



U.S. DEPARTMENT OF  
**ENERGY**



# Compute Pipelines with Pegasus: An Introduction

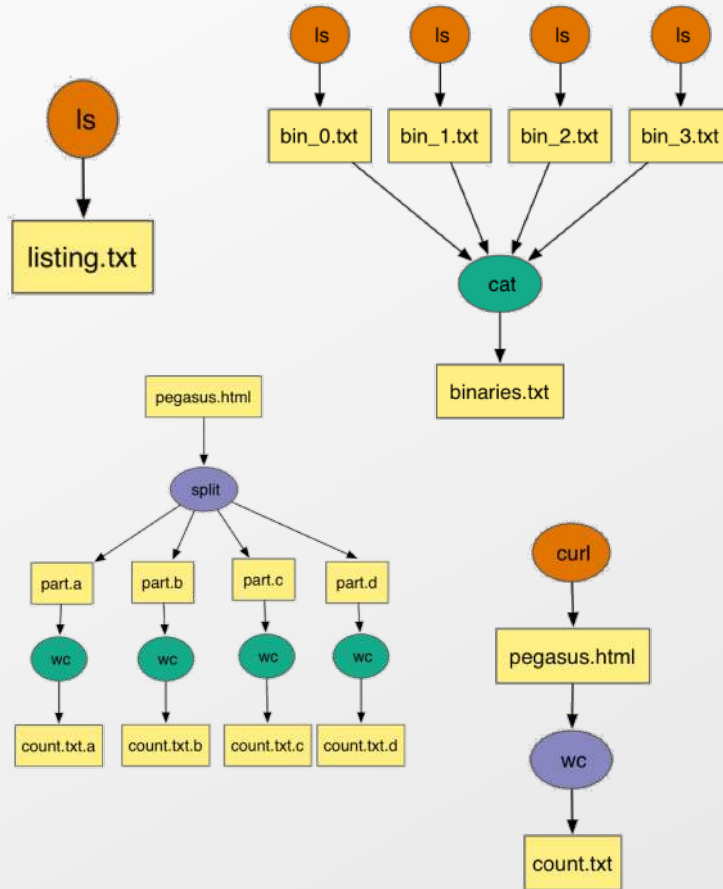
Pegasus Workflow Management System

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Karan Vahi



# Compute Pipelines Building Blocks



## Compute Pipelines

Allows scientists to connect different codes together and execute their analysis

Pipelines can be very simple (independent or parallel) jobs or complex represented as DAG's

Helps users to automate scale up

However, it is still up-to user to figure out

## Data Management

How do you ship in the small/large amounts data required by your pipeline and protocols to use?

## How best to leverage different infrastructure setups

OSG has no shared filesystem while XSEDE and your local campus cluster has one!

## Debug and Monitor Computations

Correlate data across lots of log files

Need to know what host a job ran on and how it was invoked

## Restructure Workflows for Improved Performance

Short running tasks? Data placement

# Why Pegasus ?

**Automates** complex, multi-stage processing pipelines

Enables parallel, **distributed** computations

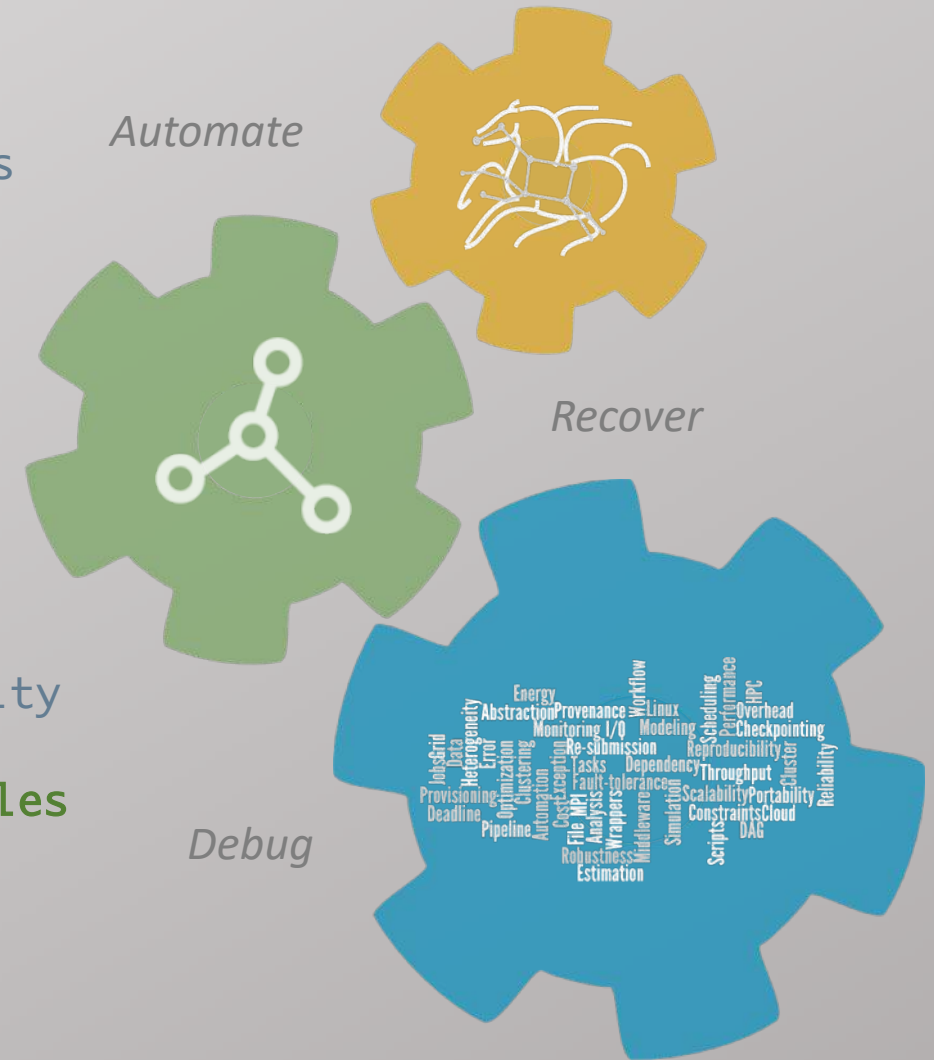
Automatically executes data transfers

Reusable, aids **reproducibility**

Records how data was produced (**provenance**)

Handles **failures** with to provide reliability

Keeps track of data and **files**



NSF funded project since 2001,  
with close collaboration with  
HTCCondor team

Some of the successful stories...

# Advanced LIGO PyCBC Workflow

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

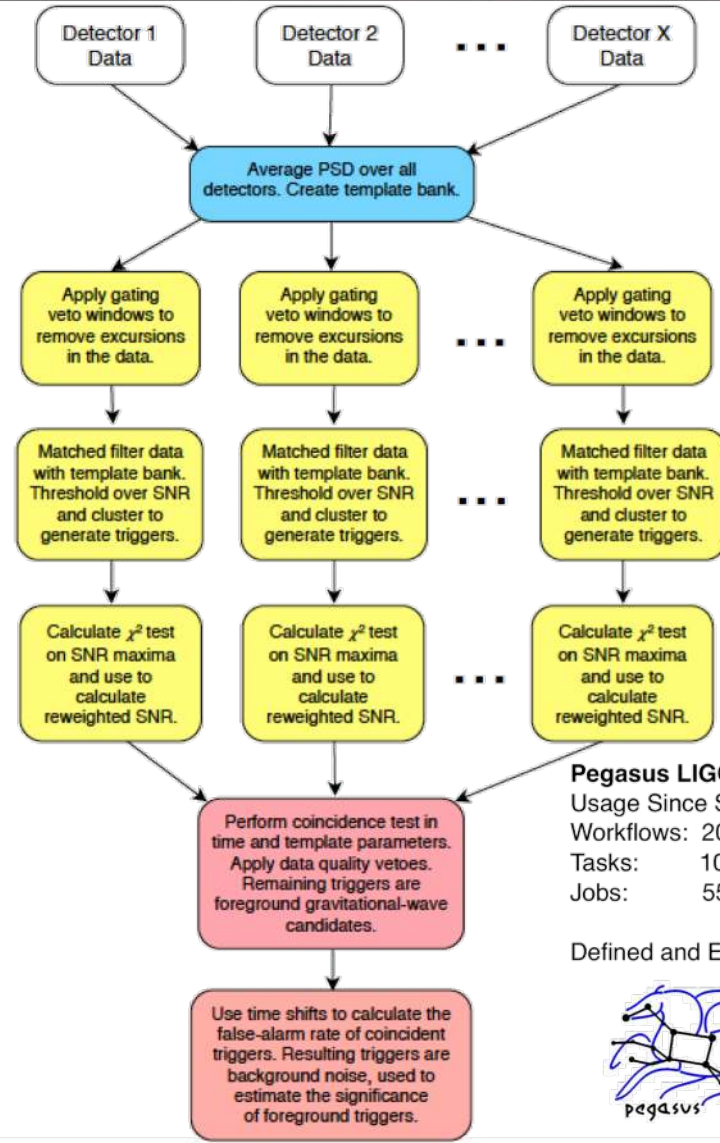
Contains **100's of thousands of jobs** and accesses on order of **terabytes of data**

Uses data from multiple detectors

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

A single run of the binary black hole + binary neutron star search through the O1 data (about 3 calendar months of data with 50% duty cycle) requires a **workflow** with **194,364 jobs**

Generating the final O1 results with all the review required for the first discovery took about **20 million core hours**



# Benefits to LIGO provided by Pegasus- Expanded Computing Horizons

- No longer limited to a single execution resource
  - Non Pegasus LIGO pipelines can often only run on LIGO clusters
  - Input is replicated out of band , in a rigid directory layout.
  - Rely on the shared filesystem to access data.
- Pegasus made it possible to leverage Non LDG Computing Resources
  - Open Science Grid
    - Dynamic – Best Effort Resource with no shared filesystem available
  - Large NSF Supercomputing Clusters XSEDE
    - No HTCondor
    - Geared for Large MPI jobs, not thousands of single node jobs
    - LIGO tried to setup XSEDE cluster as a LDG site but mismatch in setup.
    - Pegasus enabled LIGO to use XSEDE without changes at LIGO or at XSEDE
  - VIRGO Resources in Europe
    - Clusters with no shared filesystem and different storage management infrastructure than LDG
    - No HTCondor

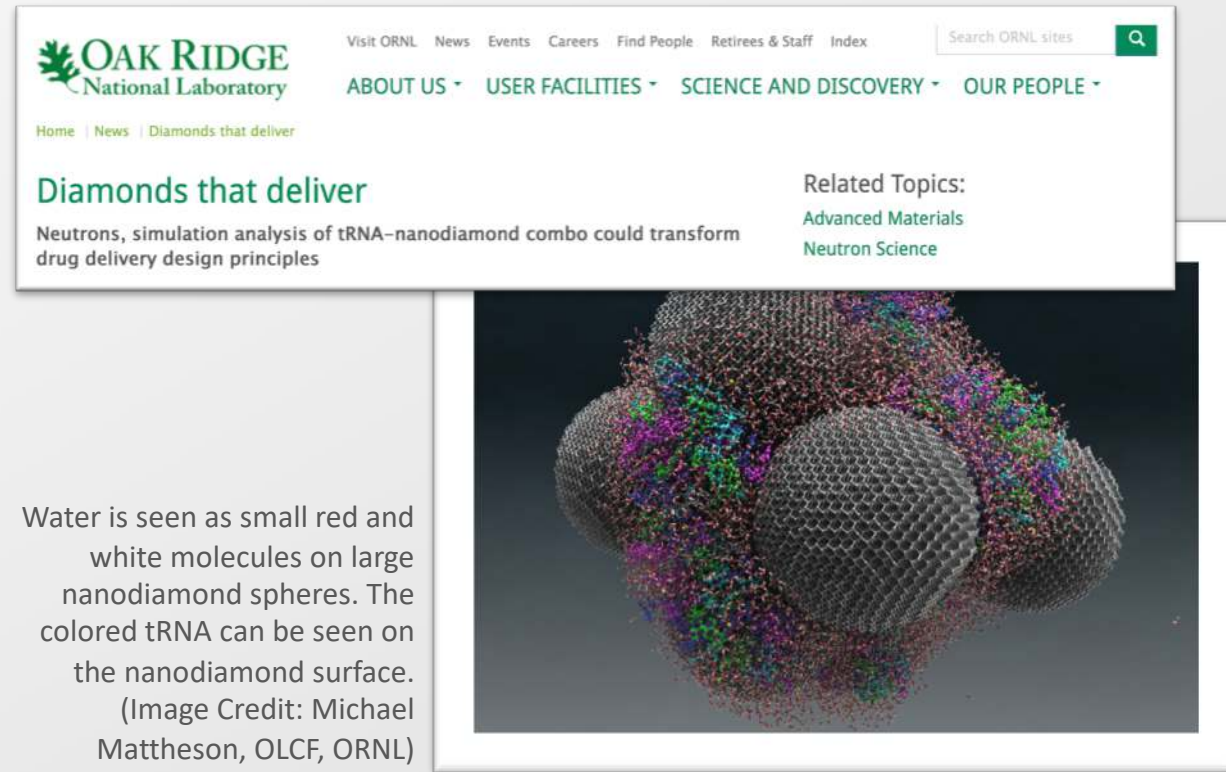


# Impact on DOE Science

Enabled cutting-edge domain science (e.g., drug delivery) through collaboration with scientists at the DoE **Spallation Neutron Source (SNS)** facility

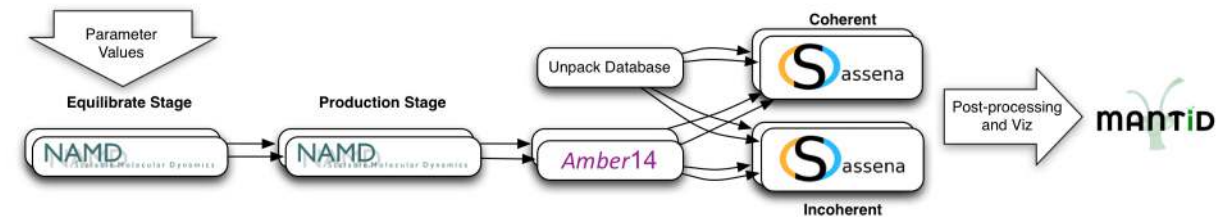
A Pegasus workflow was developed that confirmed that **nanodiamonds** can enhance the dynamics of tRNA

It compared SNS neutron scattering data with MD simulations by calculating the epsilon that best matches experimental data



The screenshot shows the Oak Ridge National Laboratory website. The main headline is "Diamonds that deliver" with a sub-headline: "Neutrons, simulation analysis of tRNA-nanodiamond combo could transform drug delivery design principles". To the right, under "Related Topics", are "Advanced Materials" and "Neutron Science". Below the text is a 3D visualization of a nanodiamond sphere (a cluster of grey spheres) with small red and white spheres (water molecules) and colored dots (tRNA) on its surface.

Water is seen as small red and white molecules on large nanodiamond spheres. The colored tRNA can be seen on the nanodiamond surface.  
(Image Credit: Michael Mattheson, OLCF, ORNL)



*An automated analysis workflow for optimization of force-field parameters using neutron scattering data.* V. E. Lynch, J. M. Borreguero, D. Bhowmik, P. Ganesh, B. G. Sumpter, T. E. Proffen, M. Goswami, *Journal of Computational Physics*, July 2017.

# Data Movement In Production Runs

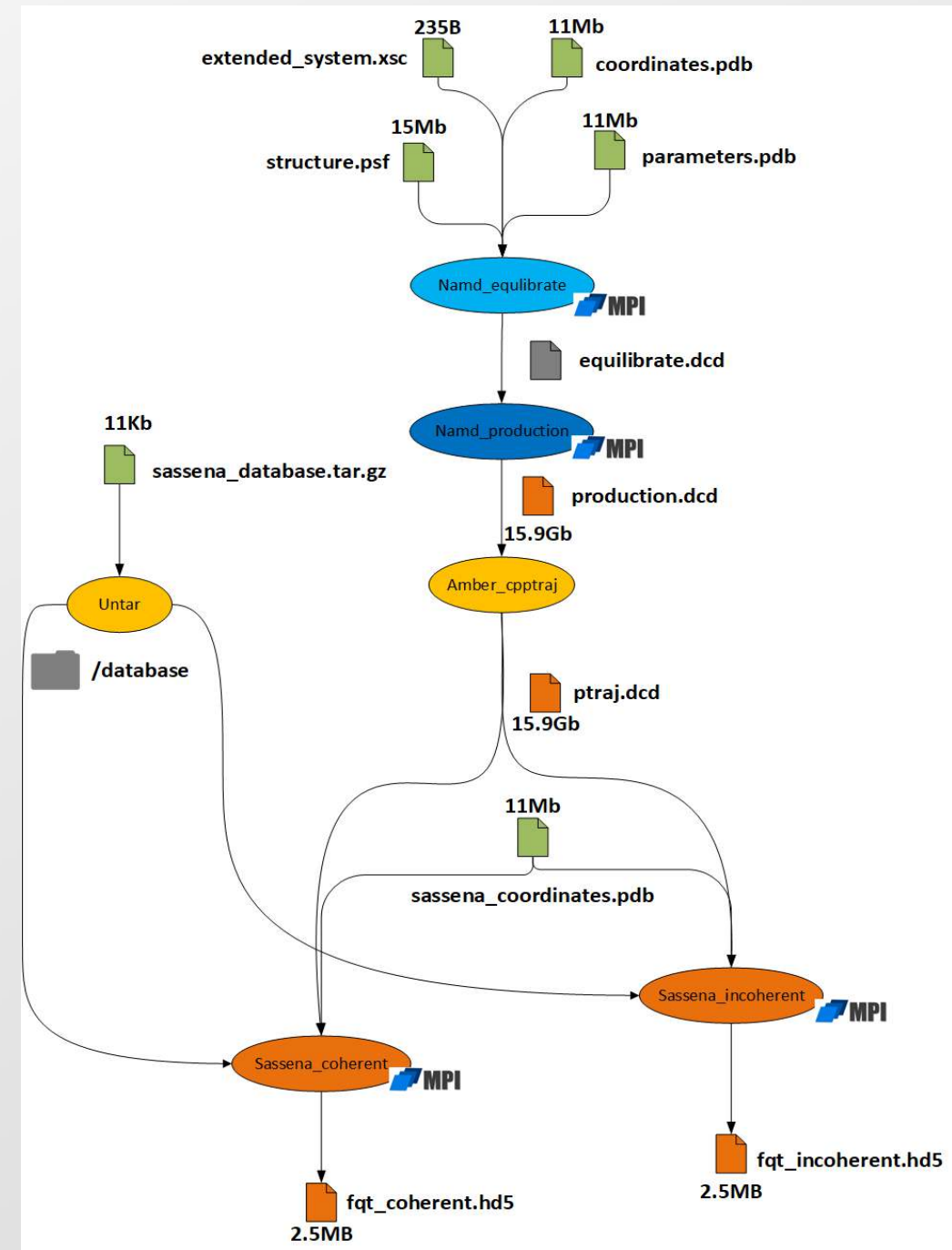
During production runs a single SNS workflow was staging in 48Mb of data (ie. input parameters) and it was generating over 30Gb of data.

Multiple runs, with variable input parameters, conducted on a Cray XE6 at NERSC using 400,000 CPU hours, and generated approximately 3TB of data.

**Green files:** Input data staged in the execution site by Pegasus

**Red files:** Output data staged out of the execution by Pegasus

**Gray files:** Temporary data





# Key Pegasus Concepts

Pegasus WMS == Pegasus planner (mapper) + DAGMan workflow engine + HTCondor scheduler/broker

Pegasus maps workflows to infrastructure

DAGMan manages dependencies and reliability

HTCondor is used as a broker to interface with different schedulers

## Workflows are DAGs

Nodes: jobs, edges: dependencies

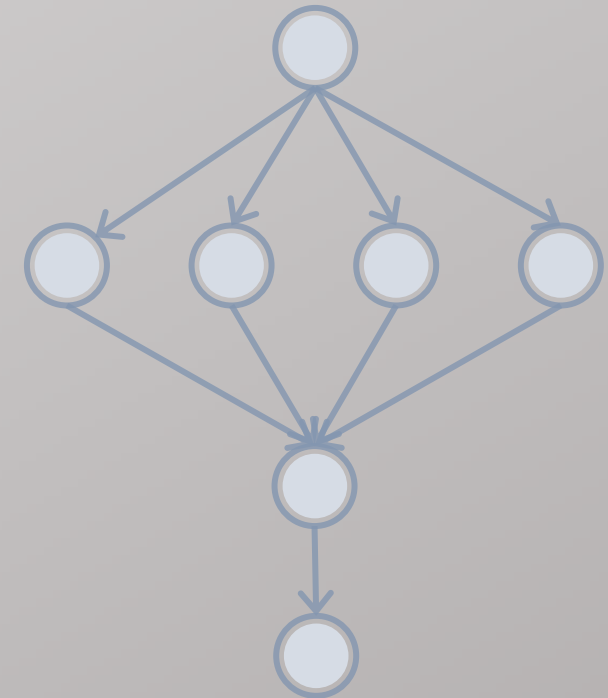
No while loops, no conditional branches

Jobs are standalone executables

Planning occurs ahead of execution

Planning converts an abstract workflow into a concrete, executable workflow

Planner is like a compiler

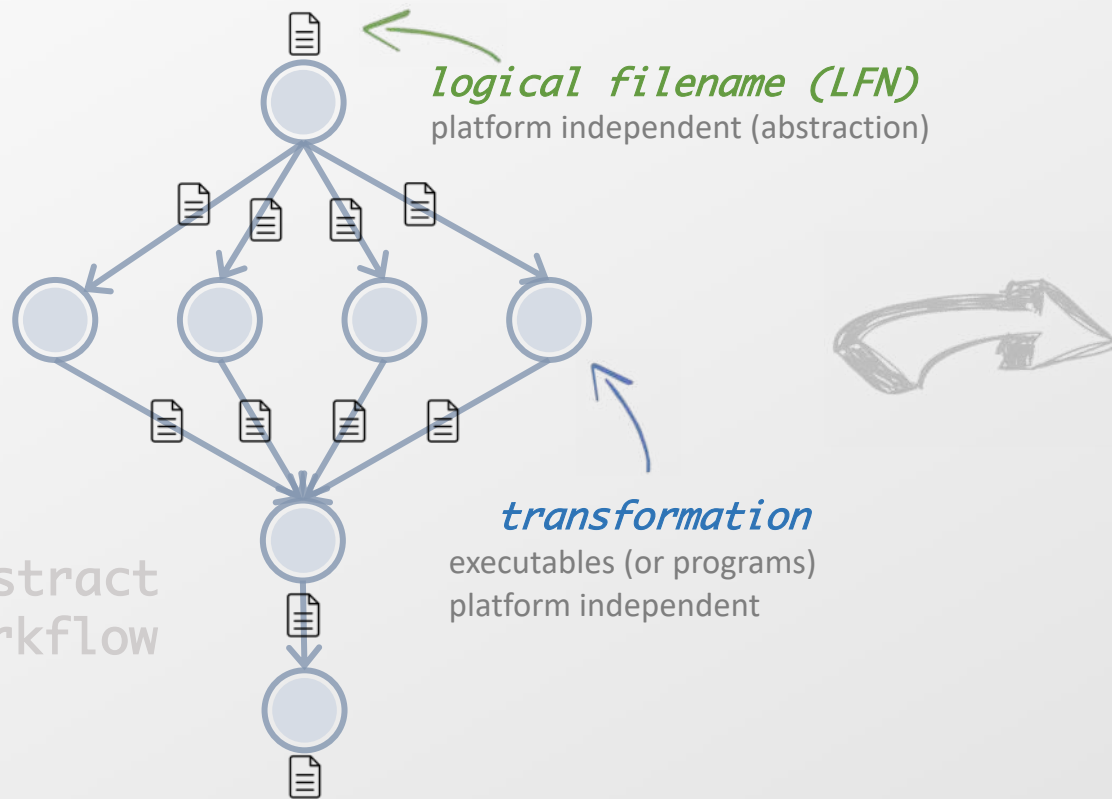


# DAX

DAG in XML

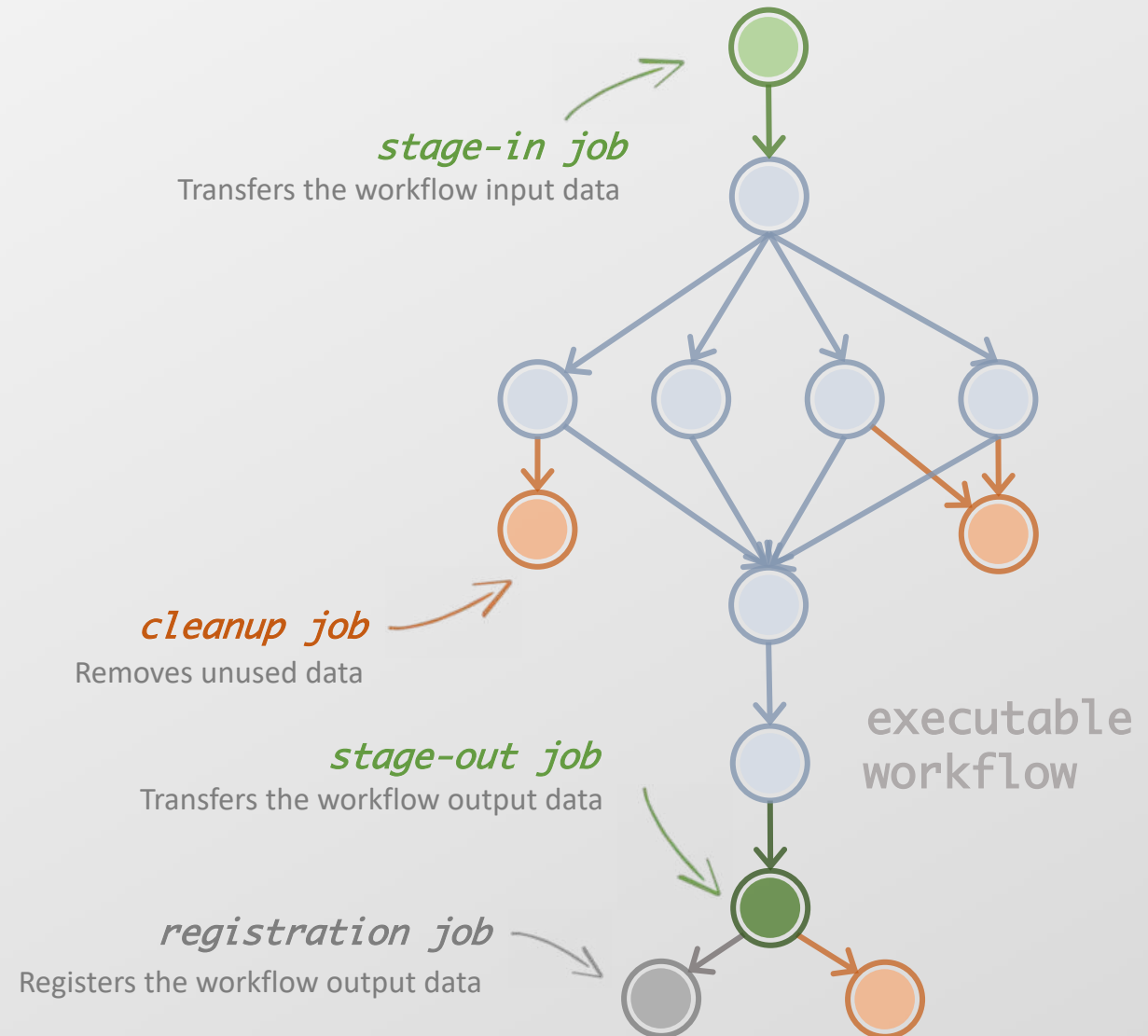
## Portable Description

Users do not worry about  
low level execution details

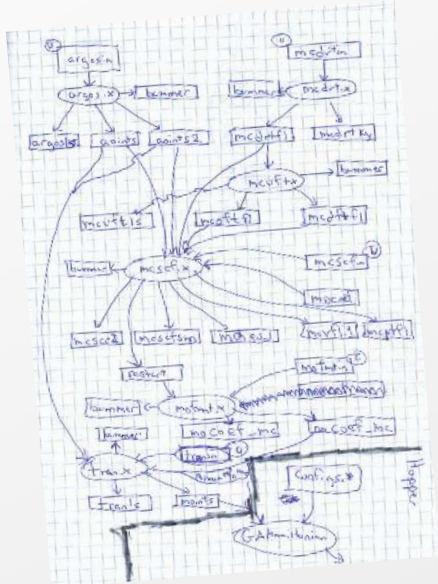


# DAG

directed-acyclic graphs



# Pegasus also provides tools to generate the abstract workflow



```
#!/usr/bin/env python

from Pegasus.DAX3 import *
import sys
import os

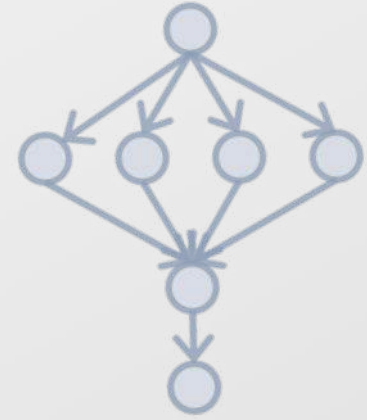
# Create an abstract dag
dax = ADAG("hello_world")

# 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

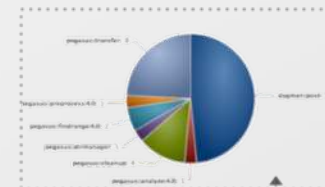




Users

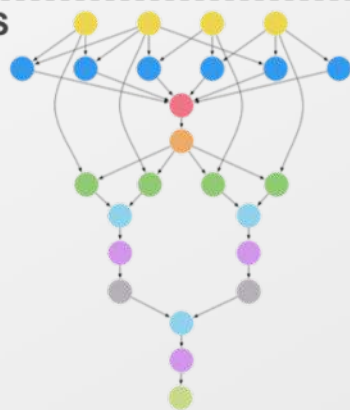
# System Architecture

## Interfaces



## APIs

### Pegasus WMS



Submit Host

Mapper

Engine

Scheduler

Pegasus Dashboard

Monitoring  
& Provenance

Logs

Notifications

Workflow DB

$j_1$   
 $j_2$   
...  
 $j_n$

Job Queue

## Clouds

Cloudware

OpenStack, Eucalyptus, Nimbus

Compute

Amazon EC2, Google Cloud,  
RackSpace, Chameleon

Storage

Amazon S3, Google Cloud Storage,  
OpenStack



Campus  
Clusters

Local Clusters

Open Science  
Grid

XSEDE

Middleware

HTCondor  
GRAM

PBS

LSF

SGE

C  
O  
M  
P  
U  
T  
E

Storage

GridFTP

HTTP

FTP

SRM

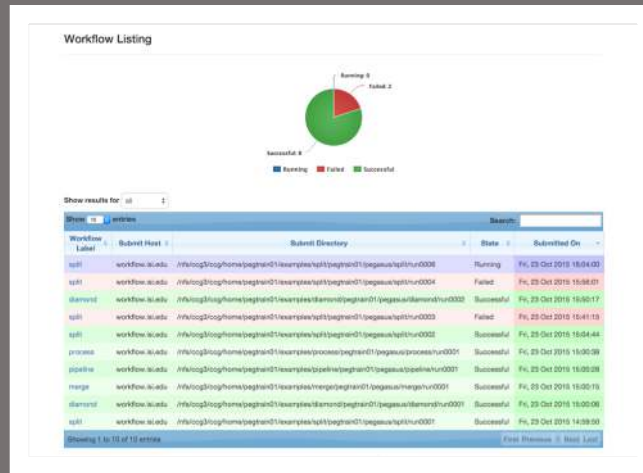
IRODS

SCP



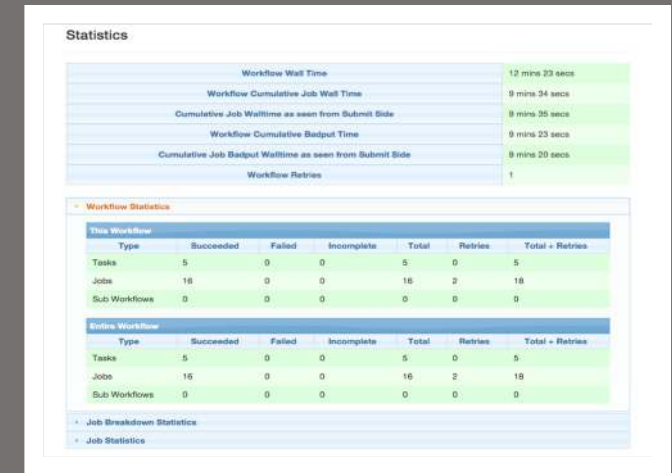
Pegasus

<http://pegasus.isi.edu>



# Pegasus dashboard

web interface for monitoring and debugging workflows



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.



Real-time Monitoring  
Reporting  
Debugging  
Troubleshooting  
RESTful API





# Pegasus dashboard

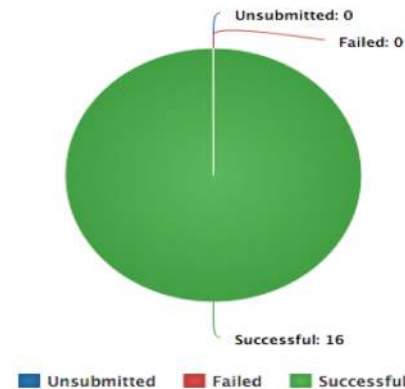
web interface for monitoring  
and debugging workflows

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.

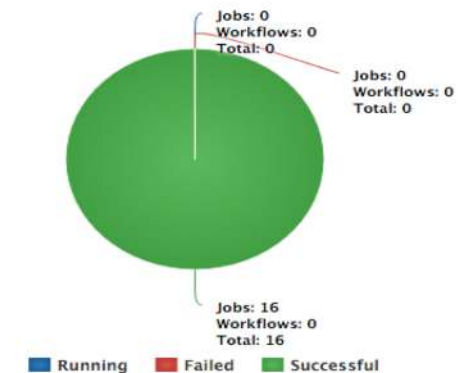
## Workflow Details 5bb4de1d-e986-42b8-9160-ab9488494ecf

|                      |  |
|----------------------|--|
| Label                | split  |
| Type                 | root-wf  |
| Progress             | Successful   |
| Submit Host          | workflow.isi.edu   |
| User                 | pegtrain01   |
| Submit Directory     | /nfs/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)







## command-line...

```
$ pegasus-status pegasus/examples/split/run0001
STAT IN_STATE JOB
Run 00:39 split-0 (/home/pegasus/examples/split/run0001)
Idle 00:03 └─split_ID0000001
Summary: 2 Condor jobs total (I:1 R:1)

UNRDY READY PRE IN_Q POST DONE FAIL %DONE STATE DAGNAME
14      0      0      1      0      2      0    11.8 Running *split-0.dag
```

```
$ pegasus-analyzer pegasus/examples/split/run0001
pegasus-analyzer: initializing...
```

```
*****Summary*****

Total jobs : 7 (100.00%)
# jobs succeeded : 7 (100.00%)
# jobs failed : 0 (0.00%)
# jobs unsubmitted : 0 (0.00%)
```

```
$ pegasus-statistics -s all pegasus/examples/split/run0001
-----
Type          Succeeded Failed Incomplete Total Retries Total+Retries
Tasks          5         0         0         5         0         5
Jobs          17         0         0        17         0        17
Sub-Workflows  0         0         0         0         0         0
-----
```

```
Workflow wall time : 2 mins, 6 secs
Workflow cumulative job wall time : 38 secs
Cumulative job wall time as seen from submit side : 42 secs
Workflow cumulative job badput wall time :
Cumulative job badput wall time as seen from submit side :
```

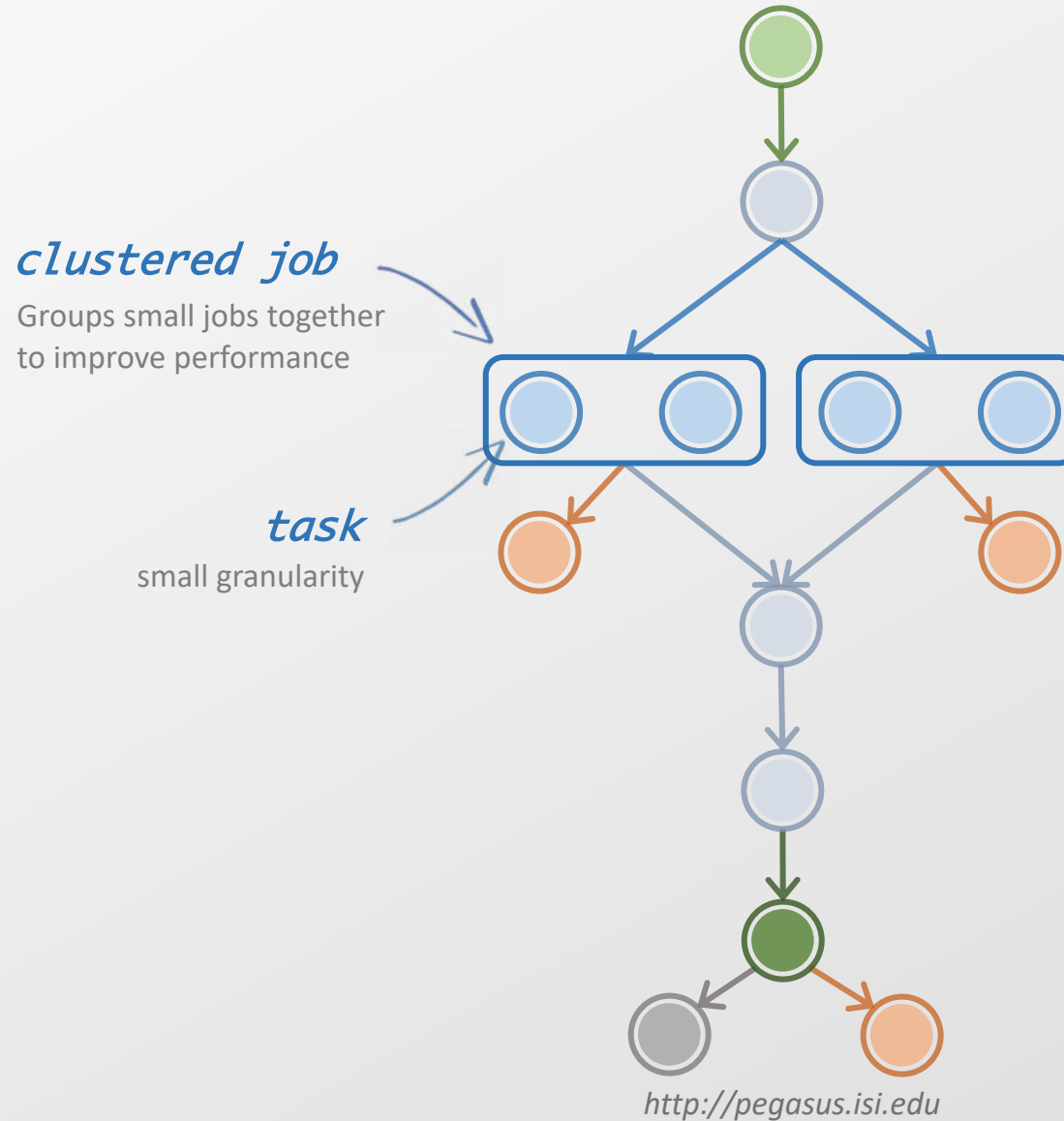
Provenance data can be  
summarized  
**pegasus-statistics**

or used for debugging  
**pegasus-analyzer**



# Performance, why not improve it?

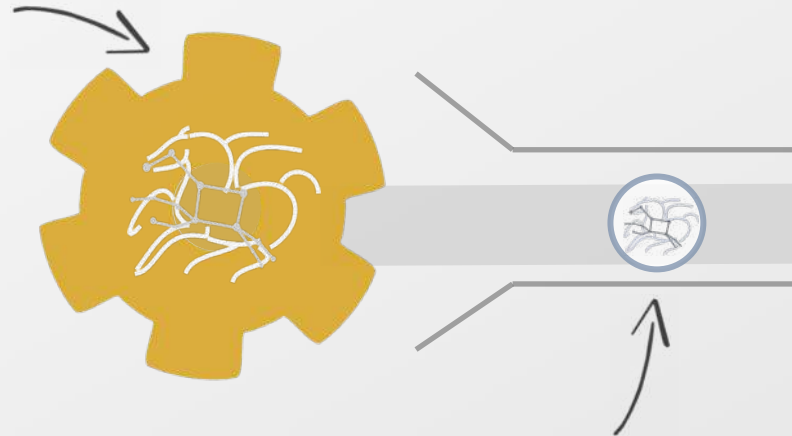
workflow restructuring  
workflow reduction  
hierarchical workflows  
pegasus-mpi-cluster



# Running fine-grained workflows on HPC systems...

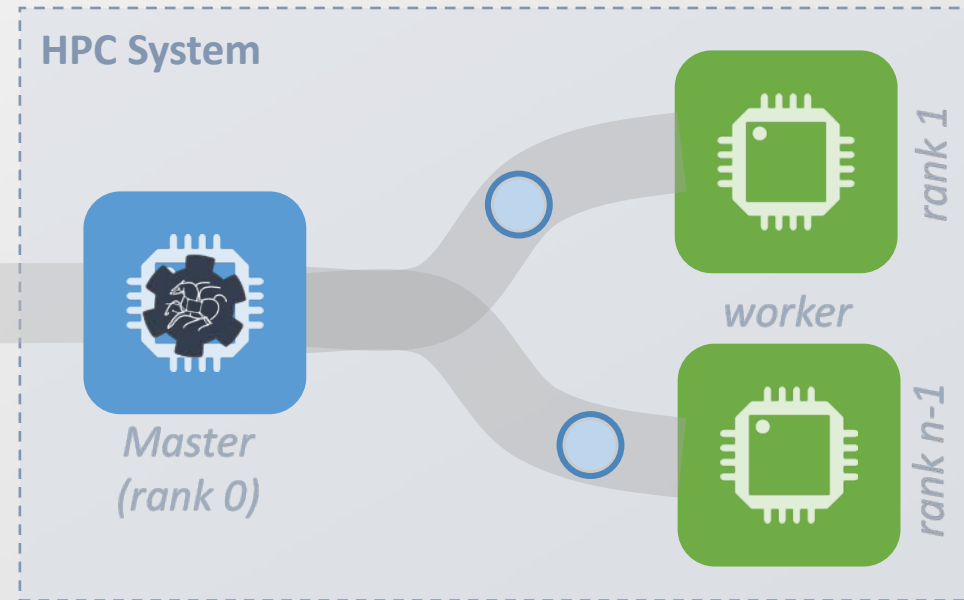
workflow restructuring  
workflow reduction  
hierarchical workflows  
pegasus-mpi-cluster

*submit host*  
(e.g., user's laptop)



*workflow wrapped as an MPI job*

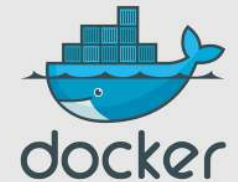
Allows sub-graphs of a Pegasus workflow to be submitted as monolithic jobs to remote resources



# Pegasus Container Support

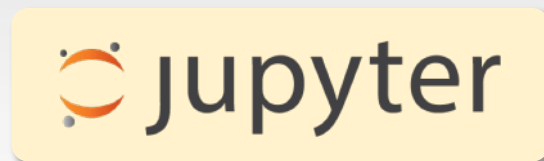
- Support for

- Docker
- Singularity – Widely supported on OSG

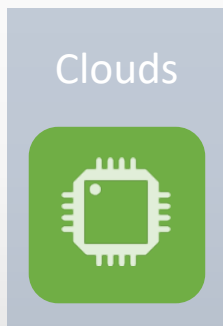
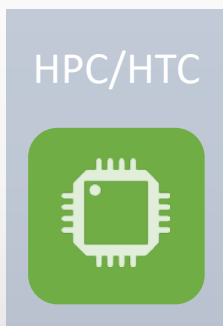


- Users can refer to **containers** in the **Transformation Catalog** with their executable preinstalled.
- Users can **refer** to a **container** they want to **use**. However, they let **Pegasus** stage their executable to the node.
  - Useful if you want to use a site recommended/standard container image.
  - Users are using generic image with executable staging.
- **Future Plans**
  - Users can **specify an image buildfile** for their jobs.
  - *Pegasus will build the Docker image as separate jobs in the executable workflow, export them at tar file and ship them around ( planned for 4.8.X )*

# Running Pegasus workflows with Jupyter



WAN LAN



Jupyter Pegasus-Tutorial-Split Last Checkpoint: 03/15/2017 (autosaved)

File Edit View Insert Cell Kernel Widgets Help Python 2

After the workflow has been submitted you can monitor it using the `status()` method. This method takes two arguments:

- `loop`: whether the status command should be invoked once or continuously until the workflow is completed or a failure is detected.
- `delay`: The delay (in seconds) the status will be refreshed. Default value is 10s.

```
In [6]: instance.status(loop=True, delay=5)
```

Progress: 100.0% (Success) (Completed: 17, Queued: 0, Running: 0, Failed: 0)

Once the workflow execution is completed, a list of the output files can be obtained 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*

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

*running a workflow*

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

*monitoring a workflow execution*

```
Progress: 100.0% (Success)    (Completed: 17, Queued: 0, Running: 0, Failed: 0)
```





# Job Submissions

## Local

*Submit Machine*

*Personal HTCondor*

*Local Campus Cluster accessible via  
Submit Machine \**

*HTCondor via Glite*

*\*\* Both Glite and BOSCO build on HTCondor BLAHP  
Support.*

*Supported schedulers*

*PBS   SGE   SLURM   MOAB*

## Remote

*BOSCO + SSH\*\**

*Each node in executable workflow  
submitted via SSH connection to  
remote cluster*

*BOSCO based Glideins\*\**

*SSH based submission of Glideins*

*PyGlidein*

*ICE Cube Glidein service*

*OSG using glideinWMS*

*CREAMCE*

*Uses CondorG*

*Globus GRAM*

*Uses CondorG*





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# Pegasus: Data Management for Scientific Workflows

Pegasus Workflow Management System

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Karan Vahi

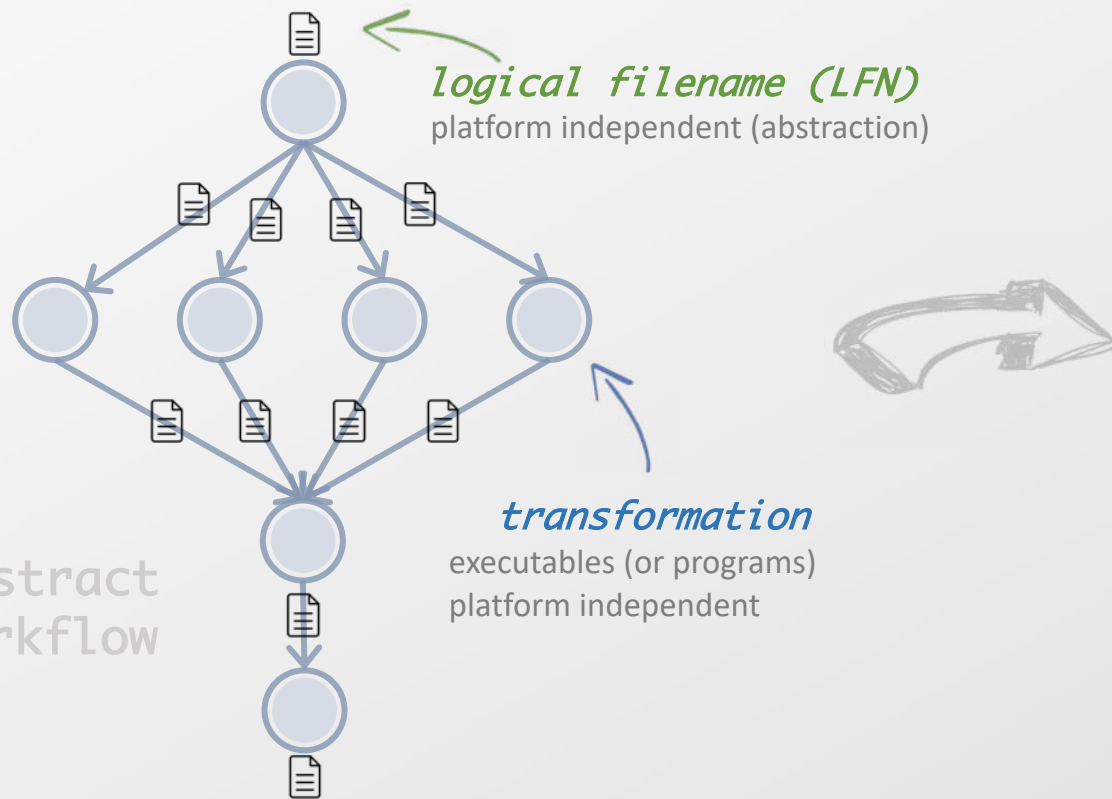


# DAX

DAG in XML

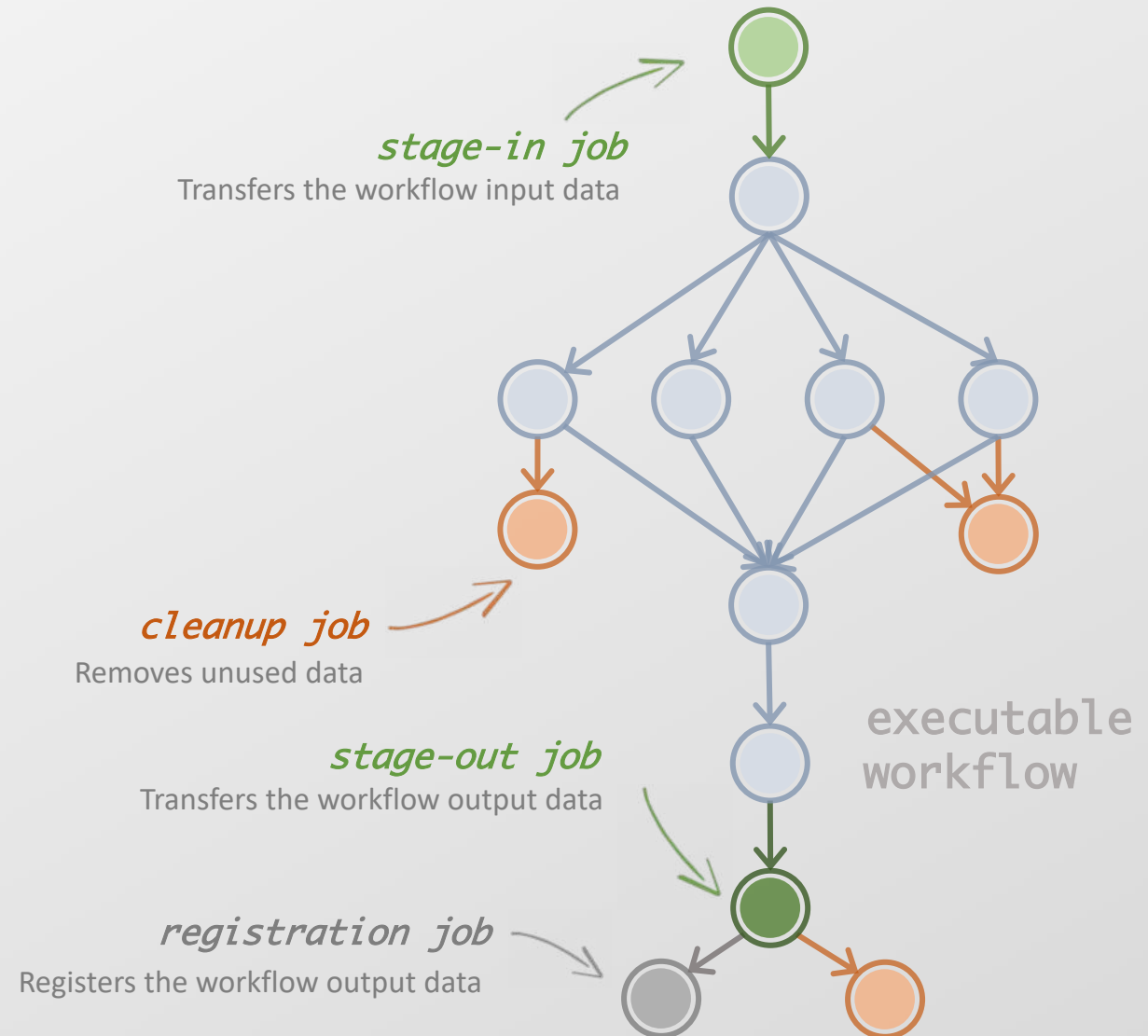
## Portable Description

Users do not worry about  
low level execution details

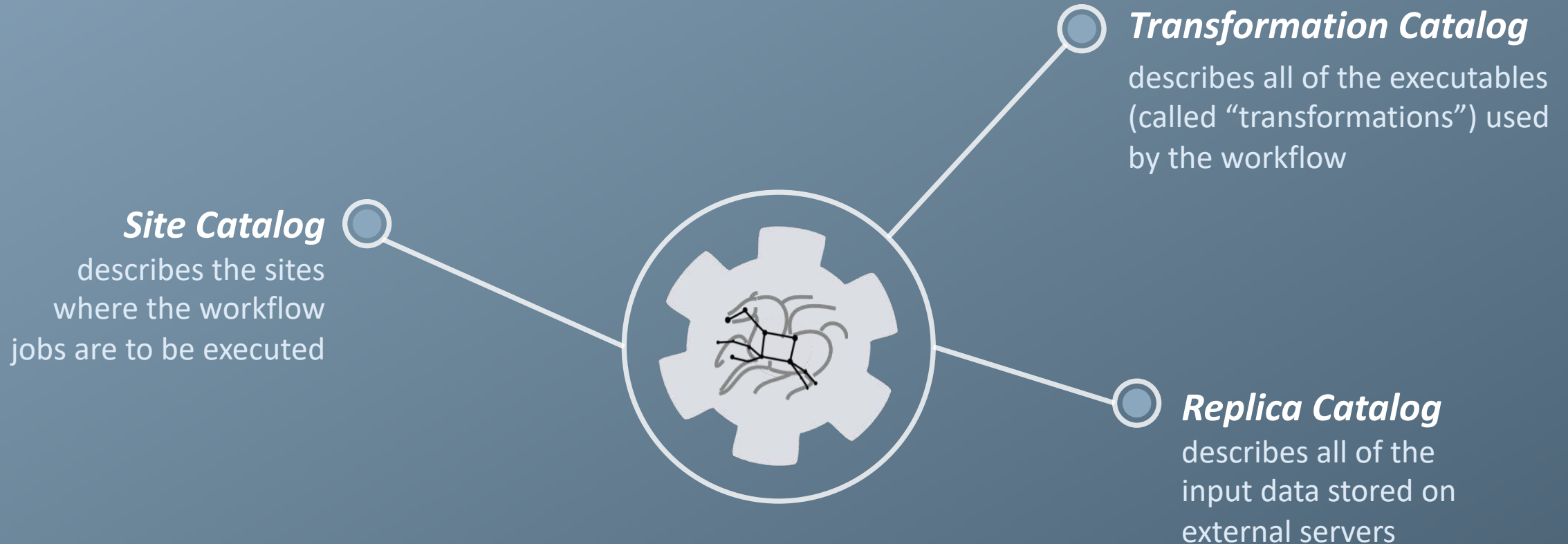


# DAG

directed-acyclic graphs



# So, what information does Pegasus need?



# How does Pegasus decide where to execute?

site catalog

transformation catalog

replica catalog

## *site description*

describes the compute resources

## *scratch*

tells where temporary data is stored

## *storage*

tells where output data is stored

## *profiles*

key-pair values associated per job level

```
<!-- The local site contains information about the submit host -->
<!-- The arch and os keywords are used to match binaries in the -->
<!-- transformation catalog -->
<site handle="local" arch="x86_64" os="LINUX">

  <!-- These are the paths on the submit host where Pegasus stores data -->
  <!-- Scratch is where temporary files go -->
  <directory type="shared-scratch" path="/home/tutorial/run">
    <file-server operation="all" url="file:///home/tutorial/run"/>
  </directory>

  <!-- Storage is where pegasus stores output files -->
  <directory type="local-storage" path="/home/tutorial/outputs">
    <file-server operation="all" url="file:///home/tutorial/outputs"/>
  </directory>

  <!-- This profile tells Pegasus where to find the user's private key -->
  <!-- for SCP transfers -->
  <profile namespace="env" key="SSH_PRIVATE_KEY">
    /home/tutorial/.ssh/id_rsa
  </profile>

</site>
```



# What if data is not local to the submit host?

site catalog

transformation catalog

replica catalog

```
# This is the replica catalog. It lists information about each of the
# input files used by the workflow. You can use this to specify locations to
# input files present on external servers.

# The format is:
# LFN PFN site="SITE"

f.a    file:///home/tutorial/examples/diamond/input/f.a    site="local"
```

*logical filename*

abstract data name

*physical filename*

data physical location on site  
different transfer protocols  
can be used (e.g., scp, http,  
ftp, gridFTP, etc.)

*site name*

in which site the file is available



# Replica catalog

## *multiple sources*

site catalog  
transformation catalog  
replica catalog

### *pegasus.conf*

```
# Add Replica selection options so that it will try URLs first, then
# XrootD for OSG, then gridftp, then anything else
pegasus.selector.replica=Regex
pegasus.selector.replica.regex.rank.1=file:///cvmfs/*.
pegasus.selector.replica.regex.rank.2=file://.*
pegasus.selector.replica.regex.rank.3=root://.*
pegasus.selector.replica.regex.rank.4=gridftp://.*
pegasus.selector.replica.regex.rank.5=.\*
```

### *rc.data*

```
# This is the replica catalog. It lists information about each of the
# input files used by the workflow. You can use this to specify locations
# to input files present on external servers.

# The format is:
# LFN PFN site="SITE"

f.a    file:///cvmfs/oasis.opensciencegrid.org/diamond/input/f.a    site="cvmfs"
f.a    file:///local-storage/diamond/input/f.a    site="prestaged"
f.a    gridftp://storage.mysite/edu/examples/diamond/input/f.a    site="storage"
```

# pegasus-transfer

*Pegasus' internal data transfer tool with support for a number of different protocols*

## Directory creation, file removal

If protocol supports, used for cleanup

## Two stage transfers

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

## Parallel transfers

## Automatic retries

## Credential management

Uses the appropriate credential for each site and each protocol (even 3<sup>rd</sup> party transfers)

HTTP  
SCP  
GridFTP  
Globus  
Online  
iRods  
Amazon S3  
Google  
Storage  
SRM  
FDT  
stashcp  
cp  
ln -s

# Data Staging Configurations

## HTCondor 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

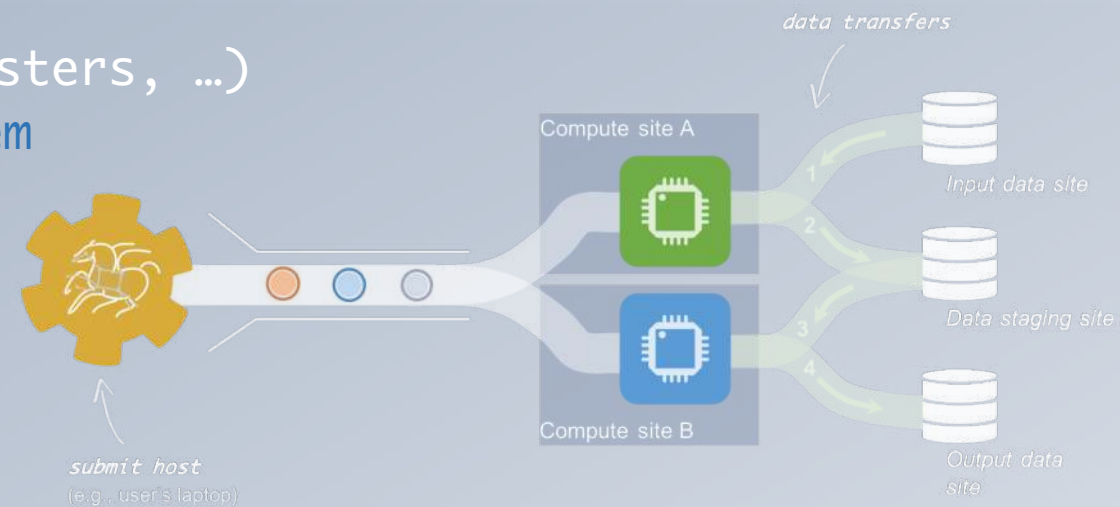
## Non-shared File System (clouds, OSG, ...)

Worker nodes do not share a file system

Data is pulled / pushed from a staging site, possibly not co-located with the computation

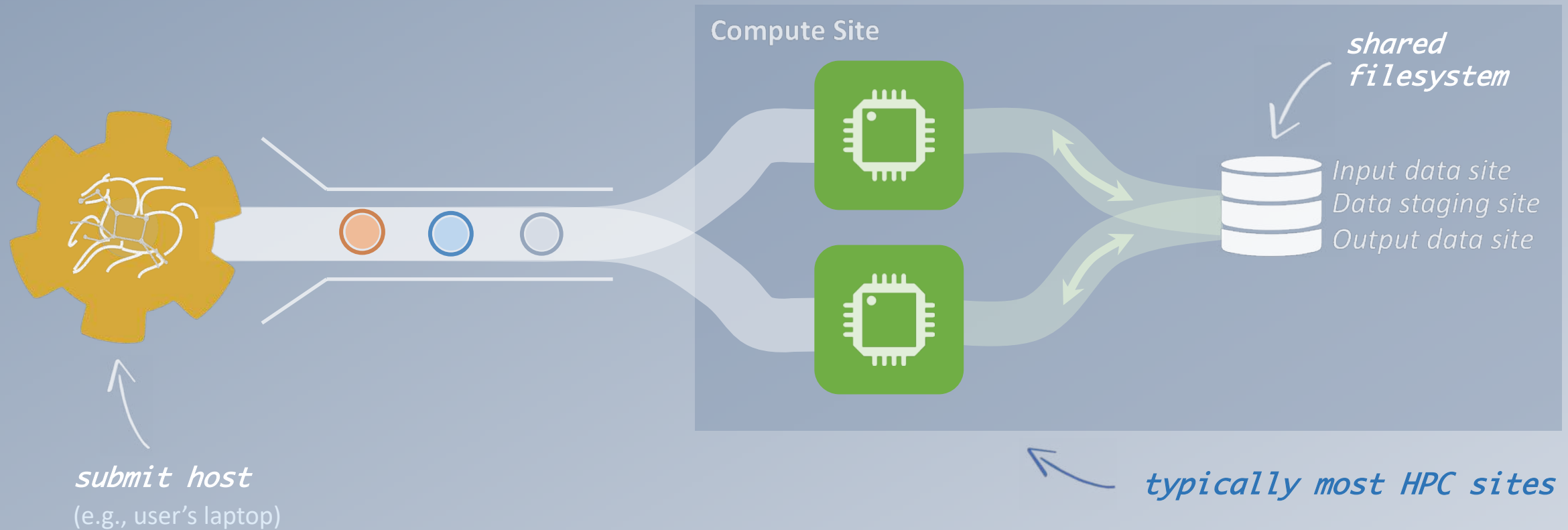
## Shared File System (HPC sites, XSEDE, Campus clusters, ...)

I/O is directly against the shared file system



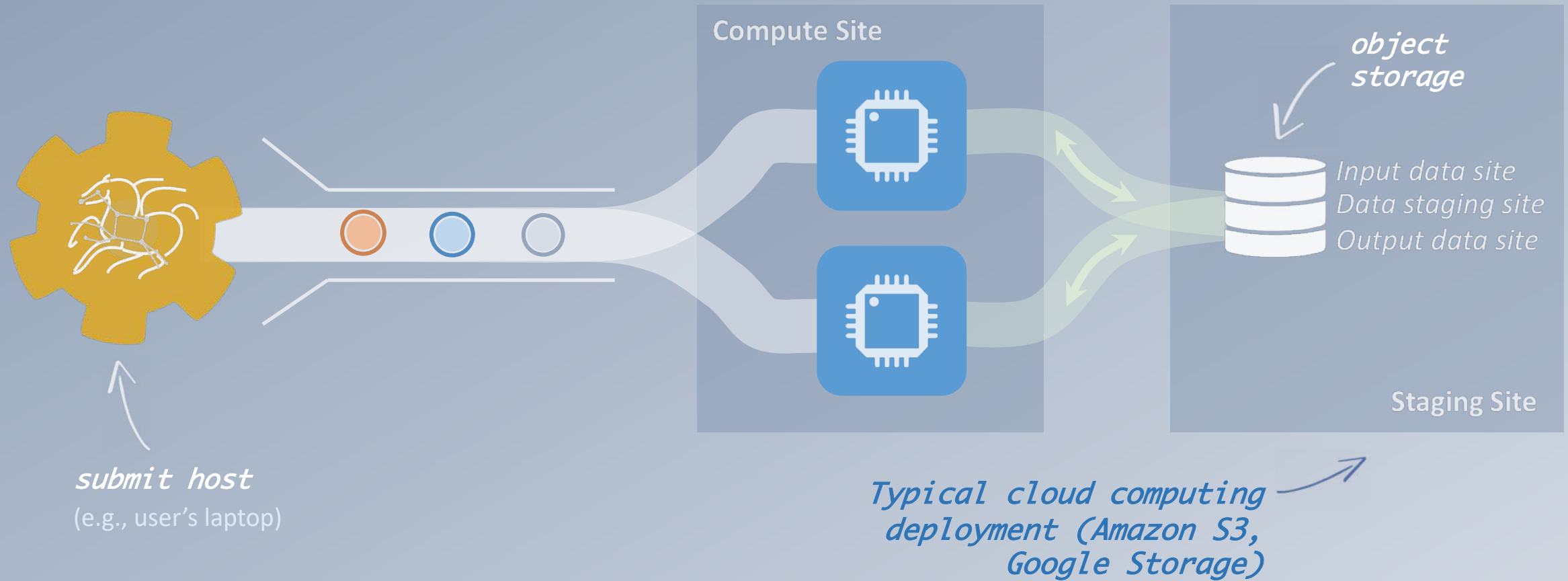
# High Performance Computing

There are several possible configurations...



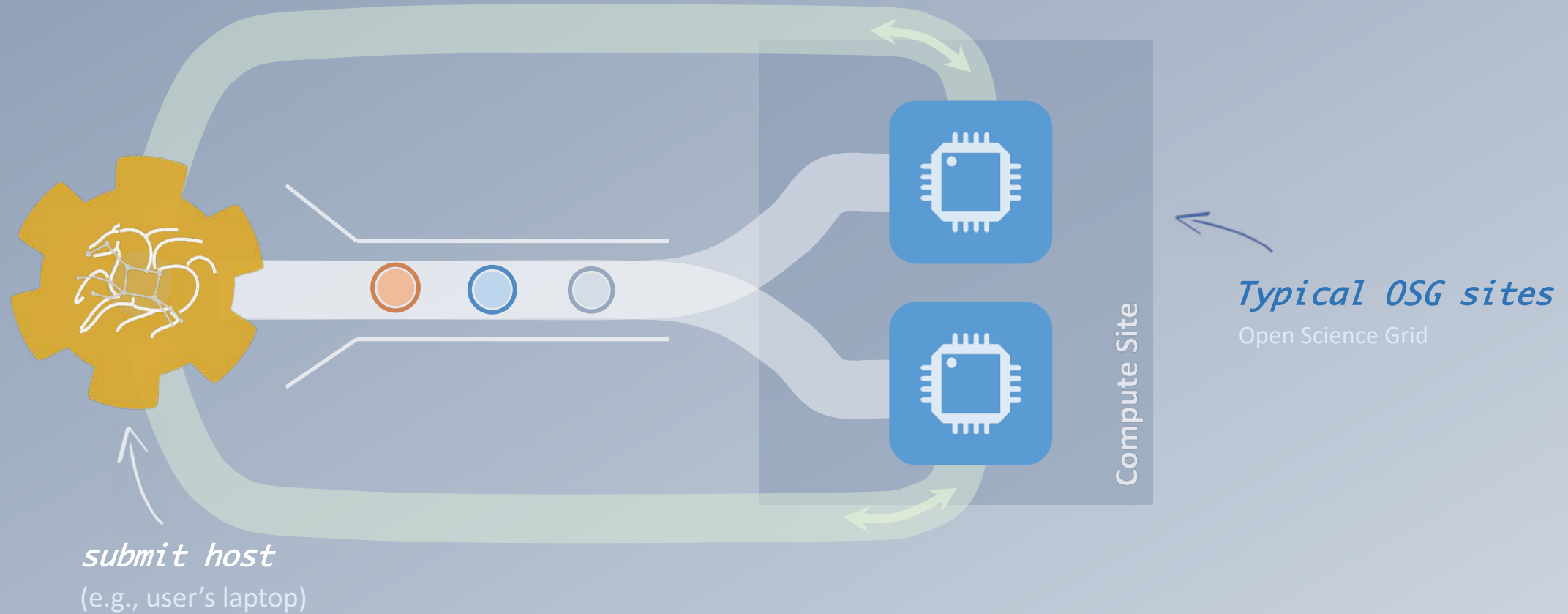
# Cloud Computing

high-scalable object storages



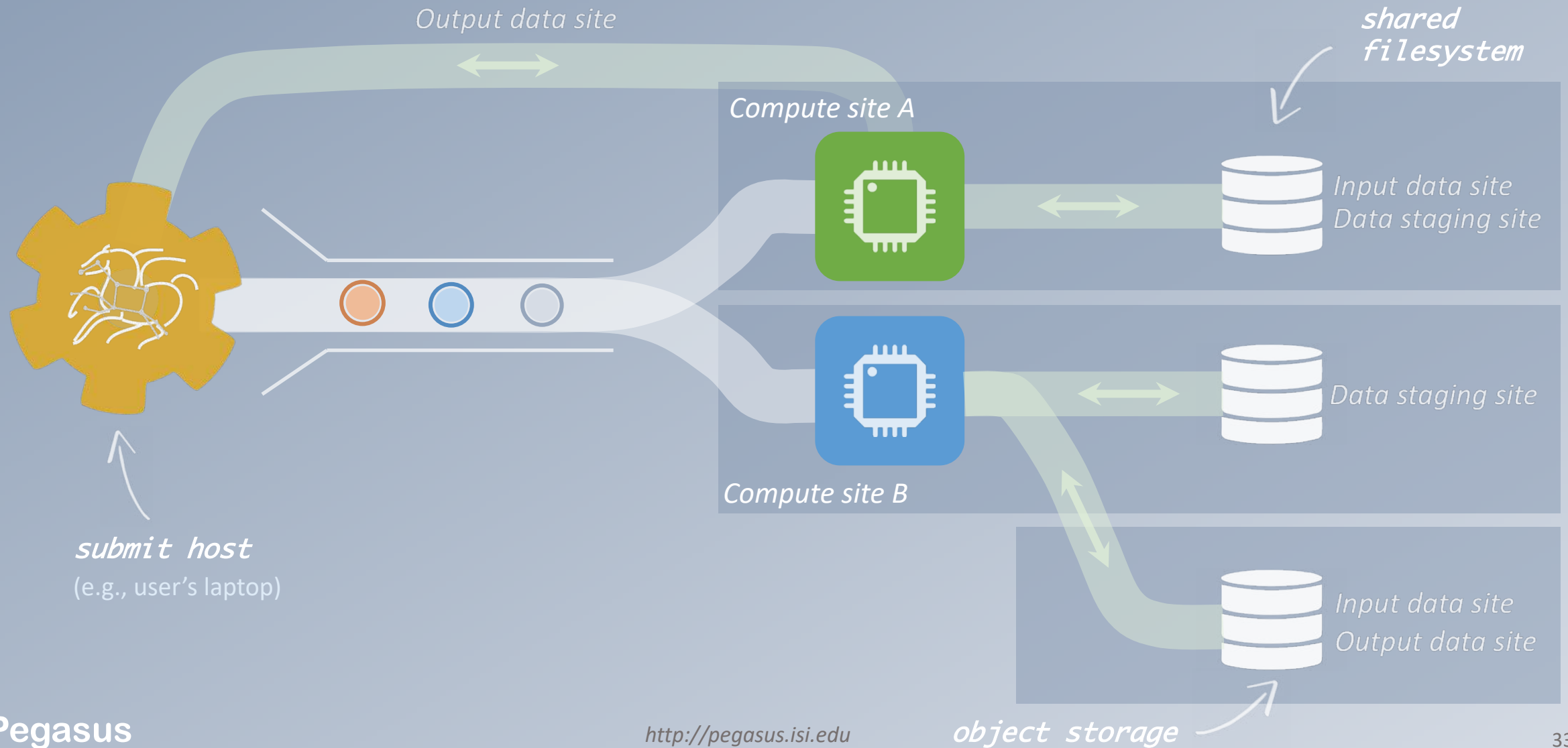
# Grid Computing

local data management



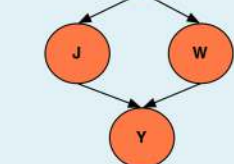


# And yes... you can mix everything!



## Data Flow for LIGO Pegasus Workflows in OSG

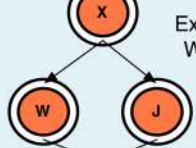
**SUBMIT HOST** Abstract Workflow



**Pegasus Planner**

Workflow Setup Job

Workflow Stagein Job

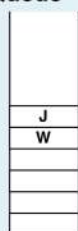


Executable Workflow

Workflow Stageout Job

Data Cleanup Job

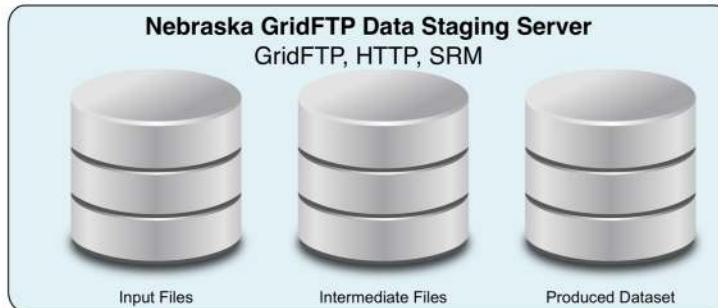
**Condor Schedd Queue**



**Condor DAGMan**



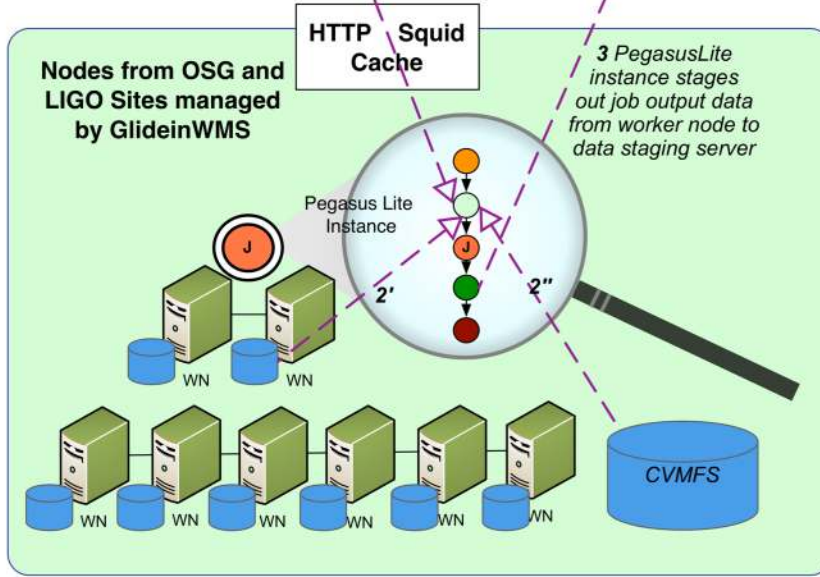
1 Workflow Stagein Job stages in the input data for workflow from user server



2 PegasusLite instance looks up input data on the compute node/ CVMFS If not present, stage-in data from remote data staging server



4 Workflow Stageout Job stages produced data from data staging server to LIGO Output Data Server



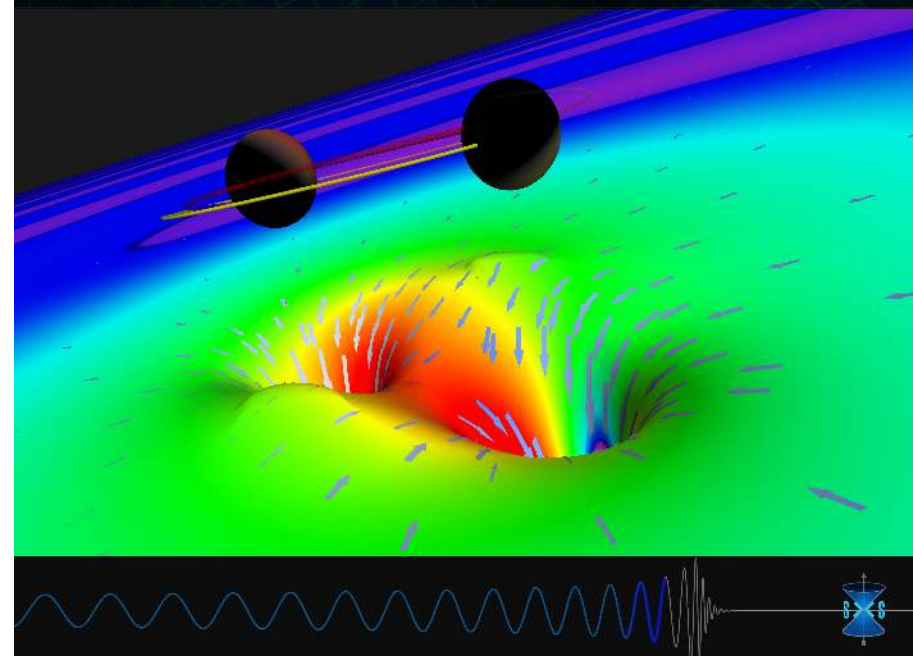
### LEGEND

- Directory Setup Job
- Data Stageout Job
- Pegasus Lite Compute Job
- Data Stagein Job
- Directory Cleanup Job
- Worker Node

## Advanced LIGO – Laser Interferometer Gravitational Wave Observatory

60,000 compute tasks  
Input Data: 5000 files (10GB total)  
Output Data: 60,000 files (60GB total)

executed on LIGO Data Grid,  
Open Science Grid and XSEDE



# Optimizing storage usage...

abstract workflow  
executable workflow  
optimizations

storage constraints

Problem?

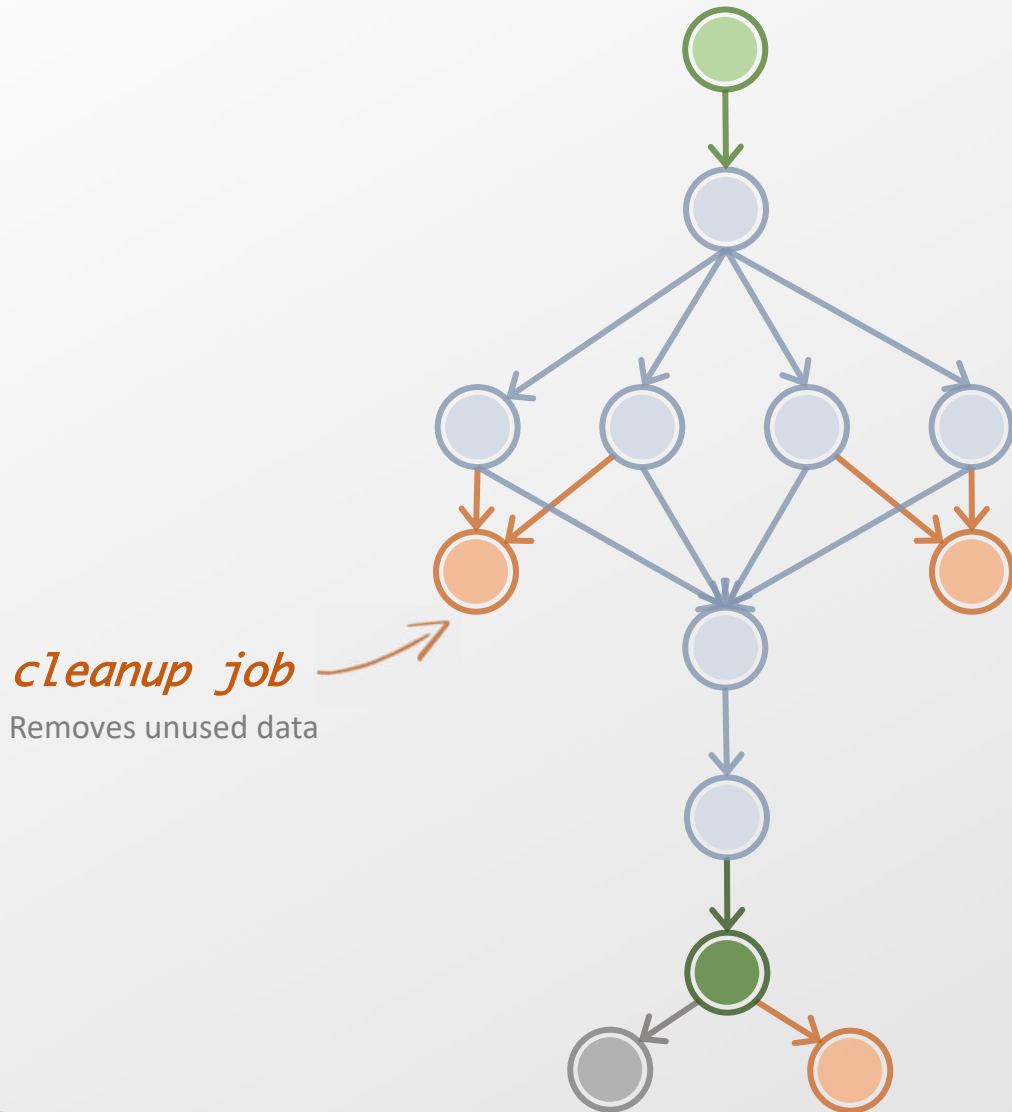
- Users run out of disk space while running workflows

Why does it occur

- Workflows could bring in huge amounts of data
- Data is generated during workflow execution
- Users don't worry about cleaning up after they are done

• Pegasus Solutions

- Add leaf cleanup nodes to cleanup after workflow finishes.
- Interleave cleanup nodes
- Cluster cleanup nodes per level to improve performance





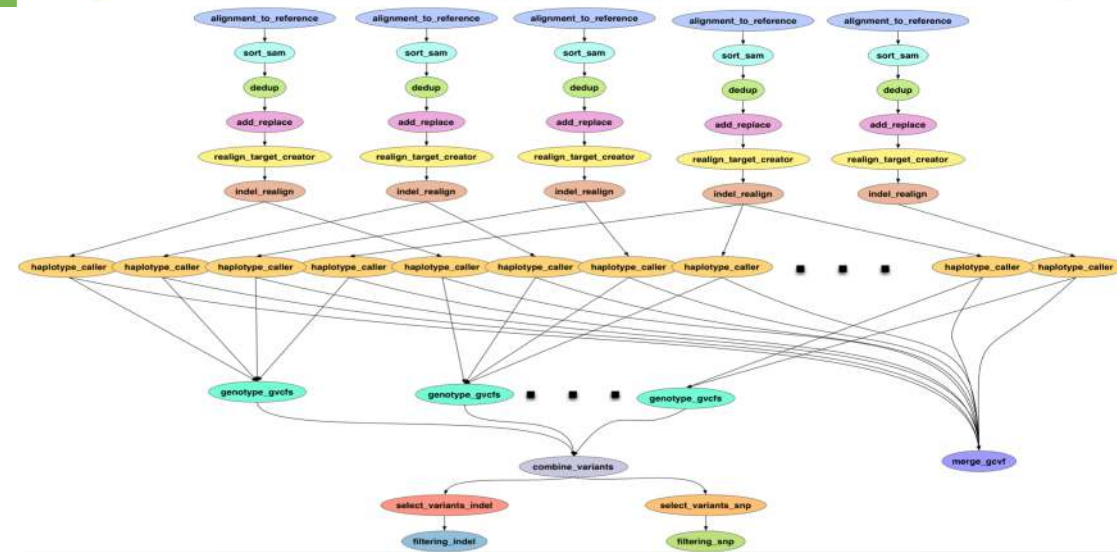
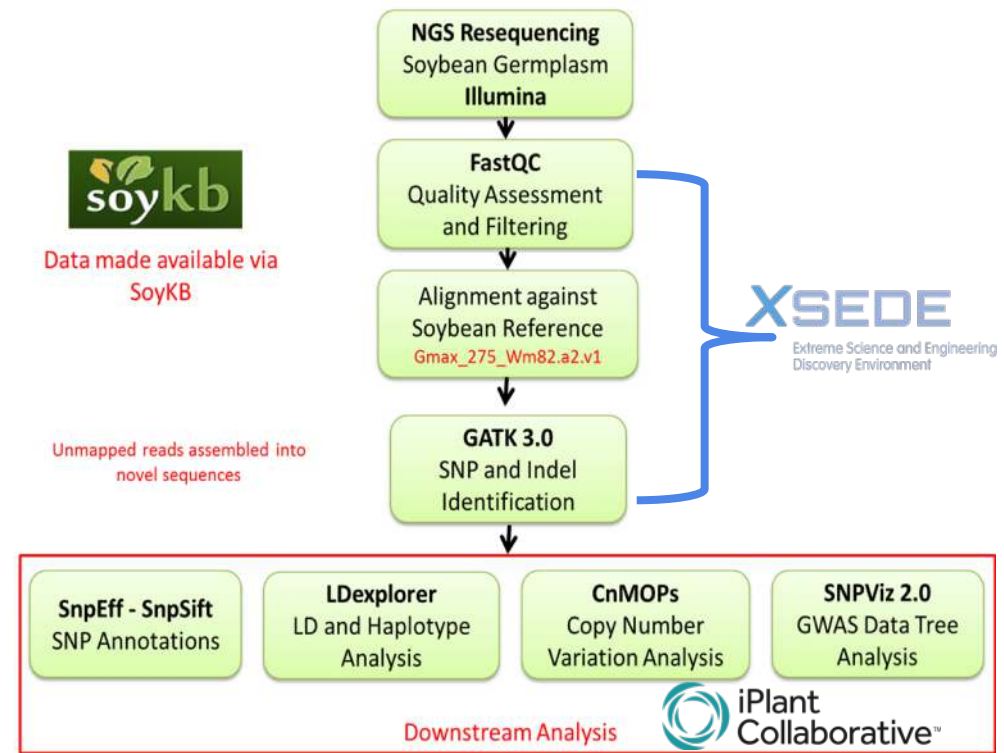
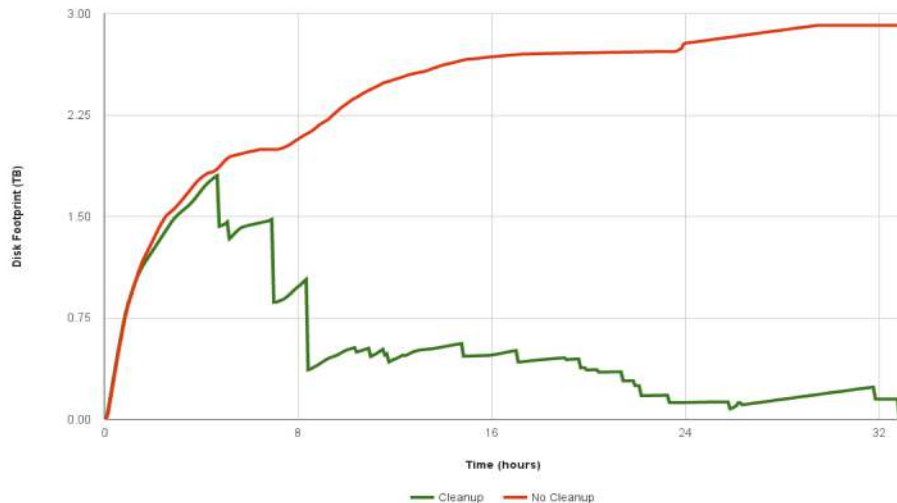
# Soybean Workflow

TACC Wrangler as Execution Environment

Flash Based Shared Storage

Switched to glideins (pilot jobs) - Brings in remote compute nodes and joins them to the HTCondor pool on the submit host - Workflow runs at a finer granularity

Works well on Wrangler due to more cores and memory per node (48 cores, 128 GB RAM)



# Metadata

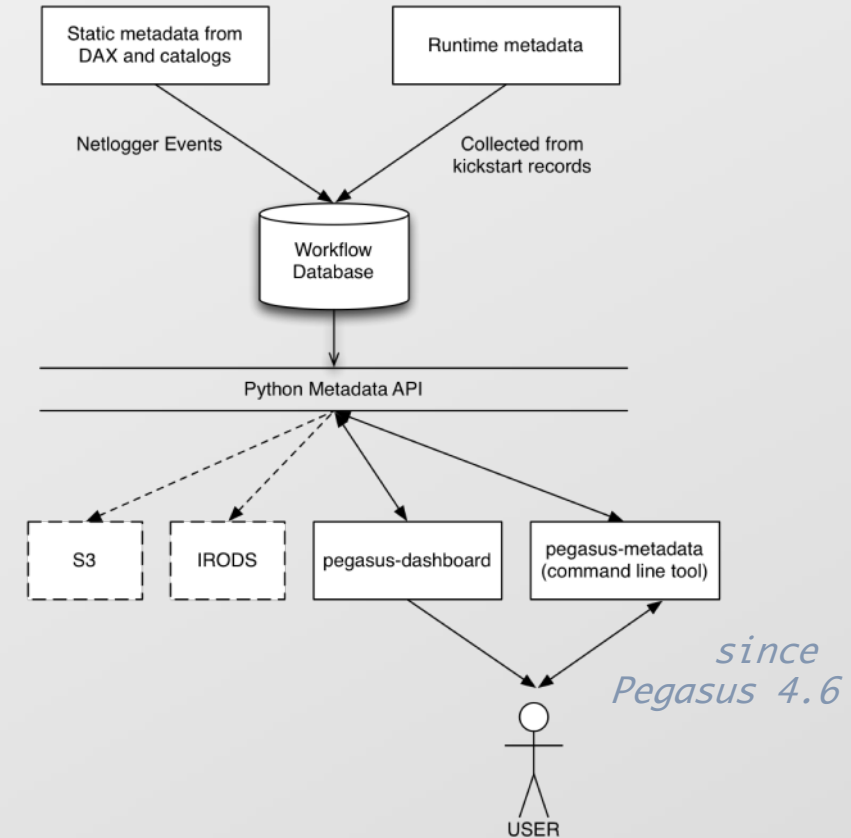
*Can associate arbitrary key-value pairs with workflows, jobs, and files*

## Data registration

*Output files get tagged with metadata on registration in the workflow database*

## Static and runtime metadata

*Static: application parameters  
Runtime: performance metrics*



```
1 <adag ...>
2   <metadata key="experiment">par_all27_prot_lipid</metadata>
3   <job id="ID0000001" name="namd">
4     <argument><file name="equilibrate.conf"/></argument>
5     <metadata key="timesteps">500000</metadata>
6     <metadata key="temperature">200</metadata>
7     <metadata key="pressure">1.01325</metadata>
8     <uses name="Q42.psf" link="input">
9       <metadata key="type">psf</metadata>
10      <metadata key="charge">42</metadata>
11    </uses>
12    ...
13    <uses name="eq.restart.coord" link="output" transfer="false">
14      <metadata key="type">coordinates</metadata>
15    </uses>
16    ...
17  </job>
18 </adag>
```

*workflow,  
job, file*

*select data  
based on metadata*

*register data  
with metadata*



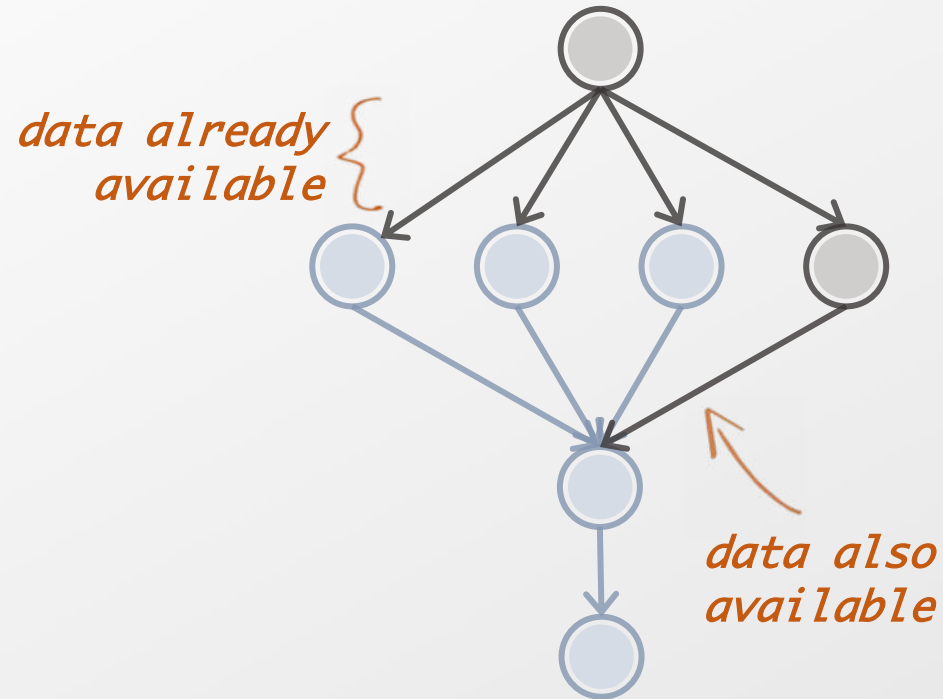
# What about data reuse?

workflow restructuring

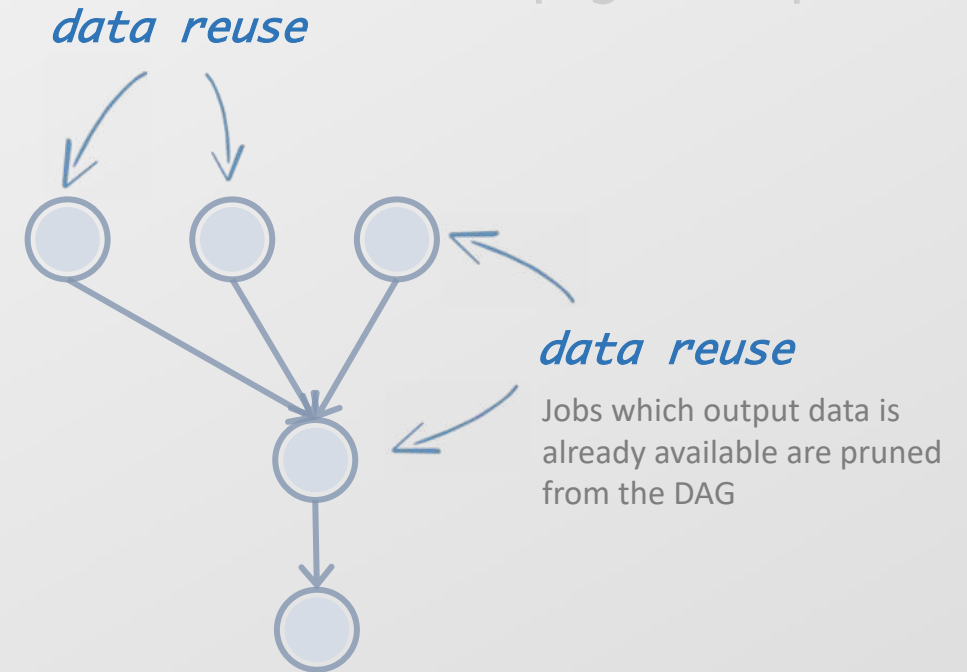
workflow reduction

hierarchical workflows

pegasus-mpi-cluster



*workflow reduction*





# Data Management for Containers

- Users can refer to container images as
  - Docker or Singularity Hub URL's
  - Docker Image exported as a TAR file and available at a server , just like any other input dataset.
- We want to avoid hitting Docker/Singularity Hub repeatedly for large workflows
  - Extend pegasus-transfer to pull image from Docker Hub and then export it as tar file, that can be shipped around in the workflow.
- Ensure pegasus worker package gets installed at runtime inside the user container.



# Pegasus

est. 2001

Automate, recover, and debug scientific computations.

## Get Started

**Pegasus Website**

<http://pegasus.isi.edu>

**Users Mailing List**

[pegasus-users@isi.edu](mailto:pegasus-users@isi.edu)

**Support**

[pegasus-support@isi.edu](mailto:pegasus-support@isi.edu)

### Pegasus Online Office Hours

<https://pegasus.isi.edu/blog/online-pegasus-office-hours/>

*Bi-monthly basis on second Friday of the month, where we address user questions and also apprise the community of new developments*

### HipChat

