Before we start

Hands on Exercises Notes	*https://pegasus.isi.edu/tutorial/CC-IN2P3/*
System	*cctbcondor09.in2p3.fr*

CC-IN2P3 Pegasus Tutorial

Pegasus Workflow Management System

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OUTLINE

Introduction *Scientific Workflows*
Pegasus Overview
Success Stories

Pegasus Overview *Basic Concepts*
Features
System Architecture

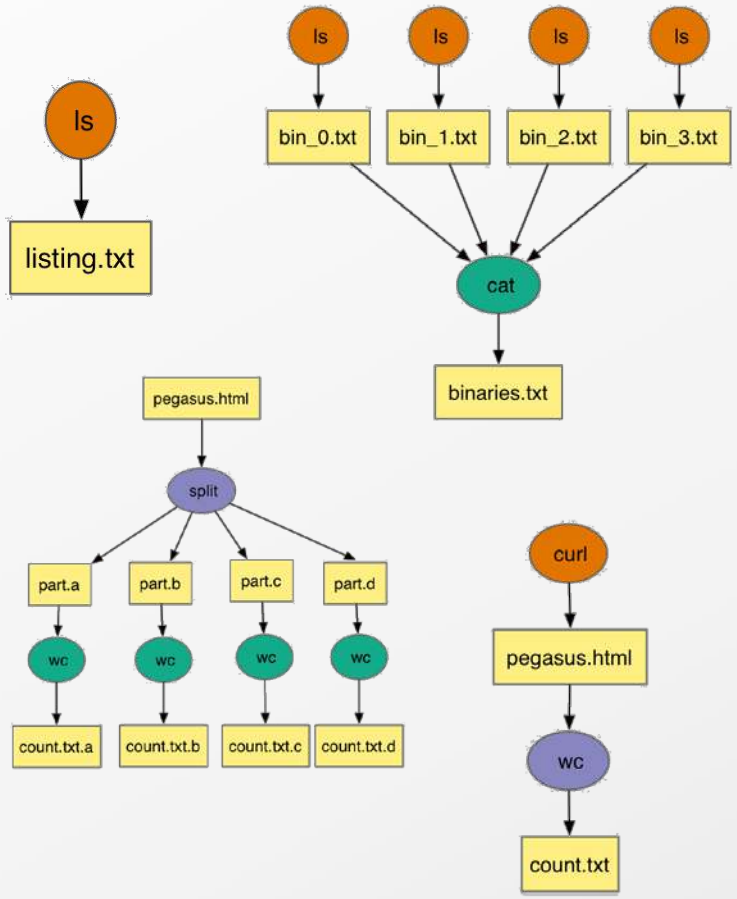
Hands-on Tutorial *Submitting a Workflow*
Workflow Dashboard and Monitoring
Generating the Workflow

Understanding Pegasus Features *Information Catalogs*
Containers

Hands-on Tutorial *Workflows with Containers*
Clustering
Fault-Tolerance

Other Features *Data Staging*
Jupyter Notebooks
Metadata, Hierarchal Workflows, Data Reuse

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

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

Filesystem, site services, endpoints, policies, …

Debug and Monitor Computations

Correlate data across lots of tasks / metadata / log files
Need to know what host a job ran on, how it was invoked, and in what environment

Restructure Workflows for Improved Performance

Short running tasks / Data placement and management / …

Why Pegasus?

Automates complex, multi-stage processing pipelines

Enables parallel, **distributed computations**

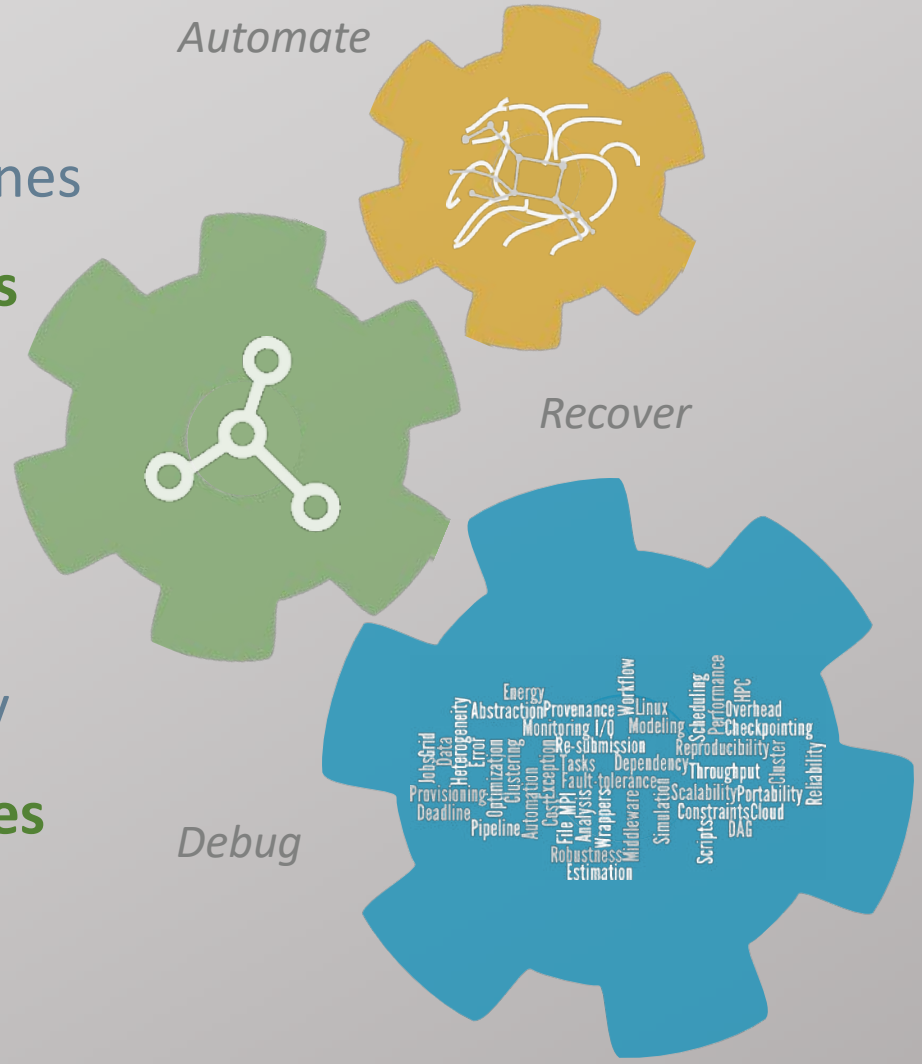
Automatically executes data transfers

Reusable, aids **reproducibility**

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

Handles **failures** with to provide reliability

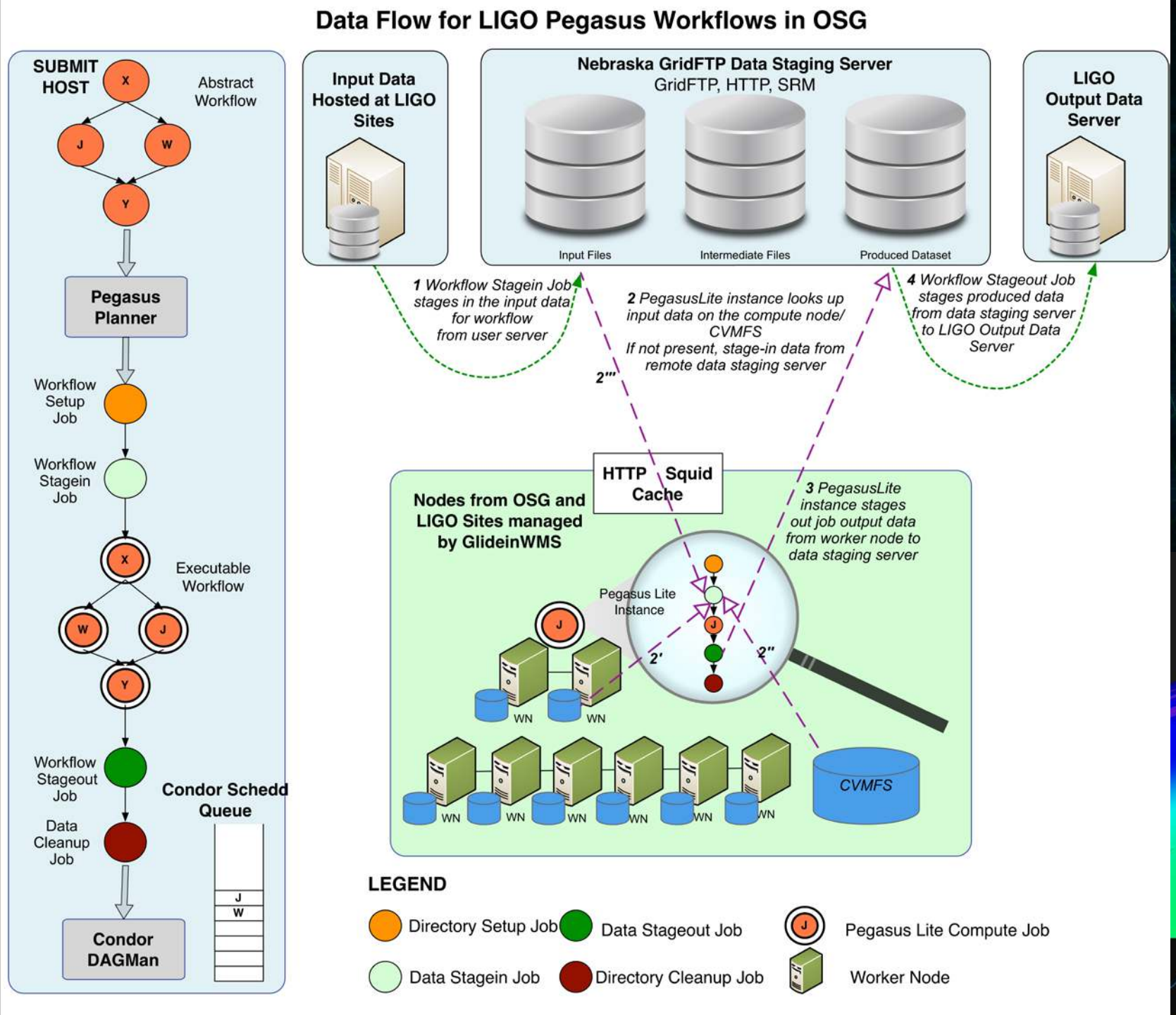
Keeps track of data and **files**



HTCondor High Throughput Computing

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

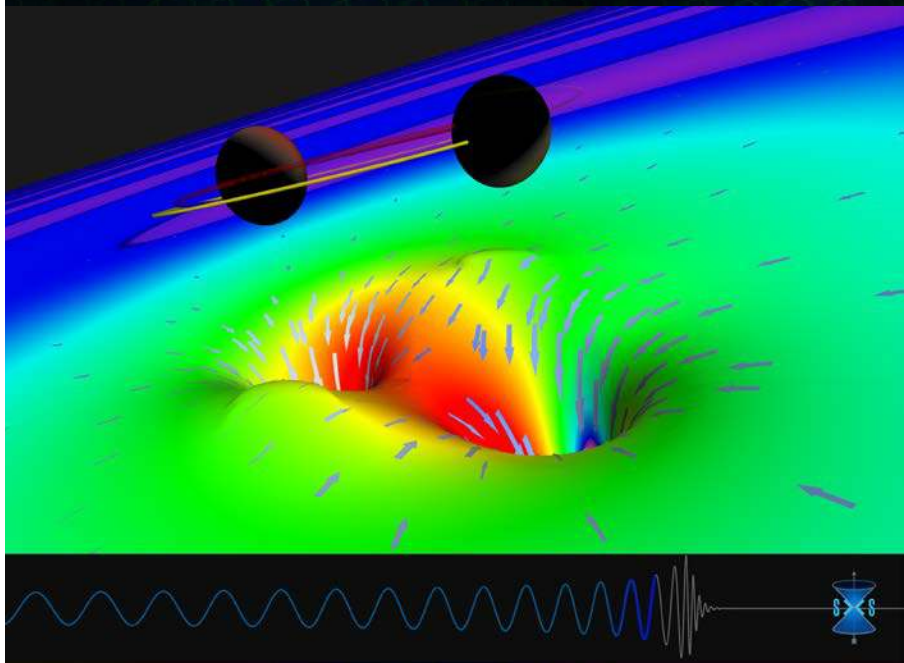
Some of the success stories…



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, EGI, Open Science Grid and XSEDE



Advanced LIGO

PyCBC Workflow

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

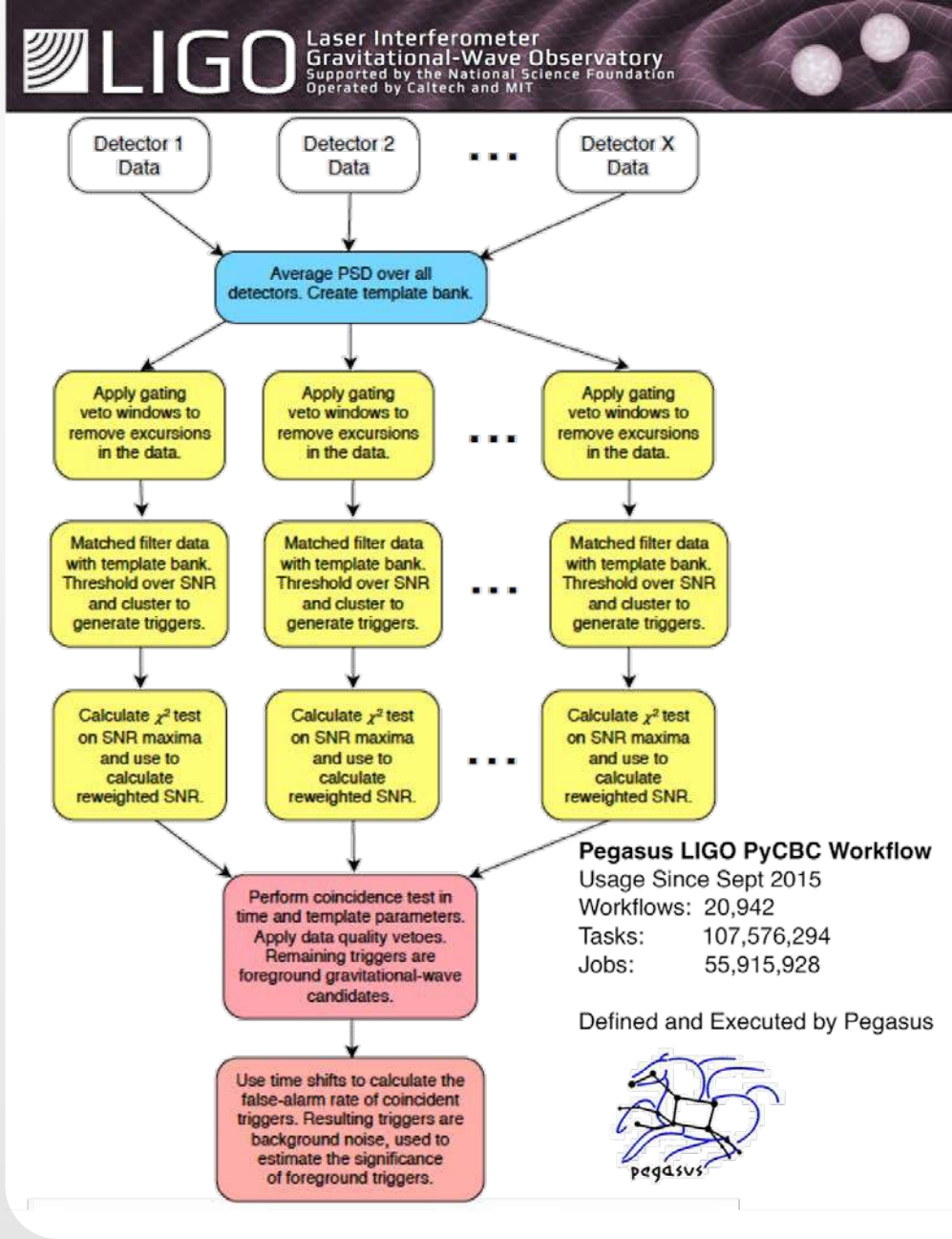
Contains **100,000s of jobs** and accesses on order of **terabytes of data**

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**



PyCBC Papers: An improved pipeline to search for gravitational waves from compact binary coalescence. *Samantha Usman, Duncan Brown et al.*
The PyCBC search for gravitational waves from compact binary coalescence, *Samantha Usman et al* (https://arxiv.org/abs/1508.02357)
PyCBC Detection GW150914: First results from the search for binary black hole coalescence with Advanced LIGO. *B. P. Abbott et al.*

Southern California Earthquake Center's CyberShake

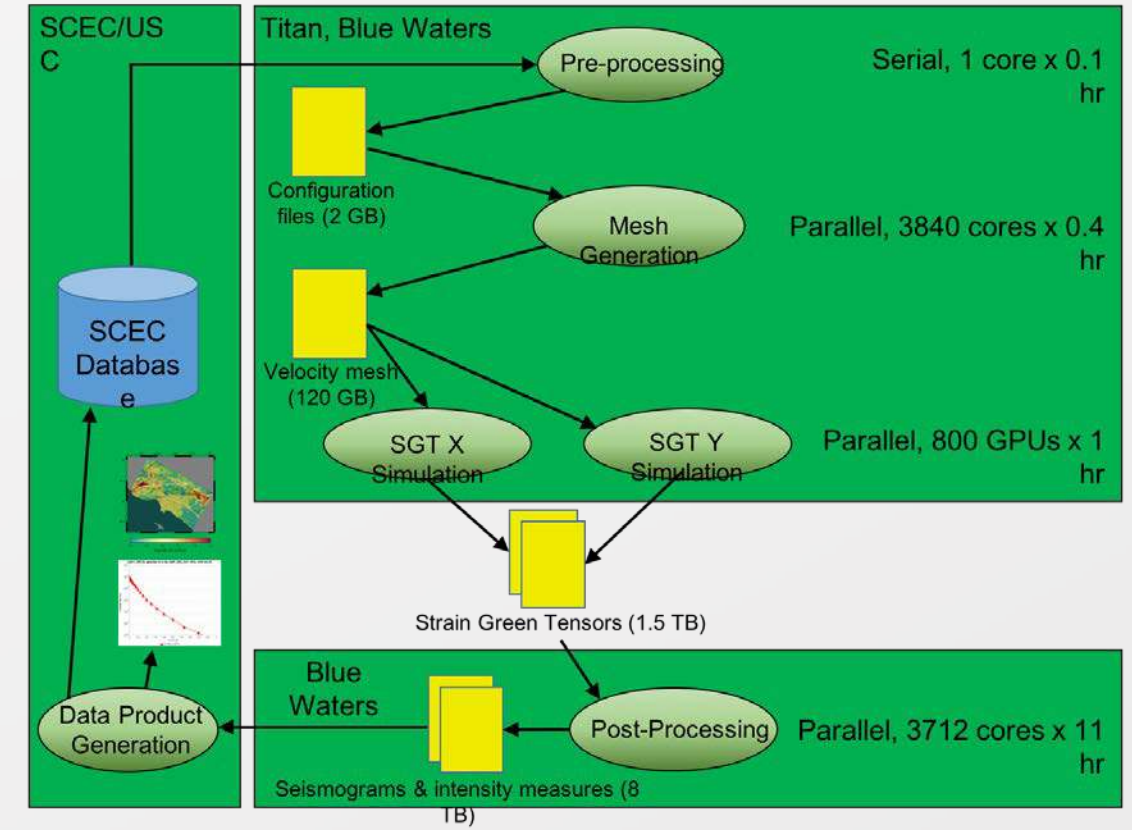
Builders ask seismologists: What will the peak ground motion be at my new building in the next 50 years?

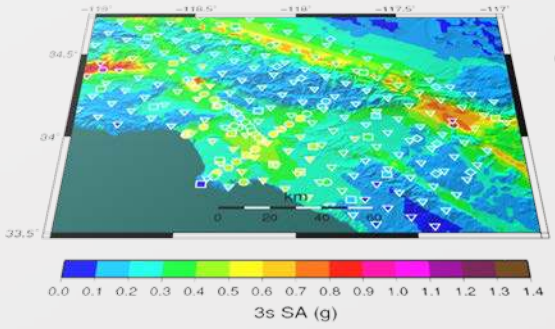
Seismologists answer this question using Probabilistic Seismic Hazard Analysis (PSHA)

CPU jobs (Mesh generation, seismogram synthesis):
1,094,000 node-hours
GPU jobs: 439,000 node-hours
- AWP-ODC finite-difference code
- 5 billion points per volume, 23,000 timesteps
- 200 GPUs for 1 hour

Titan:
- 421,000 CPU node-hours, 110,000 GPU node-hours

Blue Waters:
- 673,000 CPU node-hours, 329,000 GPU node-hours





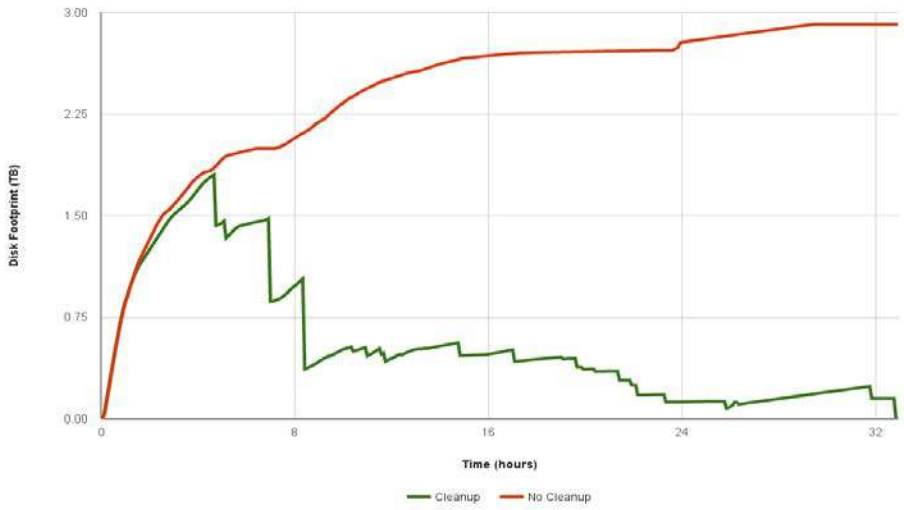
286 sites, 4 models
each workflow has **420,000 tasks**

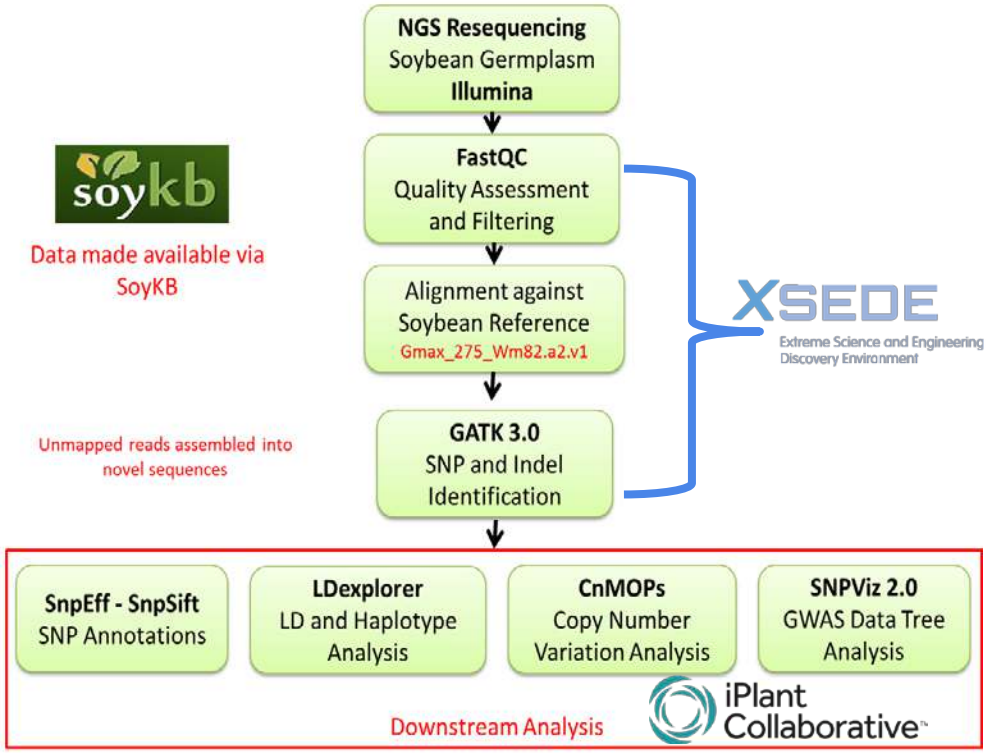
Soykb Workflow

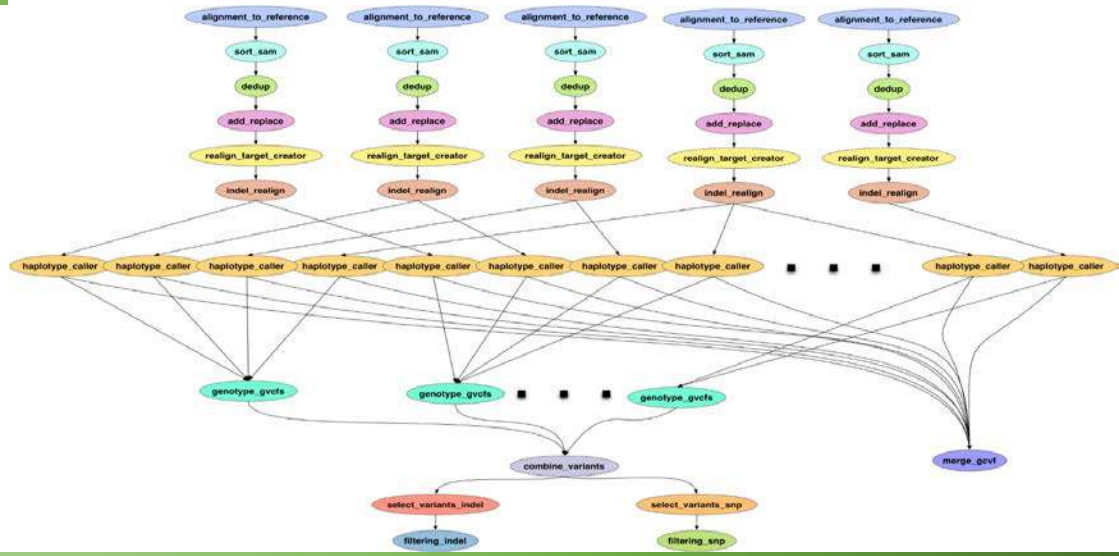
TACC Wrangler as Execution Environment

HTCondor 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 great on Wrangler due to the flash filesystem, and the memory per core (48 cores, 128 GB RAM)







XENONnT - Dark Matter Search

Two workflows: Monte Carlo simulations, and the main processing pipeline.

Workflows execute across Open Science Grid (OSG) and European Grid Infrastructure (EGI)

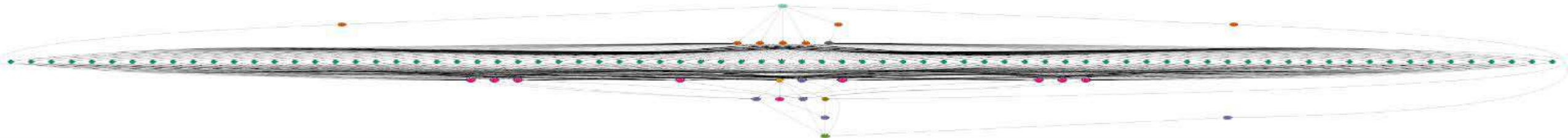
Rucio for data management

MongoDB instance to track science runs and data products.

```
------------------------------------------------------------------------------
Type           Succeeded Failed  Incomplete  Total     Retries   Total+Retries
Tasks          4000      0       0           4000      267       4267
Jobs           4484      0       0           4484      267       4751
Sub-Workflows  0         0       0           0         0         0
------------------------------------------------------------------------------

Workflow wall time                                       : 5 hrs, 2 mins
Cumulative job wall time                                 : 136 days, 9 hrs
Cumulative job wall time as seen from submit side        : 141 days, 16 hrs
Cumulative job badput wall time                          : 1 day, 2 hrs
Cumulative job badput wall time as seen from submit side : 4 days, 20 hrs
```

Main processing pipeline is being developed for XENONnT - data taking will start at the end of 2019. Workflow in development:



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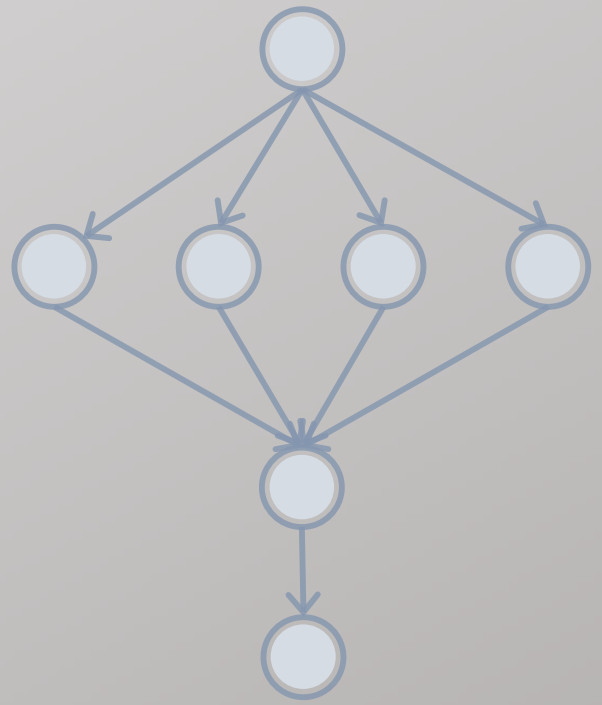
Basic concepts…

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

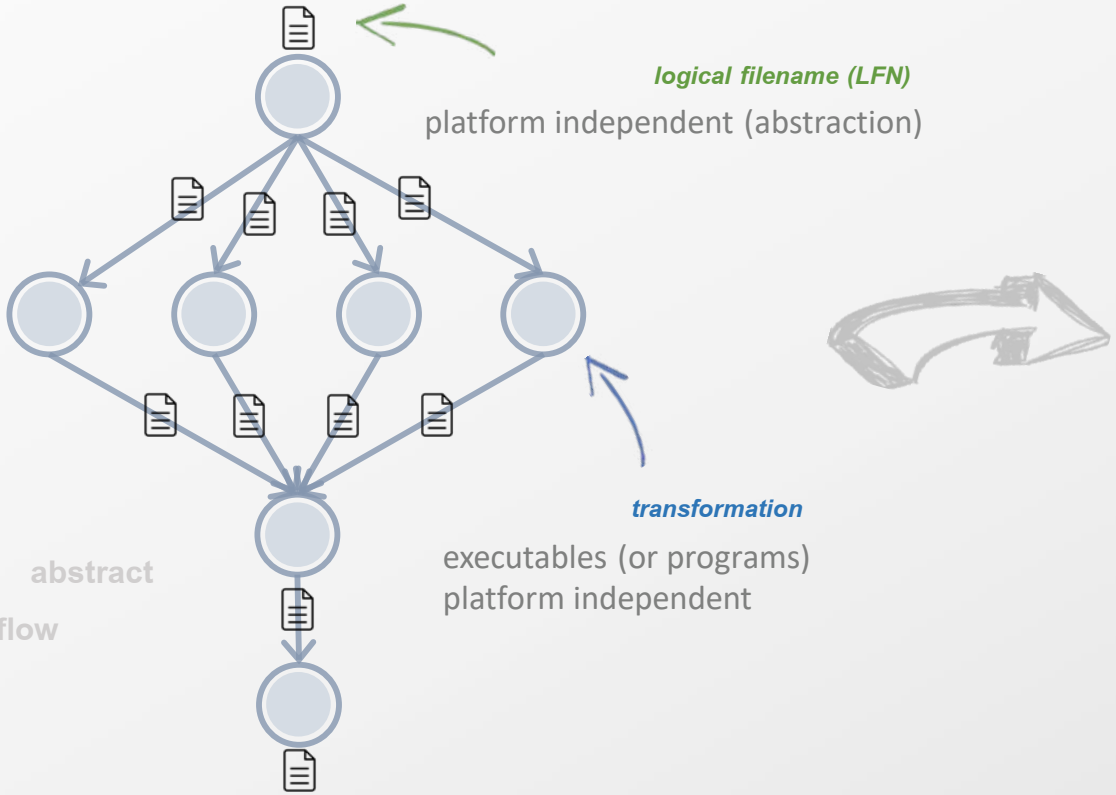
- Planner is like a compiler

DAX

DAG in XML

Portable Description

Users do not worry about low level execution details



logical filename (LFN)

platform independent (abstraction)

transformation

executables (or programs)
platform independent

abstract workflow

DAG

directed-acyclic graphs

stage-in job

Transfers the workflow input data

cleanup job

Removes unused data

stage-out job

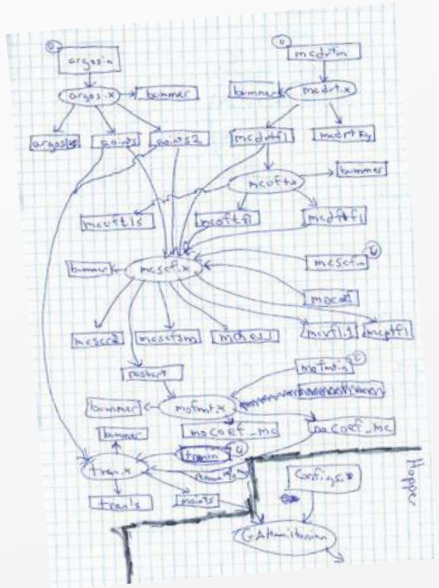
Transfers the workflow output data

registration job

Registers the workflow output data

executable workflow

Pegasus also provides tools to generate the abstract workflow



```python
#!/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)
```

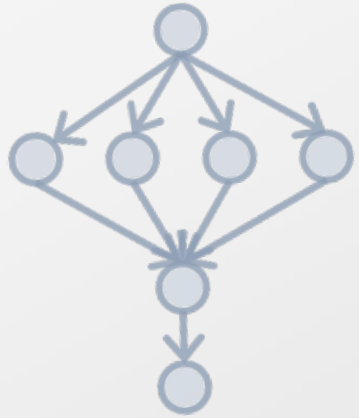
python

Java

R

perl

jupyter

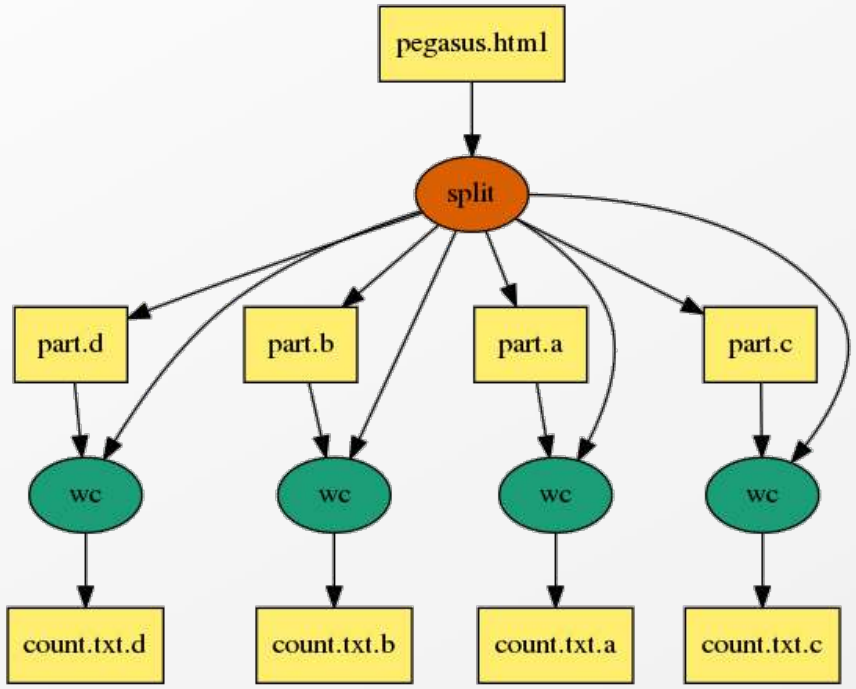


```xml
<?xml version="1.0" encoding="UTF-8"?>

<!-- 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

An example

Split Workflow



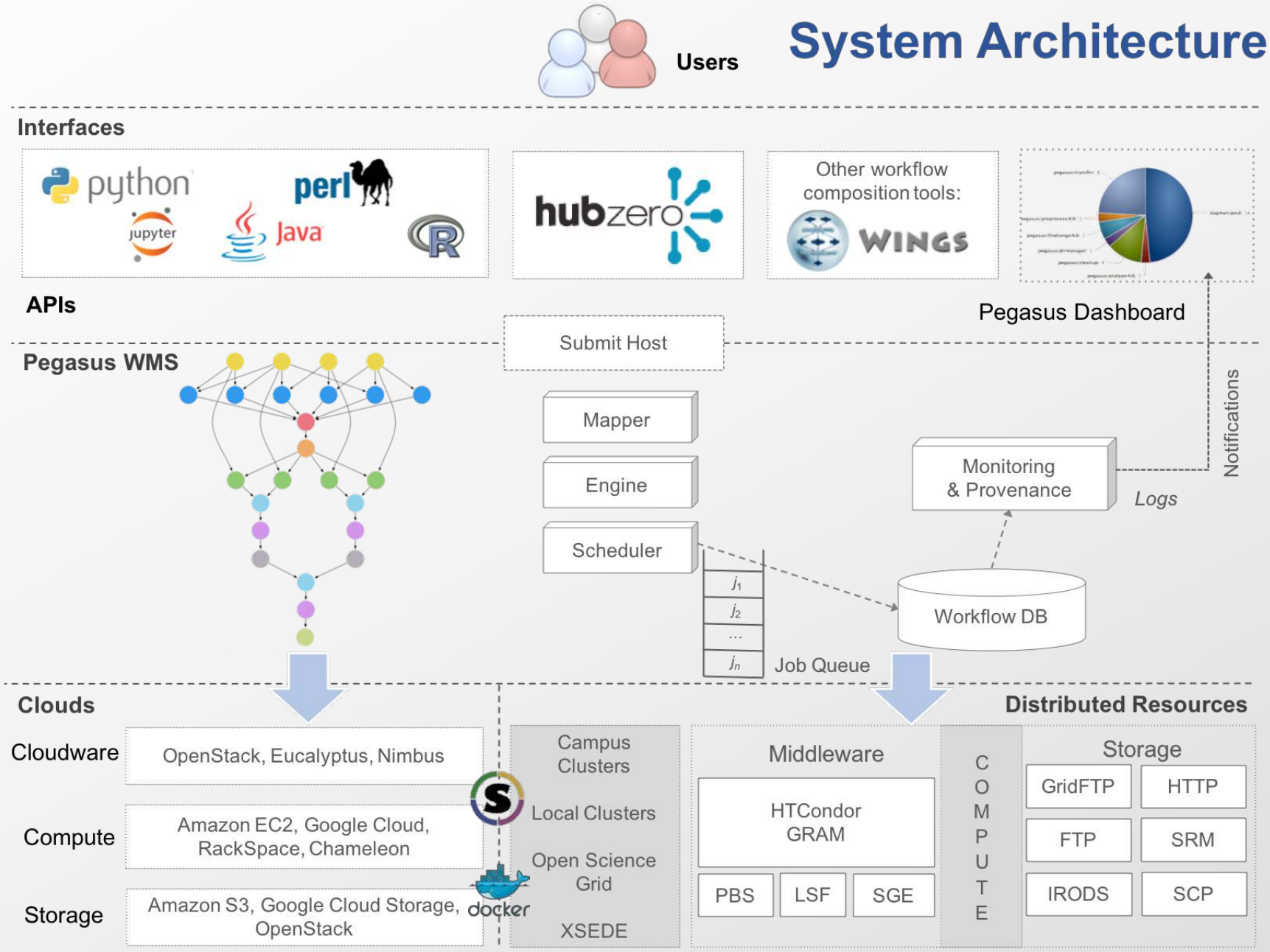
Visualization Tools:

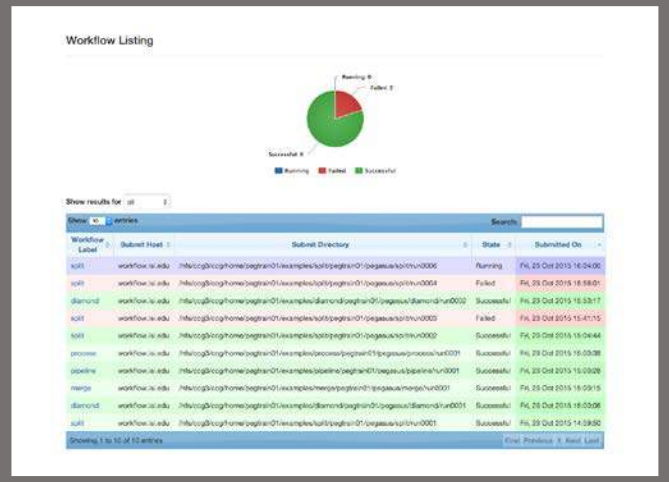
pegasus-graphviz

pegasus-plots

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

import os, pwd, sys, time
from Pegasus.DAX3 import *

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

webpage = File("pegasus.html")

# 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)
dax.addJob(split)

# we do a parmeter sweep on the first 4 chunks created
for c in "abcd":

    part = File("part.%s" % c)
    split.uses(part, link=Link.OUTPUT, transfer=False, register=False)
    count = File("count.txt.%s" % c)

    # wc job
    wc = Job("wc")
    wc.addProfile( Profile("pegasus", "label", "p1"))
    wc.addArguments("-l", part)
    wc.setStdout(count)
    wc.uses(part, link=Link.INPUT)
    wc.uses(count, link=Link.OUTPUT, transfer=True, register=True)
    dax.addJob(wc)

    # job dependency
    dax.depends(wc, split)

f = open("split.dax", "w")
dax.writeXML(f)
f.close()
```

System Architecture

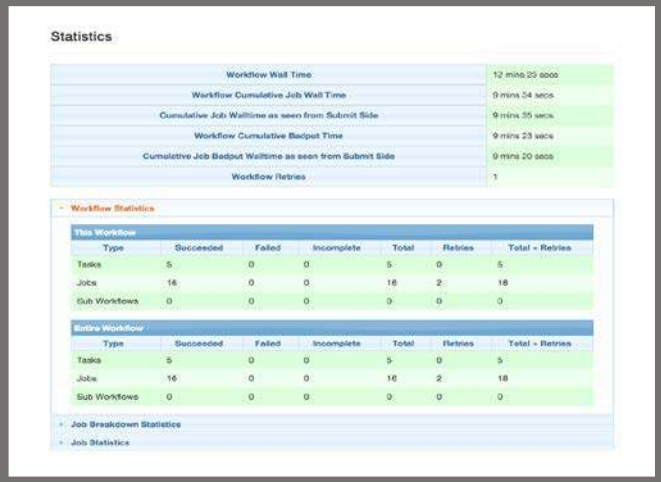




Pegasus

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

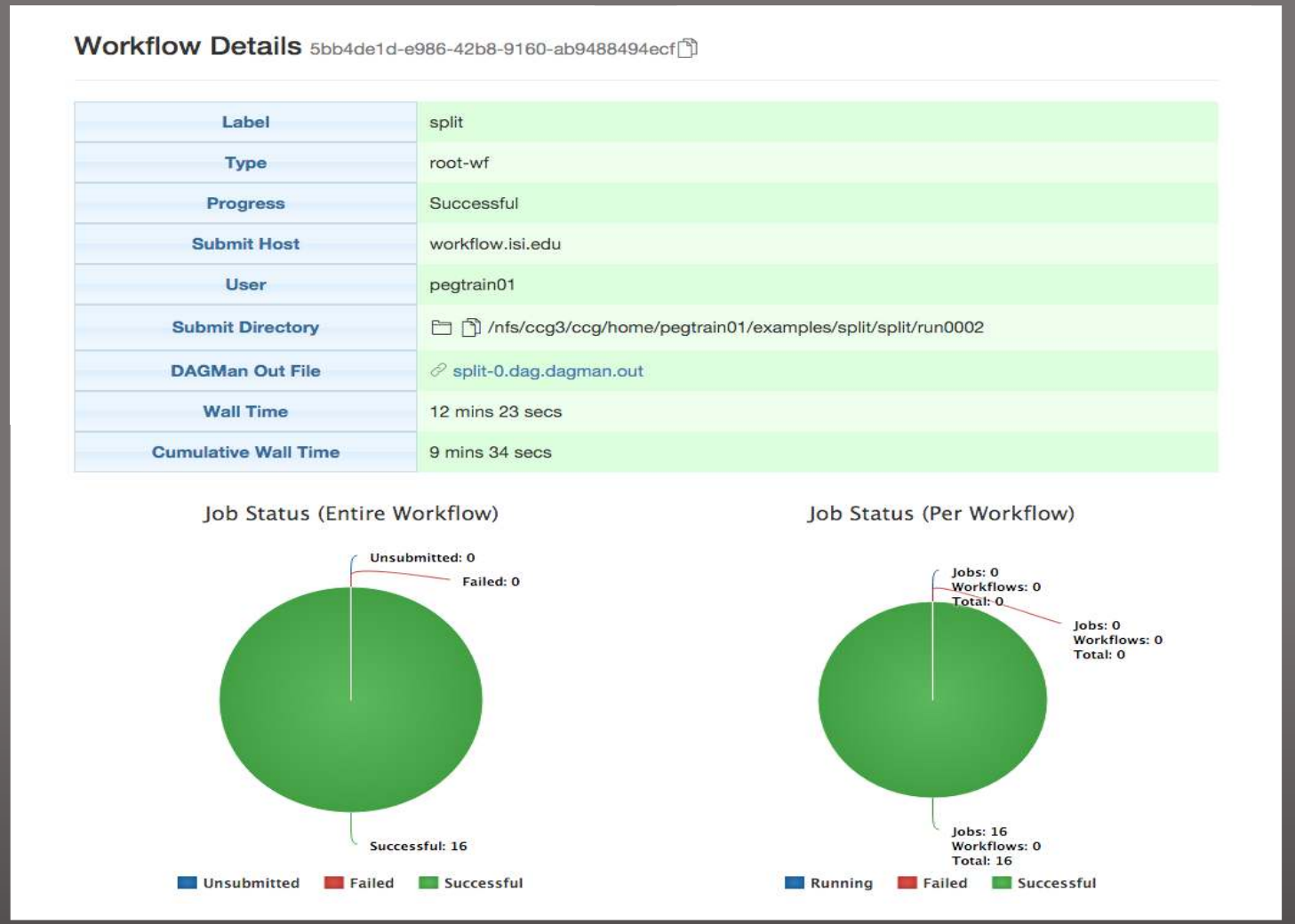
RESTful API

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.



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

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Hands-on Pegasus Tutorial…

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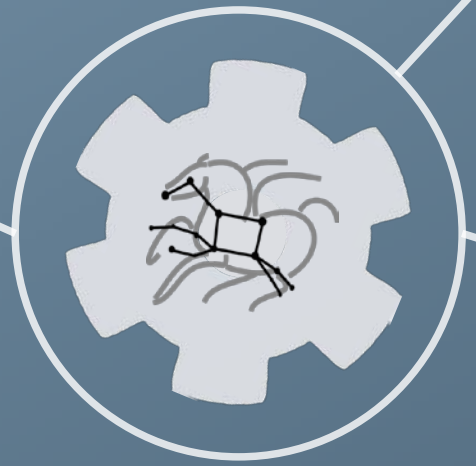
Understanding Pegasus features…

So, what information does Pegasus need?

Transformation Catalog
describes all of the executables (called “transformations”) used by the workflow

Site Catalog
describes the sites where the workflow jobs are to be executed



Replica Catalog
describes all of the input data stored on external servers

How does Pegasus decide where to execute?

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 were 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>
```

How does it know where the executables are or which ones to use?

executables description

list of executables locations per site

physical executables

mapped from logical transformations

transformation type

whether it is installed or available to stage

```
...
# This is the transformation catalog. It lists information about
# each of the executables that are used by the workflow.

tr ls {
  site PegasusVM {
    pfn "/bin/ls"
    arch "x86_64"
    os "linux"
    type "INSTALLED”
  }
}
...
```

What if data is not local to the submit host?


```
# 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

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

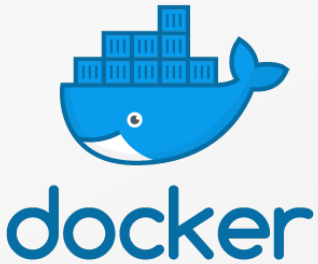
```
# This is the replica catalog. It lists information about each of the
# input files used by the workflow. You can use this to specify locations
# to input files present on external servers.

# 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 Container Support

- Support for
  - Docker
  - Singularity
  - Shifter (coming soon)



- 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)

- 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.

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Workflow Dashboard and Monitoring
Generating the Workflow

Understanding Pegasus Features *Information Catalogs*
Containers

Hands-on Tutorial *Workflows with Containers*
Clustering
Fault-Tolerance

Other Features *Data Staging*
Jupyter Notebooks
Metadata, Hierarchal Workflows, Data Reuse

A few more features…

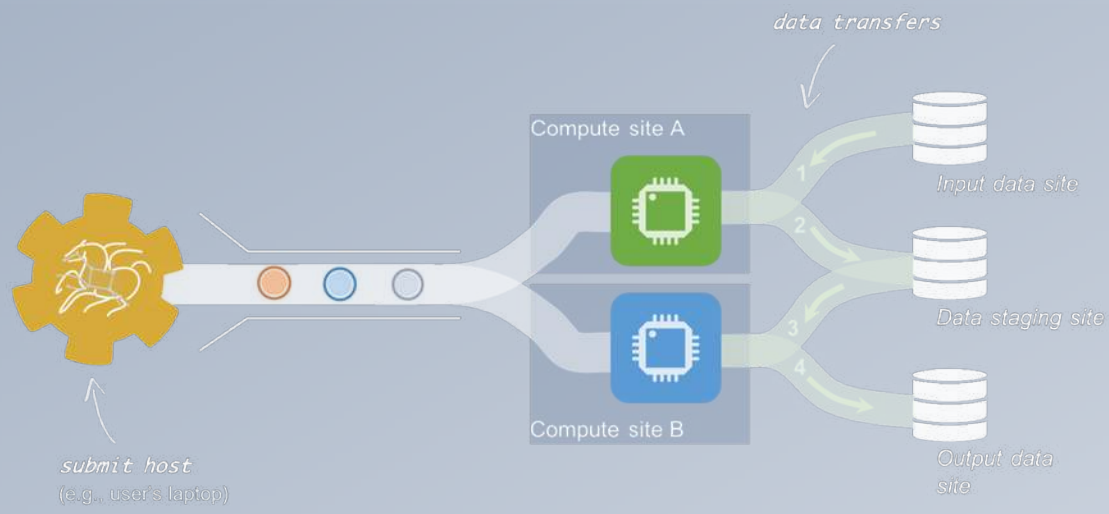
Data Staging Configurations

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

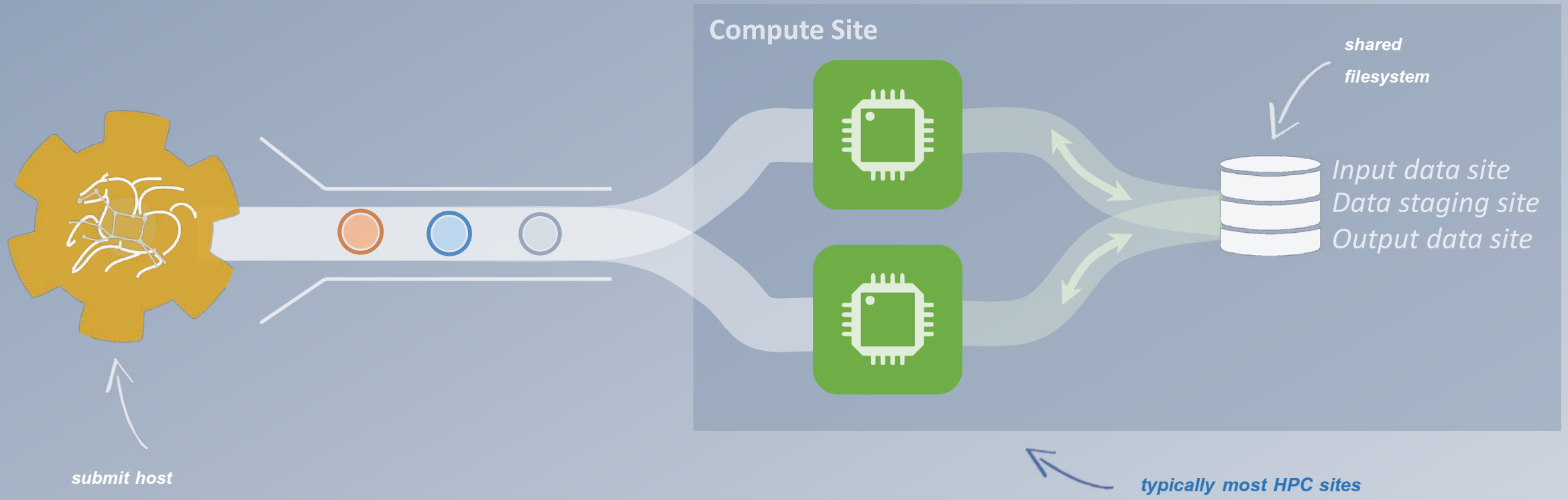


Shared File System (HPC sites, XSEDE, Campus clusters, …)

- I/O is directly against the shared file system

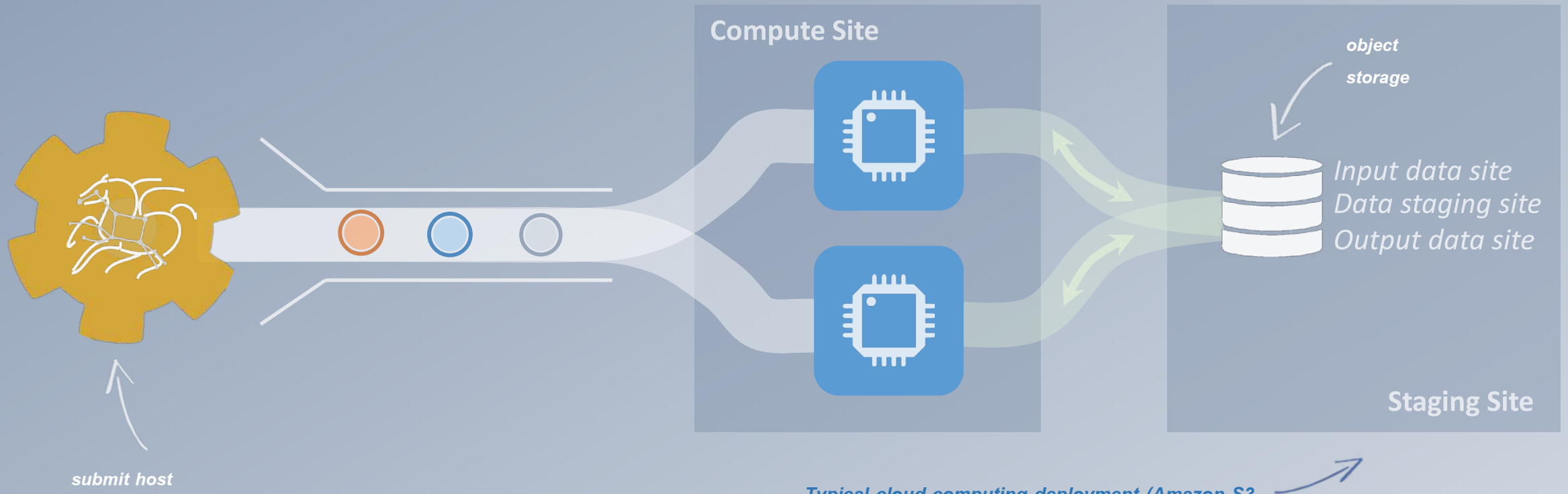
High Performance Computing

There are several possible configurations…



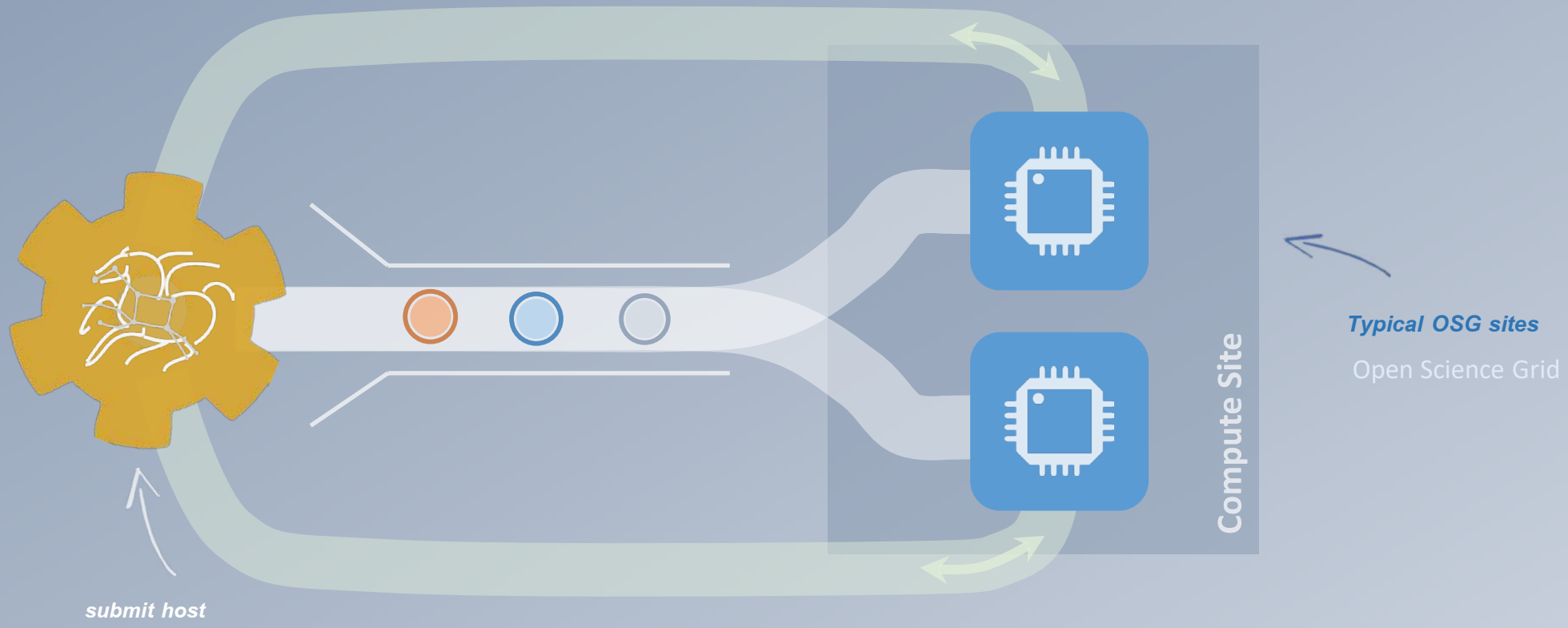
Cloud Computing

high-scalable object storages

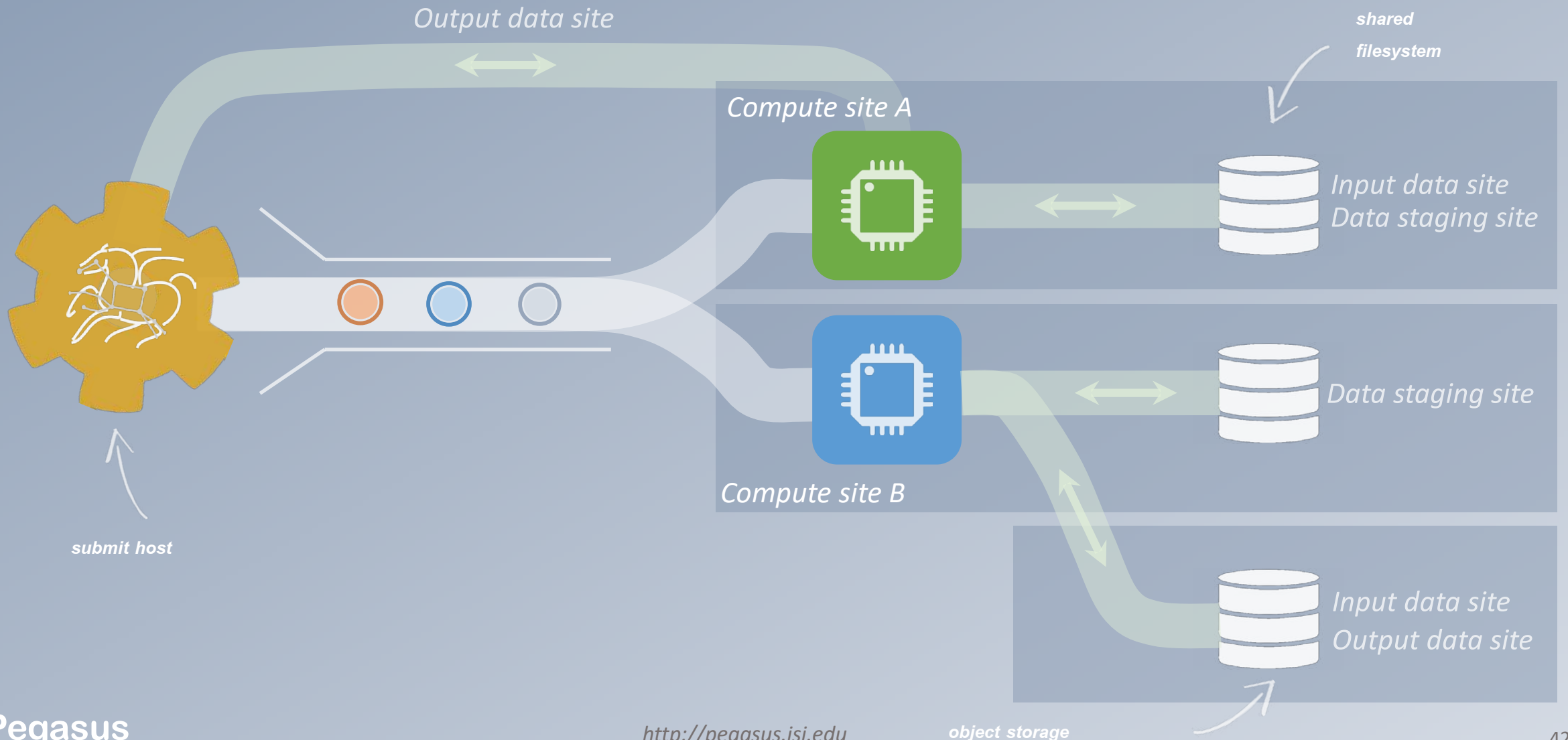


Typical cloud computing deployment (Amazon S3, Google Storage)

local data management



And yes… you can mix everything!



pegasus-transfer

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

Directory creation, file removal

If protocol can support it, also used for cleanup

Two stage transfers

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

Parallel transfers

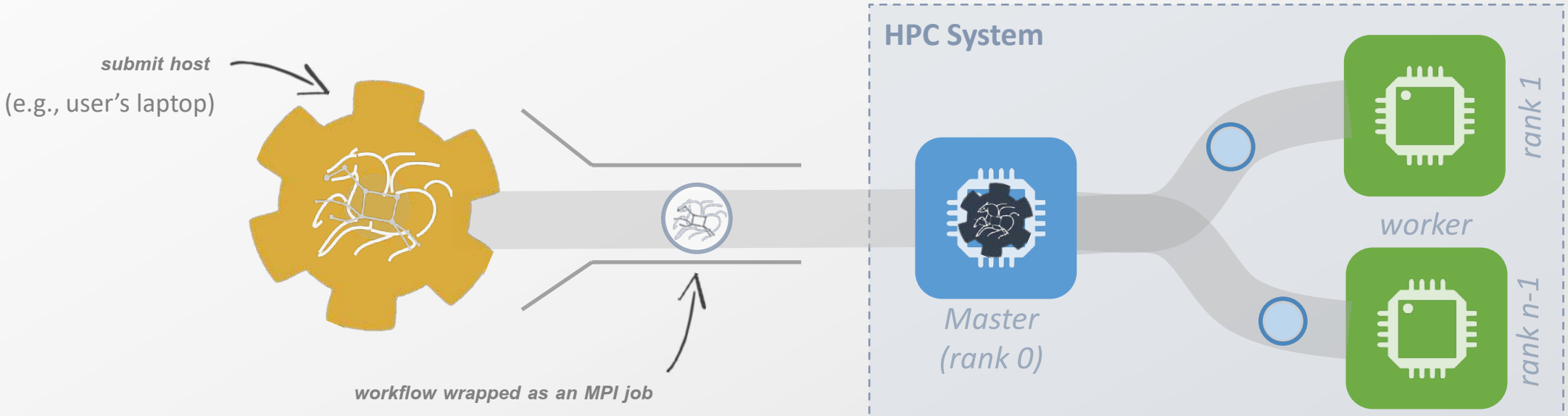
Automatic retries

Credential management

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

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

Running **fine-grained** workflows on HPC systems…



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

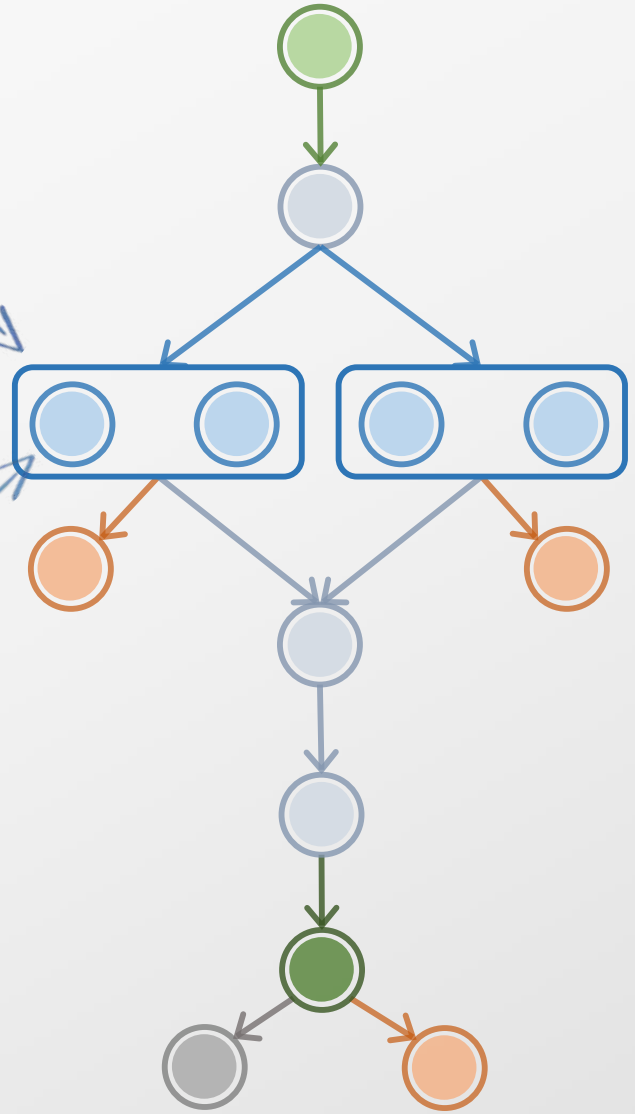
Performance, why not improve it?

clustered job

Groups small jobs together to improve performance

task

small granularity



http://pegasus.isi.edu

And if a job fails?

Job Failure Detection

detects non-zero exit code
output parsing for success or failure message
exceeded timeout
do not produced expected output files

Job Retry

helps with transient failures
set number of retries per job and run

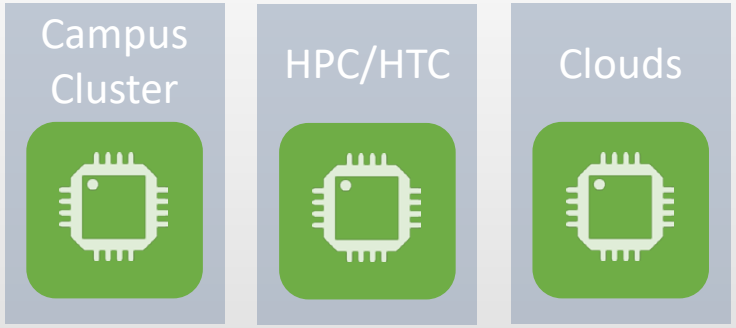
Checkpoint Files

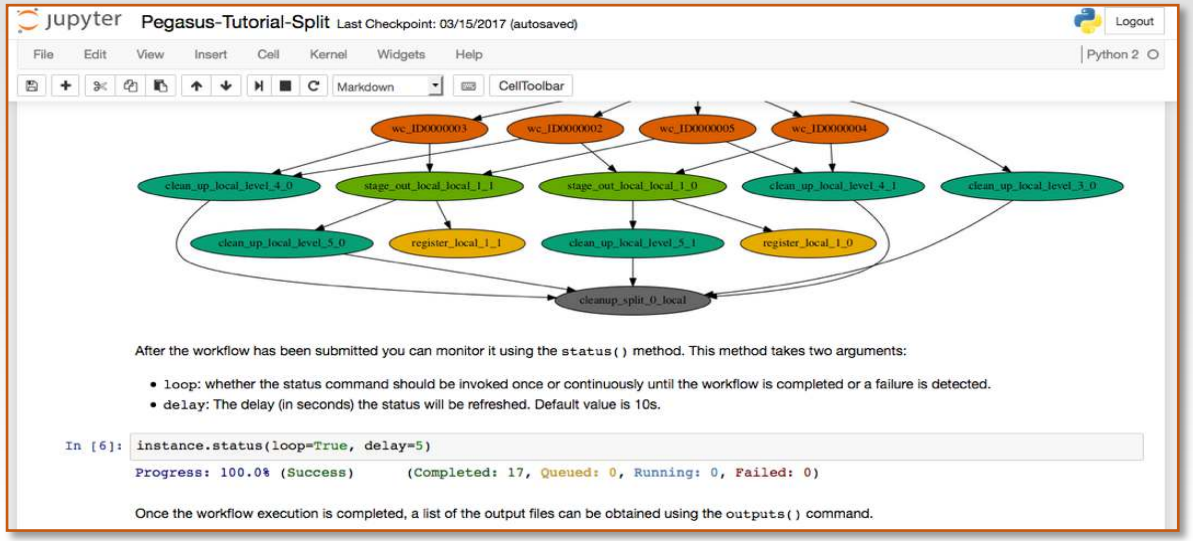
job generates checkpoint files
staging of checkpoint files is
automatic on restarts

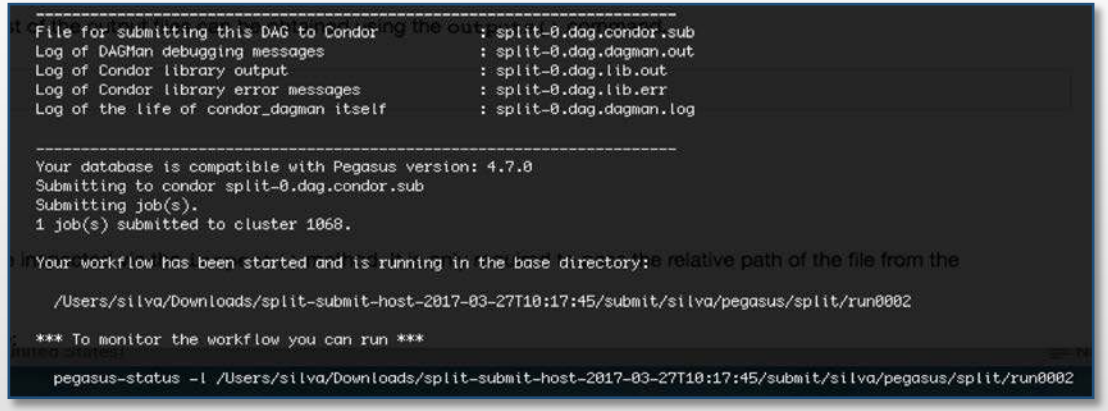
Rescue DAGs

workflow can be restarted from checkpoint file
recover from failures with minimal loss

Running Pegasus workflows with Jupyter







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)
```

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

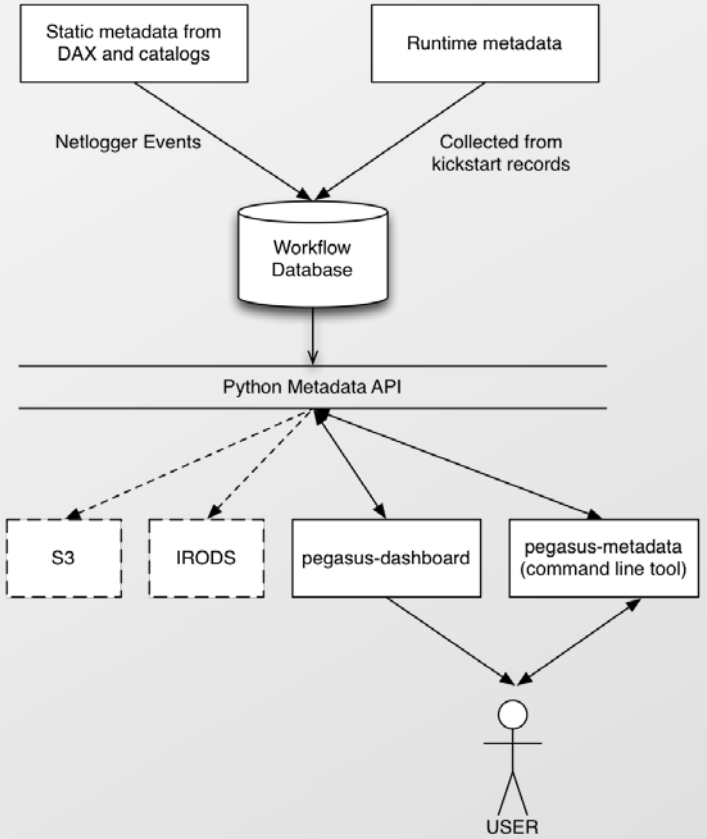
Runtime: performance metrics

```
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>
```

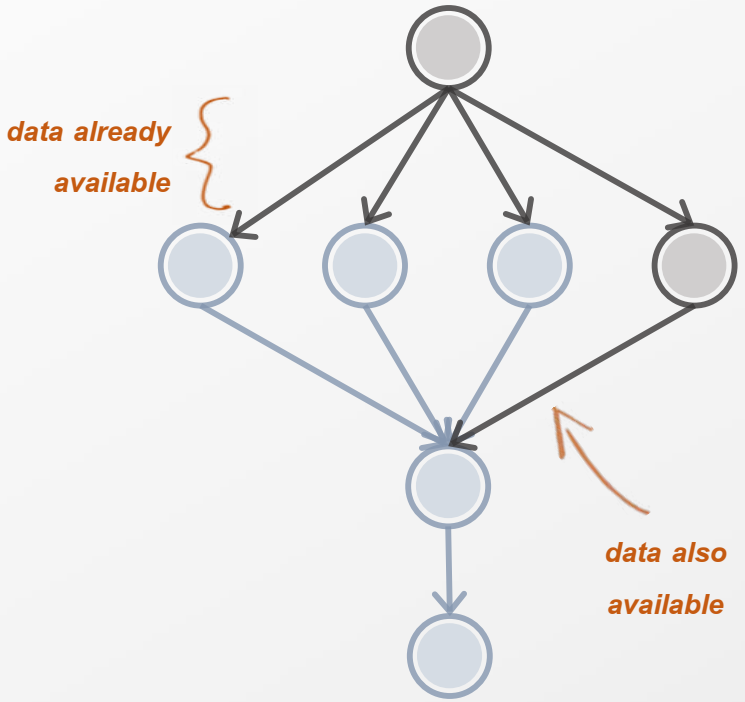
workflow, job, file

select data based on metadata

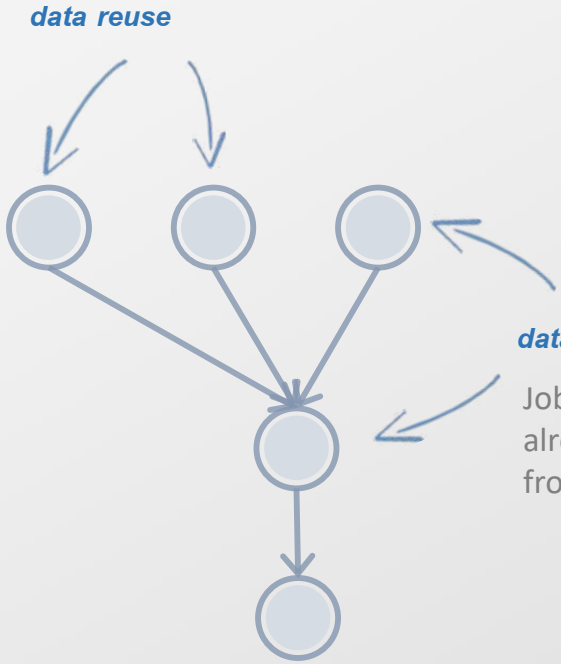
register data with metadata



What about **data reuse**?



workflow
reduction



Jobs which output data is already available are pruned from the DAG

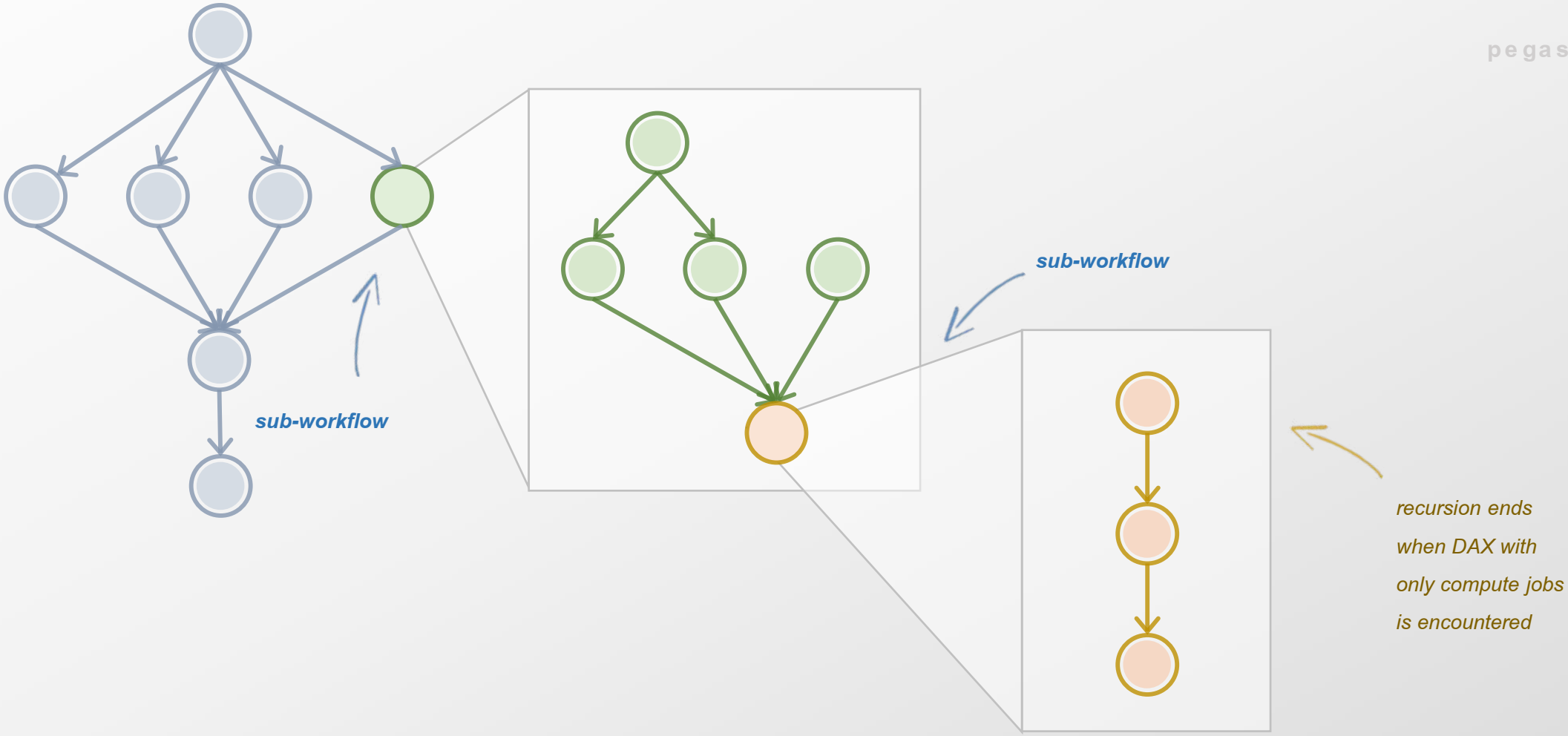
Pegasus also handles **large-scale workflows**

workflow restructuring

workflow reduction

hierarchical workflows

pegasus-mpi-cluster



Job Submissions

Local

Submit Machine

Personal HTCondor

Local Campus Cluster accessible via Submit Machine ****

HTCondor via BLAHP

Remote

BOSCO + SSH*

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

BOSCO based Glideins*

SSH based submission of glideins

PyGlidein

IceCube glidein service

OSG using glideinWMS

Infrastructure provisioned glideins

CREAMCE

Uses CondorG

Globus GRAM

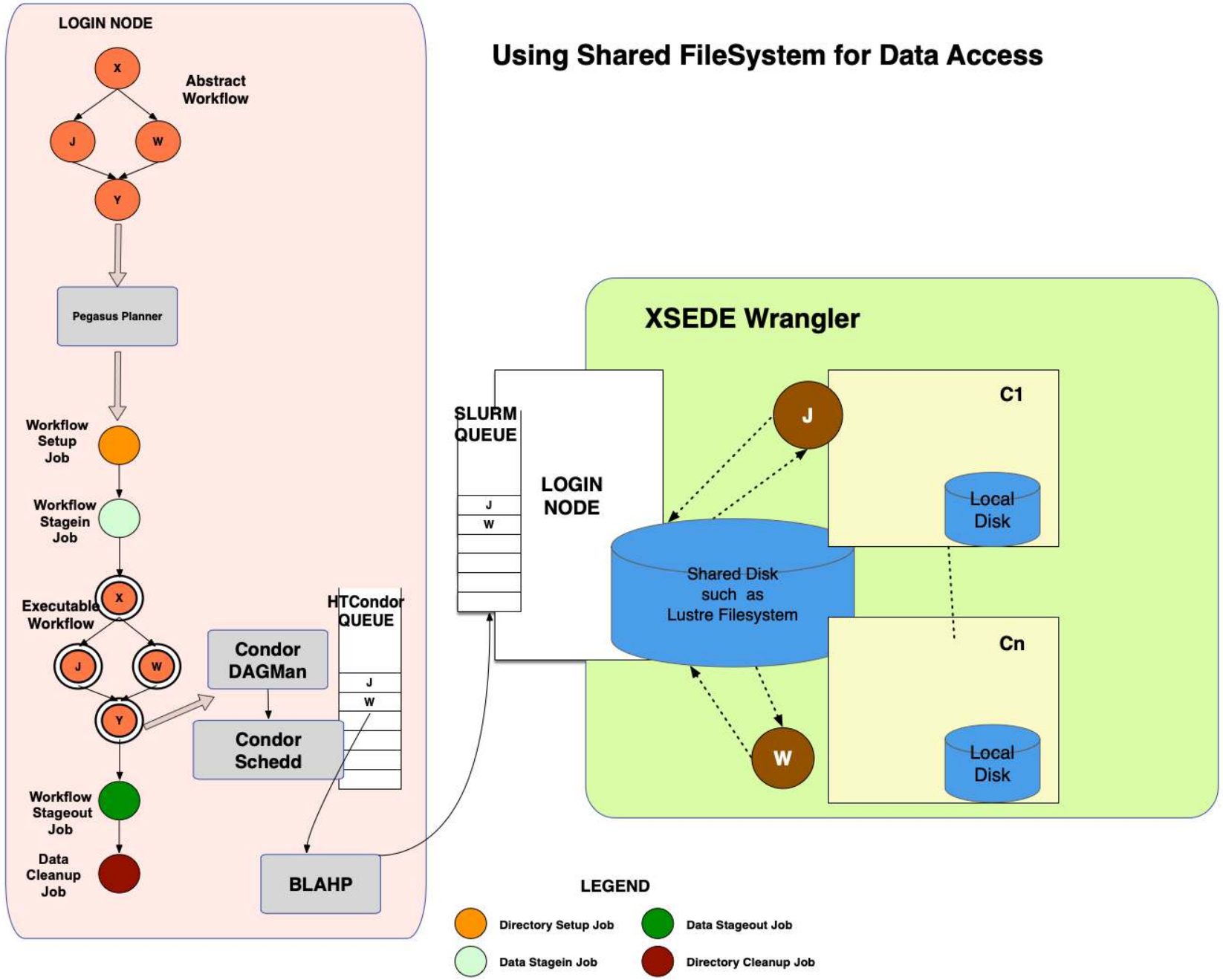
Uses CondorG

*** Both Glite and BOSCO build on HTCondor BLAHP*

Currenty supported schedulers:

SLURM SGE PBS MOAB

Using Shared FileSystem for Data Access



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

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