

Community Resources for Enabling Research in Distributed Scientific Workflows

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Information Sciences Institute

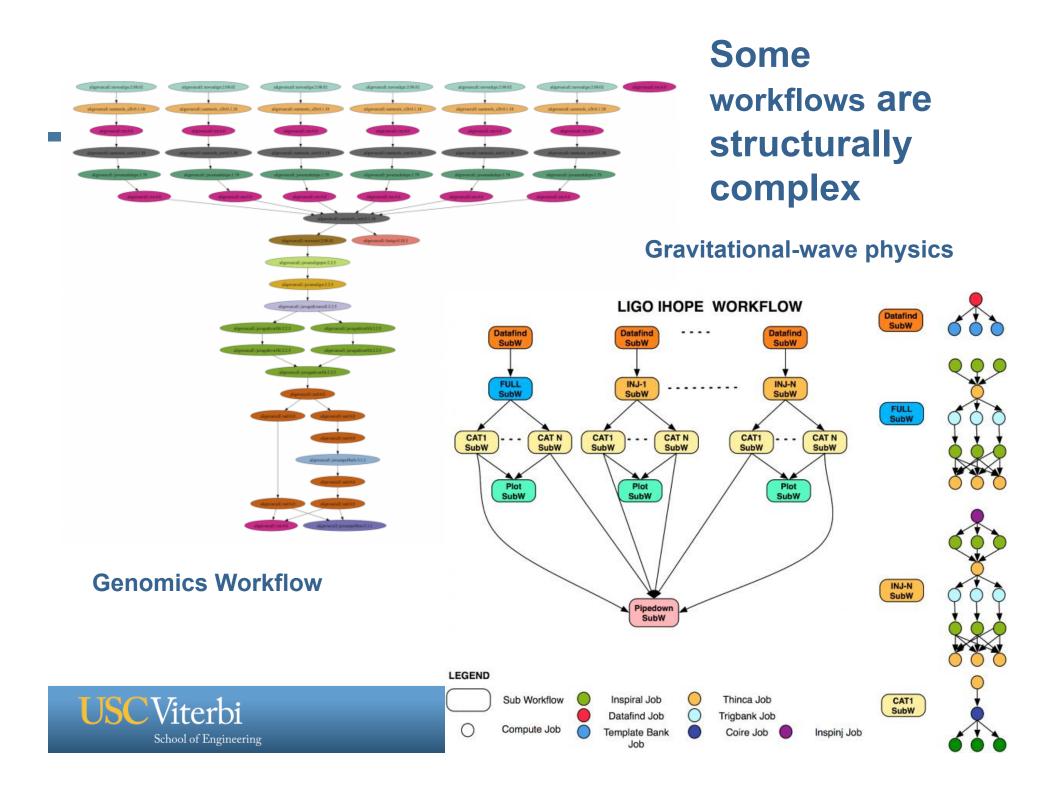
Community Resources for Enabling Scientific Workflow Research

- Execution traces
- Synthetic workflow generator
- Workflow execution simulator

www.workflowarchive.org

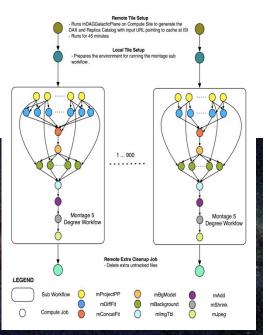






Some workflows are large-scale and data-intensive

Montage Galactic Plane Workflow



John Good (Caltech)

× 17

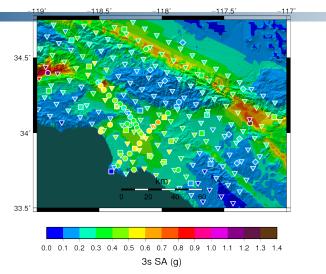
- Montage Galactic Plane Workflow
 - 18 million input images (~2.5 TB)
 - 900 output images (2.5 GB each, 2.4 TB total)
 - 10.5 million tasks (34,000 CPU hours)

Need to support hierarchical workflows and scale, workflow ensembles





Southern California Earthquake Center, T. Jordan, USC



239 Workflows

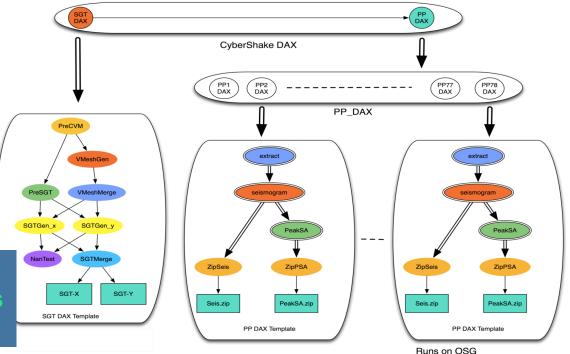
- Each site in the input map corresponds to one workflow
- Each workflow has:
- ♦ 820,000 tasks

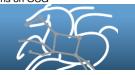
MPI codes ~ 12,000 CPU hours, Post Processing 2,000 CPU hours Data footprint ~ 800GB

Coordination between resources is needed

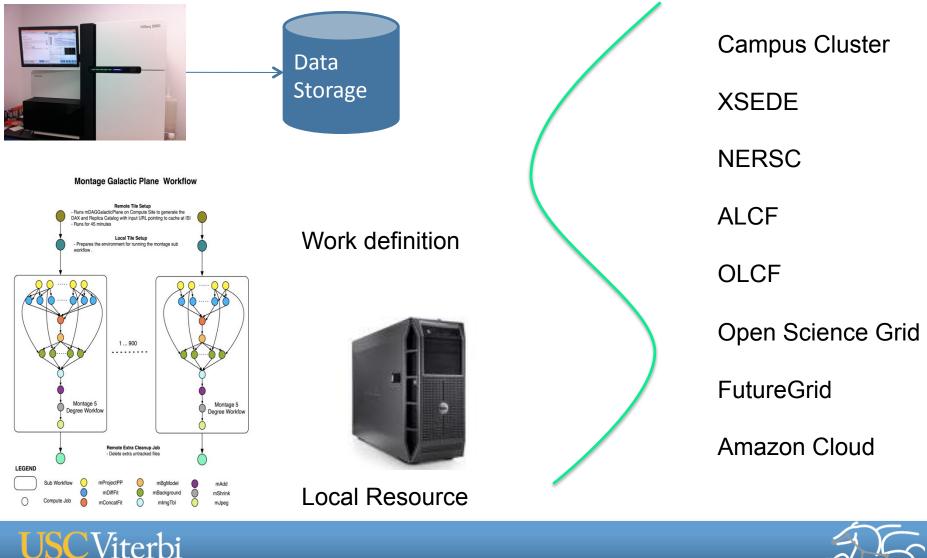
CyberShake PSHA Workflow

- Description
 - Builders ask seismologists: "What will the peak ground motion be at my new building in the next 50 years?"
 - Seismologists answer this question using Probabilistic Seismic Hazard Analysis (PSHA)





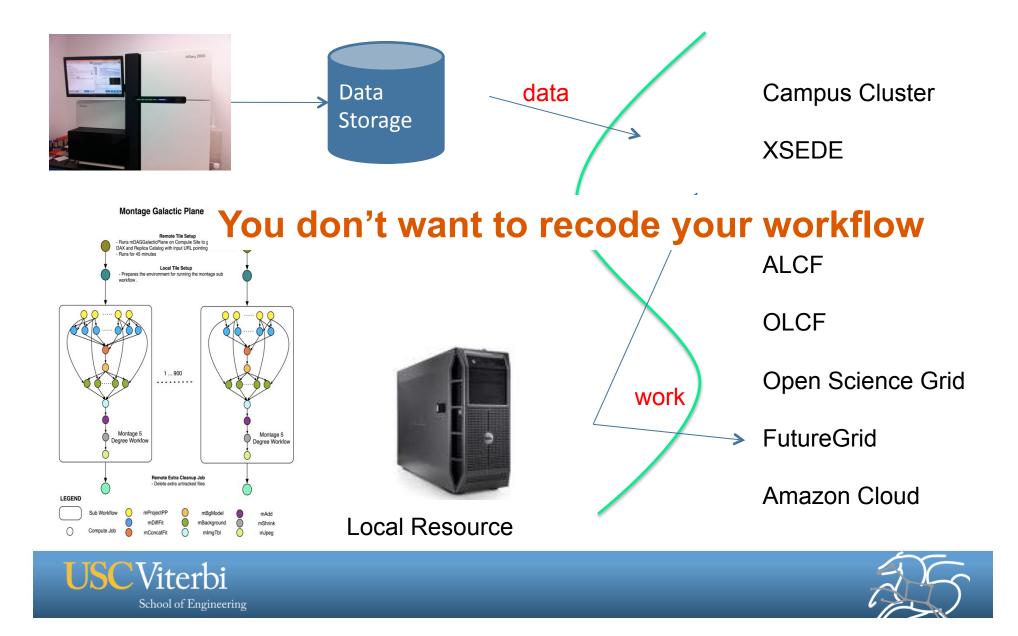
Sometimes the environment is complex







Sometime you want to change or combine resources



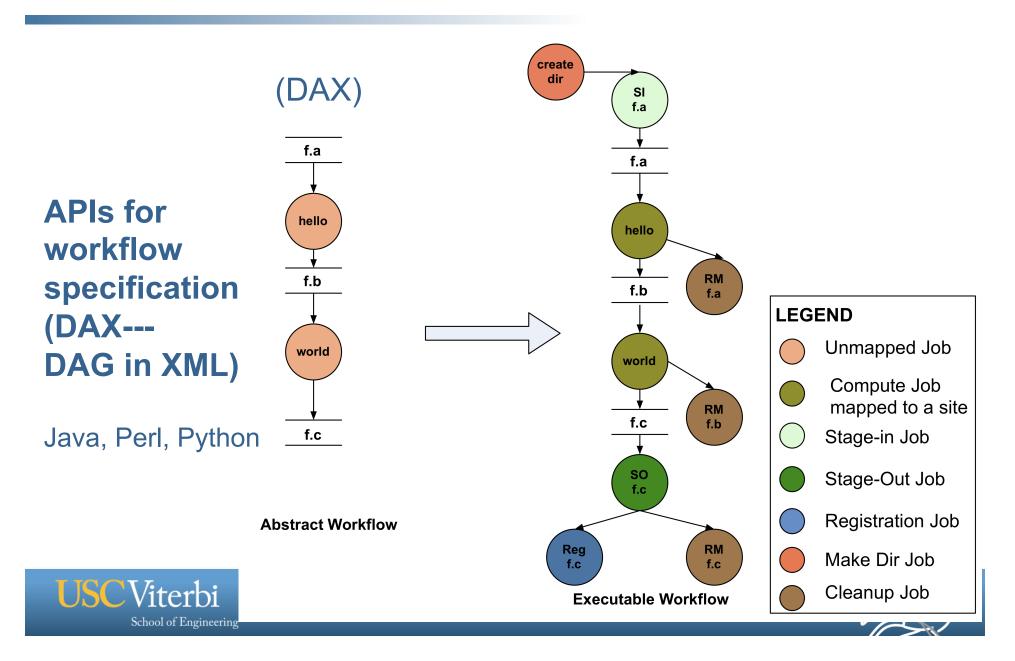
Pegasus Workflow Management System

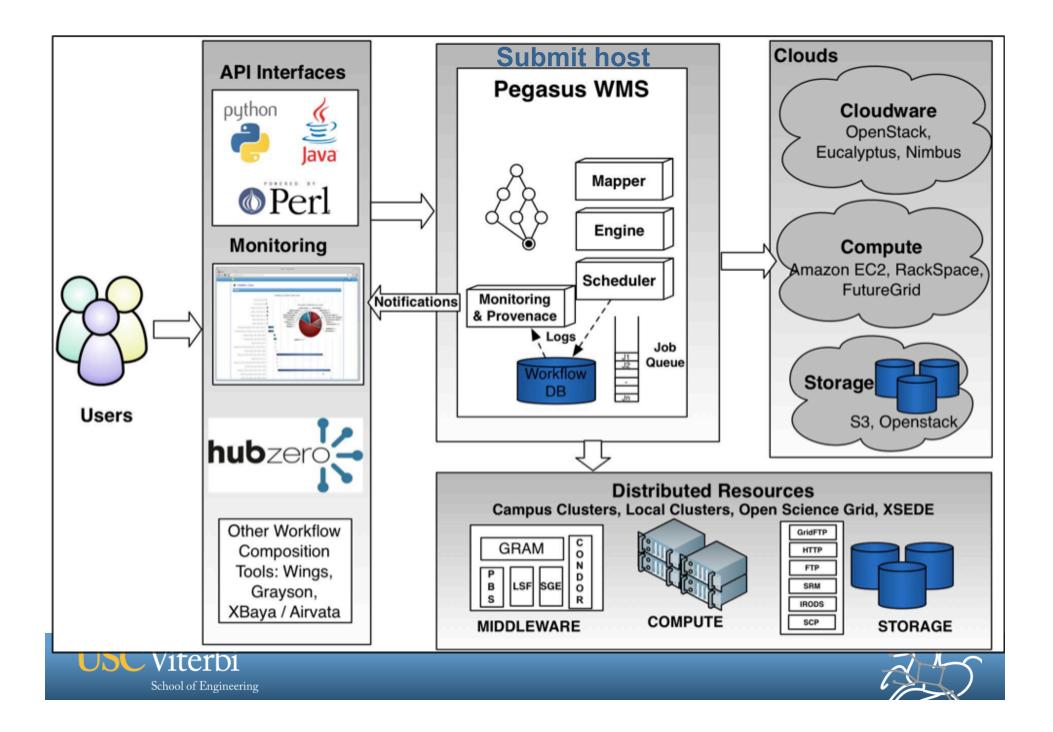
- A workflow "compiler"
 - Input: abstract workflow description, resource-independent
 - Output: executable workflow with concrete resources
 - Transforms the workflow for performance and reliability (task clustering, data cleanup, etc.)
 - Automatically locates physical locations for both workflow tasks and data
- A workflow engine (DAGMan)
 - Executes the workflow on local or distributed resources (HPC, clouds)
 - Task executables are managed by Condor schedd
- Provenance and execution traces are collected and stored
- Traces and DB can be mined for performance and overhead information





Generating executable workflows





Pegasus optimizations address issues of:

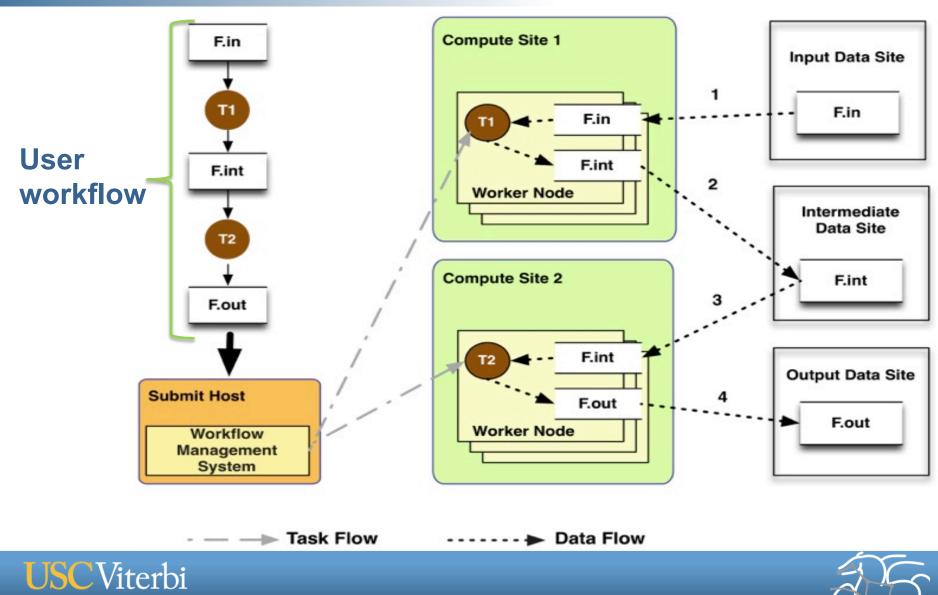
- Failures in the execution environment or application
- Data storage limitations on execution sites
- Performance
 - Small workflow tasks
- Heterogeneous execution architectures
 - Different file systems (shared/non-shared)
 - Different system architectures (Cray XT, Blue Gene, ...)





Storage limitations

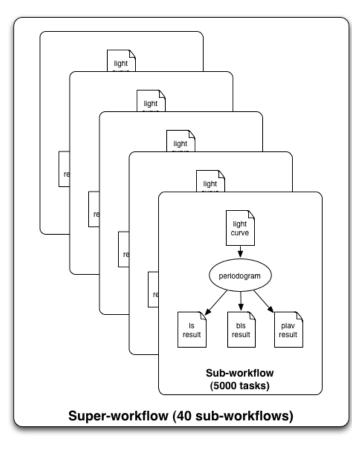
Variety of file system deployments: shared vs non-shared





Sometimes the environment is just not exactly right

Single core workload



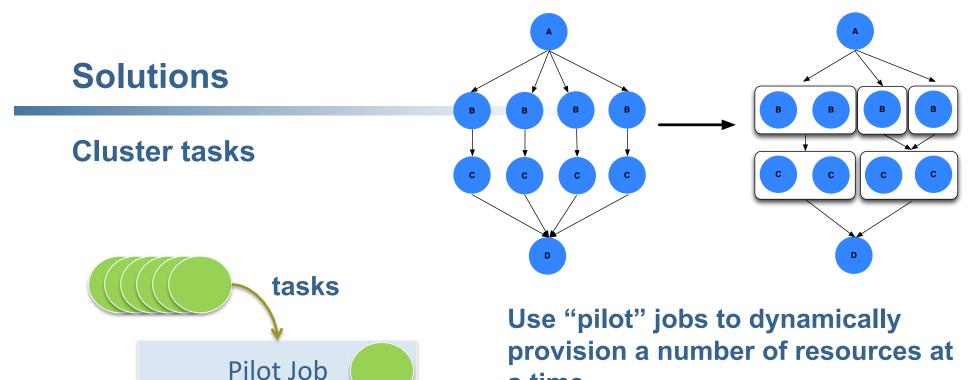


Cray XT System Environment / ALPS / aprun

• Designed for MPI codes







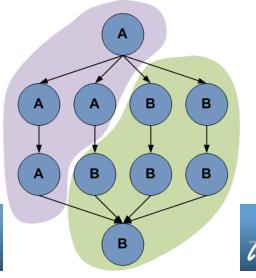
a time

Develop an MPI-based workflow management engine to manage sub-workflows

time

USC Viterbi

School of Engineering





Pegasus-kickstart

- Lightweight C based executable to launch jobs
- Captures job runtime provenance and logs it as a XML record
- Following information is captured about each job on all supported platforms
 - exit code with which the job it launched exited
 - start time and duration of the job
 - hostname and IP address of the host the job ran on
 - stdout and stderr of the job
 - arguments with which it launched the job
 - directory in which the job was launched
 - environment that was set for the job before it was launched





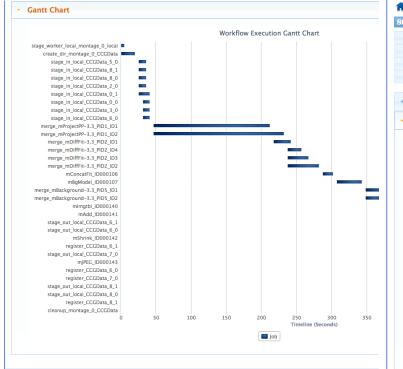
Pegasus-kickstart with extra tracing enabled

- Captures extra tracing information (optional) on Linux based hosts
- Collects, for each process in process tree
 - peak memory usage (resident set size, and vm size)
 - total I/O read and write,
 - runtime,
 - start and end time
 - Pid
 - all files accessed (total read and write per file)
- Traces also include DAGMan and Condor logs (release of jobs to the scheduling system, sending jobs to remote resources, etc..)



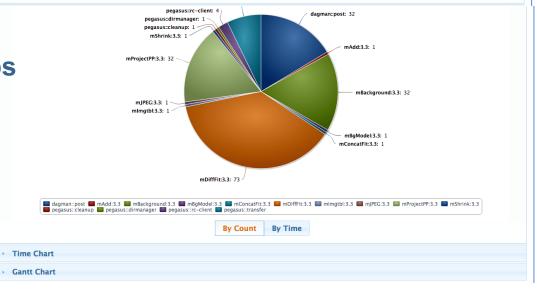


Workflow Monitoring Dashboard – pegasus-dashboard



| tistics | | | | | | | | | |
|-----------------------------------|--|---------|-------------|--------|--------|---------|----------------|--|--|
| Workflow Wall Time | | | | | | | 8 mins 53 secs | | |
| Workflow Cumulative Job Wall Time | | | | | | | 1 min 59 secs | | |
| | Cumulative Job Walltime as seen from Submit Side | | | | | | | | |
| | Workflow Retries | | | | | | | | |
| | | | | | | | | | |
| Workflow Statistics | | | | | | | | | |
| Job Breakdown Statistics | | | | | | | | | |
| | | | | | | | | | |
| Show so + entries S | | | | | | Search: | | | |
| Transformation | - Count | Succeed | ed 🌣 Failed | Min | ≎ Max | A Mean | Total | | |
| dagman::post | 32 | 32 | 0 | 5 | 6 | 5.063 | 162 | | |
| mAdd:3.3 | 1 | 1 | 0 | 1.203 | 1.203 | 1.203 | 1.203 | | |
| mBackground:3.3 | 32 | 32 | 0 | 0.054 | 0.197 | 0.130 | 4.174 | | |
| mBgModel:3.3 | 1 | 1 | 0 | 18.701 | 18.701 | 18.701 | 18.701 | | |
| mConcatFit:3.3 | 1 | 1 | 0 | 1.033 | 1.033 | 1.033 | 1.033 | | |
| mDiffFit:3.3 | 73 | 73 | 0 | 0.048 | 0.226 | 0.103 | 7.492 | | |
| mlmgtbl:3.3 | 1 | 1 | 0 | 0.107 | 0.107 | 0.107 | 0.107 | | |
| mJPEG:3.3 | 1 | 1 | 0 | 0.523 | 0.523 | 0.523 | 0.523 | | |
| mProjectPP:3.3 | 32 | 32 | 0 | 0.915 | 0.978 | 0.926 | 29.633 | | |
| mShrink:3.3 | 1 | 1 | 0 | 0.485 | 0.485 | 0.485 | 0.485 | | |
| pegasus::cleanup | 1 | 1 | 0 | 5 | 5 | 5 | 5 | | |
| pegasus::dirmanager | 1 | 1 | 0 | 10 | 10 | 10 | 10 | | |
| pegasus::rc-client | 4 | 4 | 0 | 0.706 | 0.868 | 0.783 | 3.134 | | |
| pegasus::transfer | 14 | 14 | 0 | 0 | 5.229 | 2.724 | 38.135 | | |

Status, statistics, timeline of jobs





Overview of the Community Resources

www.workflowarchive.org

- Execution Traces of a range of real workflow applications
- Synthetic Workflow Generator produces realistic workflows based on profiles extracted from execution traces (astronomy, gravitational-wave physics, bioinformatics, earthquake science)
- Workflow Simulator mimics the execution of synthetic workflows on realistic infrastructures





Workflow Traces Archive

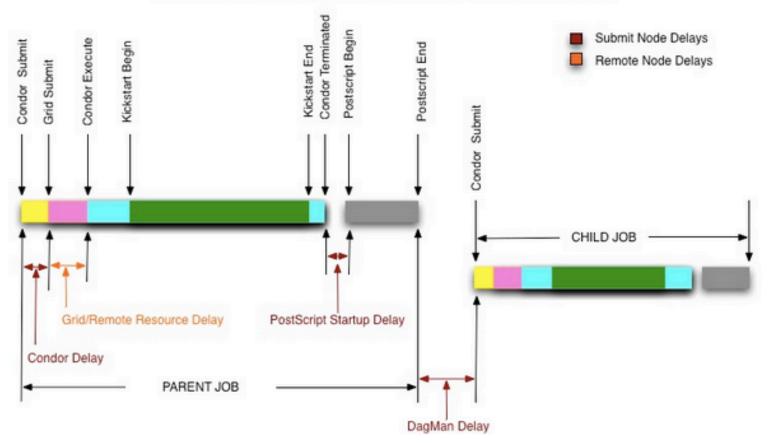
Workflow Gallery currently has 11 workflow applications, most with multiple runs

08/24 12:24:55 submitting: condor submit -a dag node name' '=' 'stage in remote usc 1 -a +DAGManJobId' '=' '11443 -a DAGManJobId' '=' '11443 -a submit event notes' '=' 'DAG' 'Node:' 'stage_in_remote_usc 1 -a +DAGParentNodeNames' '=' "create dir 61HE2AAXX 2 HSB 135 S1C R 0 usc" stage in remote usc 1.sub 08/24 12:24:55 From submit: Submitting job(s). DAGMan, Condor, Pegasus logs, 08/24 12:24:55 From submit: Logging submit event(s). submit files, stdout, stderr 08/24 12:24:55 From submit: 1 job(s 1314221995 Sam 62411024112 08/24 12:24:55 assigned Condor II 1314221995 SamToMrf SamToMrf-0-1 EXECUTE 11602.0 usc 7200 159 1314221995 SamToBam SamToBam-26-1 EXECUTE 11600.0 usc 7200 157 08/24 12:24:55 Submitting Condor N 1314222155 SamToBam SamToBam-27-1 JOB TERMINATED 11601.0 usc 08/24 12:24:55 submitting: condor s 1314222155 SamToBam SamToBam-27-1 JOB SUCCESS 0 usc 7200 158 +DAGManJobId' '=' '11443 -a DAGM 1314222155 SamToBam SamToBam-27-1 POST SCRIPT STARTED 11607 'stage in remote usc 2 -a +DAGPa 1314222160 SamToBam SamToBam-27-1 POST SCRIPT TERMINATED 1 "create dir 61HE2AAXX 2 HSB 1 1314222160 SamToBam SamToBam-27-1 POST SCRIPT SUCCESS 0 usc 08/24 12:24:55 From submit: Submit 1314222166 stage out remote usc 5 1 SUBMIT 11605.0 usc - 162 08/24 12:24:55 From submit: Loggin 1314222176 stage out remote usc 5 1 GLOBUS SUBMIT 11605.0 usc - 1 08/24 12:24:55 From submit: 1 job(s 1314222176 stage out remote usc 5 1 GRID SUBMIT 11605.0 usc - 162 08/24 12:24:55 assigned Condor II 1314222176 stage_out_remote_usc_5_1 EXECUTE 11605.0 usc - 162 08/24 12:24:55 Submitting Condor N





Traces include information about system overheads



PEGASUS WORKFLOW JOB STATES AND DELAYS





Tools to calculate job statistics

| Task Type | Count | Runtime(s) | IO Read (MB) | IO Write (MB) | Memory Peak(MB) | CPU Utilization(%) |
|-------------|-------|------------|-----------------|------------------|--------------------|-----------------------|
| mProjectPP | 2102 | 1.73 | 2.05 | 8.09 | 11.81 | 86.96 |
| mDiffFit | 6172 | 0.66 | 16.56 | 0.64 | 5.76 | 28.39 |
| mConcatFit | 1 | 143.26 | 1.95 | 1.22 | 8.13 | 53.17 |
| mBgModel | 1 | 384.49 | 1.56 | 0.10 | 13.64 | 99.89 |
| mBackground | 2102 | 1.72 | 8.36 | 8.09 | 16.19 | 8.46 |
| mImgtbl | 17 | 2.78 | 1.55 | 0.12 | 8.06 | 3.48 |
| mAdd | 17 | 282.37 | 1102 | 775.45 | 16.04 | 8.48 |
| mShrink | 16 | 66.10 | 412 | 0.49 | 4.62 | 2.30 |
| mJPEG | 1 | 0.64 | 25.33 | 0.39 | 3.96 | 77.14 |

 Table 1. Execution profile of the Montage workflow, averages calculated





Automatic Workflow Characterization

- Characterize tasks based on their estimation capability
 - Runtime, I/O write, memory peak → estimated from I/O read
- Use correlation statistics to identify statistical relationships
 between parameters
 - <u>High correlation</u> values yield <u>accurate estimations</u>, <u>Estimation based</u> on the ratio: <u>parameter/input data size</u>

| Task | Runtime | | I/O Write | | Memory Peak | | _ |
|---------------|---------|-------|-----------|----------|-------------|----------|-----------------|
| | ρ | σ | ρ | σ | ρ | σ | Constant values |
| fastqSplit | 0.98 | 9.00 | 1.00 | 297.15 | 0.00 | 0.01 | 7 |
| filterContams | -0.03 | 0.27 | 0.99 | 1.46 | 0.00 | 0.01 | |
| sol2sanger | 0.21 | 0.41 | 0.90 | 1.49 | 0.00 | 0.01 | |
| fast2bfq | 0.18 | 0.27 | 0.56 | 0.87 | 0.00 | 0.01 | Correlated if |
| map | 0.02 | 18.96 | 0.06 | 0.70 | 0.01 | 1.43 | ρ > 0.8 |
| mapMerge | 0.98 | 13.33 | 0.99 | 189.81 | -0.36 | 2.15 | |
| pileup | 0.99 | 4.73 | 0.17 | 249.78 | 0.87 | 25.70 | _ |

• Low correlation: use mean value

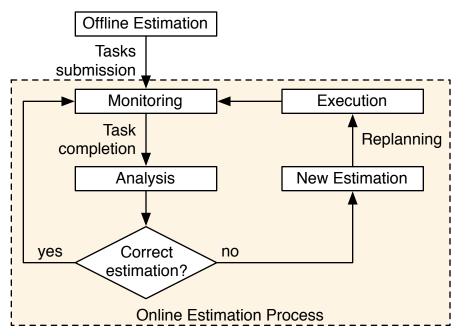
Epigenomics workflow





Workflow Resource Usage Prediction

- Profile and Characterize Workflow Execution
 - I/O, runtime, memory usage, and CPU utilization
 - Predict task runtime, e.g. using correlations based techniques
 - Predict resource usage (disk space, memory consumption) using an online estimation process



DOE project: dV/dt Accelerating the Rate of Progress towards Extreme Scale Collaborative Science





Predictive Modeling and Diagnostic Monitoring of Extreme Science Workflows

Objective: Understand complex scientific workflow applications and infrastructure behaviors and to translate this understanding into flexible, end-to-end analytical models that can effectively predict the behavior of extreme scale workflows on current and future infrastructures

Approach:

- Engage DOE science teams from simulation (e.g., Earth Systems Modeling (ESM) and instrument facilities (e.g., Spallation Neutron Source(SNS) to create example workflow scenarios
- Develop a general analytical modeling methodology that captures the endto-end performance of these workflow scenarios using a structured modeling approach;
- Validate the analytical models using empirical measurement and simulation
- Employ the analytical performance models to facilitate prototype capabilities that include anomaly detection and diagnosis, resource management and adaptation, and infrastructure design and planning.



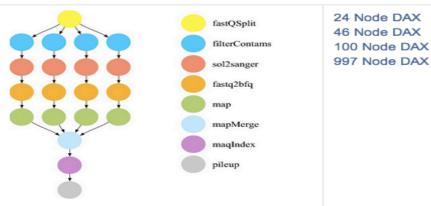


Workflow Generator Toolkit

- Inputs: the size of the workflow in number of jobs, or the input data size, or a scaling factor
- Inputs are combined with probability distributions of file sizes and runtimes from real executions of the workflow, to generate random values that are used in constructing the synthetic workflow.
- Generators have application-specific code and parameters that are designed to reproduce the structure and characteristics of the application.
- Currently supports 20 workflow applications from astronomy, earth science, bioinformatics, weather, and ocean modeling
- Pre-generated workflows: a large collection of synthetic workflow samples is available (5 workflow applications and 2,840 workflow instances)

Epigenomics

The epigenomics workflow created by the USC Epigenome Center and the Pegasus Team is used to automate various operations in genome sequence processing.





Workflow Simulator: WorkflowSim

A workflow simulator for distributed environments

- Workflow-level support (data dependency) on top of CloudSim
- Contains a model of system overheads
- Supports task failures, monitoring, task retry, task clustering
- Can be used to evaluate algorithms and techniques in task scheduling, task clustering, resource provisioning, and data placement etc.
- Input: DAX files from Synthetic Workflow Generator or other DAX generators
- Output: makespan, resource usage, cost, etc.
 Source available on github and open to contributions <u>https://github.com/WorkflowSim</u>

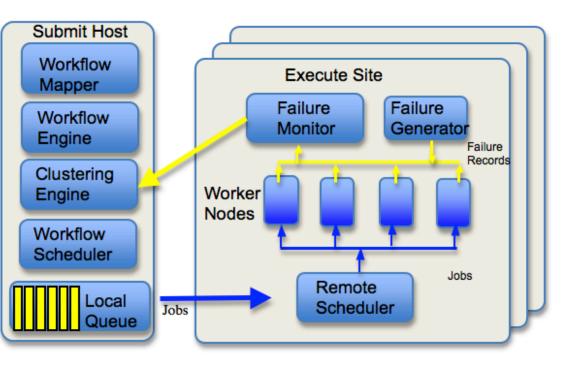




Workflow Simulator: WorkflowSim

Components

- Behavior based on Pegasus
 - Workflow Mapper/Compiler, Workflow Engine, Clustering Engine, Workflow Scheduler
- Additional features
 - Failure Generator
 - Failure Monitor
 - System Overheads
 - Monetary Cost







Simulation Usage Examples

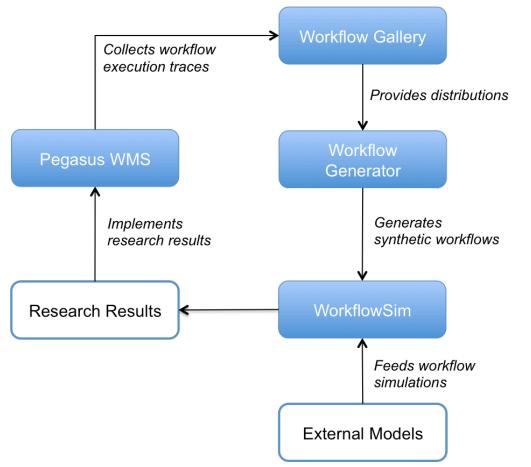
- Balanced Task Clustering: investigate the dependency and runtime imbalance problem in task clustering
 - Used synthetic workflow generator to create a large set of workflow instances
- Fault-Tolerant Task Clustering: improve the task clustering in a faulty environment
 - Relied on the generation of transient failures
 - Synthetic workflows
- Energy-Efficiency: develop an energy consumption model for large-scale infrastructure





Conclusion

- A collection of tools and data that have enabled research in new methods and systems
 - Execution traces
 - Synthetic workflow generator
 - Workflow simulator
- We use these tools to
 - Generate traces
 - Analyze and profile traces
 - Vary system configurations and workflow instances
 - Evaluate the results in simulator
 - Implement promising approaches in Pegasus
- The tools are not limited to the Pegasus community







Current Community Resources

Contributions Welcome!

- Pegasus Workflow Management System: <u>http://pegasus.isi.edu</u>
- Workflow Archive and Workflow Generator: <u>www.workflowarchive.org</u>
- WorkflowSim: <u>www.workflowsim.org</u> and <u>https://github.com/WorkflowSim</u>



