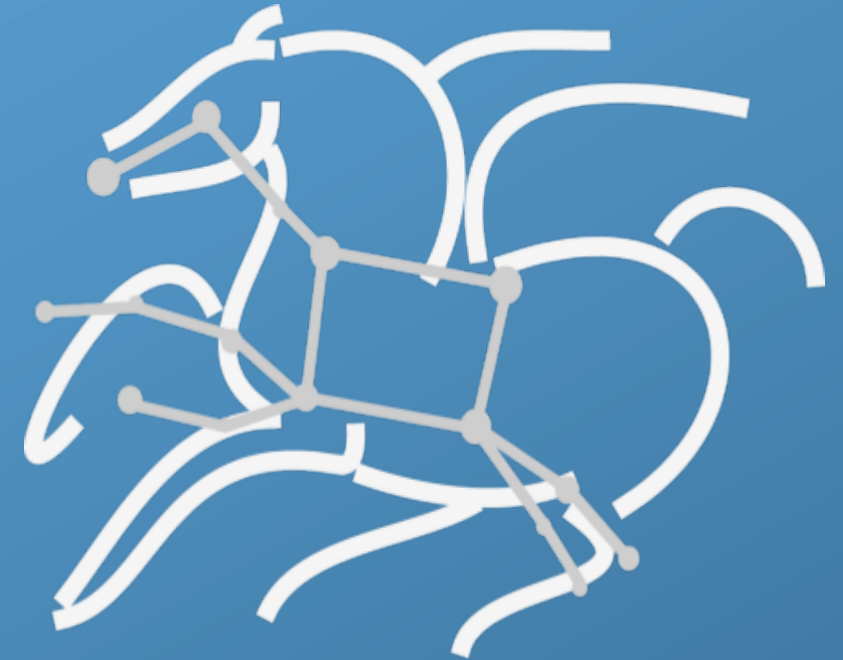




U.S. DEPARTMENT OF
ENERGY

NIH

Challenges of Managing Scientific Workflows in High-Throughput and High-Performance Computing Environments



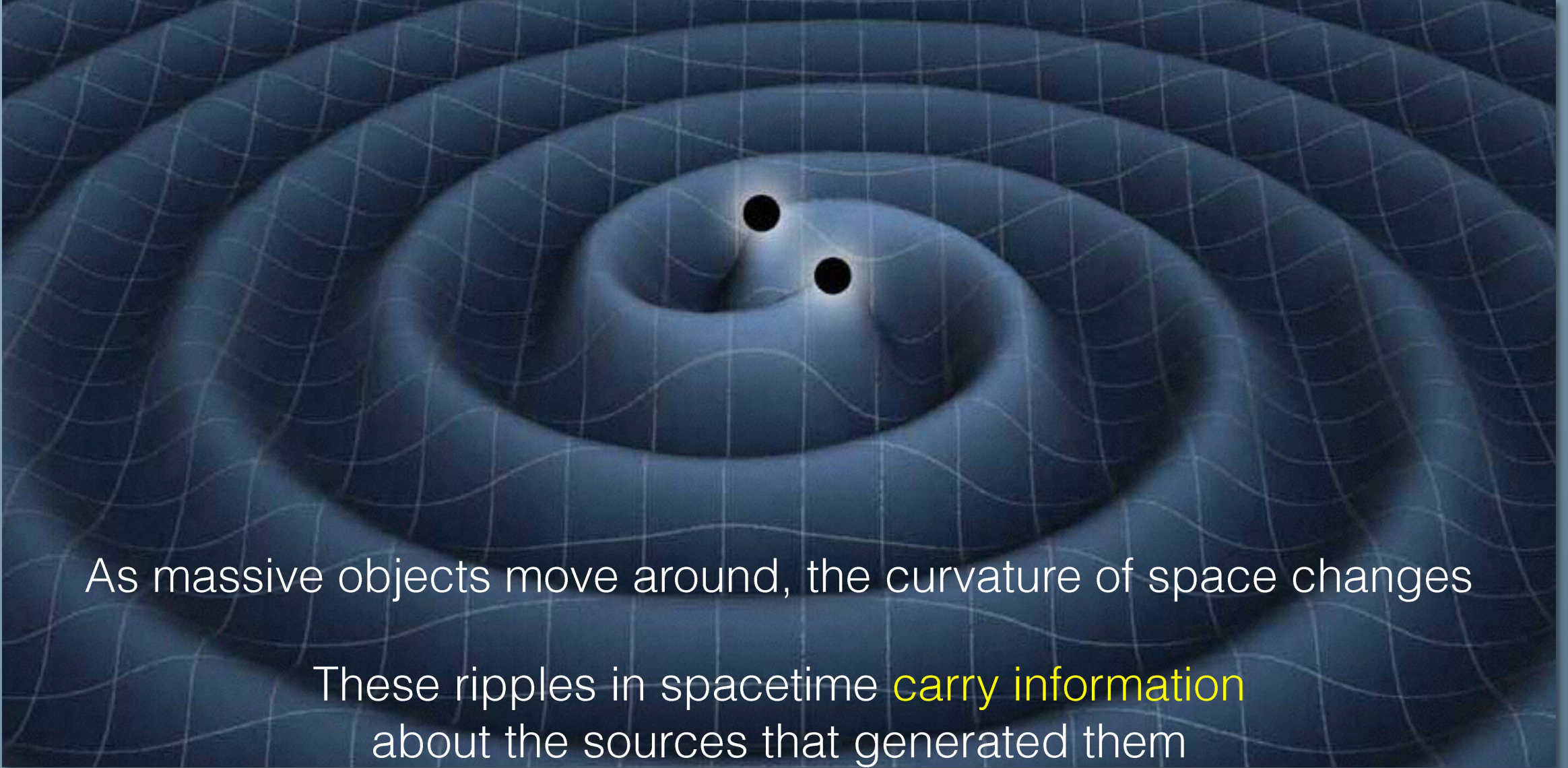
Ewa Deelman, Ph.D.

USC Viterbi

School of Engineering
Information Sciences Institute

<http://pegasus.isi.edu>

LIGO Experiment: Searching for Gravitational Waves



As massive objects move around, the curvature of space changes

These ripples in spacetime **carry information** about the sources that generated them

Image courtesy of LSC

LIGO (Laser Interferometer Gravitational-Wave Observatory)

LSC (LIGO Scientific Collaboration)

- Collaboration involved in research of the data coming out of the detectors
- 1000 scientists from universities in US and 14 other countries
- 250 students
- Responsible for developing analysis methodologies and detector technology.

Background

- Largest ever NSF funded project
- Two 4km long detectors in the US (Hanford, Washington, and Livingston, Louisiana)



Aerial View of the LIGO Livingston Laboratory

Image Credit: Caltech/MIT/LIGO Lab

Phase I

(Initial LIGO 2002 – 2010)

- No gravitational waves detected
- But a lot of analysis pipelines and computing infrastructure were setup
- **Late 2010 – Passed Blind Injection Test**

Upgrade of the detectors

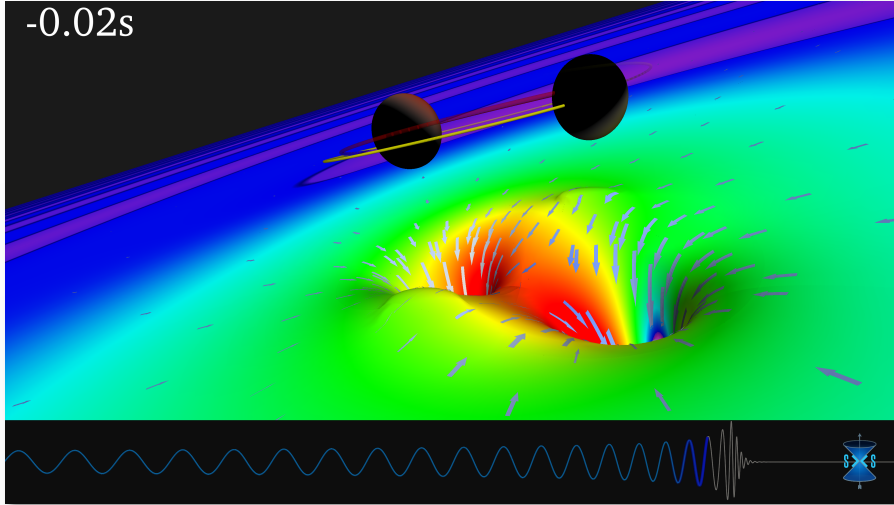
- Designed to be 10 times more sensitive than Phase I

Phase II

- Currently operating at 4 times the Initial LIGO sensitivity

(Advanced LIGO September 2015 onwards)

LIGO's Gravitational Wave Detection



LIGO announced first ever detection of gravitational waves
Feb 2016

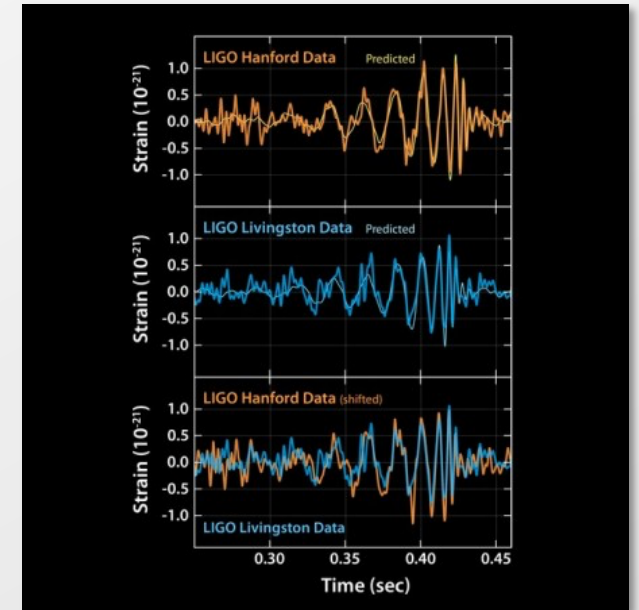
Created as a result of coalescence of a pair of dense, massive black holes

Confirms major prediction of **Einstein Theory of Relativity**

Detection Event

Detected by both of the operational Advanced LIGO detectors
(4km long L shaped interferometers)

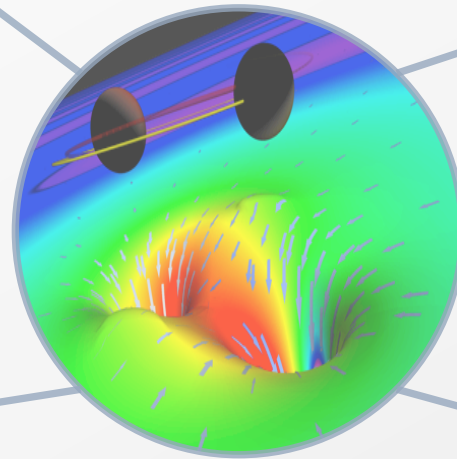
Event occurred at September 14, 2015 at 5:51 a.m. Eastern Daylight Time



*Image Credits: 0.2 Second before the black holes collide: SXS/LIGO
Signals of Gravitational Waves Detected: Caltech/MIT/LIGO Lab*

A variety of complex analysis pipelines were executed

Some were low latency that initially alerted people to look at a specific piece of data containing the signal



However, to verify that signal is a valid candidate

Pipelines/Workflows are mainly executed on LSC Data Grid

- A large amount of data needed to be analyzed*
- Statistical significance of the detection should be at 5-sigma level*

- Consists of approximately 11 large clusters at various LIGO institutions and affiliates*
- Data is replicated at sites in the US and Europe*
- Each cluster has Grid middleware and HTCondor installed*
- GridFTP used for data transfers*

Advanced LIGO PyCBC Workflow

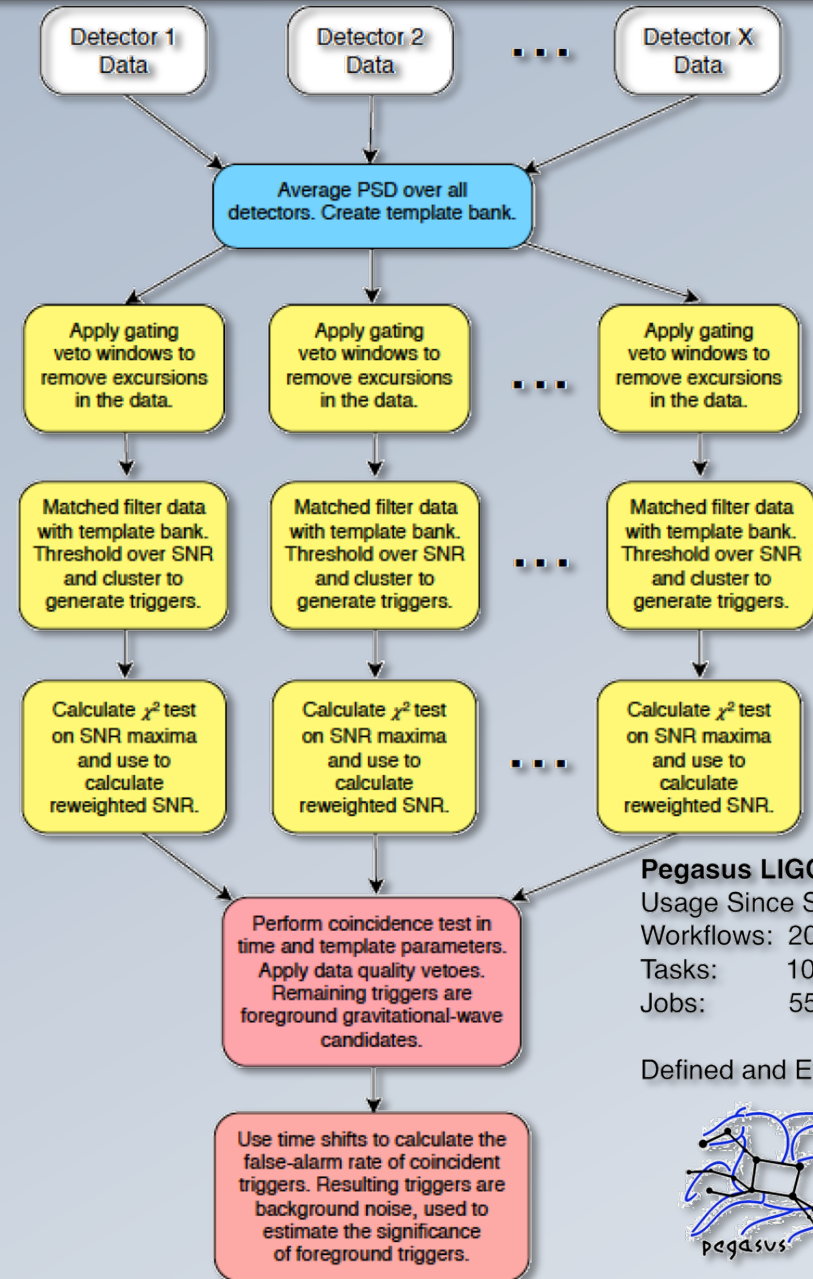
One of the main pipelines to measure the statistical significance of data needed for discovery

Contains 100's of thousands of jobs and accesses on order of terabytes of data

Uses data from multiple detectors

For the detection, the pipeline was executed on Syracuse and Albert Einstein Institute Hannover

Use our Pegasus software to automate the execution of tasks and data access



Pegasus LIGO PyCBC Workflow
Usage Since Sept 2015
Workflows: 20,942
Tasks: 107,576,294
Jobs: 55,915,928

Defined and Executed by Pegasus



Outline

1

Example Pegasus Workflows

2

Pegasus Workflow Management System

3

Challenges and solutions for workflow execution in clusters, distributed systems, and clouds

4

Future Directions

Why Scientific Workflows?

Automates complex, multi-stage processing pipelines

Enables parallel, distributed computations

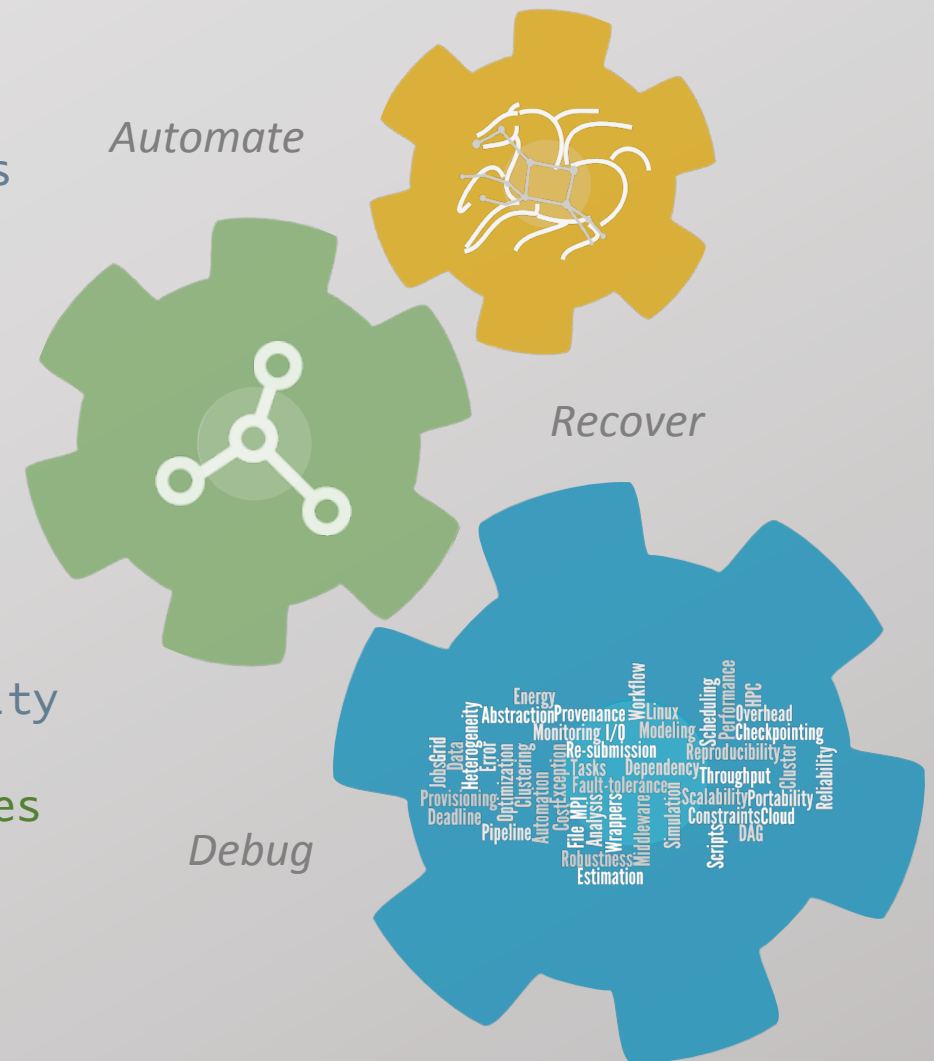
Automatically executes data transfers

Reusable, aids reproducibility

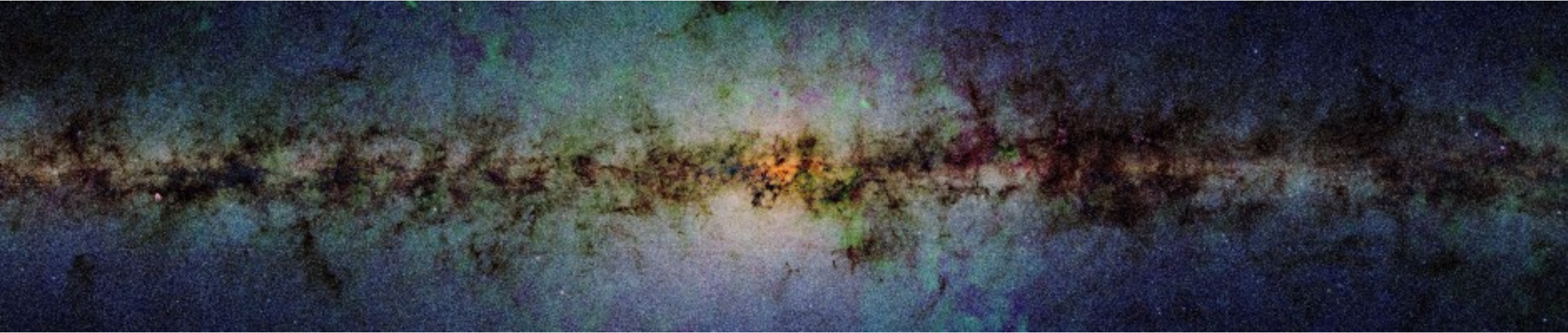
Records how data was produced (provenance)

Handles failures with to provide reliability

Keeps track of data and files



Community Archives: Galactic Plane Atlas



- 18 million input images (~2.5 TB)
- 900 output images (2.5 GB each, 2.4 TB total)
- Measuring the global star formation rate in the galaxy
- Studying the energetics of the interaction of molecular clouds with the interstellar medium
- Determining whether coagulation or fragmentation governs the formation of massive stars
- Assessing the supernova rate in the Galaxy

} × 17

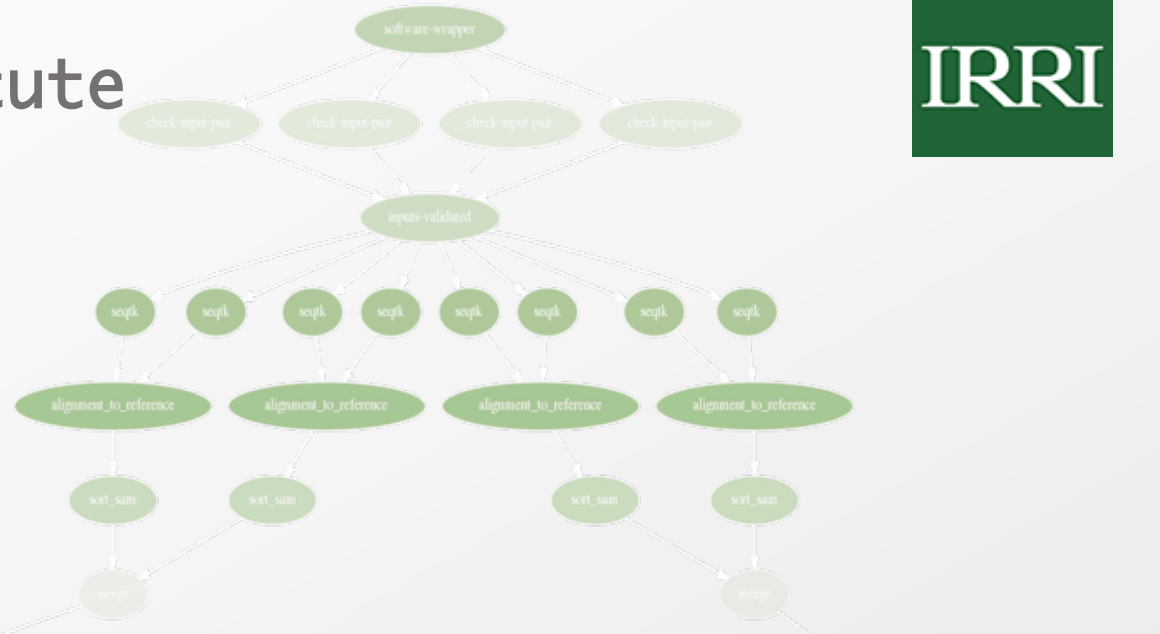
International Rice Research Institute

Liya Wang



The 3000 rice genome: ~15.4 TBs of 83 bp paired-end genomic reads for a diverse set of rice varieties

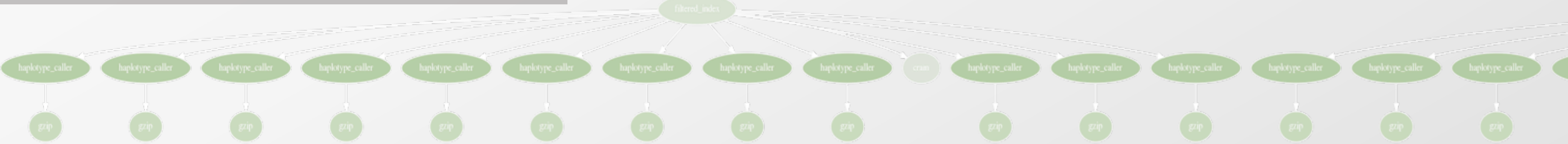
Want to capture genetic differences using well known bioinformatics applications



Workflow supports 3 different execution environments

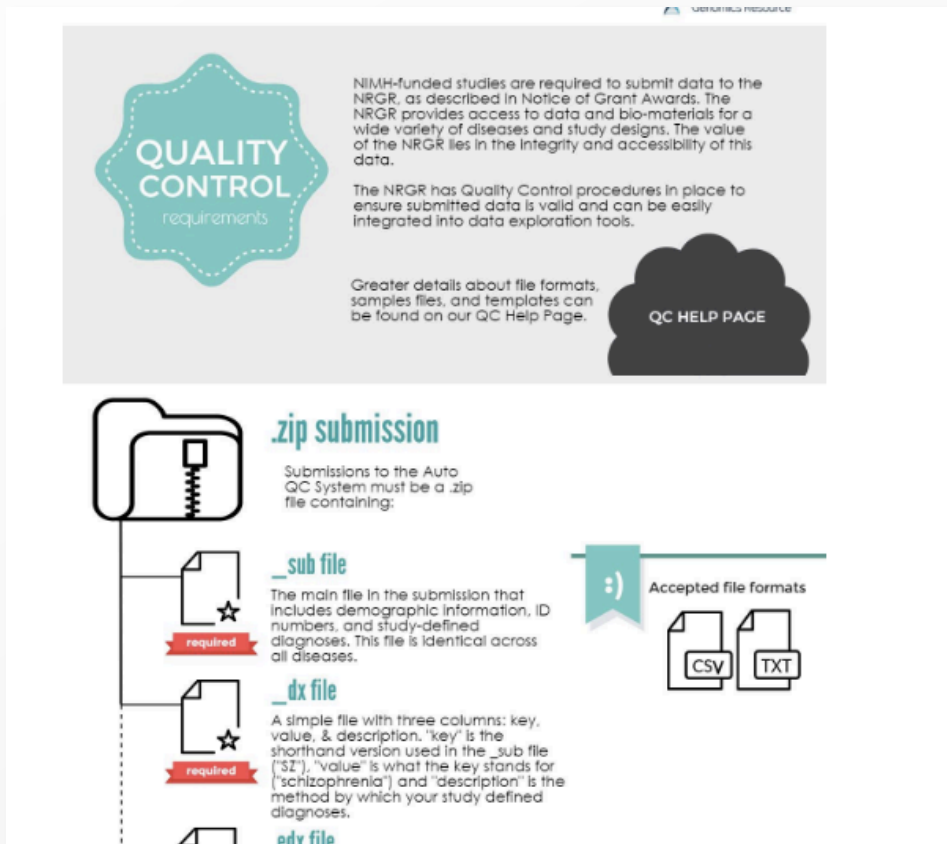
- SDSC Comet (glideins)
- TACC Stampede (pegasus-mpi-cluster)
- Distributed (local HTCondor pool)

Custom glideins on demand workflow.isi.edu as submit host



Sometimes you want to “hide” the workflow...

Automated QC Workflow, Pedigree checks, Consistency checks



QUALITY CONTROL requirements

NIMH-funded studies are required to submit data to the NRGR, as described in Notice of Grant Awards. The NRGR provides access to data and bio-materials for a wide variety of diseases and study designs. The value of the NRGR lies in the integrity and accessibility of this data.

The NRGR has Quality Control procedures in place to ensure submitted data is valid and can be easily integrated into data exploration tools.

Greater details about file formats, samples files, and templates can be found on our QC Help Page.

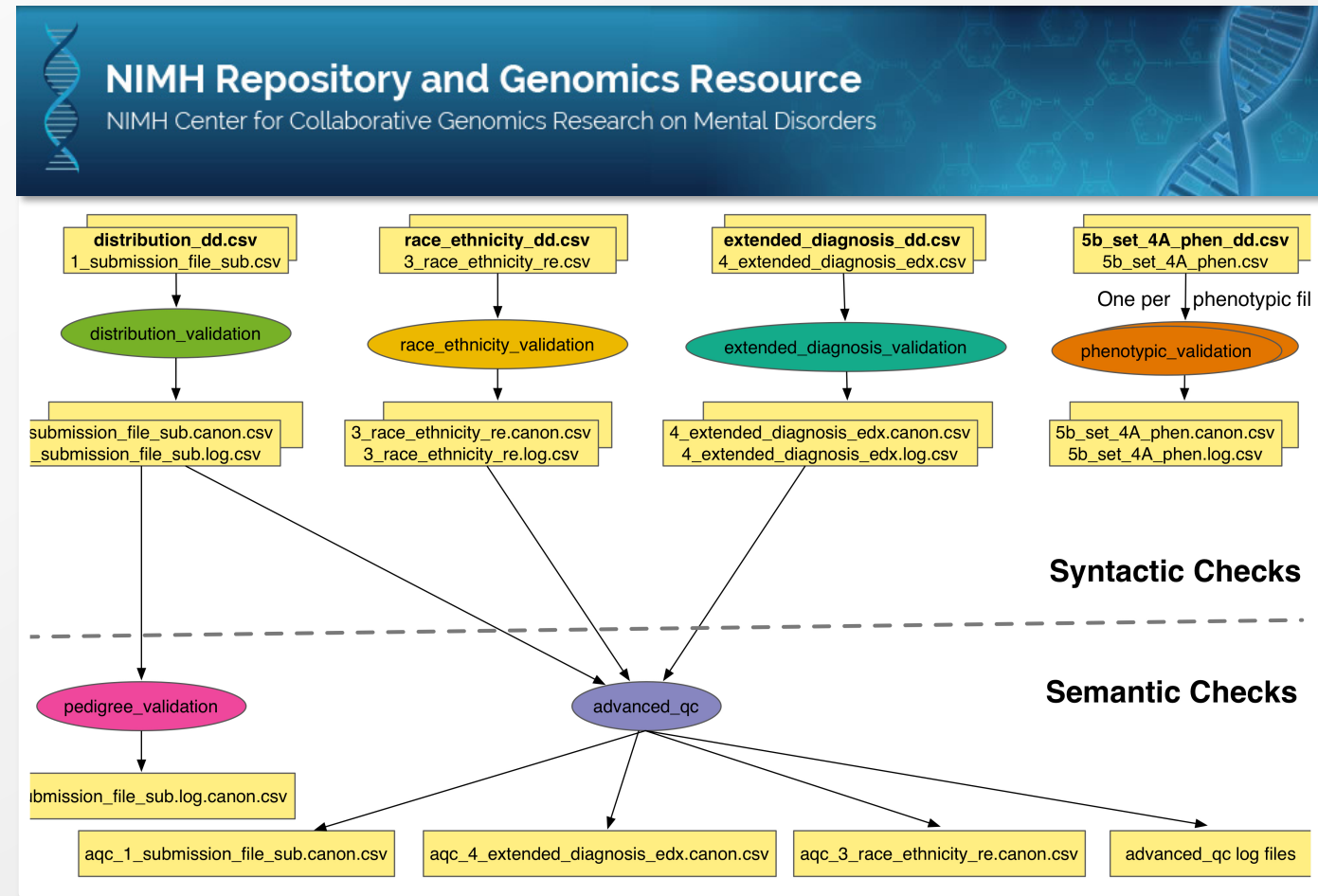
QC HELP PAGE

zip submission

Submissions to the Auto QC System must be a .zip file containing:

- _sub file** (required): The main file in the submission that includes demographic information, ID numbers, and study-defined diagnoses. This file is identical across all diseases.
- _dx file** (required): A simple file with three columns: key, value, & description. "key" is the shorthand version used in the _sub file ("SZ"); "value" is what the key stands for ("schizophrenia") and "description" is the method by which your study defined diagnoses.
- edx file**

Accepted file formats: CSV, TXT



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Pegasus Workflow Management System

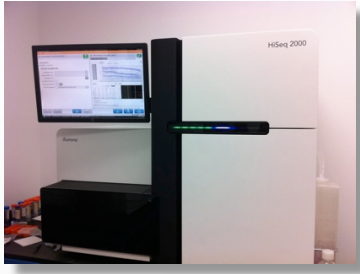
3

Challenges and solutions for workflow execution in clusters, distributed systems, and clouds

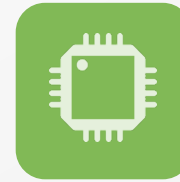
4

Future Directions

Sometimes the environment is complex...



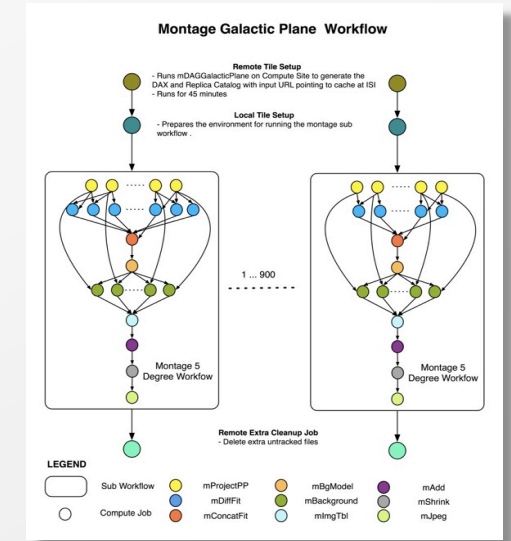
Data
Storage



Local
Resource



Work Definition



Campus Cluster

XSEDE

NERSC

ALCF

OLCF

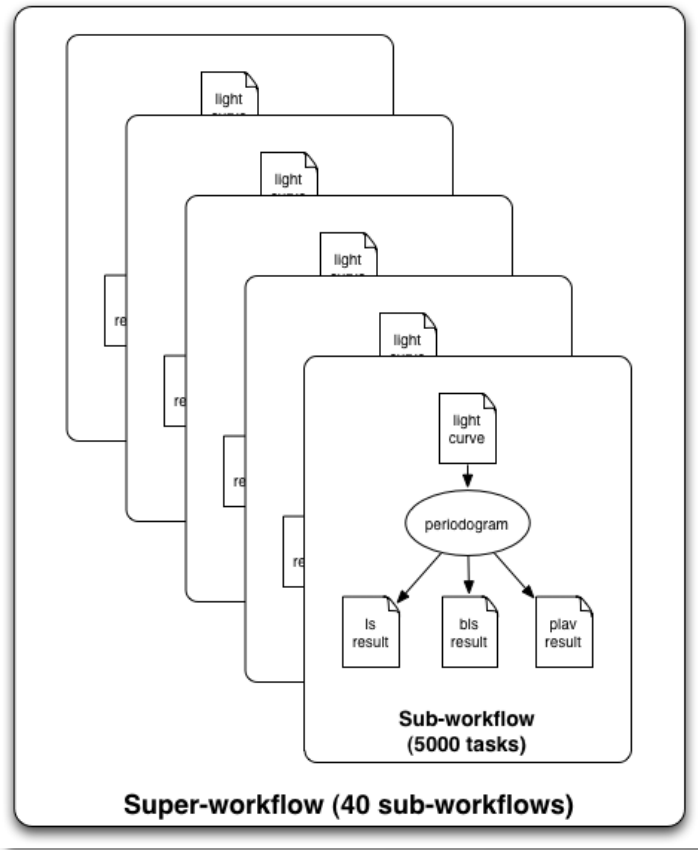
OSG

Chameleon

Amazon Cloud

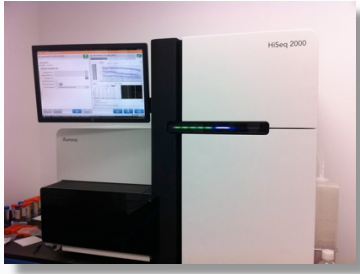
Sometimes the environment is just not exactly right

Single core workload

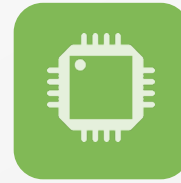


Cray XK7 System Environment / Designed for MPI codes

Sometimes you want to change or combine resources



Data Storage

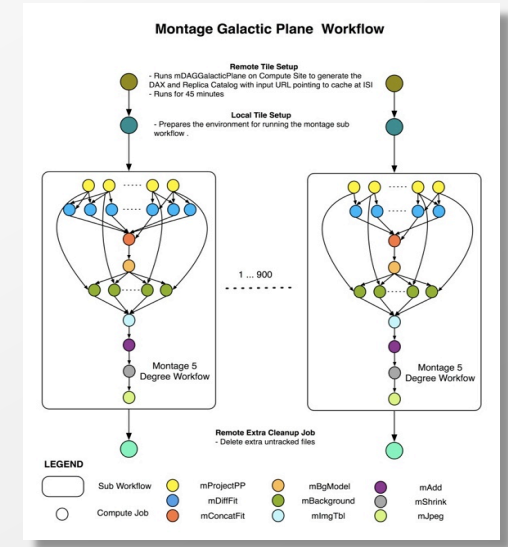


Local Resource

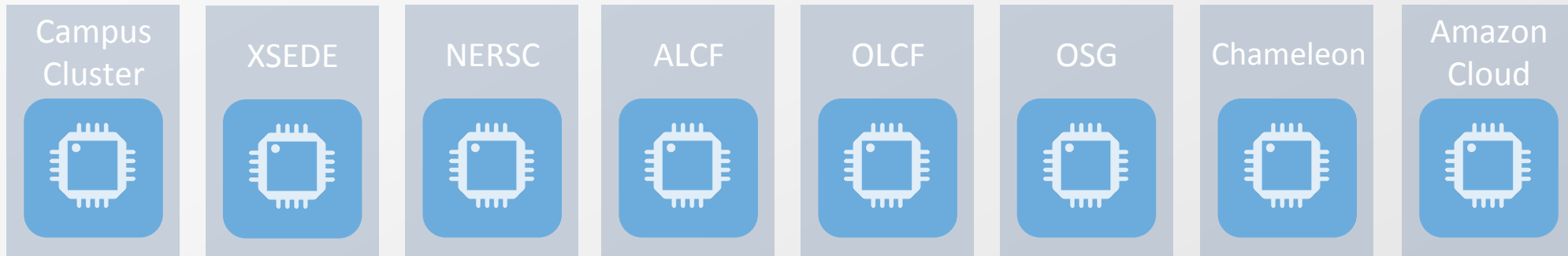
data

Work Definition

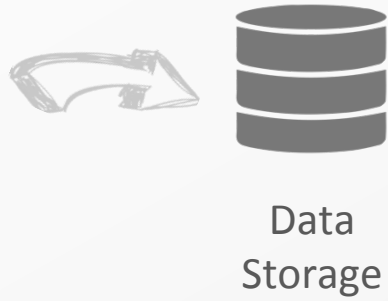
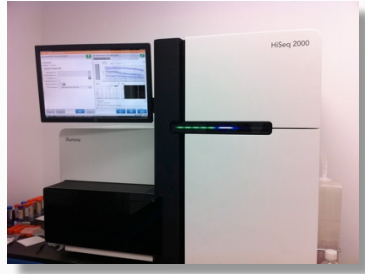
work



You don't want to recode your workflow



Our Approach: Submit locally, Compute globally



Local Resource

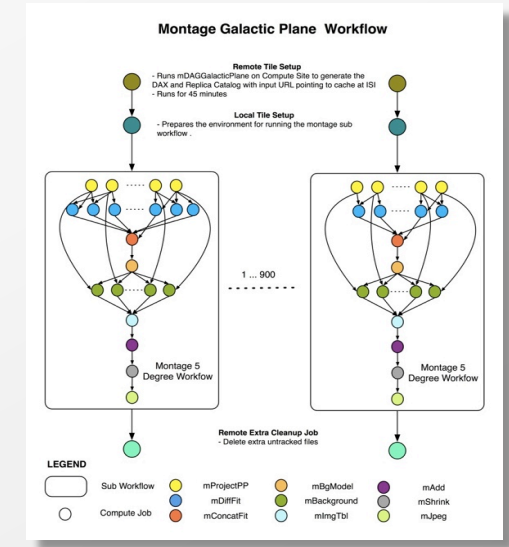
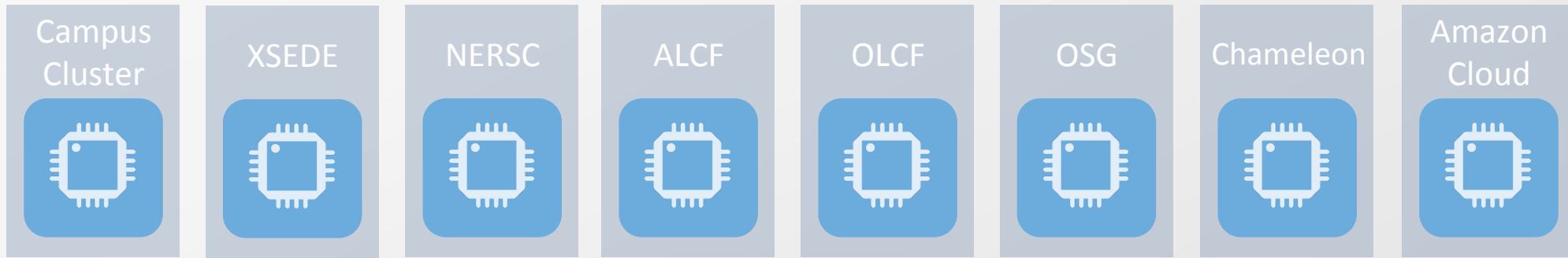


Workflow Management System

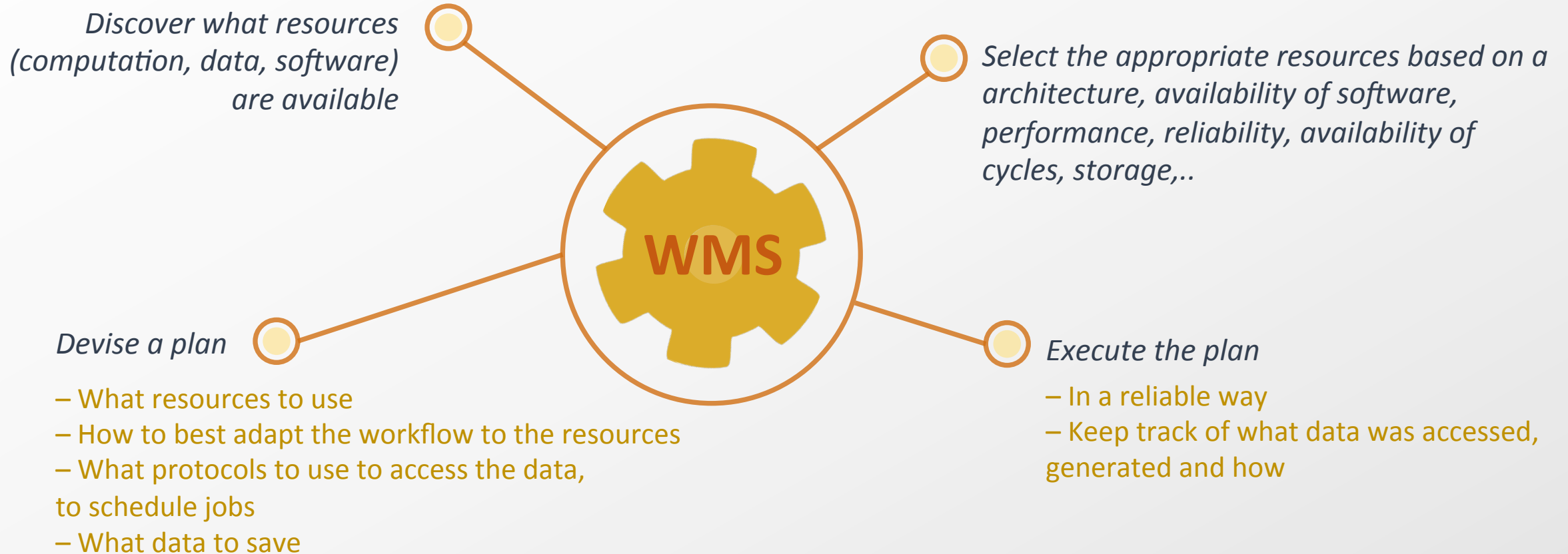


Work Definition

work



Workflow Management System (WMS) Functions



Currently outside of the WMS functions

- Resource provisioning

Pegasus Workflow Management System (est. 2001)

Collaboration with HTCondor, UW Madison

A workflow “compiler”/planner

- Input: abstract workflow description, resource-independent
- Auxiliary Info (catalogs): available resources, data, codes
- Output: executable workflow with concrete resources
- Automatically locates physical locations for both workflow tasks and data
- Transforms the workflow for performance and reliability

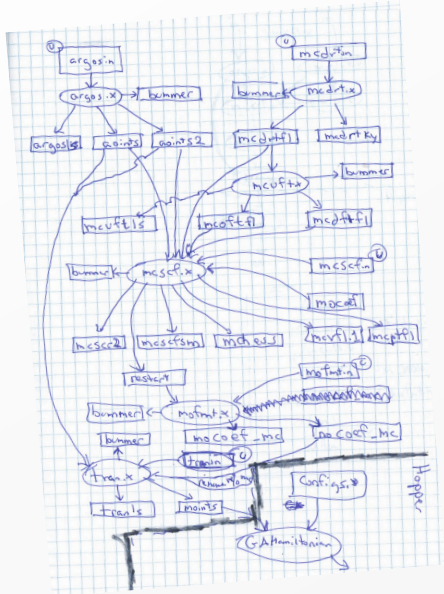
A workflow engine (DAGMan)

- 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*

Pegasus provides tools to generate the abstract workflow



```
#!/usr/bin/env python
from Pegasus.DAX3 import *
import sys
import os

# Create a abstract dag
dax = ADAG("hello_world")

# Add the hello job
hello = Job(namespace="hello_world",
            name="hello", version="1.0")
b = File("f.b")
hello.uses(a, link=Link.INPUT)
hello.uses(b, link=Link.OUTPUT)
dax.addJob(hello)

# Add the world job (depends on the hello job)
world = Job(namespace="hello_world",
            name="world", version="1.0")
c = File("f.c")
world.uses(b, link=Link.INPUT)
world.uses(c, link=Link.OUTPUT)
dax.addJob(world)

# Add control-flow dependencies
dax.addDependency(Dependency(parent=hello,
                             child=world))

# Write the DAX to stdout
dax.writeXML(sys.stdout)
```

```
<?xml version="1.0" encoding="UTF-8"?>
<!-- generator: python -->
<adag xmlns="http://pegasus.isi.edu/schema/DAX"
      version="3.4" name="hello_world">

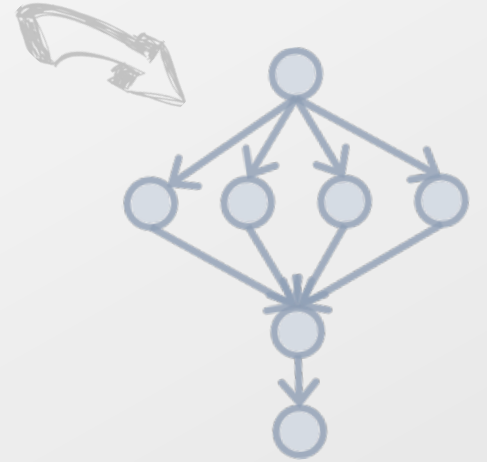
  <!-- describe the jobs making
  up the hello world pipeline -->
  <job id="ID0000001" namespace="hello_world"
       name="hello" version="1.0">

    <uses name="f.b" link="output"/>
    <uses name="f.a" link="input"/>
  </job>

  <job id="ID0000002" namespace="hello_world"
       name="world" version="1.0">

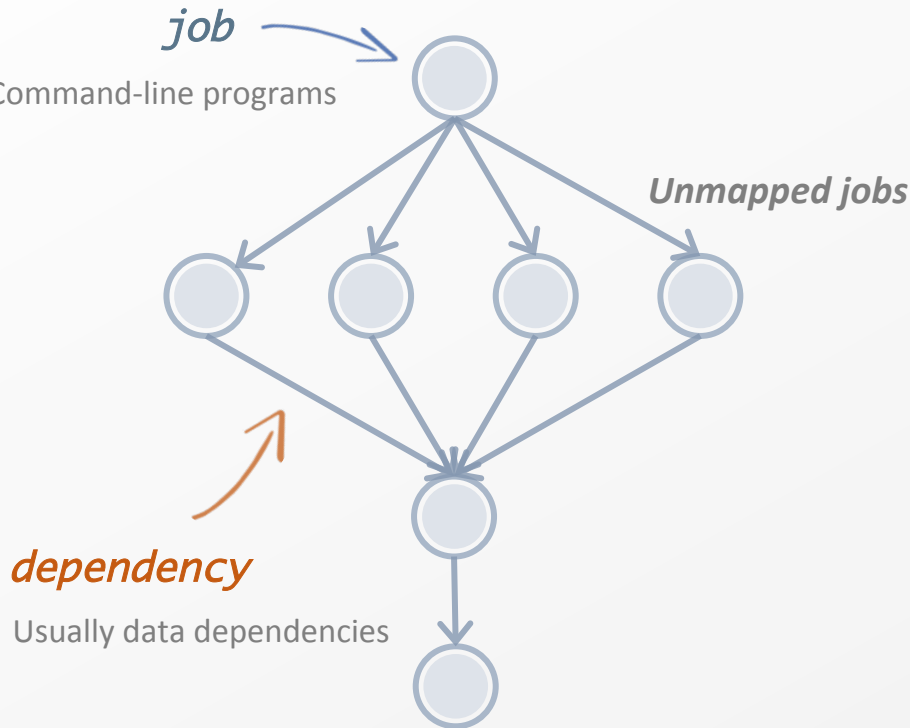
    <uses name="f.b" link="input"/>
    <uses name="f.c" link="output"/>
  </job>

  <!-- describe the edges in the DAG -->
  <child ref="ID0000002">
    <parent ref="ID0000001"/>
  </child>
</adag>
```



DAG in XML

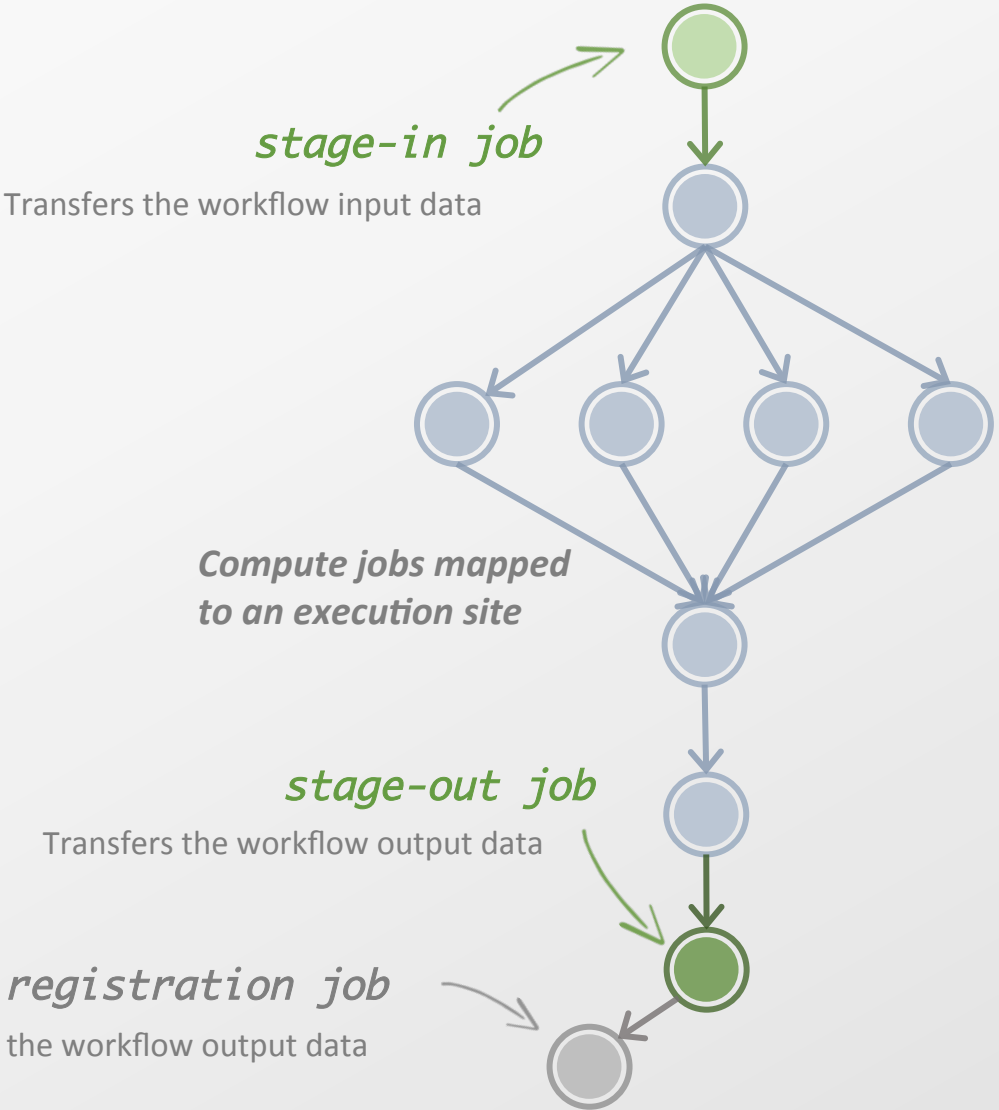
From the abstraction to execution!



abstract workflow

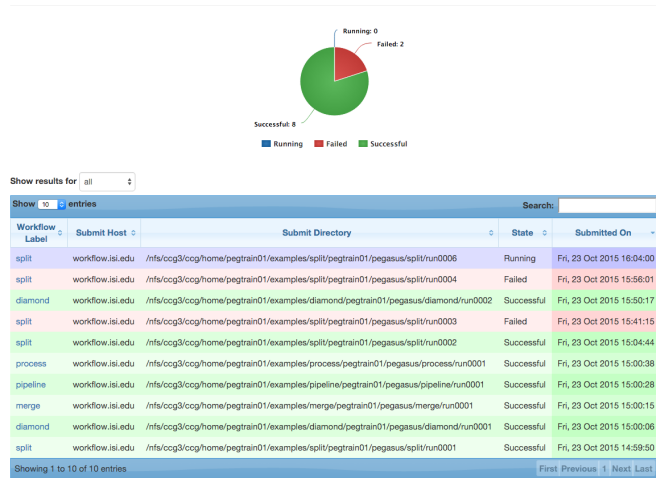


Information Catalogs



executable workflow

Workflow Listing



Pegasus dashboard

web interface for monitoring and debugging workflows

Statistics

Workflow Wall Time	12 mins 23 secs
Workflow Cumulative Job Wall Time	9 mins 34 secs
Cumulative Job Walltime as seen from Submit Side	9 mins 35 secs
Workflow Cumulative Badput Time	9 mins 23 secs
Cumulative Job Badput Walltime as seen from Submit Side	9 mins 20 secs
Workflow Retries	1

This Workflow						
Type	Succeeded	Failed	Incomplete	Total	Retries	Total + Retries
Tasks	5	0	0	5	0	5
Jobs	16	0	0	16	2	18
Sub Workflows	0	0	0	0	0	0

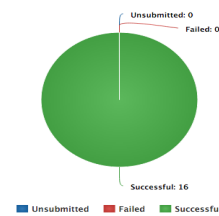
Entire Workflow						
Type	Succeeded	Failed	Incomplete	Total	Retries	Total + Retries
Tasks	5	0	0	5	0	5
Jobs	16	0	0	16	2	18
Sub Workflows	0	0	0	0	0	0

Real-time monitoring of workflow executions. It shows the status of the workflows and jobs, job characteristics, statistics and performance metrics. Provenance data is stored into a relational database.

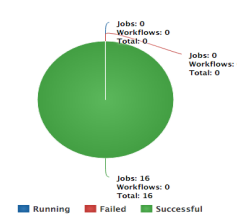
Workflow Details

Label	split
Type	root-wf
Progress	Successful
Submit Host	workflow.isi.edu
User	pegtrain01
Submit Directory	/afs/ccg3/ccg/home/pegtrain01/examples/split/split/run0002
DAGMan Out File	split-0.dag.dagman.out
Wall Time	12 mins 23 secs
Cumulative Wall Time	9 mins 34 secs

Job Status (Entire Workflow)



Job Status (Per Workflow)



Real-time Monitoring
Reporting
Debugging
Troubleshooting
RESTful API

Tools to calculate job statistics

Workflow makespan, Cumulative time

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

Execution profile of the Montage workflow, averages calculated

Outline

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Example Pegasus Workflows

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Pegasus Workflow Management System

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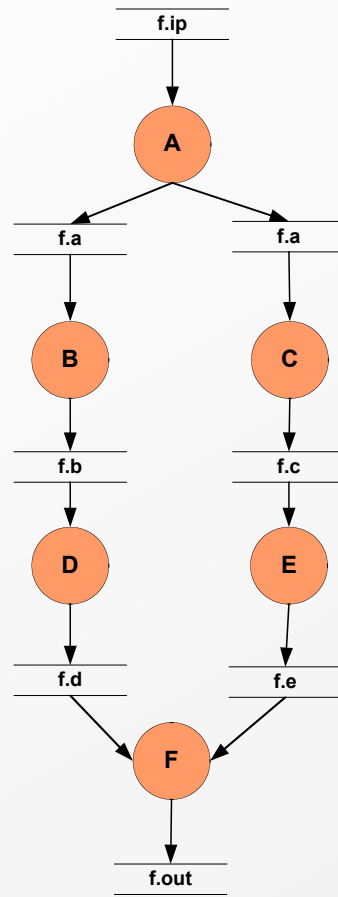
Challenges and solutions for workflow execution in clusters, distributed systems, and clouds

4

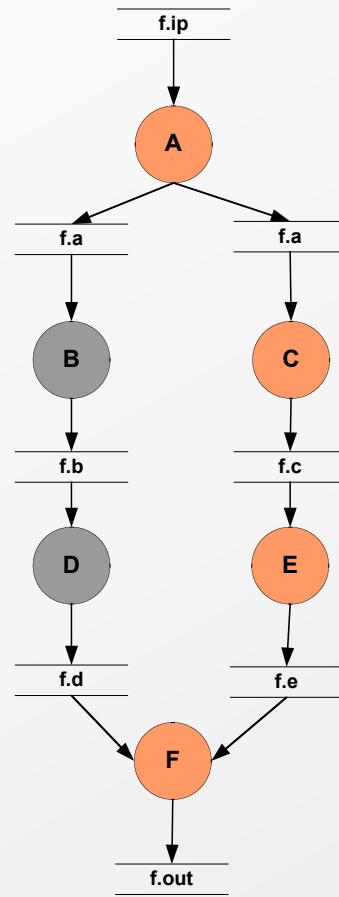
Future Directions

Sometimes fatal errors occur during workflow execution

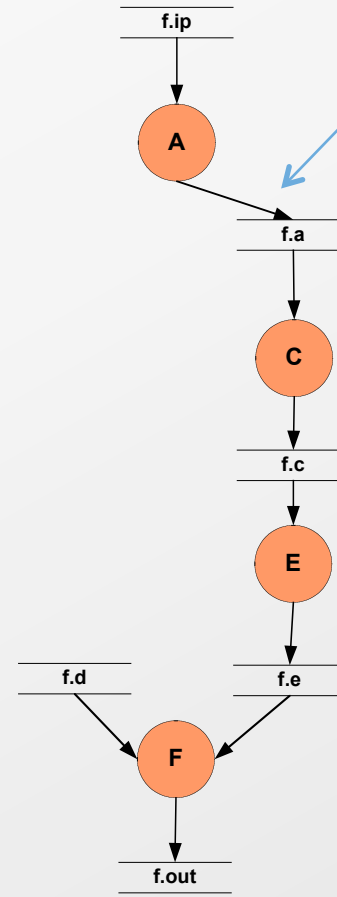
Want to restart the workflow from where it left off
Sometimes intermediate data is already available



Abstract Workflow



File f.d exists somewhere.
Reuse it.
Mark Jobs D and B to delete



Delete Job D and Job B

○ *workflow reduction*

○ *data reuse*

○ *workflow-level checkpointing*

Data Staging Configurations

Condor I/O (HTCondor pools, OSG, ...)

- Worker nodes do not share a file system
- Data is pulled from / pushed to the submit host via HTCondor file transfers
- Staging site is the submit host

Non-shared File System (clouds, OSG)

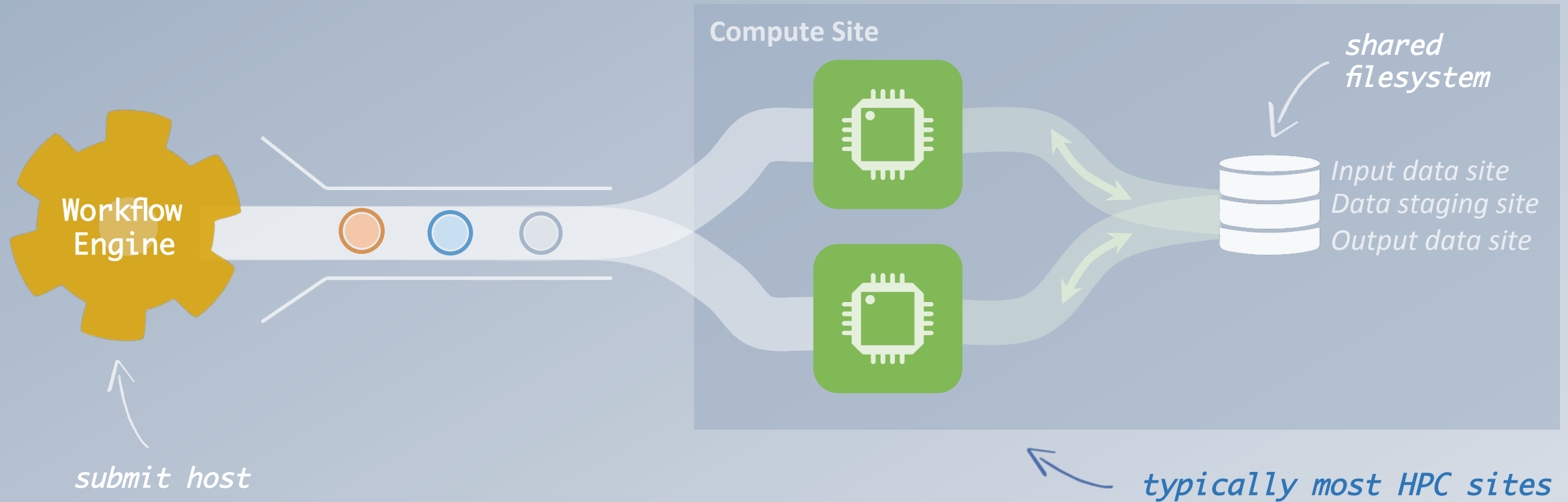
- Worker nodes do not share a file system
- Data is pulled / pushed from a staging site, possibly not co-located with the computation

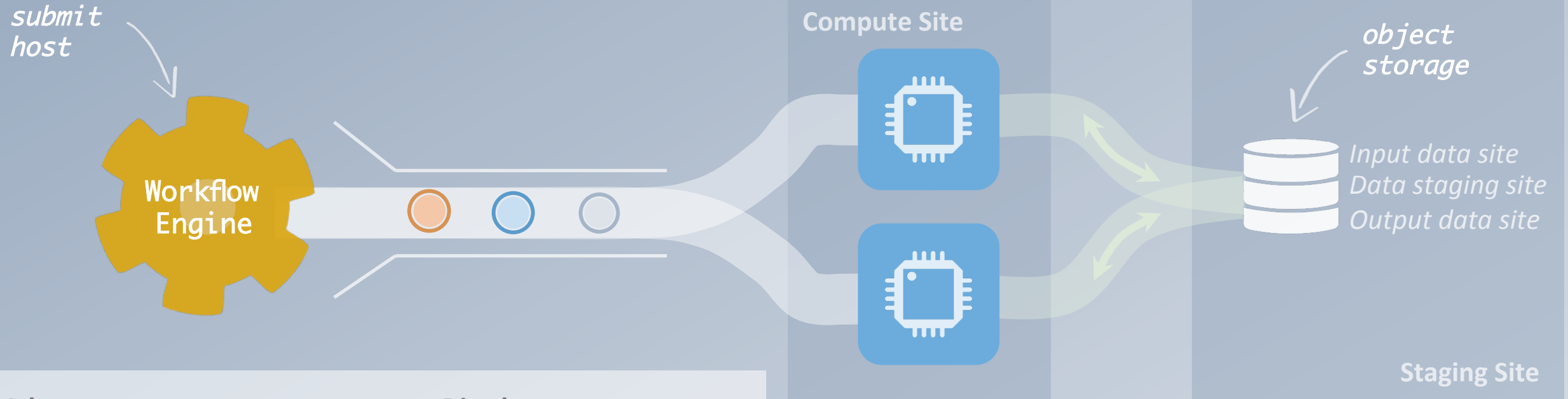
Shared File System (HPC sites, XSEDE, Campus clusters, ...)

- I/O is directly against the shared file system

High Performance Computing

There are several possible configurations...





Advantages

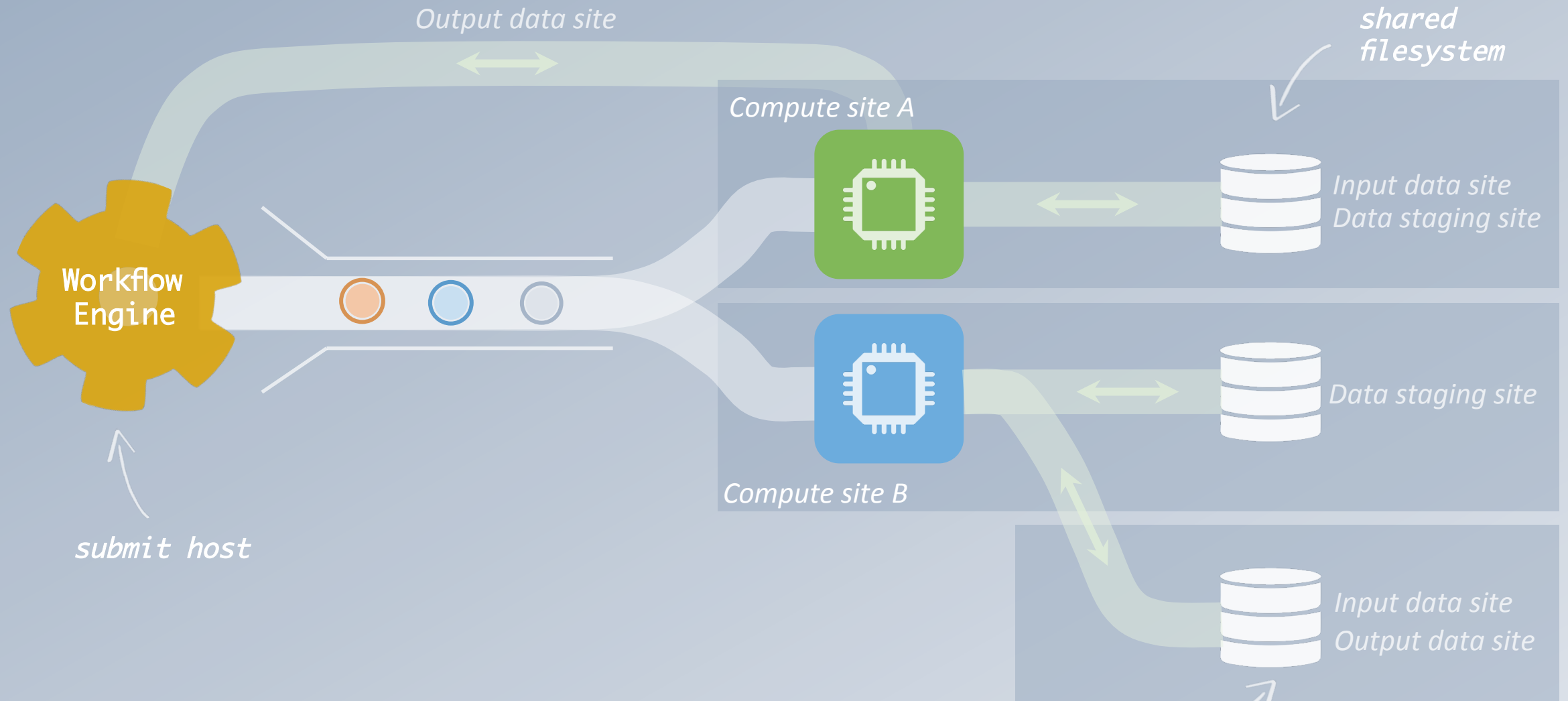
- Can leverage scalable stores
- Distribute computations across resources, such as supporting spillover from local resources to cloud resources
- Great bandwidth

Disadvantages

- Duplicate Transfers
- Latencies in transferring large number of files
- Added costs for duplicate transfers

Typical cloud computing deployment (Amazon S3, Google Storage)

And yes... you can mix everything!



pegasus-transfer

subsystem for various storage systems

Pegasus' internal data transfer tool

Supports many different protocols

Directory creation, file removal

– If protocol supports, used for cleanup

Credential management

– Uses the appropriate credential for each site and each protocol (even 3rd party transfers)

Parallel transfers

Automatic retries

Checkpoint and restart transfers

Two stage transfers

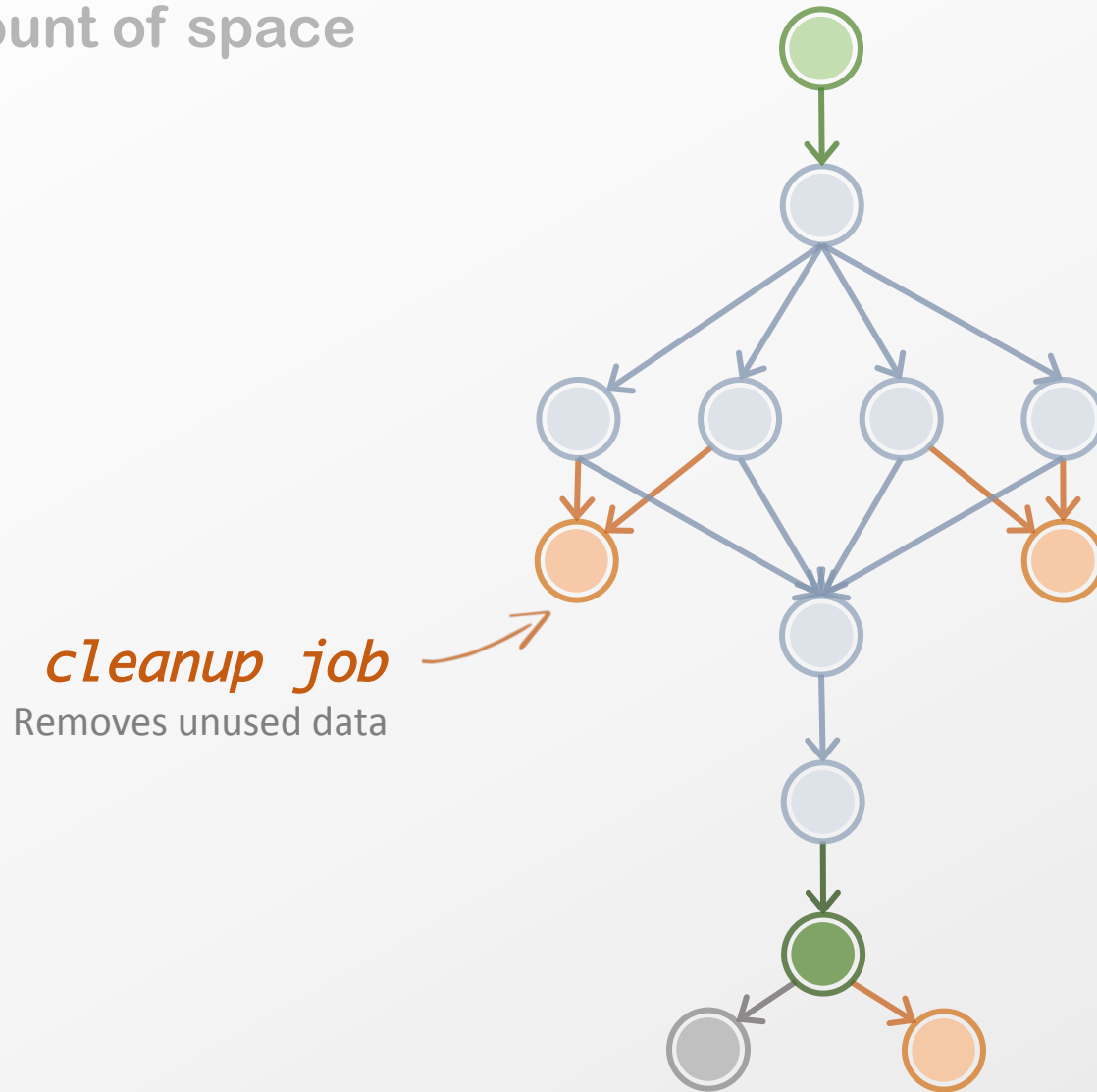
*– e.g. GridFTP to S3 = GridFTP to local file,
local file to S3*

PROTOCOLS

HTTP **SCP** GridFTP **iRods** AmazonS3 **Google Storage** SRM **FDT** stashcp **cp** In -s

Optimizing storage usage...

Small amount of space

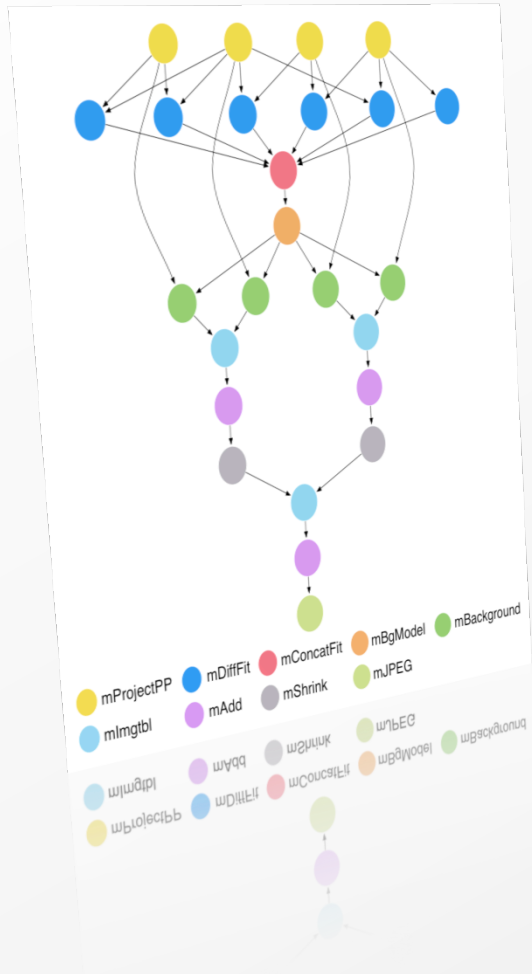


Automatically add tasks to “clean up” data no longer needed

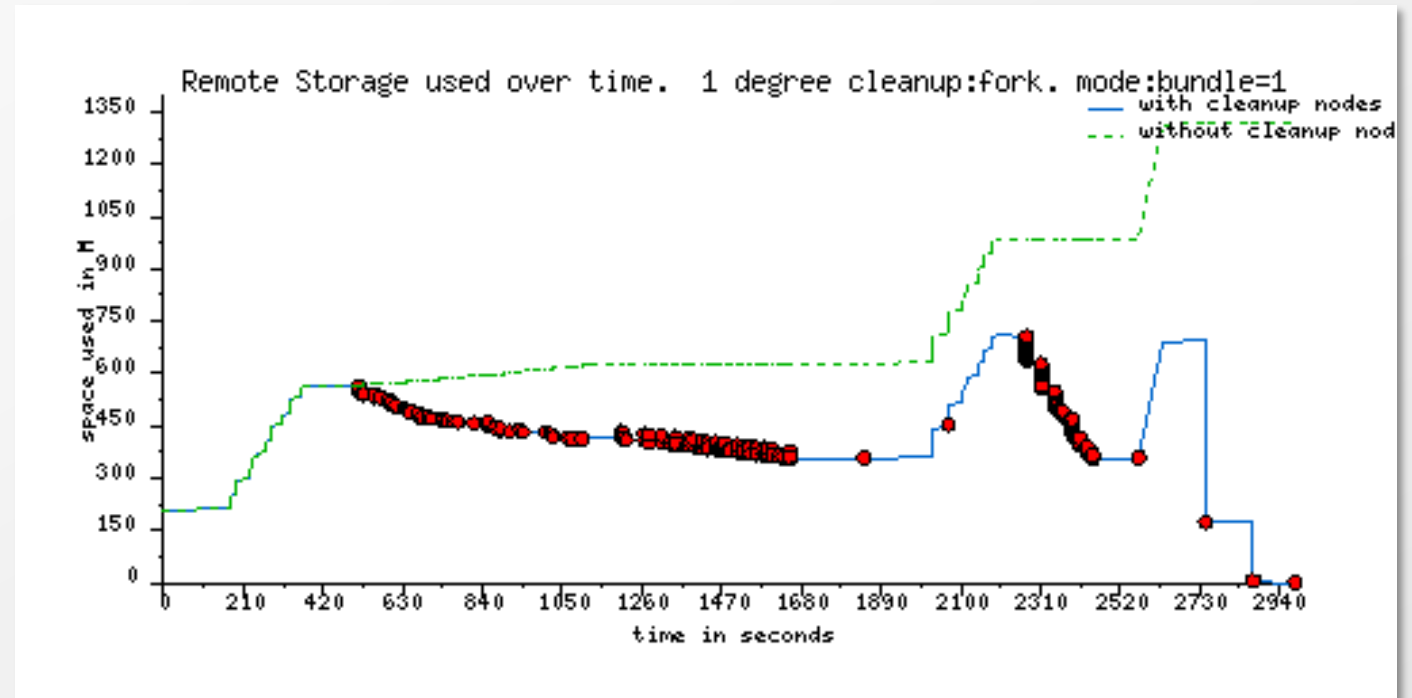
LIGO was running on Open Science Grid resources, processing TBs of data within a single workflow

Optimizing storage usage...

Example of the Montage Astronomy Workflow



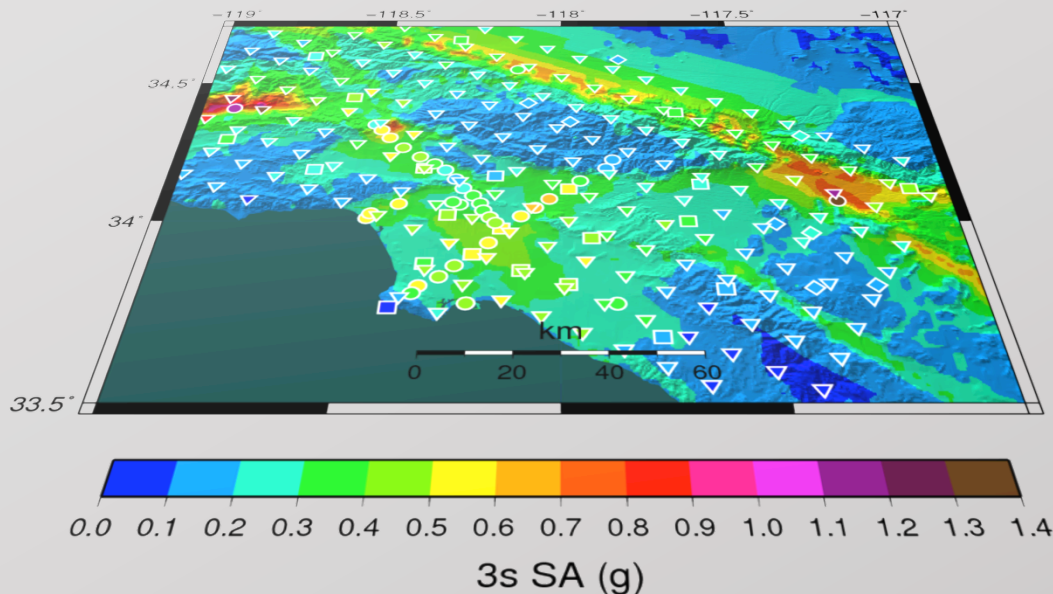
1.25GB versus 700 MB



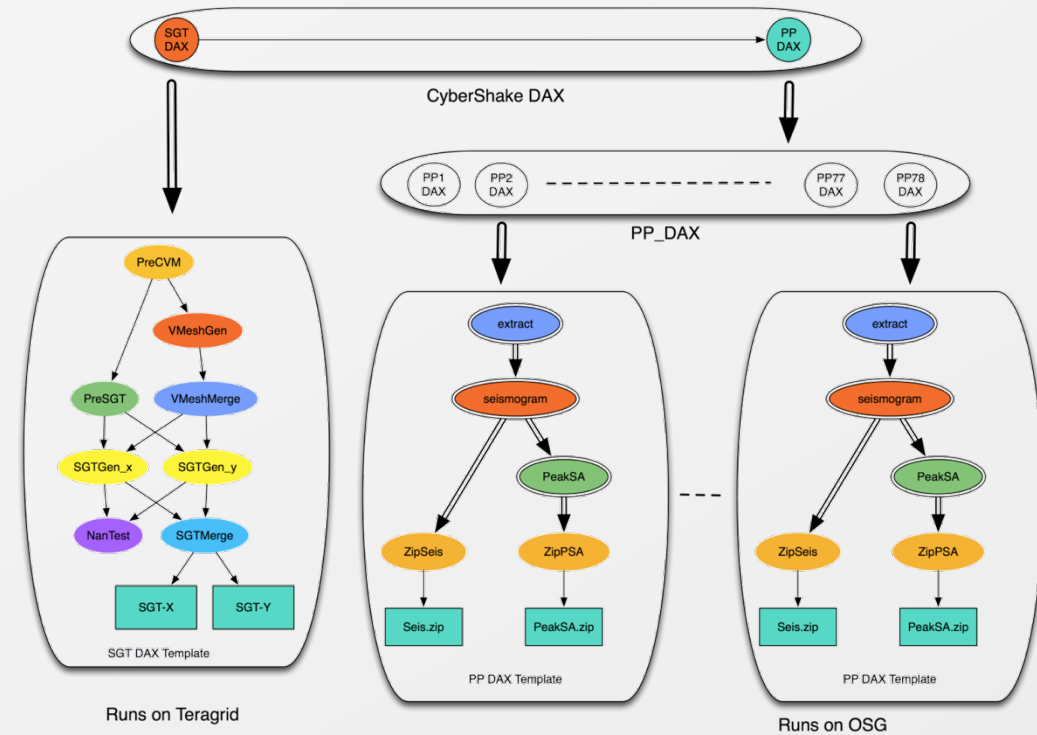
Southern California Earthquake Center's CyberShake PSHA Workflow

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)



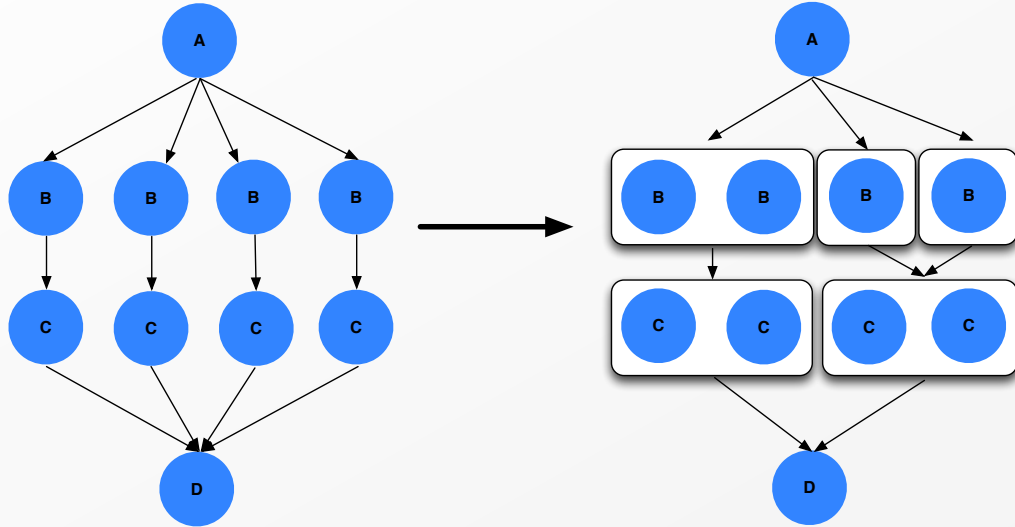
Workload does not match the infrastructure



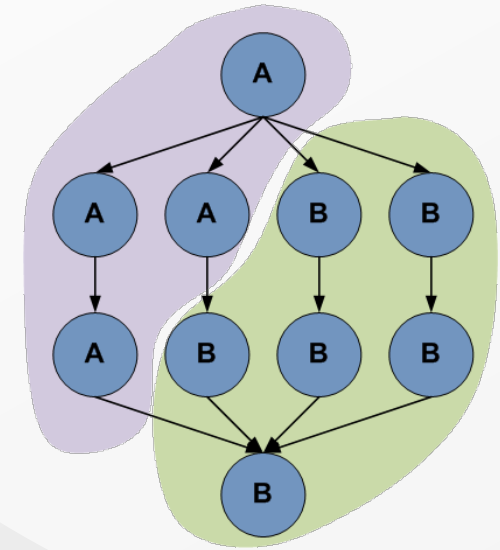
293 workflows
each workflow has 820,000 tasks

Solutions:

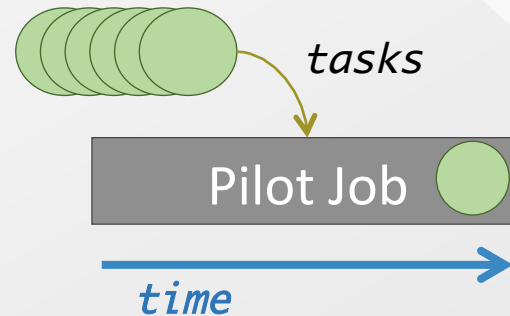
Task clustering



Partition the workflow into sub-workflows and send them for execution to the target system

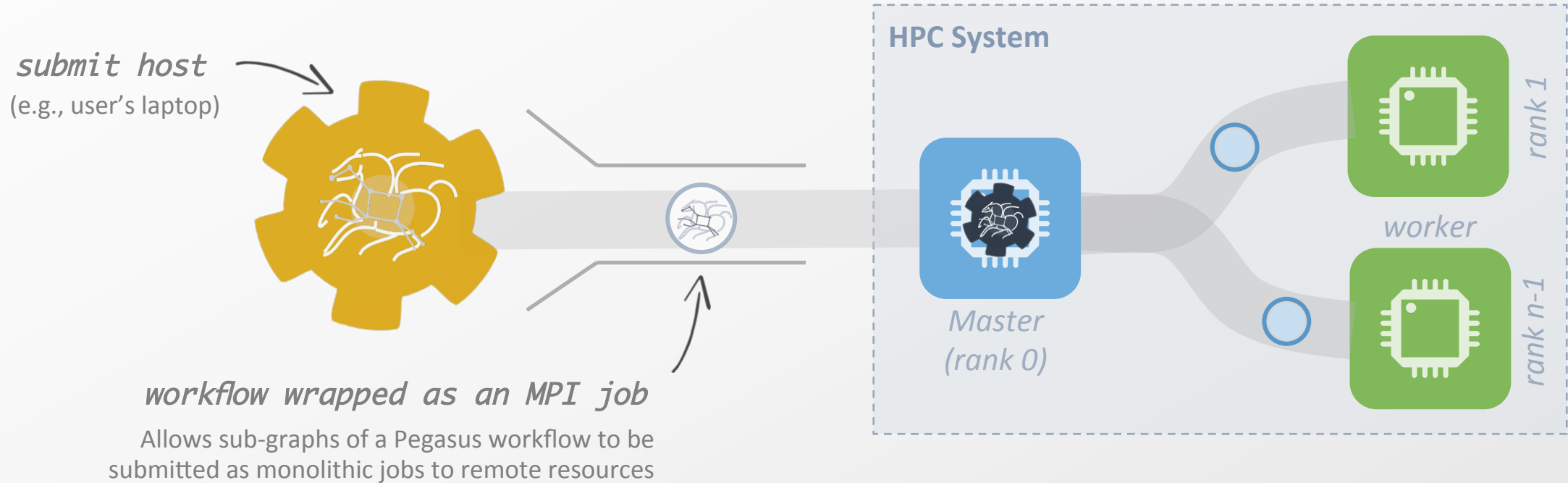


Use "pilot" jobs to dynamically provision a number of resources at a time



Running fine-grained workflows on HPC systems...

Specialized Workflow Engines Needed for Different Execution Sites



Pegasus MPI-Cluster

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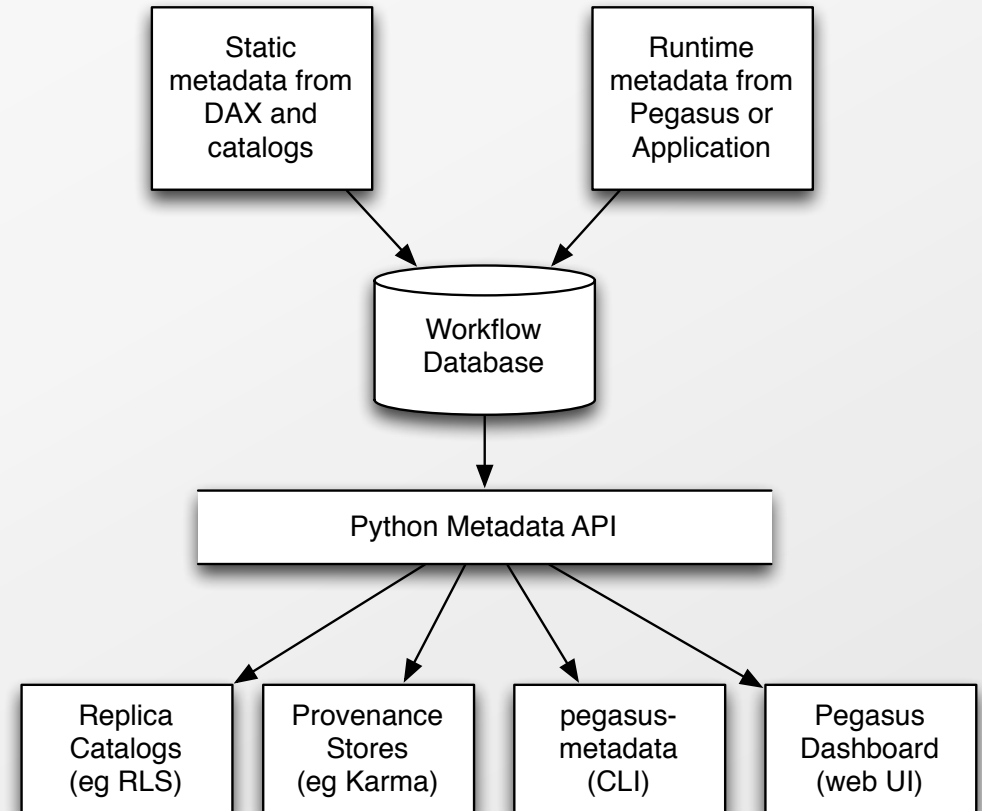
Challenges and solutions for workflow execution in clusters, distributed systems, and clouds

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Future Directions

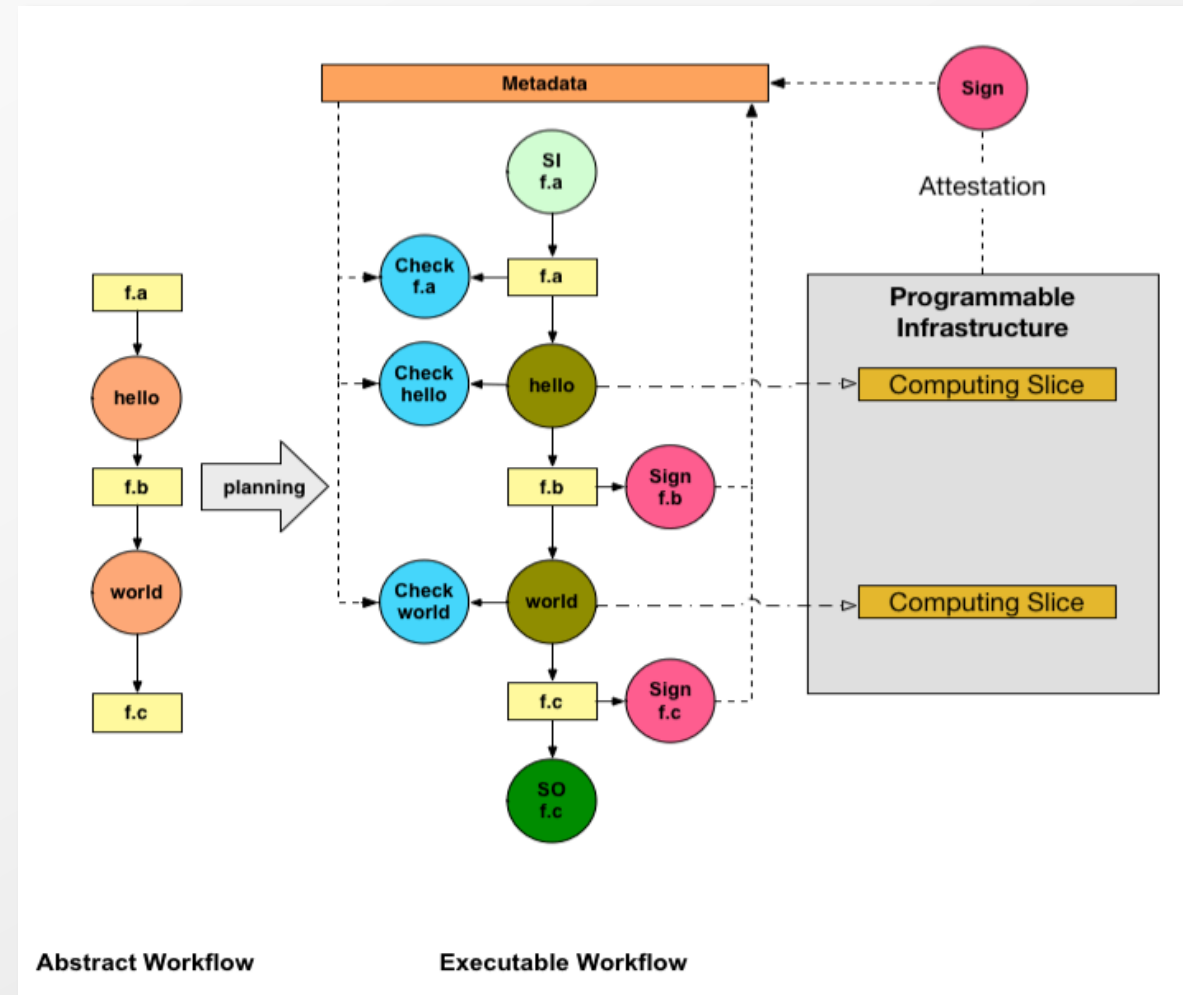
Metadata

- Can associate arbitrary key-value pairs with workflows, jobs, and files
- Replica selection
 - Input files are selected based on metadata attributes
- Data registration
 - Output files get tagged with metadata on registration
- Static and runtime metadata
 - Static: application parameters
 - Runtime: performance metrics



Scientific Workflow Integrity with Pegasus

- Provide additional assurances that a scientific workflow is not accidentally or maliciously tampered with during its execution
- Allow for detection of modification to its data or executables at later dates to facilitate reproducibility
- Integrate cryptographic support for data integrity into the Pegasus Workflow Management System.



Collaboration with Von Welch (IU) and Ilya Baldin (RENCI)

Simple tool to quickly bring up a HTCondor/Pegasus cluster within Jetstream: Bootstraps master/compute nodes

Maintains configuration/credentials using SaltStack

No autoscaling, but nodes can be added/removed at runtime manually

Used by Upendra Kumar Devisett and Susan Miller to run a workflow derived from the OSG Gene Expression Matrix

Future directions in clouds

Support for containers



Better management of elasticity of cloud resources

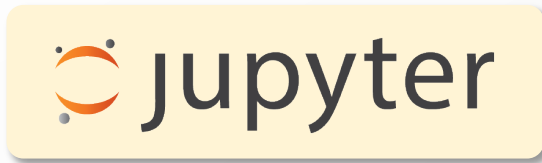
- Worrying about runaway resources
- Develop monitoring algorithms for scaling up and down based on upcoming workflow needs

On the fly deployment through workflows

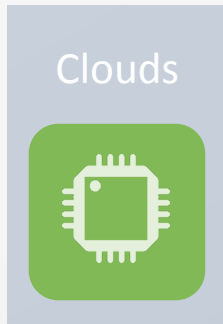
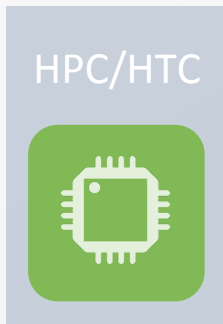
Develop a “cloud cost” calculator to help estimate the cost of workflow execution on the cloud

- Including different types of resources
- Including workflow ensembles

Running Pegasus workflows with Jupyter



WAN LAN



The screenshot shows a Jupyter notebook interface with a menu bar (File, Edit, View, Insert, Cell, Kernel, Widgets, Help) and a toolbar. The main content area displays a Directed Acyclic Graph (DAG) for a workflow named 'Pegasus-Tutorial-Split'. The DAG consists of several nodes: four orange nodes at the top (we_ID000003, we_ID000002, we_ID000005, we_ID000004), several green nodes (clean_up_local_level_4_0, stage_out_local_local_1_1, stage_out_local_local_1_0, clean_up_local_level_4_1, clean_up_local_level_3_0), two yellow nodes (register_local_1_1, register_local_1_0), and one grey node at the bottom (cleanup_split_0_local). Arrows indicate the flow between these nodes. Below the DAG, there is text explaining how to monitor the workflow using the `status()` method, with a list of arguments: `loop` and `delay`. A code cell shows the command `instance.status(loop=True, delay=5)` and its output: `Progress: 100.0% (Success) (Completed: 17, Queued: 0, Running: 0, Failed: 0)`. Further text explains how to retrieve output files using the `outputs()` command.

```
File for submitting this DAG to Condor: split-0.dag.condor.sub
Log of DAGMan debugging messages: split-0.dag.dagman.out
Log of Condor library output: split-0.dag.lib.out
Log of Condor library error messages: split-0.dag.lib.err
Log of the life of condor_dagman itself: split-0.dag.dagman.log

-----
Your database is compatible with Pegasus version: 4.7.0
Submitting to condor split-0.dag.condor.sub
Submitting job(s).
1 job(s) submitted to cluster 1068.

Your workflow has been started and is running in the base directory:
/Users/silva/Downloads/split-submit-host-2017-03-27T10:17:45/submit/silva/pegasus/split/run0002

*** To monitor the workflow you can run ***

pegasus-status -l /Users/silva/Downloads/split-submit-host-2017-03-27T10:17:45/submit/silva/pegasus/split/run0002
```

Pegasus-Jupyter Python API

```
from Pegasus.jupyter.instance import *
```

importing the API

```
instance = Instance(dax)
```

creating an instance of the DAX

```
instance.run(site='condorpool')
```

running a workflow

```
# Create an abstract dag
```

```
dax = ADAG("split")
```

```
# the split job that splits the webpage into smaller chunks
```

```
split = Job("split")
```

```
split.addArguments("-l", "100", "-a", "1", webpage, "part.")
```

```
split.uses(webpage, link=Link.INPUT)
```

```
# associate the label with the job. All jobs with same label
```

```
# are run with PMC when doing job clustering
```

```
split.addProfile( Profile("pegasus", "label", "p1"))
```

```
dax.addJob(split)
```

using the Pegasus DAX3 API to write a workflow



```
instance.status(loop=True, delay=5)
```

monitoring a workflow execution

```
Progress: 100.0% (Success)
```

```
(Completed: 17, Queued: 0, Running: 0, Failed: 0)
```

Το βε ρελεασεδ ωιτη:

 Pegasus 4.8

Ease of use and data focus

Enhancing ease of use of tools

- Workflow composition via R – available now
- Easier reuse
- Exploring integration with Jupyter Notebook

Enhanced data management

- Collecting and archiving data from sensors and instruments
- Adding data management primitives

Focus on *live* processing

- Analysis of instrumental data on the fly
- Coupling simulation and data mining/visualization “in-situ” – within an HPC system

Reproducibility, transparency, reuse

- Explore how we can capture, quantify, publish workflows in a reproducible way



Pegasus est. 2001

Automate, recover, and debug scientific computations.

Get Started

Pegasus Website

<http://pegasus.isi.edu>

Users Mailing List

pegasus-users@isi.edu

Support

pegasus-support@isi.edu

We welcome the opportunity to work with new applications and enhance our solutions based on user's needs.

HipChat

