

Building Community Resources For Scientific Workflow Research

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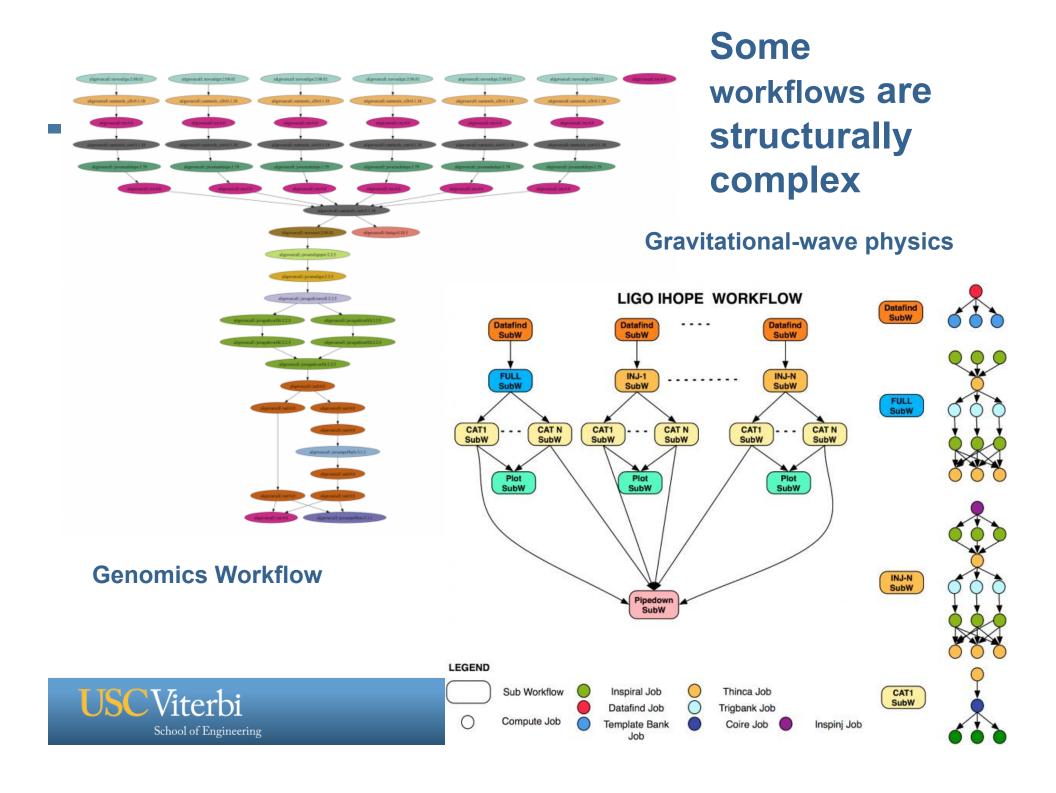
Funding from NSF and DOE



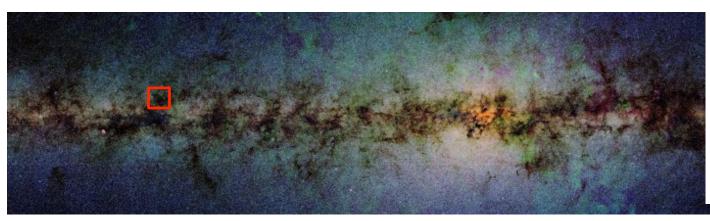
Community Resources for Enabling Scientific Workflow Research

- Execution traces
- Synthetic workflow generator
- Workflow execution simulator

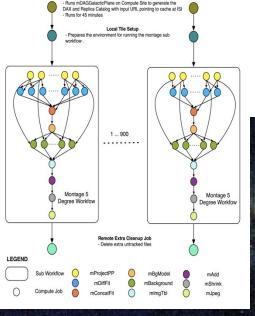




Some workflows are large-scale and data-intensive



Montage Galactic Plane Workflow



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)

John Good (Caltech)

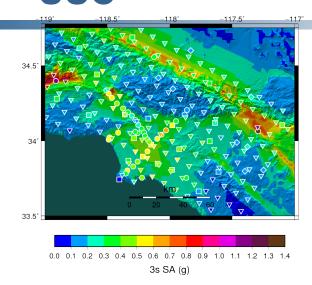
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 Need to support hierarchical workflows and scale, workflow ensembles





Southern California Earthquake Center, T. Jordan, USC

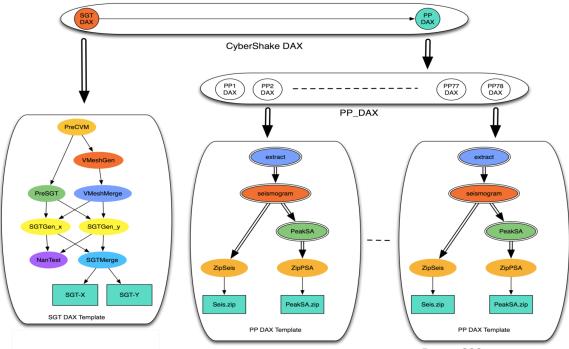


1,144 geographic locations
Uses Pegasus with execution on
TACC's Stampede
~ 470 million tasks total
Over 739 hours of computing
45 TB of data
12 TB being staged back for
archiving

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)







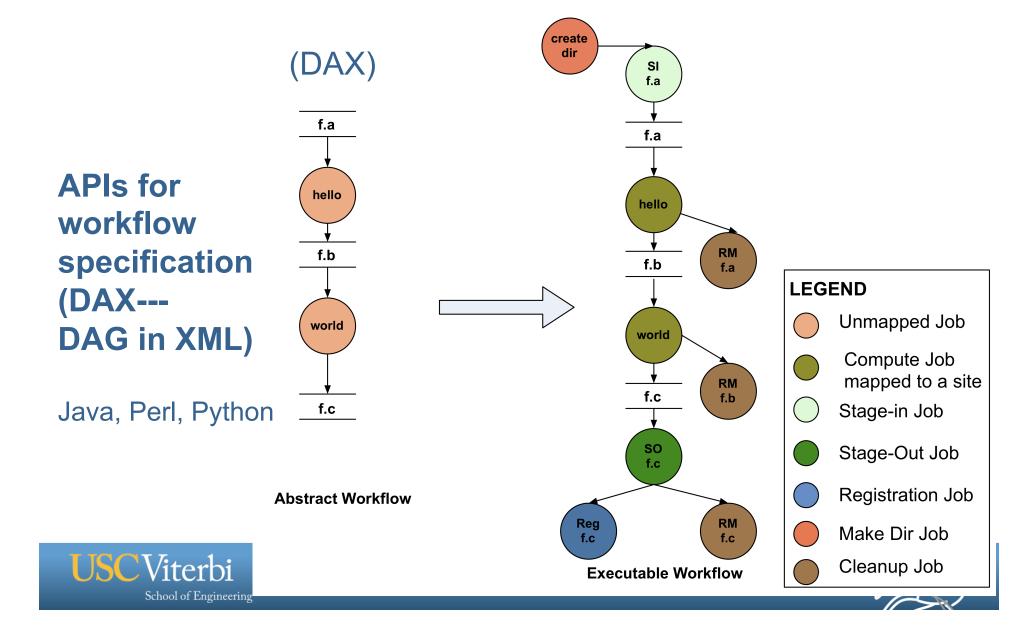
Pegasus Workflow Management System

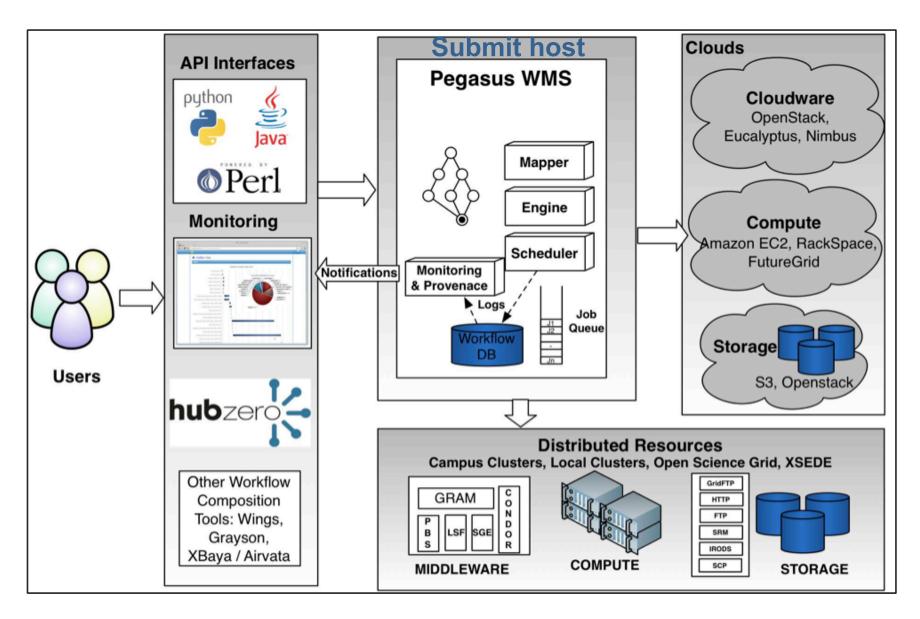
- A workflow "compiler"
 - Input: abstract workflow description, resource-independent
 - Output: executable workflow with concrete resources
 - Transforms the workflow for performance and reliability (task clustering, data cleanup, etc.)
 - Automatically locates physical locations for both workflow tasks and data
- A workflow engine (DAGMan)
 - Executes the workflow on local or distributed resources (HPC, clouds)
 - Task executables are wrapped with pegasus-kickstart and 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-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





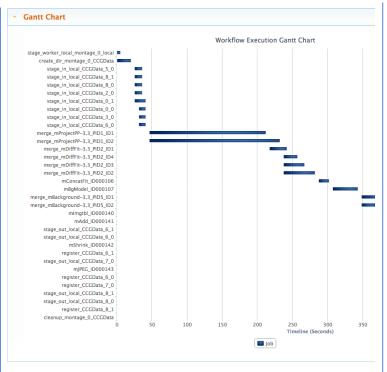
Pegasus-kickstart with extra tracing enabled

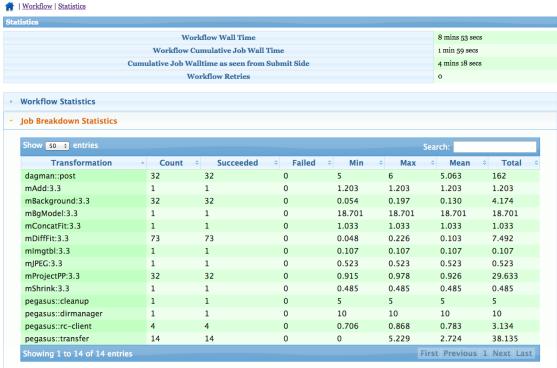
- Captures extra tracing information (optional) on Linux based hosts
- Traces each process that the job launches
 - Using LD_PRELOAD library interposition (faster, less accurate),
 - ptrace() system call interposition (slower, more accurate)
- Collects, for each process in process tree
 - peak memory 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

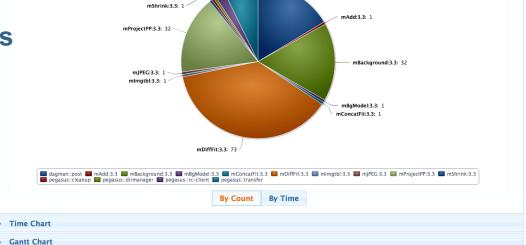




pegasus::rc-client: 4

pegasus::dirmanager: 1 pegasus::cleanup: 1

Status, statistics, timeline of jobs



dagman::post: 32



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

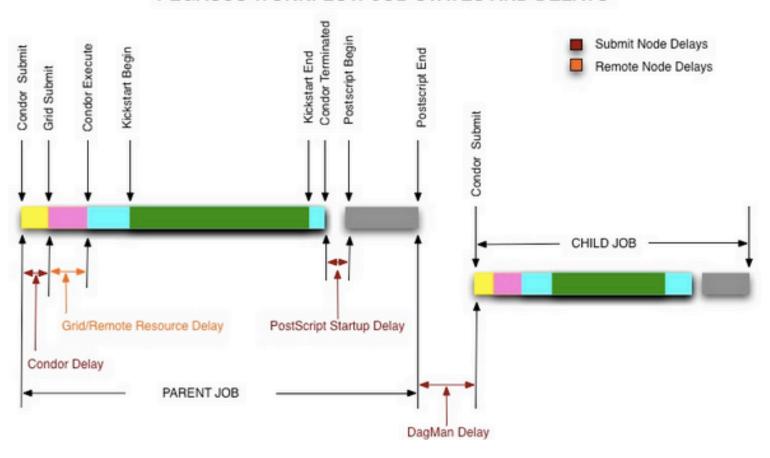
```
08/24 12:24:55 submitting: condor submit -a dag node name' '=' 'stage in remote usc 1 -a
+DAGManJobId' '=' '11443 -a DAGManJobId' '=' '11443 -a submit event notes' '=' 'DAG' 'Node:'
'stage_in_remote_usc 1 -a +DAGParentNodeNames' '='
"create dir 61HE2AAXX 2 HSB 135 S1C R 0 usc" stage in remote usc 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 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 11601
'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 uso
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

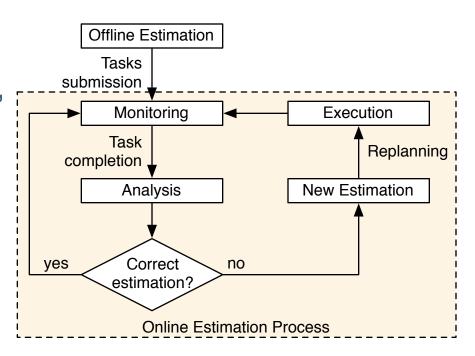
Table 1. Execution profile of the Montage workflow, averages calculated





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





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
 - High correlation values yield <u>accurate estimations</u>, <u>Estimation based</u>
 on the ratio: <u>parameter/input data size</u>
 - Low correlation: use mean value

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 Sometant values
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	$\rho > 0.8$
mapMerge	0.98	13.33	0.99	189.81	-0.36	2.15	μ στο
pileup	0.99	4.73	0.17	249.78	0.87	25.70	

Epigenomics workflow





Task Characterization/Execution

- Understand the resource needs of a task
- Establish expected values and limits for task resource consumption
- Launch tasks on the correct resources
- Monitor task execution and resource consumption, interrupt tasks that reach resource limits
- Possibly re-launch tasks on different resources
- Task characterization needs to be an online process
- New DOE project to improve the modeling of workflow behavior including data handling (Vetter, Tierney, Mandal, Carothers) "Predictive Modeling and Diagnostic Monitoring of Extreme Science Workflows;"





Results: Average Estimation Errors - Montage

		Dti	I/O Weite	Managemen
		Runtime	I/O Write	Memory
Task	Estimation	Avg. Error	Avg.Error	Avg.Error
		(%)	(%)	(%)
mProjectPP	Offline	18.95	1.63	2.80
	Online	18.95	1.63	2.80
mDiffFit	Offline	191.02	159.46	91.07
	Online	46.52	69.14	73.72
mConcatFit	Offline	4.38	0.00	7.62
	Online	4.03	0.00	6.22
mBgModel	Offline	23.83	0.00	22.08
	Online	1.17	0.00	3.43
mBackground	Offline	65.13	102.80	104.62
	Online	44.90	1.23	1.84
mImgtbl	Offline	61.27	127.29	126.58
	Online	29.15	5.53	8.35
mAdd	Offline	9.67	113.14	110.20
	Online	9.31	3.43	9.06
mShrink	Offline	13.72	0.34	0.00
	Online	7.61	0.33	0.00
mJPEG	Offline	1.61	0.00	19.09
	Online	1.37	0.00	11.40

Poor output data estimations leads to a chain of estimation errors in scientific workflows

Offline Process

Avg. Runtime Error: 43% Avg. I/O Write Error: 56% Avg. Memory Error: 53%

Online Process

Avg. Runtime Error: 18% Avg. I/O Write Error: 9% Avg. Memory Error: 13%

Online strategy counterbalances the propagation of estimation errors





Workflow Generator Toolkit

Allows to explore more application configurations

- Uses randomization and parameter sweeps to create different workflow instances
 - Generate task runtimes and data sizes based on patterns observed in execution profiles.
 - Generate workflow structure based on the targeted application: pipelines, data distribution, aggregation, or redistribution
 - Montage: number of inputs is based on the degree square of the final image, e.g.
- Outputs DAX (DAG in XML) files that can be used by Workflow Simulators



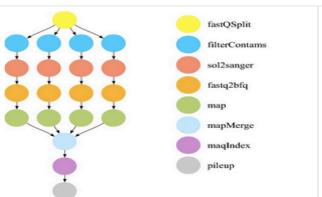


Workflow Generator Toolkit

- 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.



24 Node DAX 46 Node DAX 100 Node DAX 997 Node DAX



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.

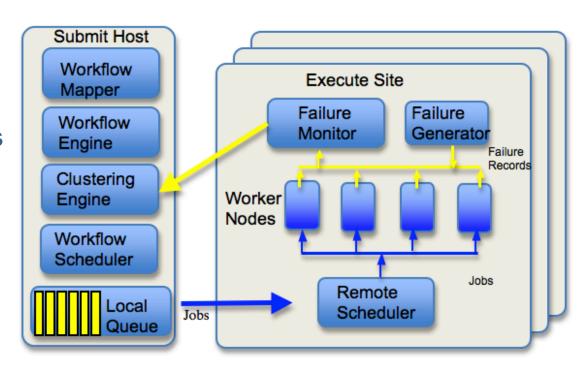




Workflow Simulator: WorkflowSim

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

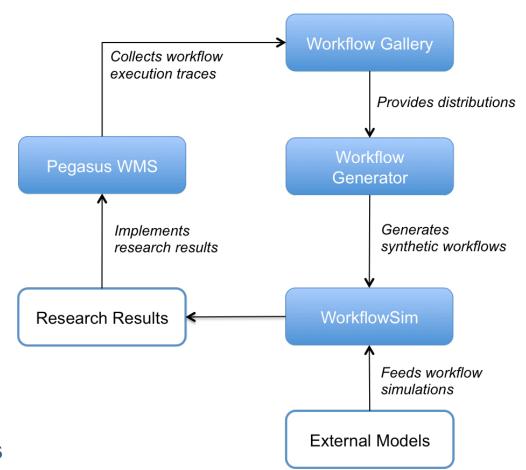
- Balanced Task Clustering: investigate the dependency and runtime imbalance problem in task clustering
 - Used synthetic workflow generator to create a large set of workflow instances
- Fault-Tolerant Task Clustering: improve the task clustering in a faulty environment
 - Relied on the generation of 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: http://pegasus.isi.edu
- Workflow Archive and Workflow Generator: www.workflowarchive.org
- WorkflowSim: <u>www.workflowsim.org</u> and <u>https://github.com/WorkflowSim</u>



