Galaxy Farm

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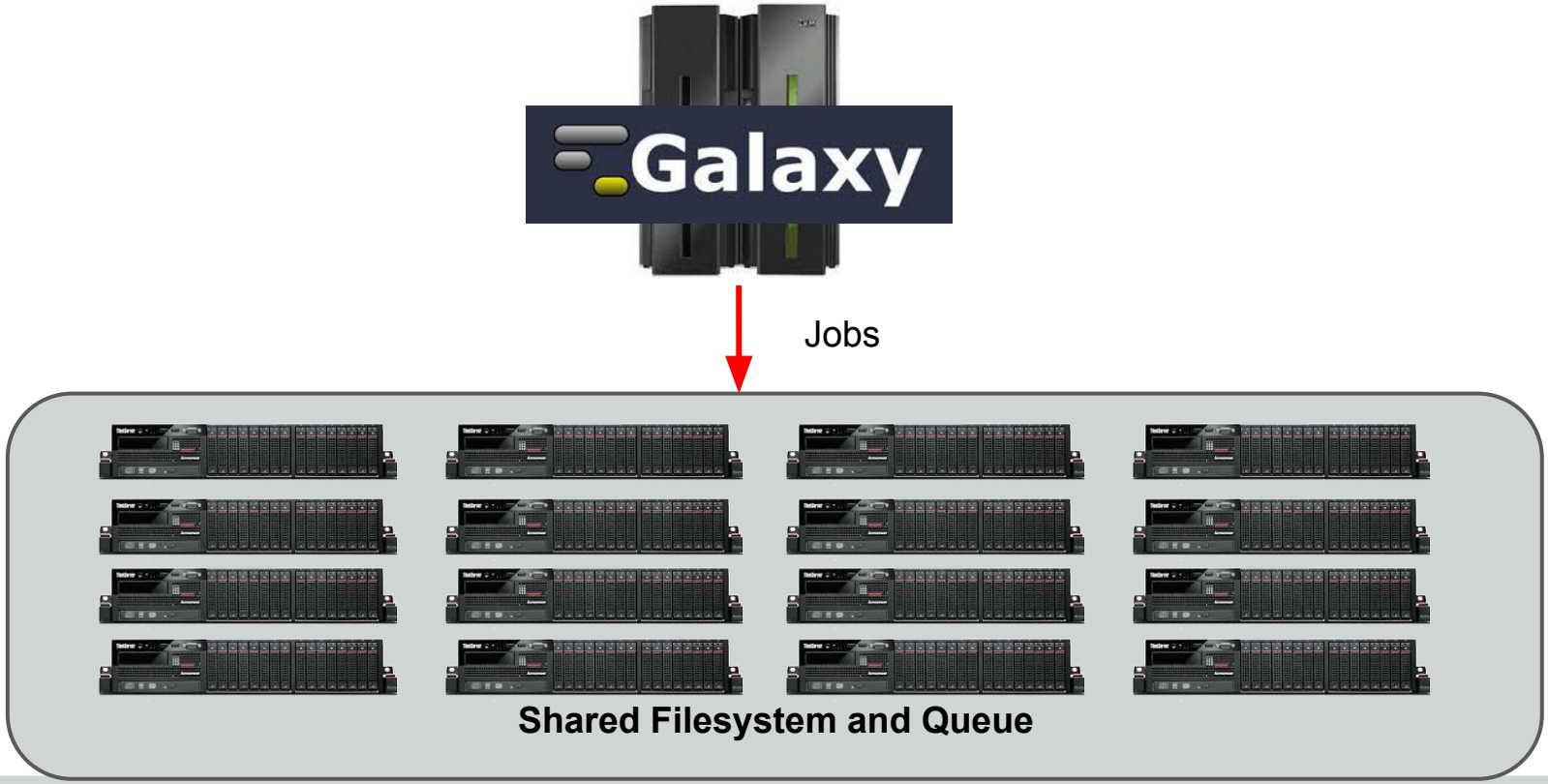
Current Clustering



For High Performance

For large scale genomics using network shared drives doesn't scale

Galaxy needs a concept of data locality

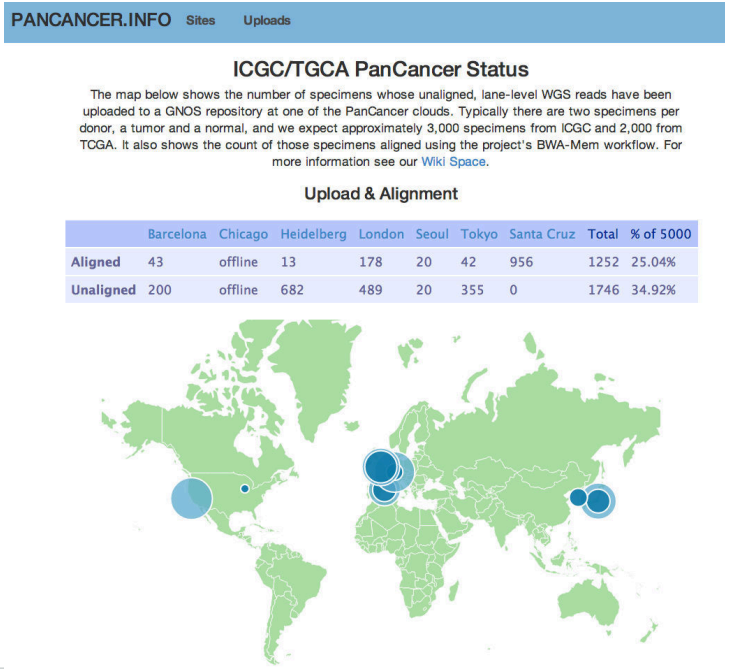
Be able to do workflow end-to-end on remote node, only transfer back the required results

What kind of high performance

Applying standardized pipelines to massive data sets

Example:

Run standard re-alignment pipeline on every TCGA WGS



Farming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Workflow
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Things that need to move around

- Work
- Workflows
- Tools
- Data
- Provenance

What do you need

Essentials

- Workflow Request Batches
- UUIDs (on everything)
- Data Referrals (UUID resolution)
- Standardized Job/Workflow/Tool/Provenance Transfer

Fancy Stuff

- Docker
- Gossip Protocols
- Peer Authentication

What's Done? What's needed?

Done:

- Dataset UUID are now on by default
- Workflow Batches Implemented
- Mesos based launching

Needed:

- Workflow Request Transfer
- Auto History transfer

Going forward?

Get a working prototype running

Do a large scale run

The tools that you need for farming are the same ones you need for federation...

Extra Slides

Workflow Request Batch

In the Galaxy DB, we need to seperate the idea of a Workflow Request and a Workflow Instance

Add the concept of Batches, that can be schduled at the same time (with common scheduling configurations)

UUID resolution

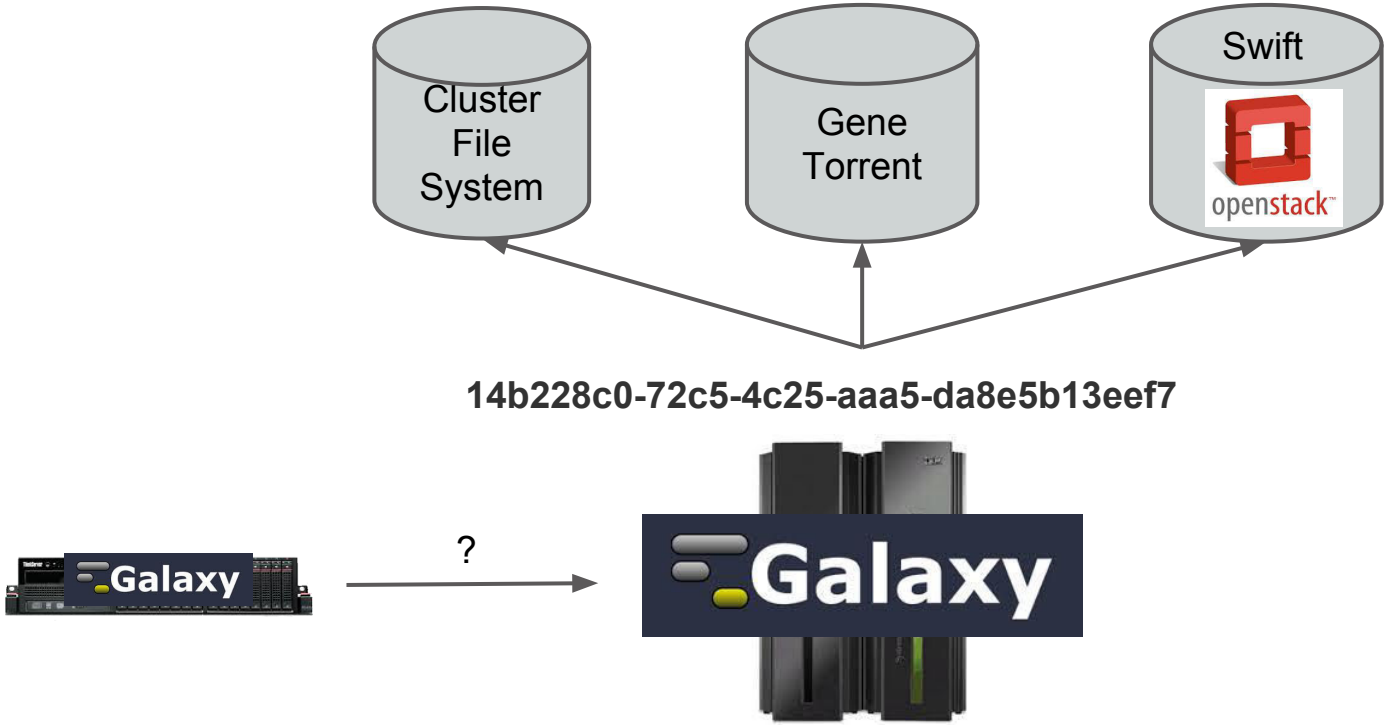
14b228c0-72c5-4c25-aaa5-da8e5b13eef7

Cancer Genomics Hub Browser Cart (0) Batch search Help Accessibility Search **Data Browser**

Item details for Analysis Id 14b228c0-72c5-4c25-aaa5-da8e5b13eef7

Study	TCGA
Barcode	TCGA-A6-A567-01A-31D-A28G-10
Disease	COAD
Disease Name	Colon adenocarcinoma
Sample Type	TP
Sample Type Name	01
Analyte Type	DNA
Library Type	WGS
Center	BCM
Center Name	Baylor College of Medicine
Platform	ILLUMINA
Platform Name	Illumina
Assembly	GRCh37-lite
Filename	TCGA-A6-A567-01A-31D-A28G-10_wgs_Illumina.bam
Filesize	519.58 GB

Data Referral



Job Offloading

Work and Data Transfers

Galaxy

Galaxy