Connecting Galaxy to a Data Repository

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In collaboration with

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Goals

Support data analysis on large collections of samples

Both on private and public data sets

Support efficient deployment of new algorithms and tools

For collaborators to run analyses on their data without our help

For the general public as supplement to publications

Support exploration and visualization of analysis results

With interactive, browser-based visualization tools

Difficulties with Goals

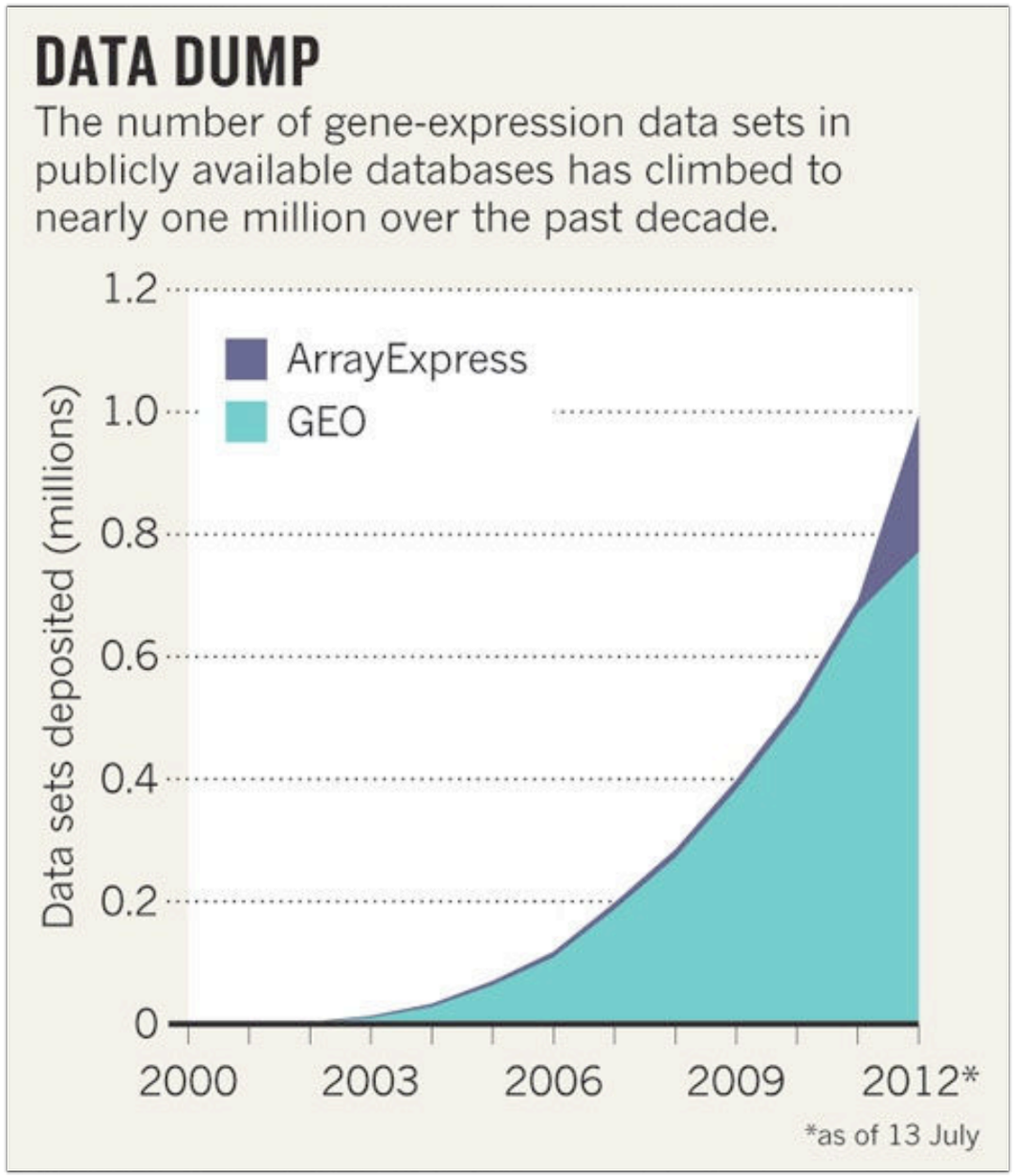
Searching/Finding relevant data

Downloading and processing data

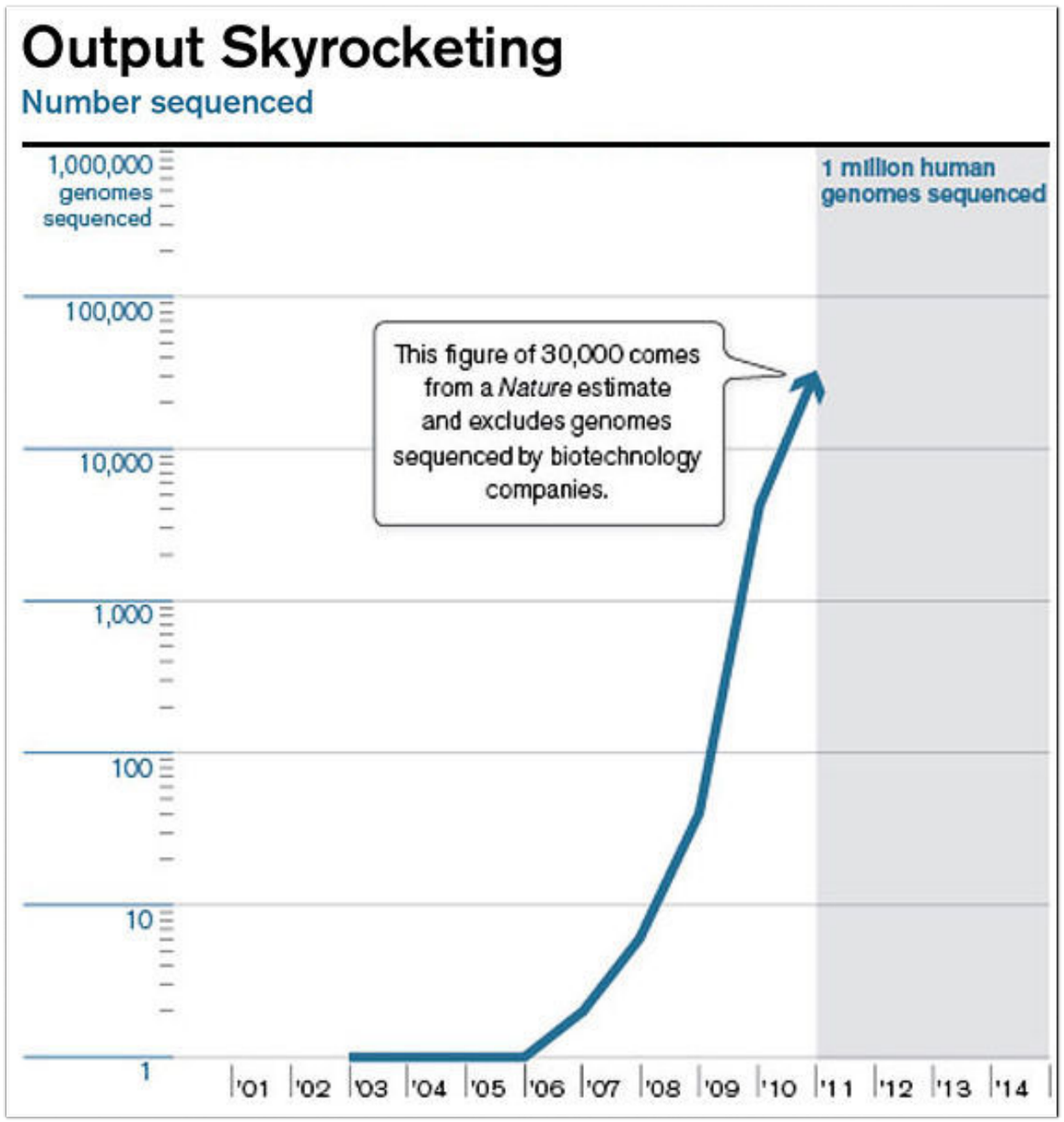
Dealing with the magnitude of data

Sharing analyses and data

Explosion of Big Data



Baker et al. "Gene data to hit milestone." Nature. 2012 Jul 18



Source: U.S. National Human Genome Research Institute, Nature

Explosion of Big Data

Sequence Read Archive (SRA) (7/25/2012)

Open: 255 terabases, 295 TB

Total: 608 terabases, 506 TB

Cancer Genomics Hub (CGHub) (7/16/2012)

Current: 31 TB, 22,760 files

Planned: 20k cases, 200 GB / case, 100TB

Gene Expression Omnibus (GEO) (7/25/2012)

10,314 platforms, 777,398 samples

2,720 datasets, 31,544 series

EBI ArrayExpress (7/25/2012)

31,465 experiments

914,184 assays

Sequence Read Archive

GEO Gene Expression Omnibus

ARRAYEXPRESS

"... a production facility composed of a group of [...] processes [...] refining certain materials or **converting raw material into products of value** ..."

Source: Wikipedia & *geekly on Flickr*

Implementation

Refinery web application is built on top of Django

Django is a popular Python web application framework

Using Postgresql database as backend

Long running tasks are managed through Celery & RabbitMQ

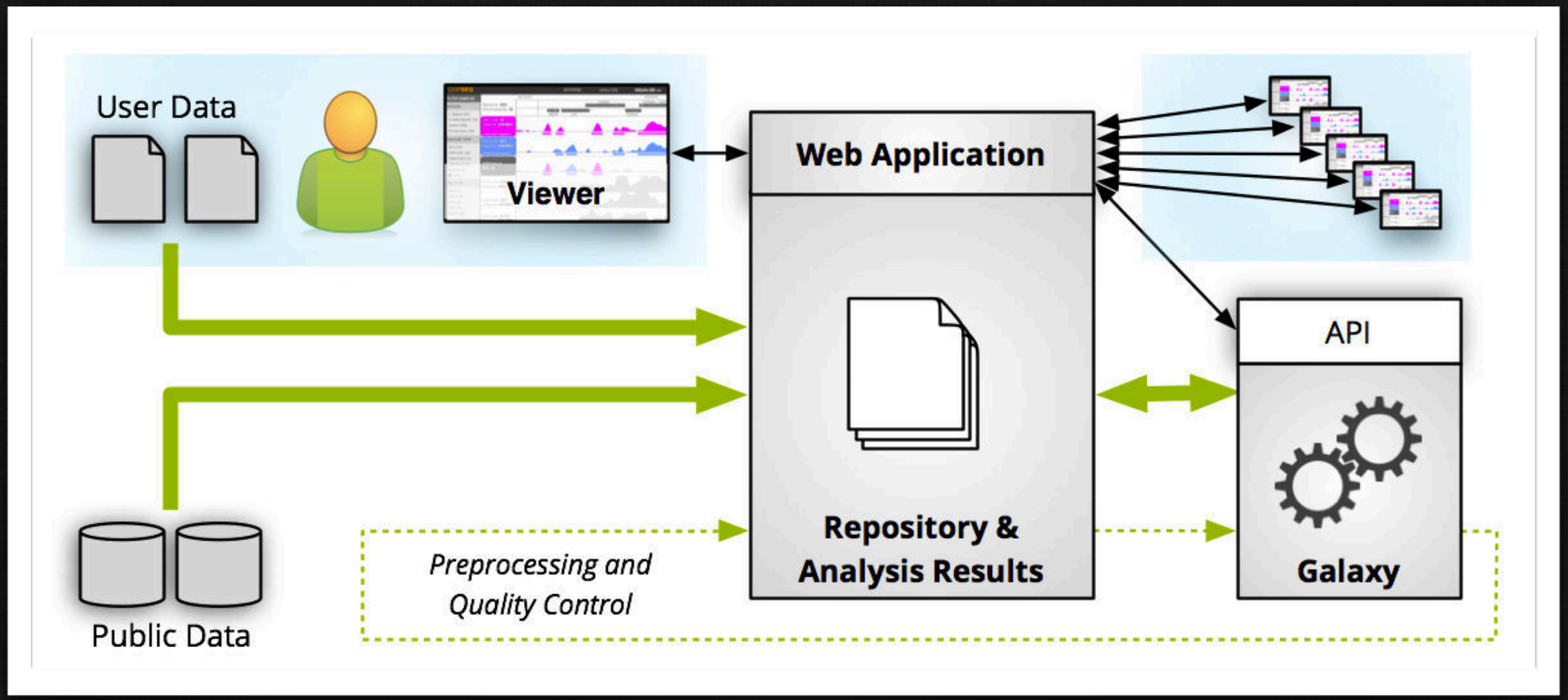
Search enhanced using Apache Solr

Typeahead functionality, Facets to find and filter for similar experiments

Web application controls Galaxy through its API

Refinery and Galaxy need to be able to access the same disk space

Overview


User Data
Viewer
Web Application
API
Repository &
Analysis Results
Galaxy
Public Data
Preprocessing and
Quality Control

Repository

Meta information stored in ISA-TAB format

Automated import of public data from ArrayExpress/GEO and SRAs

Automated import from Harvard Stem Cell Commons (Hide Lab)

Private data sets and analysis results stored locally

e.g. BAM files and intermediate results

Public data stored remotely

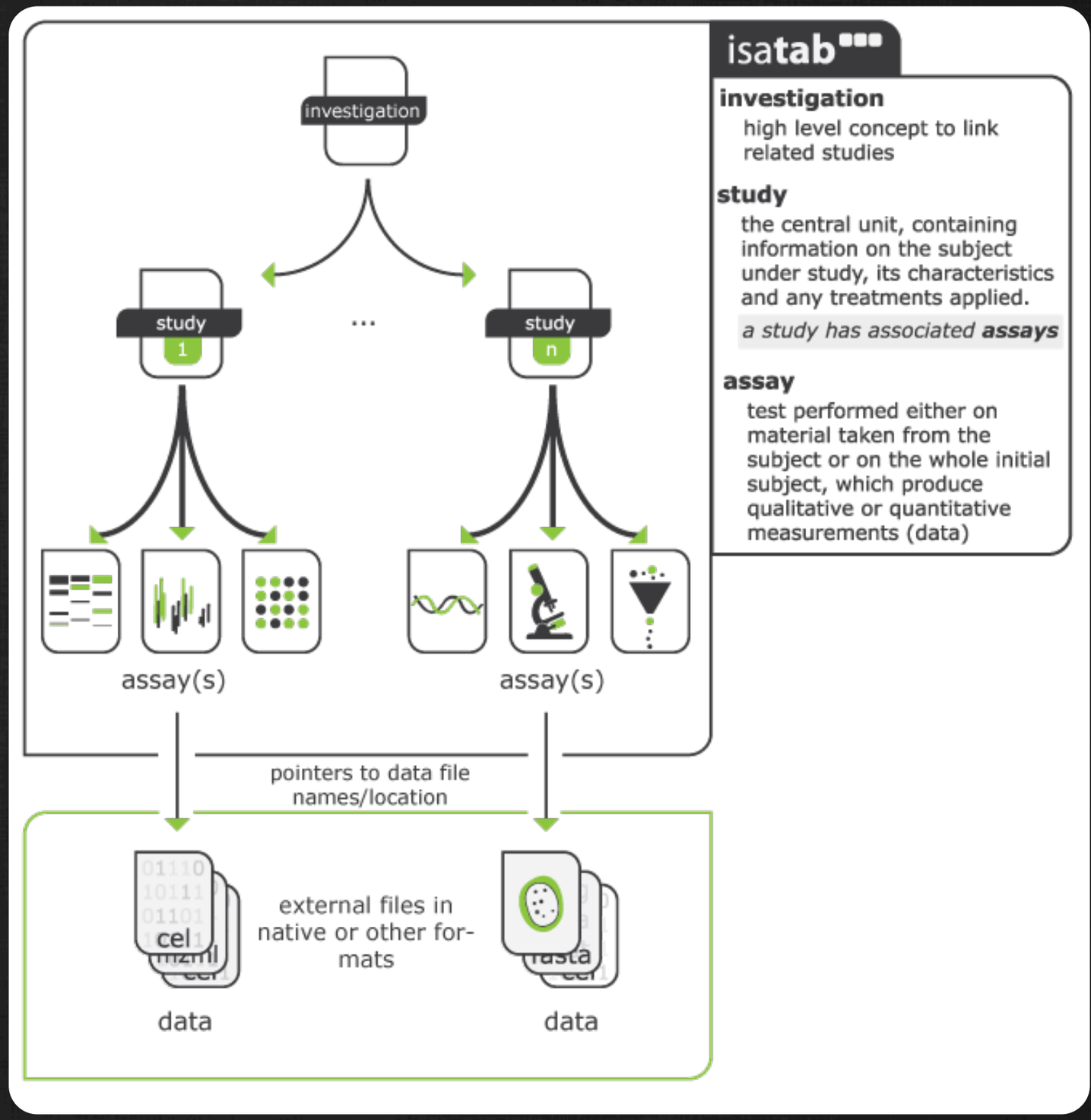
Previews available, automated download for analyses or loaded from local cache

Repository

The **Investigation**, **Study**, **Assay** (**ISA**) **tab-delimited** (**TAB**) format is a framework to collect and communicate complex metadata

Builds on the existing **MAGE-TAB** format

Adopted by: Pride (proteomics), ENA (genomics), ArrayExpress (transcriptomics), Novartis Institutes for BioMedical Research, NCI caBIG, etc...



Sansone et al.. The first RSBI (ISA-TAB) workshop: “Can a simple format work for complex studies?”. OMICS 2008;12:143-149.

Why not (just) use Galaxy?

Lacks support to store structured meta information about studies

Becomes an issue when data sets contain large numbers of samples with complex relationships

Difficulty with large number of samples

Significant manual intervention required to load 100s of files. Difficult to organize and keep track of outputs.

Hard to estimate progress of long running analyses

Extensions to Galaxy API

Additional features

Workflows can be downloaded and imported

Dynamic workflows are generated based on the number of inputs

Tool parameters are configurable (*to some degree*)

Selected output files from workflows are stored

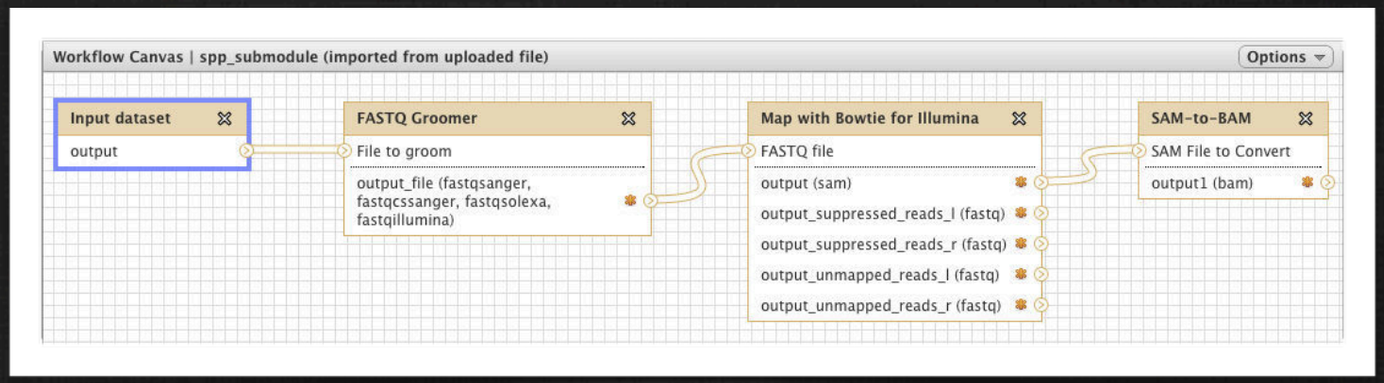
Improved support through Python class

Creation and deletion of libraries and histories

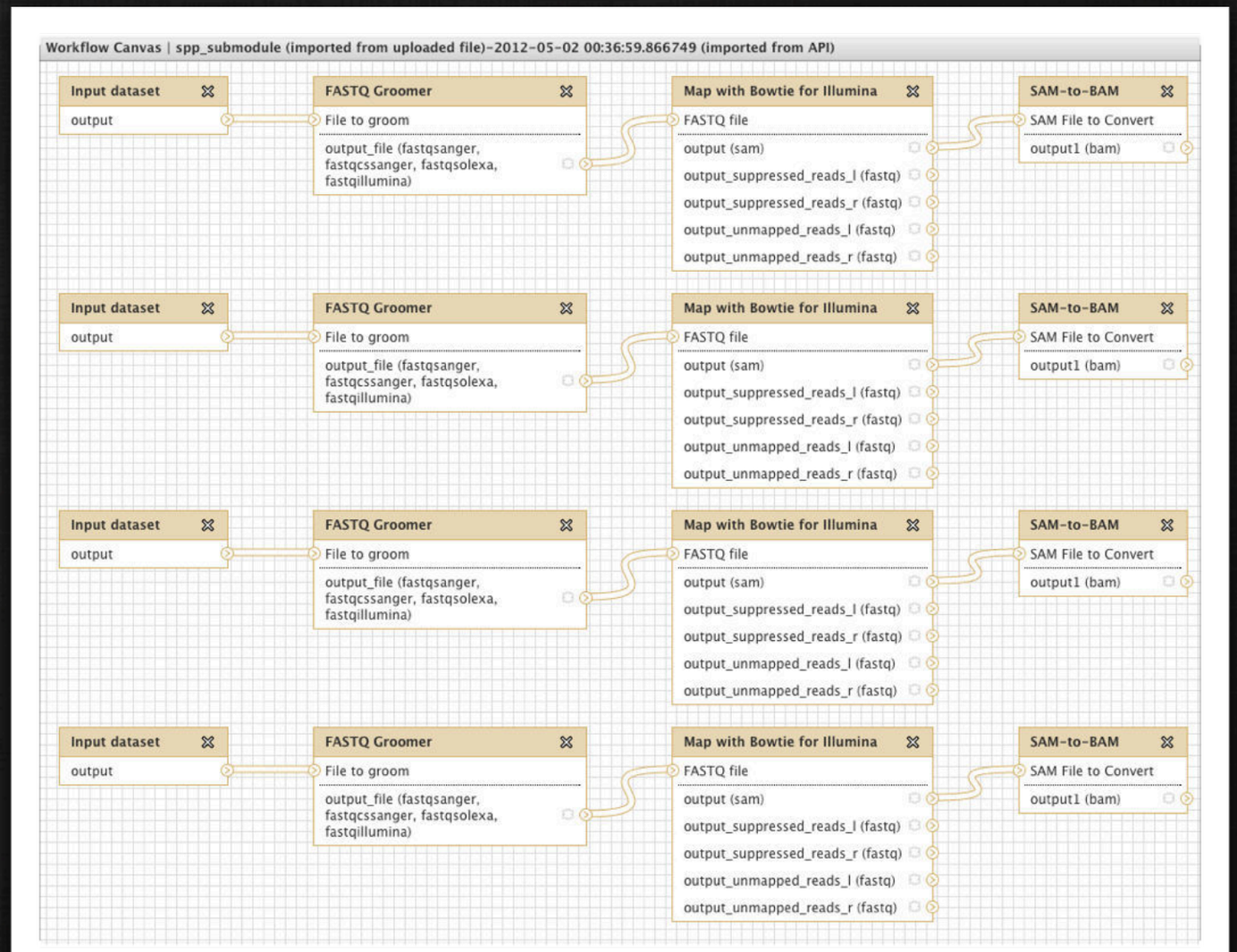
Monitoring of workflow progress through API (using history information)

Galaxy Workflow (Expansion)

Original (1x)

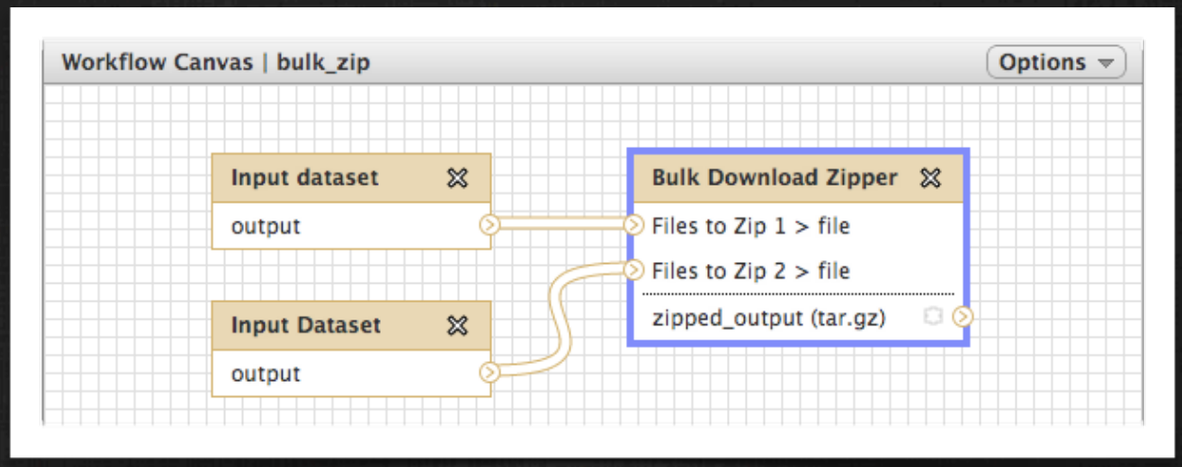


Expanded (4x)

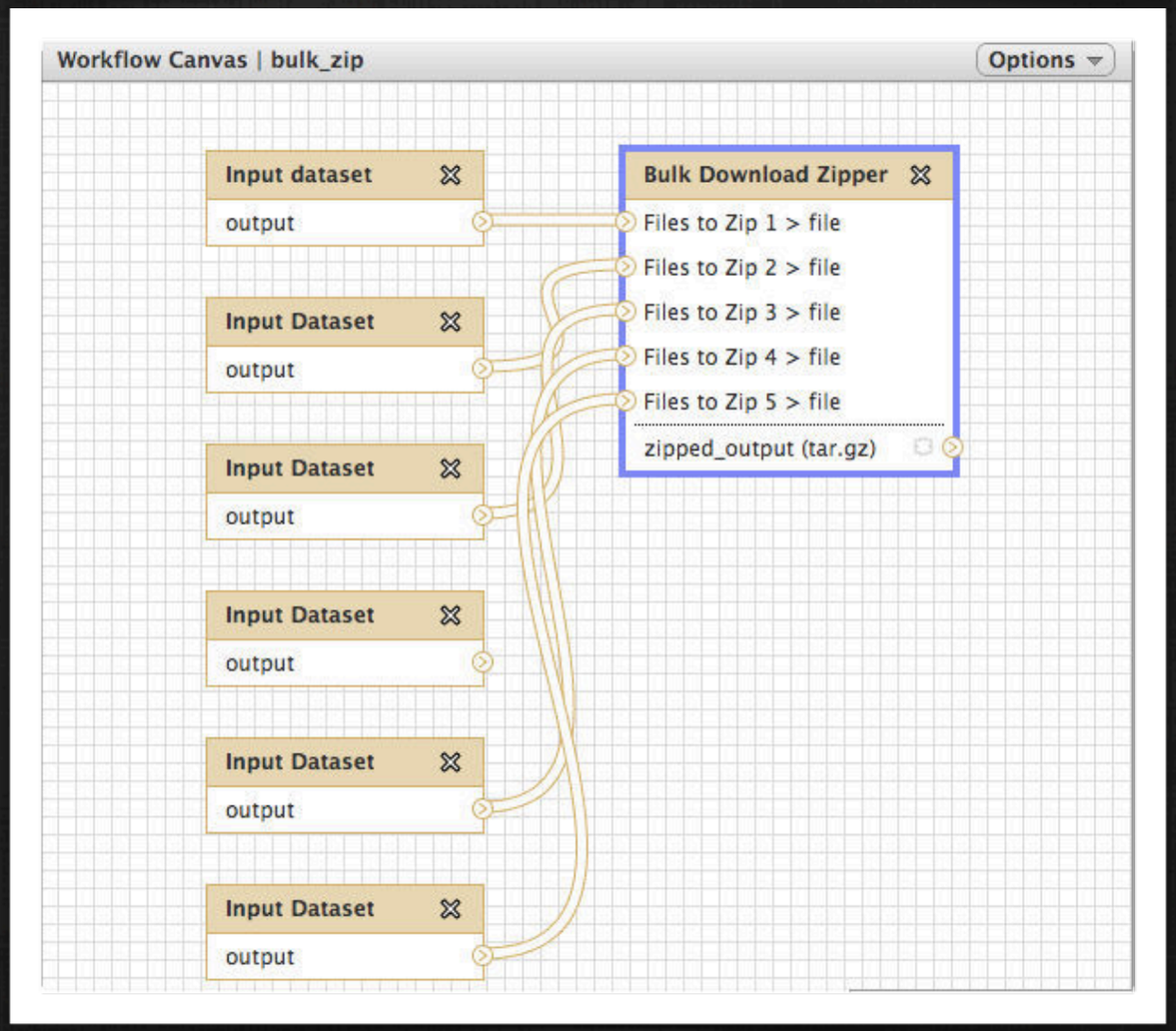


Galaxy Workflow (Reduction)

Original



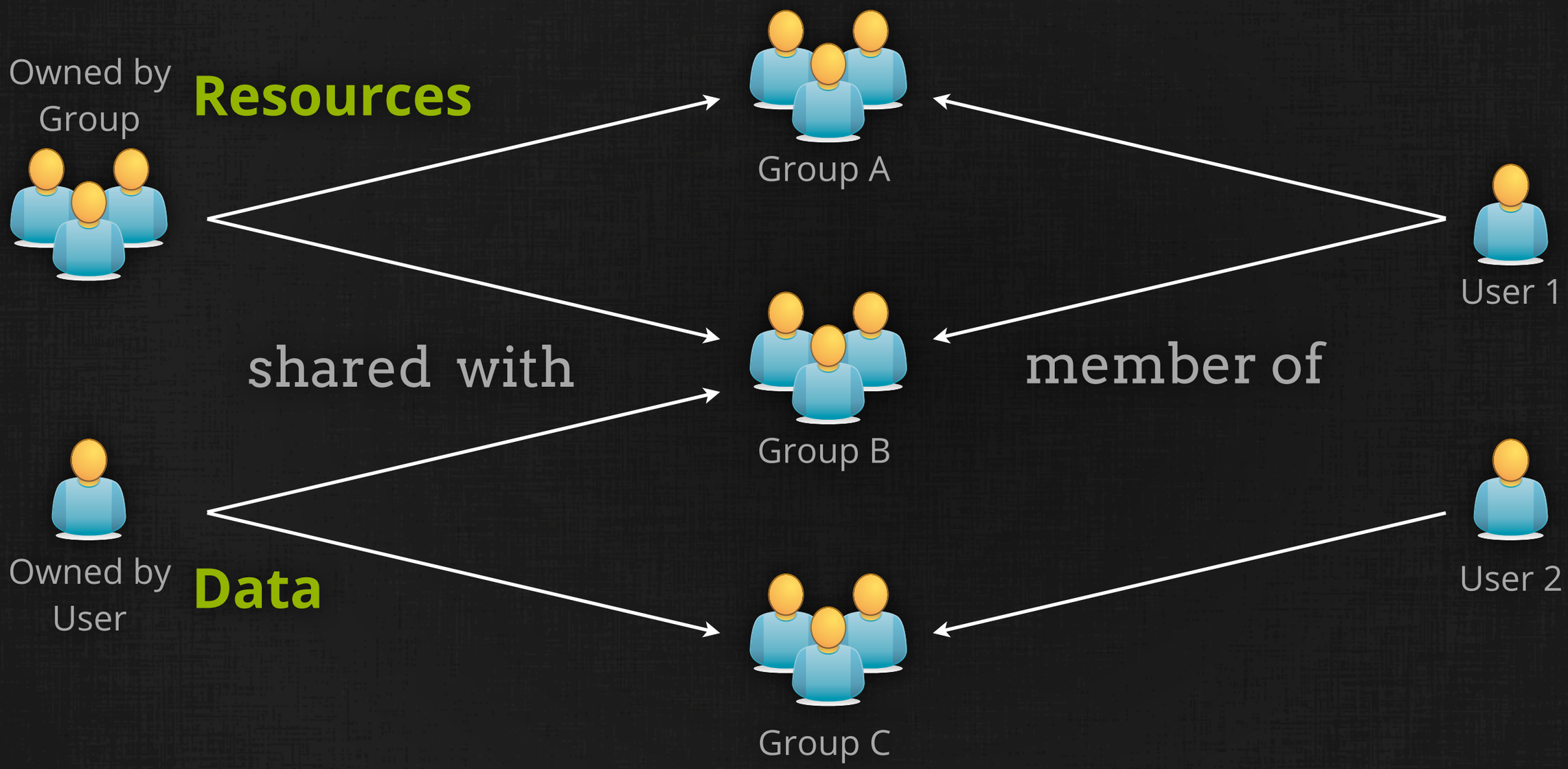
Reduction (6x)



Data and resource **sharing is a central concept** in Refinery.

Source: *f-r-a-n-k on Flickr*

Sharing

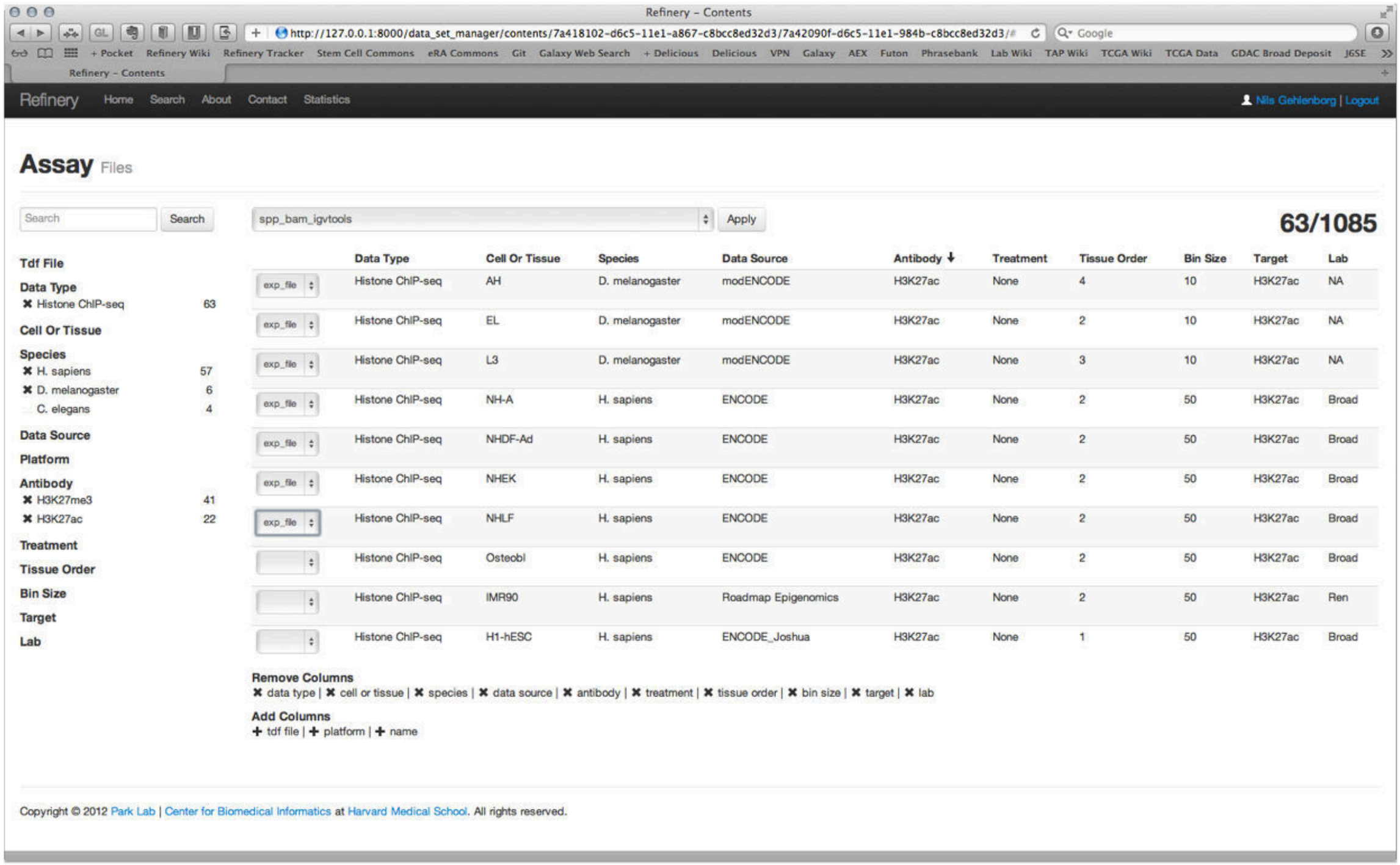


Group Ownership

Resources owned by a group are managed by one or more group managers.

Refinery PLATFORM

DEMO



Next Steps

Release an open source alpha version

Development still very much IN PROGRESS

Integrate Galaxy API extensions into Galaxy code base

Any help from the Galaxy team would be appreciated

Implement a version on our cluster

Allowing collaborators an initial version to use

Refinery PLATFORM

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- Nils Gehlenborg
- Richard Park
- Psalm Haseley
- Joe Luquette
- Peter J Park

Hide Lab @ HSPH

- Shannan Ho Sui
- Ilya Sytchev
- Winston Hide

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