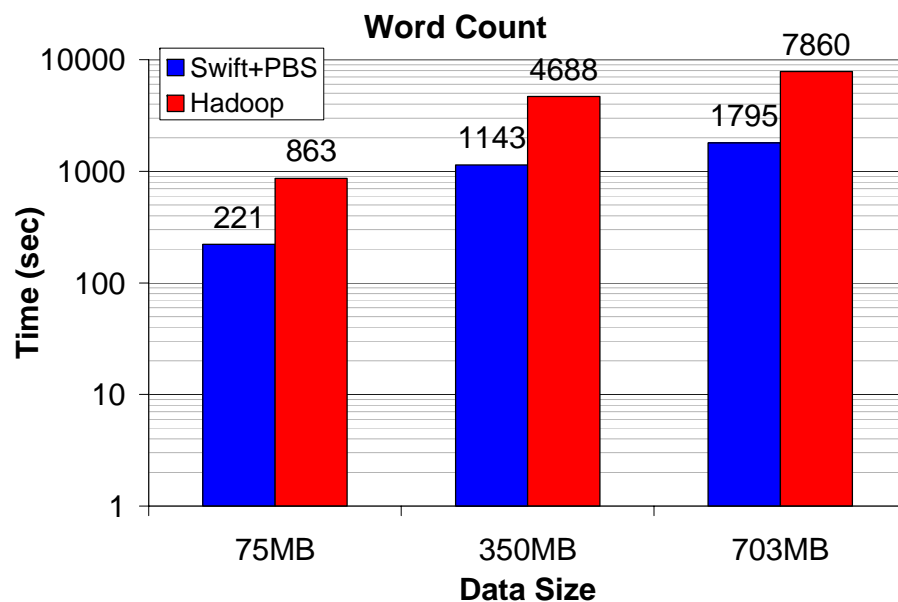
- 250K tasks on 128 processors
 - 10MB read, 10ms compute
- Comparing GPFS with data diffusion
 - 5011 sec vs. 1427 sec (ideal is 1415 sec)



Hadoop vs. Swift



- Classic benchmarks for MapReduce
 - Word Count
 - Sort
- Swift performs similar or better than Hadoop (on 32 processors)



Mythbusting



- ~~Embarrassingly~~ Happily parallel apps are trivial to run
 - Logistical problems can be tremendous
- Loosely coupled apps do not require “supercomputers”
 - Total computational requirements can be enormous
 - Individual tasks may be tightly coupled
 - Workloads frequently involve large amounts of I/O
 - Make use of idle resources from “supercomputers” via backfilling
 - Costs to run “supercomputers” per FLOP is among the best
 - BG/P: 0.35 gigaflops/watt (**higher is better**)
 - SiCortex: 0.32 gigaflops/watt
 - BG/L: 0.23 gigaflops/watt
 - x86-based HPC systems: an order of magnitude lower
- Loosely coupled apps do not require specialized system software
- Shared file systems are good for all applications
 - They don’t scale proportionally with the compute resources
 - Data intensive applications don’t perform and scale well

Features Scientific Workflow Systems should Have!



- **Parallelism**
 - Support for both explicit and implicit parallelism
- **Performance and Scalability**
 - Million to billions of tasks
 - Handle 100s~1000s of tasks/sec
- **Data management**
 - Reduce reliance on shared file systems
 - Scale with processing power
 - Data-aware scheduling
- **Reliability**
 - Self healing
 - Efficient and scalable monitoring
- **Provenance**

Solutions

(we have experience with)

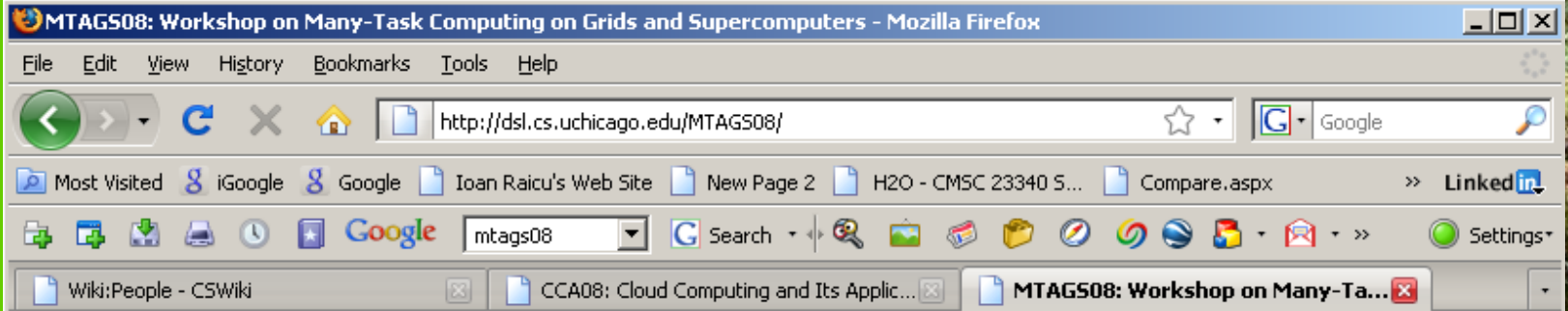


- **Falkon**
 - A Fast and Light-weight task executiON framework
 - Globus Incubator Project
 - <http://dev.globus.org/wiki/Incubator/Falkon>
- **Swift**
 - Parallel programming tool for rapid and reliable specification, execution, and management of large-scale science workflows
 - <http://www.ci.uchicago.edu/swift/index.php>
- **Environments:**
 - *Clusters*: TeraPort (TP)
 - *Grids*: Open Science Grid (OSG), TeraGrid (TG)
 - *Specialized large machines*: SiCortex 5732
 - *Supercomputers*: IBM BlueGene/P (BG/P)

More Information



- More information:
 - Personal research page: <http://people.cs.uchicago.edu/~iraicu/>
 - Falkon: <http://dev.globus.org/wiki/Incubator/Falkon>
 - Swift: <http://www.ci.uchicago.edu/swift/index.php>
- Collaborators:
 - Ian Foster, The University of Chicago & Argonne National Laboratory
 - Alex Szalay, The Johns Hopkins University
 - Rick Stevens, The University of Chicago & Argonne National Laboratory
 - Yong Zhao, Microsoft
 - Mike Wilde, Computation Institute, University of Chicago & Argonne National Laboratory
 - Catalin Dumitrescu, Fermi National Laboratory
 - Zhao Zhang, The University of Chicago
 - Jerry C. Yan, NASA, Ames Research Center
 - Kamil Iskra, Argonne National Laboratory
 - Pete Beckman, Argonne National Laboratory
 - Mihael Hategan, The University of Chicago
 - Ben Clifford, The University of Chicago
 - Veronika Nefedova, Argonne National Laboratory
 - Tiberiu Stef-Praun, The University of Chicago
 - Daniela Stan Raicu, DePaul University
 - Gabriela Turcu, The University of Chicago
 - Atilla S. Balkir, The University of Chicago
 - Jing Tie, The University of Chicago
 - Quan T. Pham, The University of Chicago
 - Sarah Kenny, The University of Chicago
 - Gregor von Laszewski, Rochester Institute of Technology
 - Jim Gray, Microsoft Research
 - Julian Bunn, California Institute of Technology



MTAGS

Workshop on Many-Task Computing on Grids and Supercomputers

co-located with ACM/IEEE SC08 (International Conference for High Performance, Networking, Storage and Analysis)
Austin, Texas -- November 17th, 2008

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[Registration](#)

[Workshop Program](#)

Important Dates

Papers Due:	August 15th, 2008
Notification of Acceptance:	October 1st, 2008
Camera Ready Papers Due:	October 15th, 2008
Workshop Date:	November 17th, 2008

Committee Members

Workshop Chairs

Yong Zhao, Microsoft
Ian Foster, University of Chicago & Argonne National Laboratory
Ioan Raicu, University of Chicago

Technical Committee

Ian Foster, University of Chicago & Argonne National Laboratory
Dan Ardelean, Google
Bob Grossman, University of Illinois at Chicago
Indranil Gupta, University of Illinois at Urbana Champaign
Tevfik Kosar, Louisiana State University

Handling Megajobs BOF at SC08



- More and more people need to run thousands to millions of closely related jobs that are associated with individual projects. Scientists seek convenient means to specify and manage many jobs, arranging inputs, aggregating outputs, identifying successful and failed jobs and repairing failures. System administrators seek methods to process extraordinary numbers of jobs for multiple users without overwhelming queuing systems or disrupting fair-share usage policies. And, grid developers are producing a new generation of queuing and scheduling systems as well as auxiliary systems for use with existing queuing and scheduling systems. This Birds-of-feather session provides a venue for the exchange of information about processing large numbers of jobs. Short presentations of an invited sample of projects will be followed by discussion.
- For more information, contact:
 - Marlon Pierce: mpierce@cs.indiana.edu
 - Dick Repasky: rrepasky@indiana.edu
 - Ioan Raicu: iraicu@cs.uchicago.edu