Galaxy Community Update

Plant and Animal Genome XXIV (PAG 2016)
January 13, 2016

Dave Clements
Galaxy Team
Johns Hopkins University
http://galaxyproject.org/

#usegalaxy @galaxyproject

Agenda

A quick stroll through the Galaxy

User Facing Features

Admin / Developer Features

Galaxy Ecosystem Update

http://galaxyproject.org

What is Galaxy?

Keith Bradnam's definition:

"A web-based platform that provides a simplified interface to many popular bioinformormatics tools."

From

"13 Questions You May Have About Galaxy"

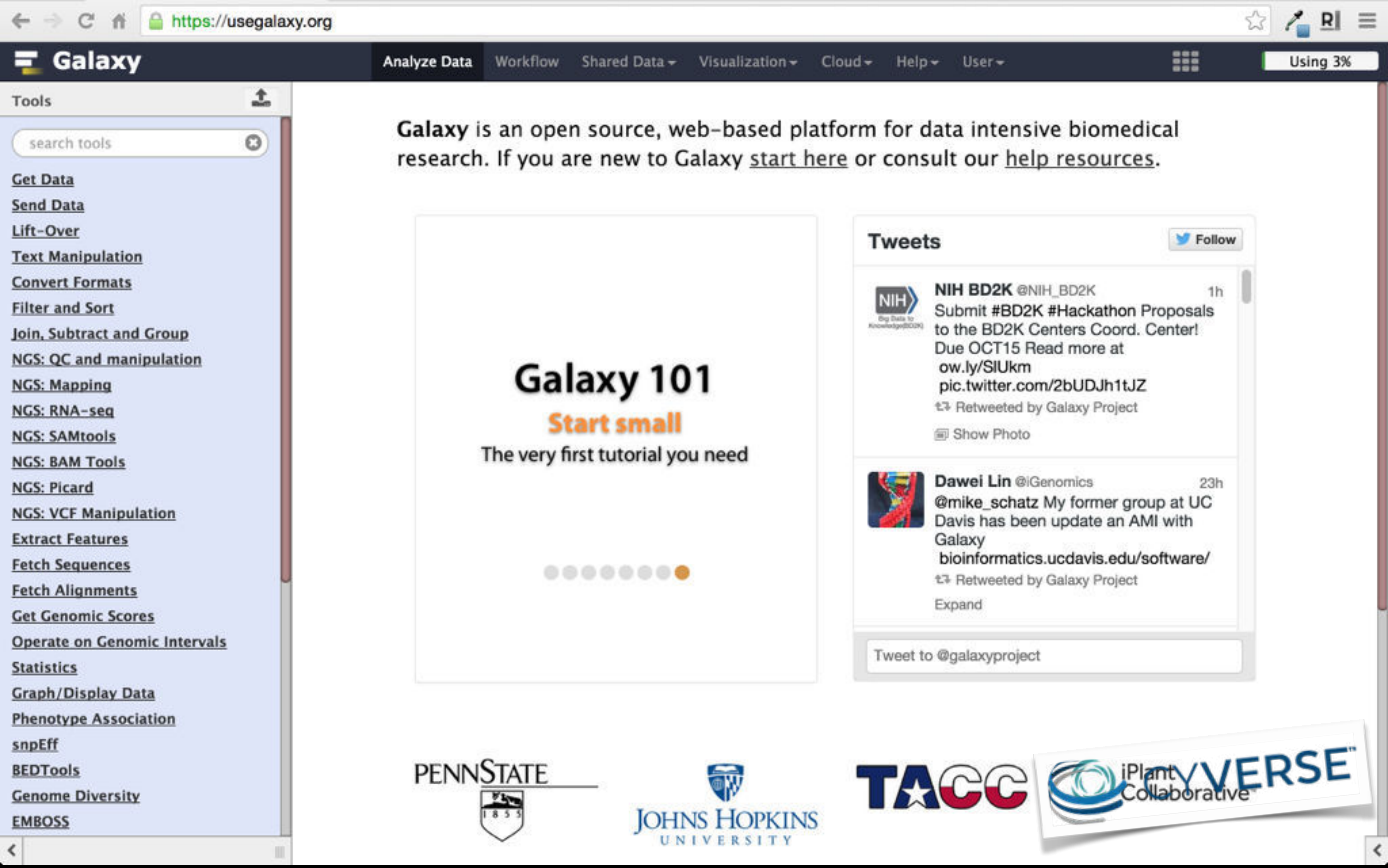
http://bit.ly/13questions

http://galaxyproject.org

Galaxy is available several ways ...

http://galaxyproject.org

As a free for everyone service on the web: usegalaxy.org



Galaxy is an open source, web-based platform for data intensive biomedical research. If you are new to Galaxy start here or consult our help resources.

Galaxy 101

Start small

The very first tutorial you need

NIH BD2K @NIH_BD2K 1h

Submit #BD2K #Hackathon Proposals to the BD2K Centers Coord. Center! Due OCT15 Read more at ow.ly/SIUkm pic.twitter.com/2bUDJh1tJZ

Retweeted by Galaxy Project

Show Photo

Dawei Lin @iGenomics 23h

@mike_schatz My former group at UC Davis has been update an AMI with Galaxy bioinformatics.ucdavis.edu/software/

Retweeted by Galaxy Project

Expand

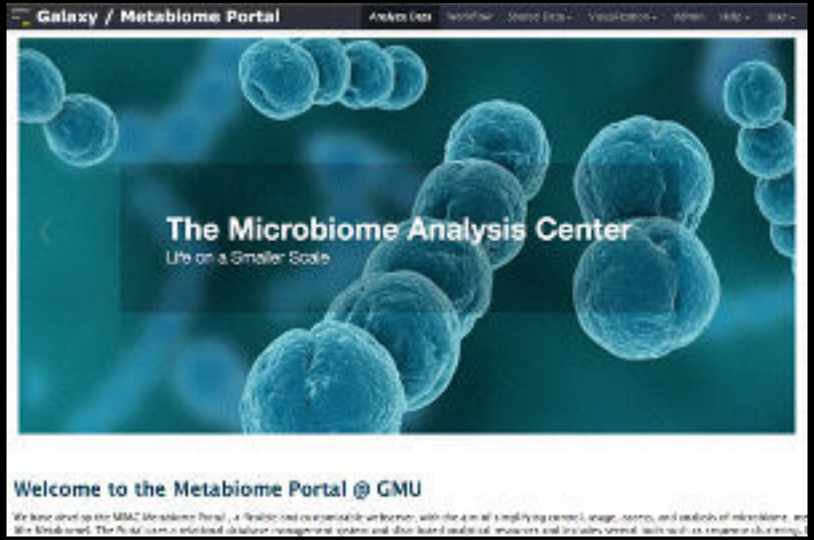
Tweet to @galaxyproject

Explore the Galaxy with

RNA-Rocket

PATHOGENPORTAL

THE BIOINFORMATICS RESOURCE CENTERS PORTAL



The Microbiome Analysis Center

Life on a Smaller Scale

Welcome to the Metabiome Portal @ GMU

香港中文大學 - 華大基因跨組學創新研究院

CUHK-BGI Innovation Institute of Trans-Omics

华大基因 BGI

$(\mathrm{GIGA})^n$ Galaxy

by CBIIT

Integrated publishing of workflows from $(\mathrm{GIGA})^n$ SCIENCE

Cistrome

A Galaxy Server dedicated to ChIP-* analysis

070+

Public Galaxy Servers

and *still* counting

The Genomic HyperBrowser

Powered by Galaxy

SCDE

STEM CELL DISCOVERY ENGINE

Experiments Connected

Whale Shark Galaxy!

South Green

bioinformatics platform

Genomic analysis tools for southern and Mediterranean plants

bit.ly/gxyServers

Galaxy is available as Open Source Software

Galaxy is installed in locations around the world.

http://getgalaxy.org

Galaxy is available on the Cloud

openstack™
CLOUD SOFTWARE

amazon
web services™

OpenNebula.org
The Open Source Toolkit for Cloud Computing

globus
genomics

http://aws.amazon.com/education
http://globus.org/
http://wiki.galaxyproject.org/Cloud

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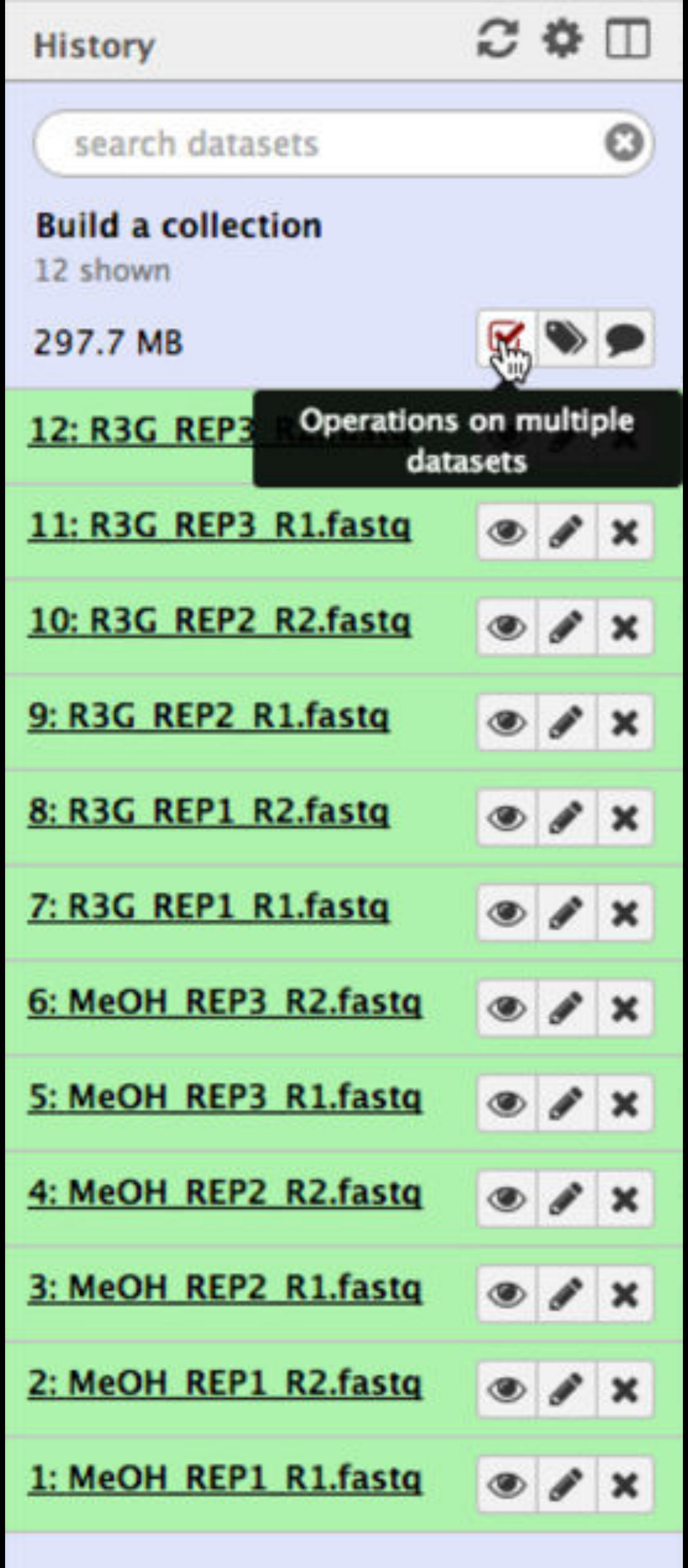
Dataset collections!

Dataset Collections give Galaxy semantic knowledge about dataset relationships.

Tools can then take advantage of this knowledge.

Dataset collections


History

search datasets

Build a collection

12 shown

297.7 MB

Operations on multiple datasets

- 12: R3G_REP3
- 11: R3G_REP3_R1.fastq
- 10: R3G_REP2_R2.fastq
- 9: R3G_REP2_R1.fastq
- 8: R3G_REP1_R2.fastq
- 7: R3G_REP1_R1.fastq
- 6: MeOH_REP3_R2.fastq
- 5: MeOH_REP3_R1.fastq
- 4: MeOH_REP2_R2.fastq
- 3: MeOH_REP2_R1.fastq
- 2: MeOH_REP1_R2.fastq
- 1: MeOH_REP1_R1.fastq


History

search datasets

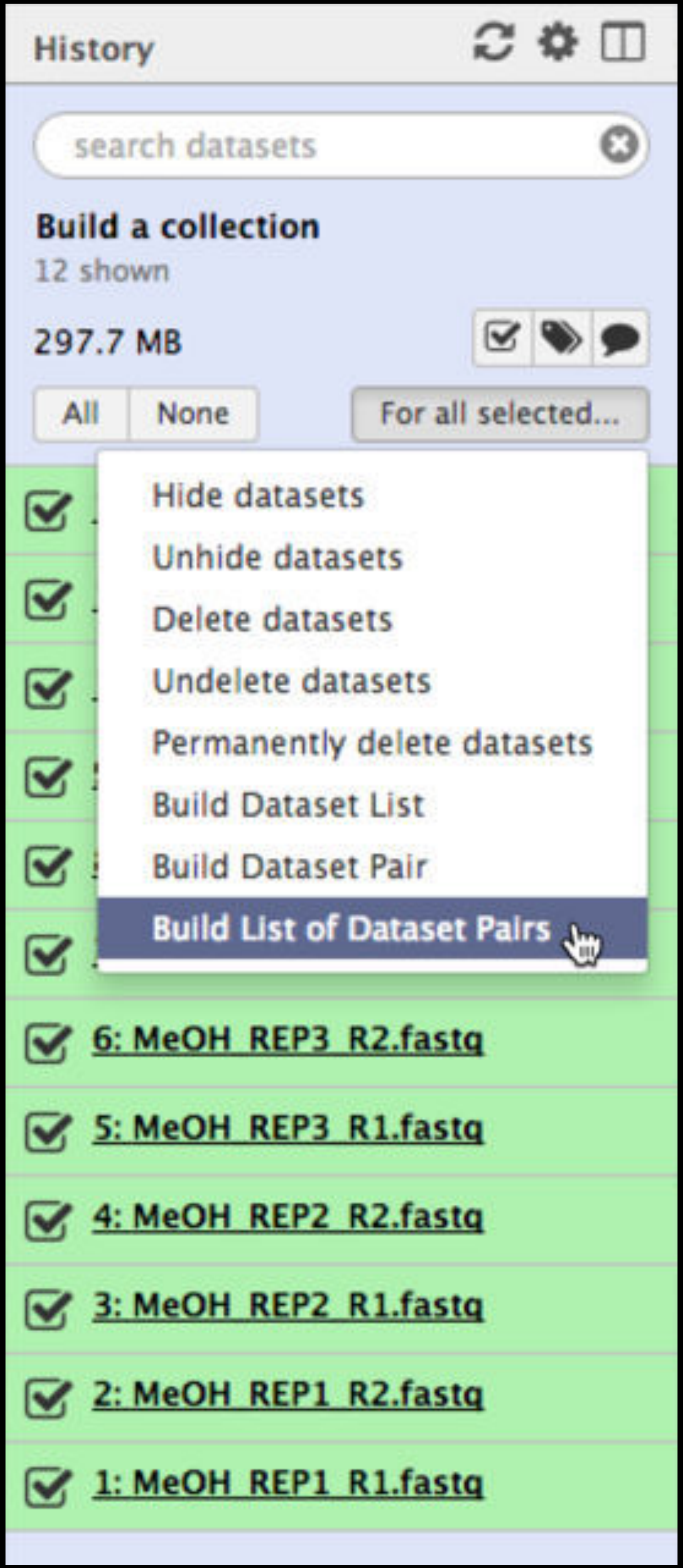
Build a collection

12 shown

297.7 MB

All | None | For all selected...

- ☐ 12: R3G_REP3_R2.fastq
- ☐ 11: R3G_REP3_R1.fastq
- ☐ 10: R3G_REP2_R2.fastq
- ☐ 9: R3G_REP2_R1.fastq
- ☐ 8: R3G_REP1_R2.fastq
- ☐ 7: R3G_REP1_R1.fastq
- ☐ 6: MeOH_REP3_R2.fastq
- ☐ 5: MeOH_REP3_R1.fastq
- ☐ 4: MeOH_REP2_R2.fastq
- ☐ 3: MeOH_REP2_R1.fastq
- ☐ 2: MeOH_REP1_R2.fastq
- ☐ 1: MeOH_REP1_R1.fastq


History

search datasets

Build a collection

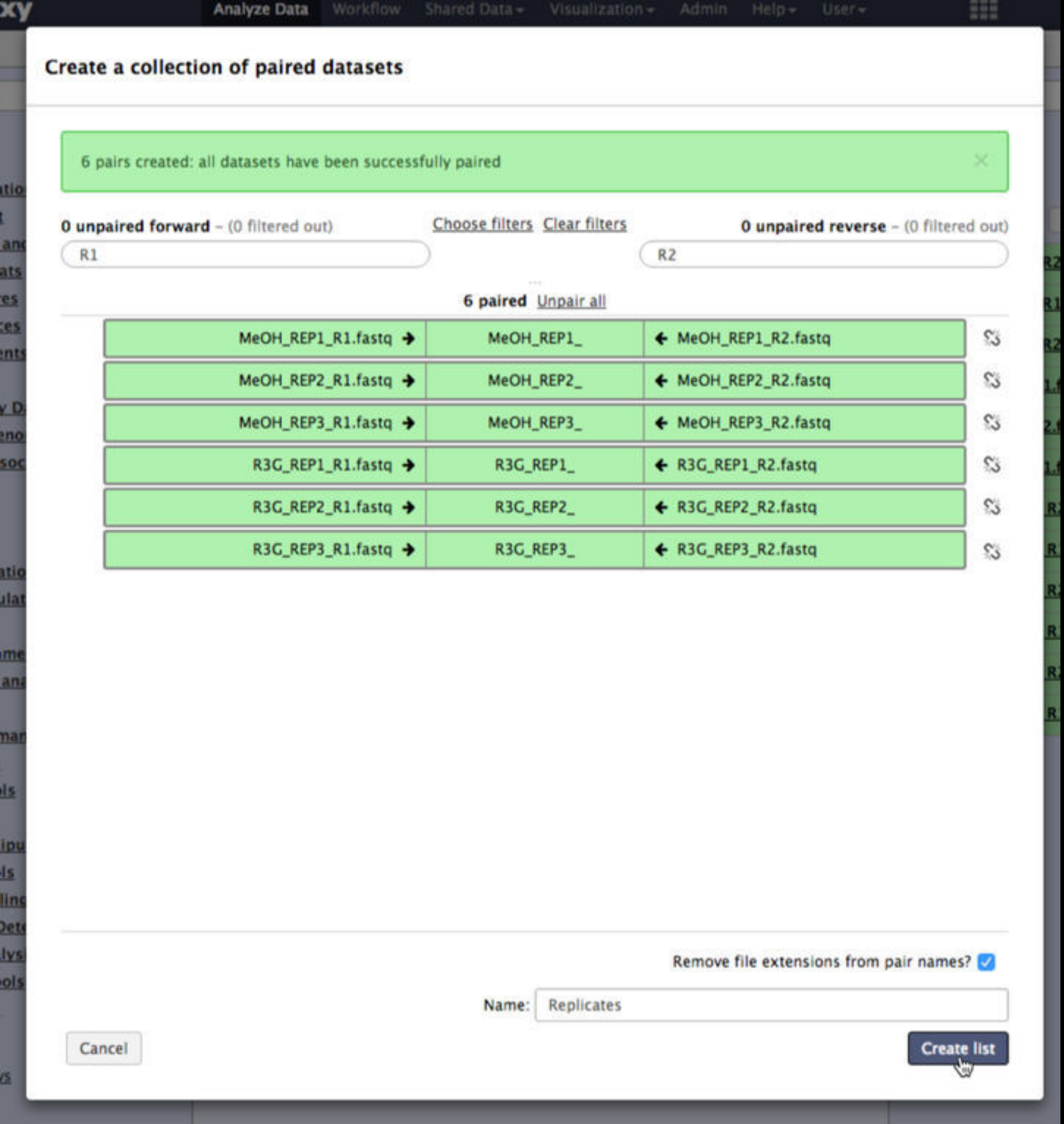
12 shown

297.7 MB

All | None | For all selected...

- Hide datasets
- Unhide datasets
- Delete datasets
- Undelete datasets
- Permanently delete datasets
- Build Dataset List
- Build Dataset Pair
- **Build List of Dataset Pairs**

- ☑
- ☑
- ☑
- ☑
- ☑
- ☑
- ☑ 6: MeOH_REP3_R2.fastq
- ☑ 5: MeOH_REP3_R1.fastq
- ☑ 4: MeOH_REP2_R2.fastq
- ☑ 3: MeOH_REP2_R1.fastq
- ☑ 2: MeOH_REP1_R2.fastq
- ☑ 1: MeOH_REP1_R1.fastq



Create a collection of paired datasets

6 pairs created: all datasets have been successfully paired

0 unpaired forward – (0 filtered out)

Choose filters Clear filters

0 unpaired reverse – (0 filtered out)

R1

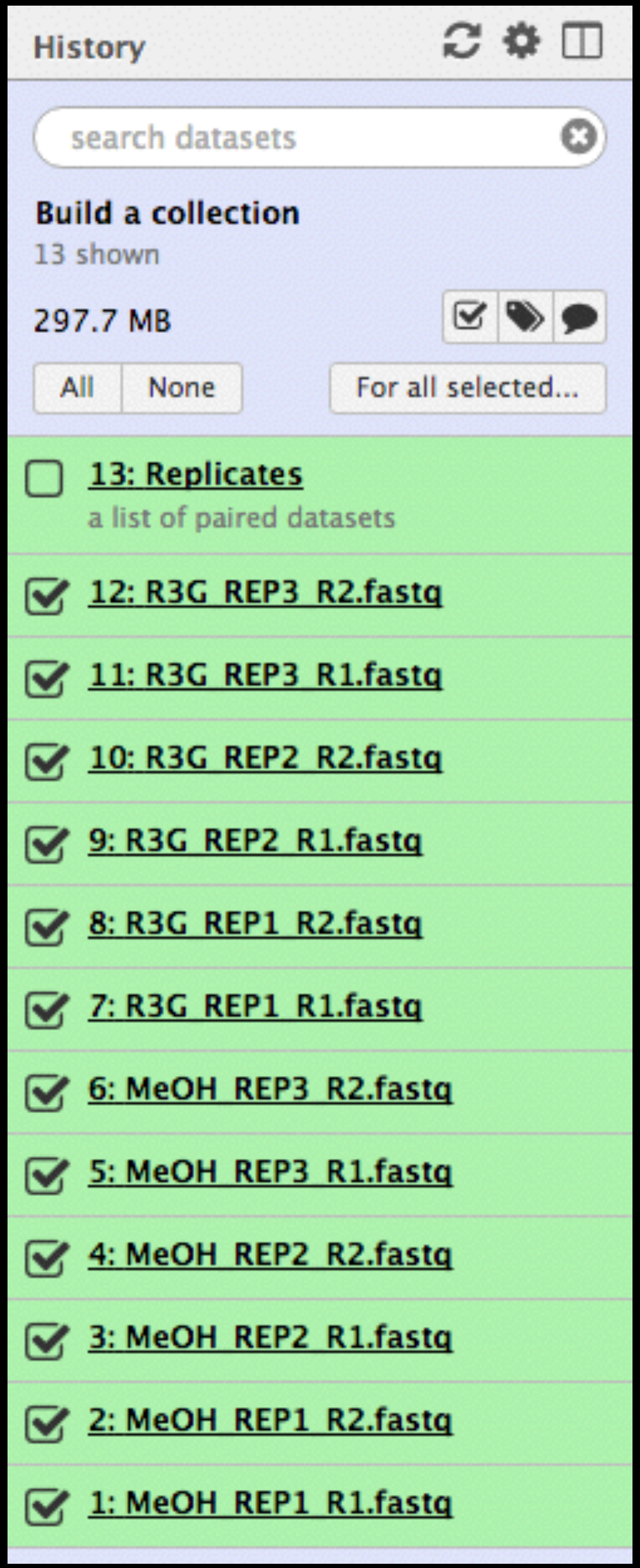
R2

6 paired Unpair all

Forward	Name	Reverse
MeOH_REP1_R1.fastq →	MeOH_REP1_	← MeOH_REP1_R2.fastq
MeOH_REP2_R1.fastq →	MeOH_REP2_	← MeOH_REP2_R2.fastq
MeOH_REP3_R1.fastq →	MeOH_REP3_	← MeOH_REP3_R2.fastq
R3G_REP1_R1.fastq →	R3G_REP1_	← R3G_REP1_R2.fastq
R3G_REP2_R1.fastq →	R3G_REP2_	← R3G_REP2_R2.fastq
R3G_REP3_R1.fastq →	R3G_REP3_	← R3G_REP3_R2.fastq

Remove file extensions from pair names? ☑

Name: Replicates



Build a collection

13 shown

297.7 MB

☐ 13: Replicates

a list of paired datasets

☑ 12: R3G_REP3_R2.fastq

☑ 11: R3G_REP3_R1.fastq

☑ 10: R3G_REP2_R2.fastq

☑ 9: R3G_REP2_R1.fastq

☑ 8: R3G_REP1_R2.fastq

☑ 7: R3G_REP1_R1.fastq

☑ 6: MeOH_REP3_R2.fastq

☑ 5: MeOH_REP3_R1.fastq

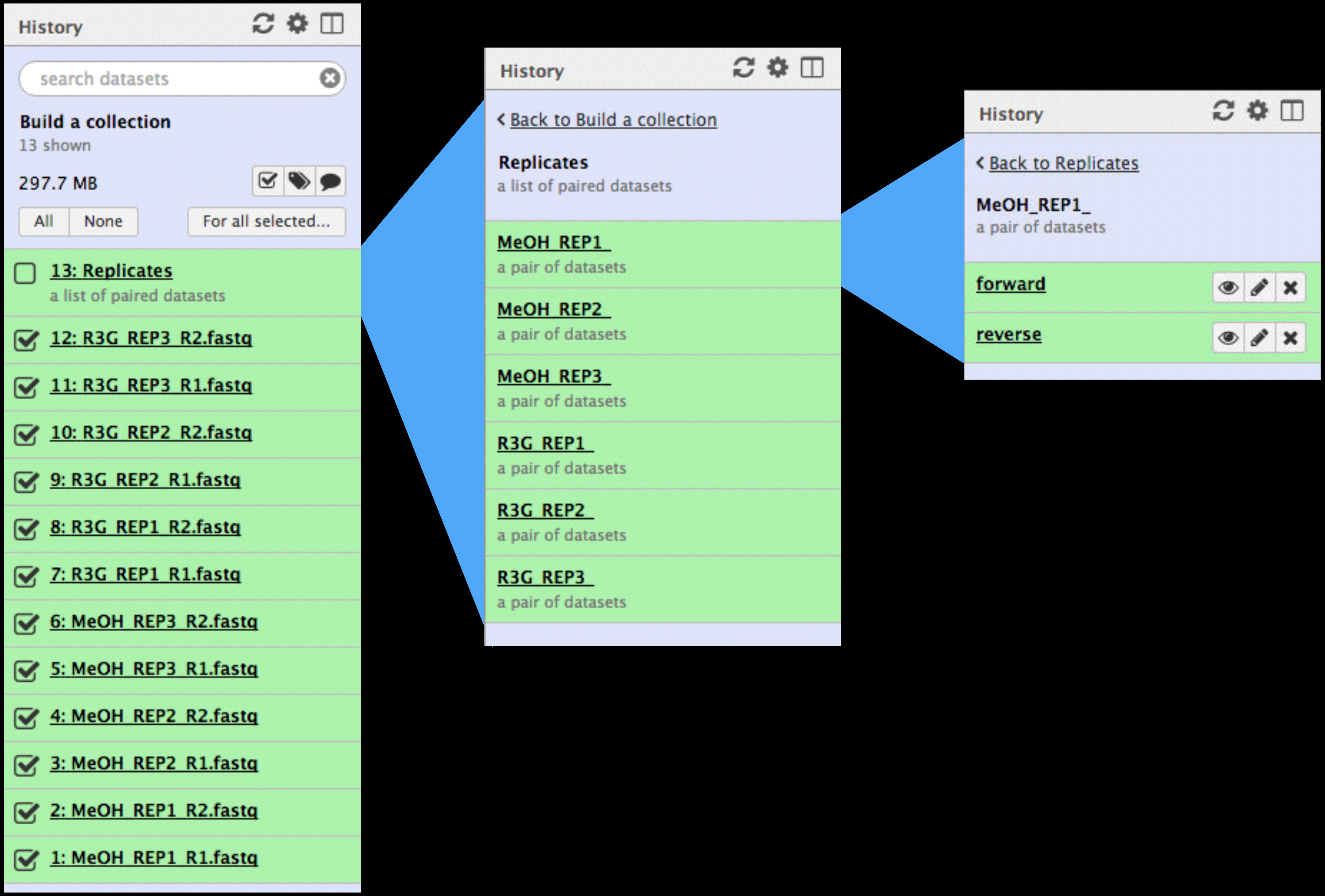
☑ 4: MeOH_REP2_R2.fastq

☑ 3: MeOH_REP2_R1.fastq

☑ 2: MeOH_REP1_R2.fastq

☑ 1: MeOH_REP1_R1.fastq

Dataset collections



Build a collection
13 shown

297.7 MB

- ☐ 13: Replicates
  a list of paired datasets
- ☑ 12: R3G_REP3_R2.fastq
- ☑ 11: R3G_REP3_R1.fastq
- ☑ 10: R3G_REP2_R2.fastq
- ☑ 9: R3G_REP2_R1.fastq
- ☑ 8: R3G_REP1_R2.fastq
- ☑ 7: R3G_REP1_R1.fastq
- ☑ 6: MeOH_REP3_R2.fastq
- ☑ 5: MeOH_REP3_R1.fastq
- ☑ 4: MeOH_REP2_R2.fastq
- ☑ 3: MeOH_REP2_R1.fastq
- ☑ 2: MeOH_REP1_R2.fastq
- ☑ 1: MeOH_REP1_R1.fastq

< Back to Build a collection

Replicates
a list of paired datasets

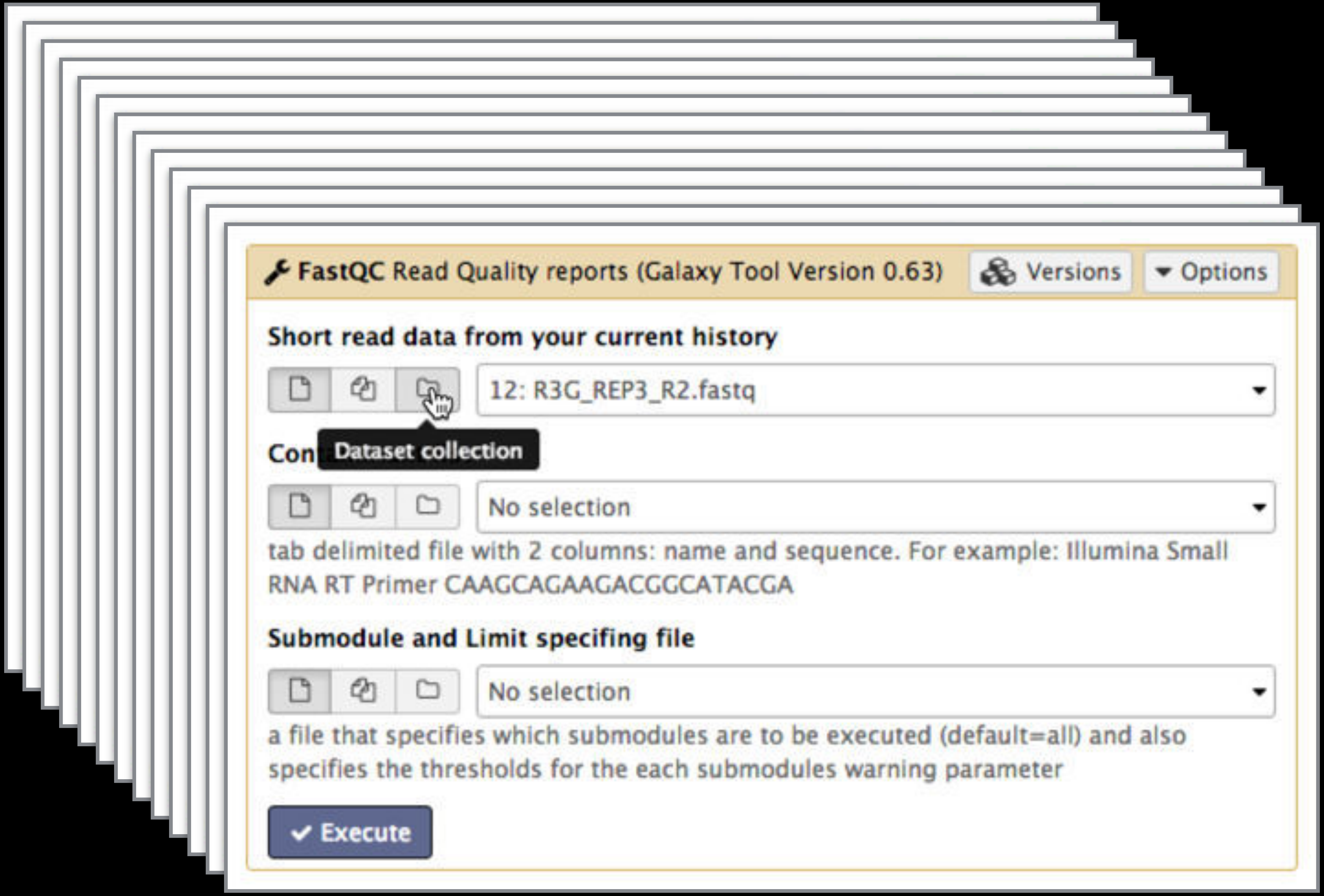
- MeOH_REP1_
  a pair of datasets
- MeOH_REP2_
  a pair of datasets
- MeOH_REP3_
  a pair of datasets
- R3G_REP1_
  a pair of datasets
- R3G_REP2_
  a pair of datasets
- R3G_REP3_
  a pair of datasets

< Back to Replicates

MeOH_REP1_
a pair of datasets

- forward
- reverse

Dataset collections



FastQC Read Quality reports (Galaxy Tool Version 0.63)

Short read data from your current history

12: R3G_REP3_R2.fastq

Con

No selection

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

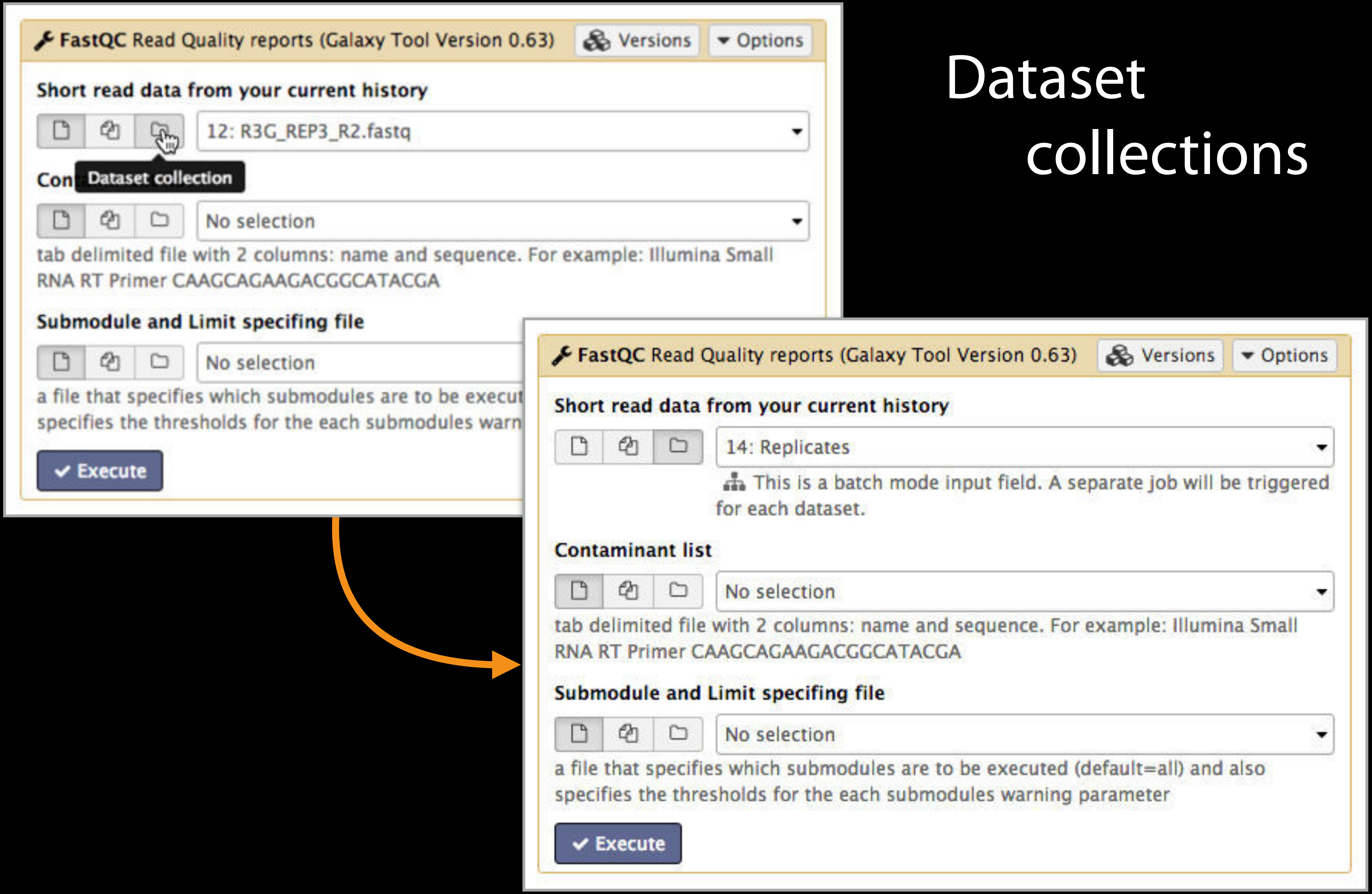
Submodule and Limit specifing file

No selection

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

Old: x 12

Dataset collections



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No selection

a file that specifies which submodules are to be execut
specifies the thresholds for the each submodules warn

FastQC Read Quality reports (Galaxy Tool Version 0.63)

Short read data from your current history

14: Replicates

This is a batch mode input field. A separate job will be triggered for each dataset.

Contaminant list

No selection

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer CAAGCAGAAGACGGCATACGA

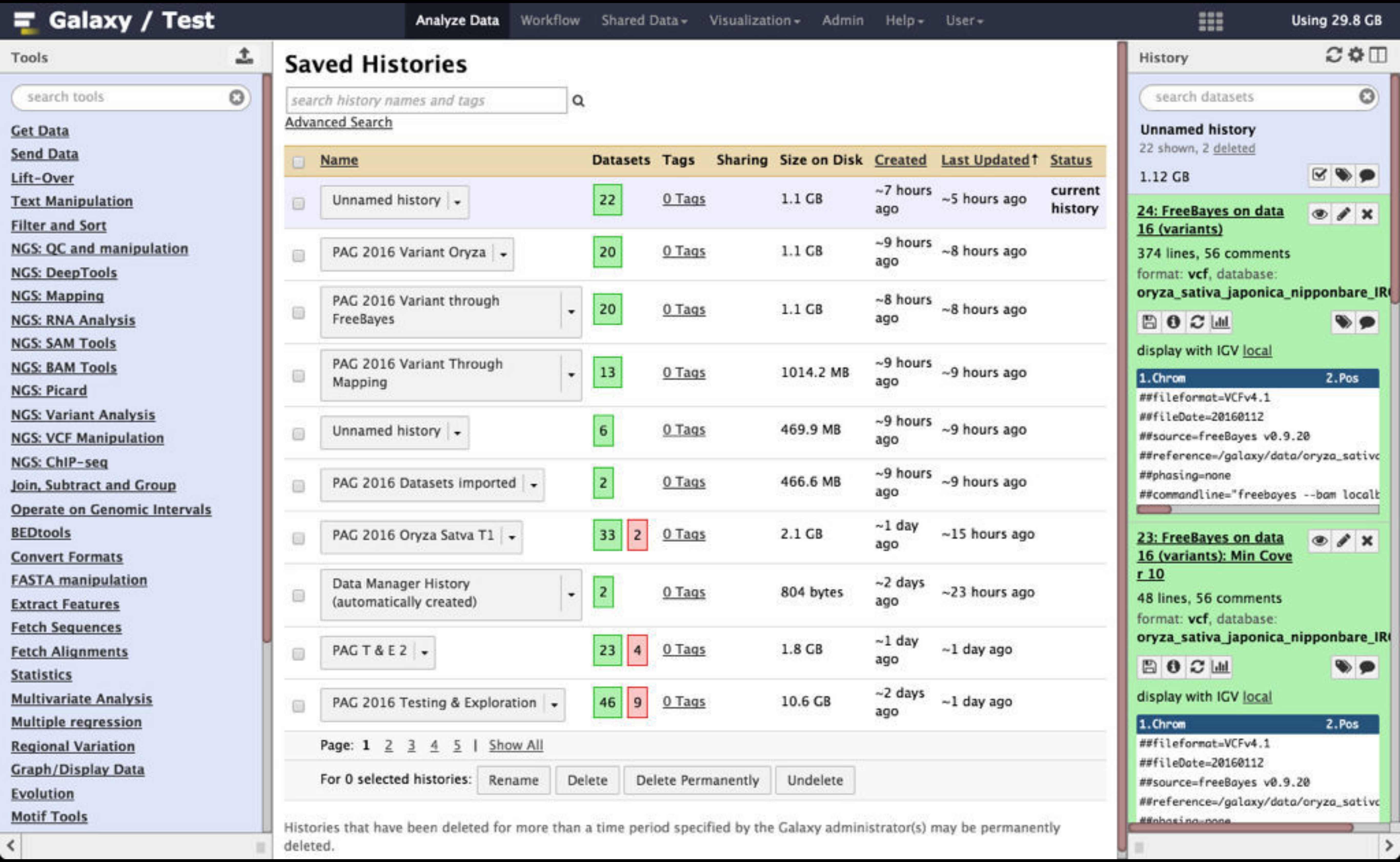
Submodule and Limit specifing file

No selection

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

New: x 1

Saved History View



Saved Histories

search history names and tags

Advanced Search

☐	Name	Datasets	Tags	Sharing	Size on Disk	Created	Last Updated↑	Status
☐	Unnamed history	22	0 Tags		1.1 GB	~7 hours ago	~5 hours ago	current history
☐	PAG 2016 Variant Oryza	20	0 Tags		1.1 GB	~9 hours ago	~8 hours ago	
☐	PAG 2016 Variant through FreeBayes	20	0 Tags		1.1 GB	~8 hours ago	~8 hours ago	
☐	PAG 2016 Variant Through Mapping	13	0 Tags		1014.2 MB	~9 hours ago	~9 hours ago	
☐	Unnamed history	6	0 Tags		469.9 MB	~9 hours ago	~9 hours ago	
☐	PAG 2016 Datasets imported	2	0 Tags		466.6 MB	~9 hours ago	~9 hours ago	
☐	PAG 2016 Oryza Satva T1	33 2	0 Tags		2.1 GB	~1 day ago	~15 hours ago	
☐	Data Manager History (automatically created)	2	0 Tags		804 bytes	~2 days ago	~23 hours ago	
☐	PAG T & E 2	23 4	0 Tags		1.8 GB	~1 day ago	~1 day ago	
☐	PAG 2016 Testing & Exploration	46 9	0 Tags		10.6 GB	~2 days ago	~1 day ago	

Page: 1 2 3 4 5 | Show All

For 0 selected histories:

Histories that have been deleted for more than a time period specified by the Galaxy administrator(s) may be permanently deleted.

Unnamed history

22 shown, 2 deleted

1.12 GB

24: FreeBayes on data 16 (variants)

374 lines, 56 comments

format: **vcf**, database: **oryza_sativa_japonica_nipponbare_IR**

display with IGV local

```
1.Chrom                 2.Pos
##fileformat=VCFv4.1
##fileDate=20160112
##source=freeBayes v0.9.20
##reference=/galaxy/data/oryza_sativ
##phasing=none
##commandline="freebayes --bam localt
```

23: FreeBayes on data 16 (variants): Min Cover 10

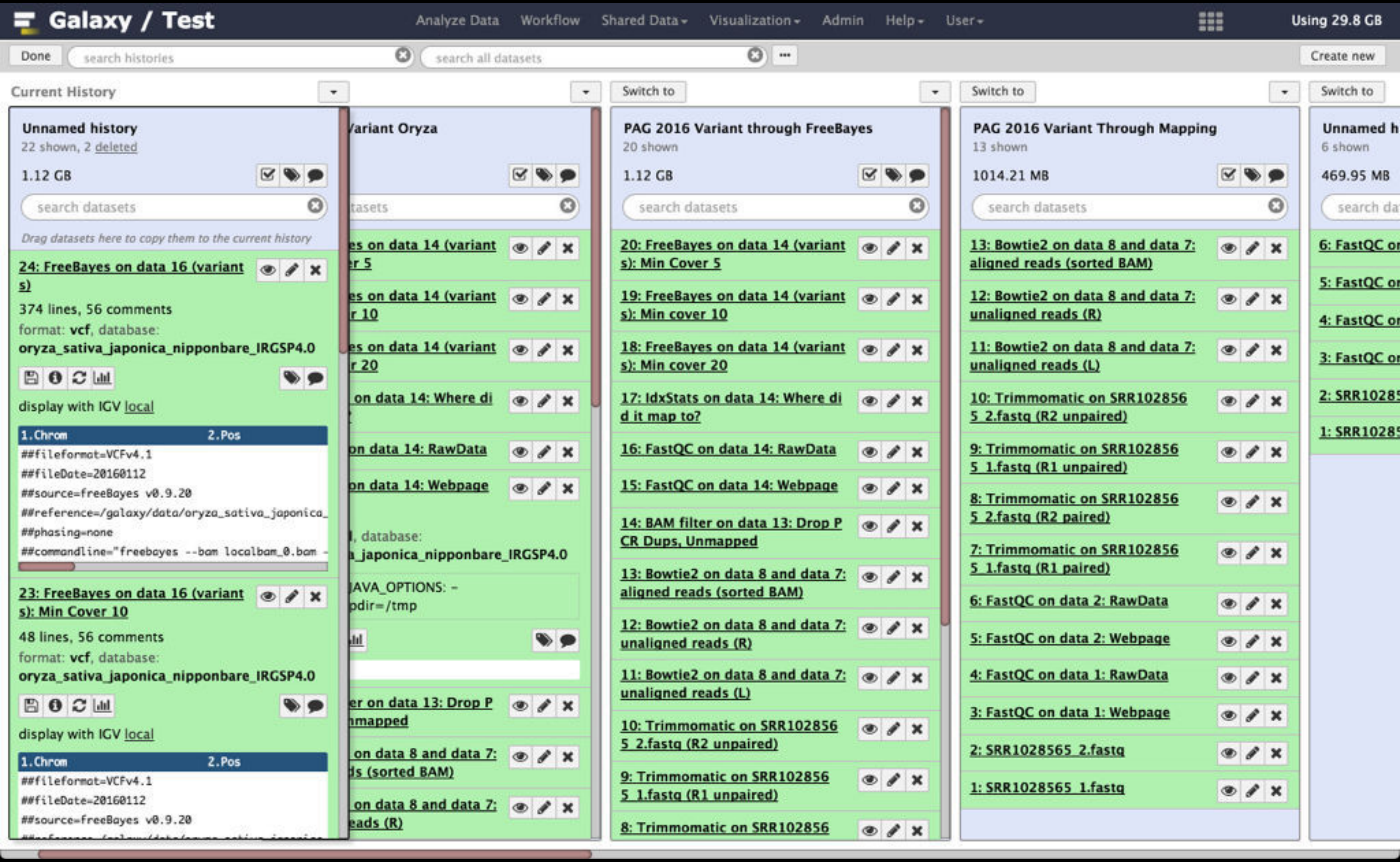
48 lines, 56 comments

format: **vcf**, database: **oryza_sativa_japonica_nipponbare_IR**

display with IGV local

```
1.Chrom                 2.Pos
##fileformat=VCFv4.1
##fileDate=20160112
##source=freeBayes v0.9.20
##reference=/galaxy/data/oryza_sativ
```

New All Histories View



Unnamed history
22 shown, 2 deleted
1.12 GB

Drag datasets here to copy them to the current history

24: FreeBayes on data 16 (variants)
374 lines, 56 comments
format: **vcf**, database:
oryza_sativa_japonica_nipponbare_IRGSP4.0
display with IGV local

```
1.Chrom            2.Pos
##fileformat=VCFv4.1
##fileDate=20160112
##source=freeBayes v0.9.20
##reference=/galaxy/data/oryza_sativa_japonica_
##phasing=none
##commandline="freebayes --bam localbam_0.bam -
```

23: FreeBayes on data 16 (variants): Min Cover 10
48 lines, 56 comments
format: **vcf**, database:
oryza_sativa_japonica_nipponbare_IRGSP4.0
display with IGV local

```
1.Chrom            2.Pos
##fileformat=VCFv4.1
##fileDate=20160112
##source=freeBayes v0.9.20
```

ariant Oryza

es on data 14 (variant r 5
es on data 14 (variant r 10
es on data 14 (variant r 20
on data 14: Where di
on data 14: RawData
on data 14: Webpage
, database:
a_japonica_nipponbare_IRGSP4.0
JAVA_OPTIONS: -
pdir=/tmp
er on data 13: Drop P nmapped
on data 8 and data 7: ds (sorted BAM)
on data 8 and data 7: eads (R)

PAG 2016 Variant through FreeBayes
20 shown
1.12 GB

20: FreeBayes on data 14 (variants): Min Cover 5
19: FreeBayes on data 14 (variants): Min cover 10
18: FreeBayes on data 14 (variants): Min cover 20
17: IdxStats on data 14: Where did it map to?
16: FastQC on data 14: RawData
15: FastQC on data 14: Webpage
14: BAM filter on data 13: Drop PCR Dups, Unmapped
13: Bowtie2 on data 8 and data 7: aligned reads (sorted BAM)
12: Bowtie2 on data 8 and data 7: unaligned reads (R)
11: Bowtie2 on data 8 and data 7: unaligned reads (L)
10: Trimmomatic on SRR1028565 2.fastq (R2 unpaired)
9: Trimmomatic on SRR1028565 1.fastq (R1 unpaired)
8: Trimmomatic on SRR102856

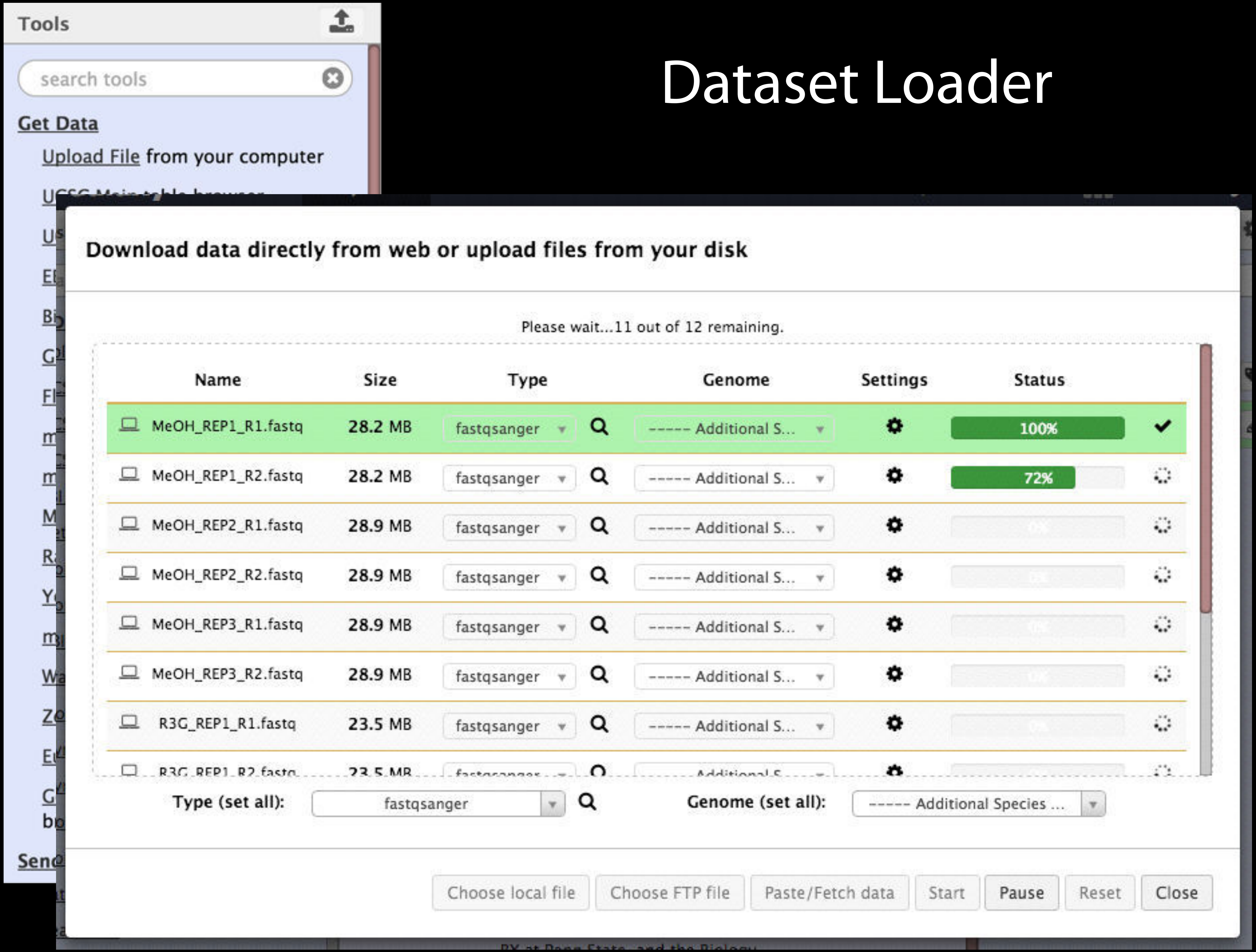
PAG 2016 Variant Through Mapping
13 shown
1014.21 MB

13: Bowtie2 on data 8 and data 7: aligned reads (sorted BAM)
12: Bowtie2 on data 8 and data 7: unaligned reads (R)
11: Bowtie2 on data 8 and data 7: unaligned reads (L)
10: Trimmomatic on SRR1028565 2.fastq (R2 unpaired)
9: Trimmomatic on SRR1028565 1.fastq (R1 unpaired)
8: Trimmomatic on SRR1028565 2.fastq (R2 paired)
7: Trimmomatic on SRR1028565 1.fastq (R1 paired)
6: FastQC on data 2: RawData
5: FastQC on data 2: Webpage
4: FastQC on data 1: RawData
3: FastQC on data 1: Webpage
2: SRR1028565 2.fastq
1: SRR1028565 1.fastq

Unnamed h
6 shown
469.95 MB

6: FastQC o
5: FastQC o
4: FastQC o
3: FastQC o
2: SRR10285
1: SRR10285

Dataset Loader



Get Data

Upload File from your computer

Download data directly from web or upload files from your disk

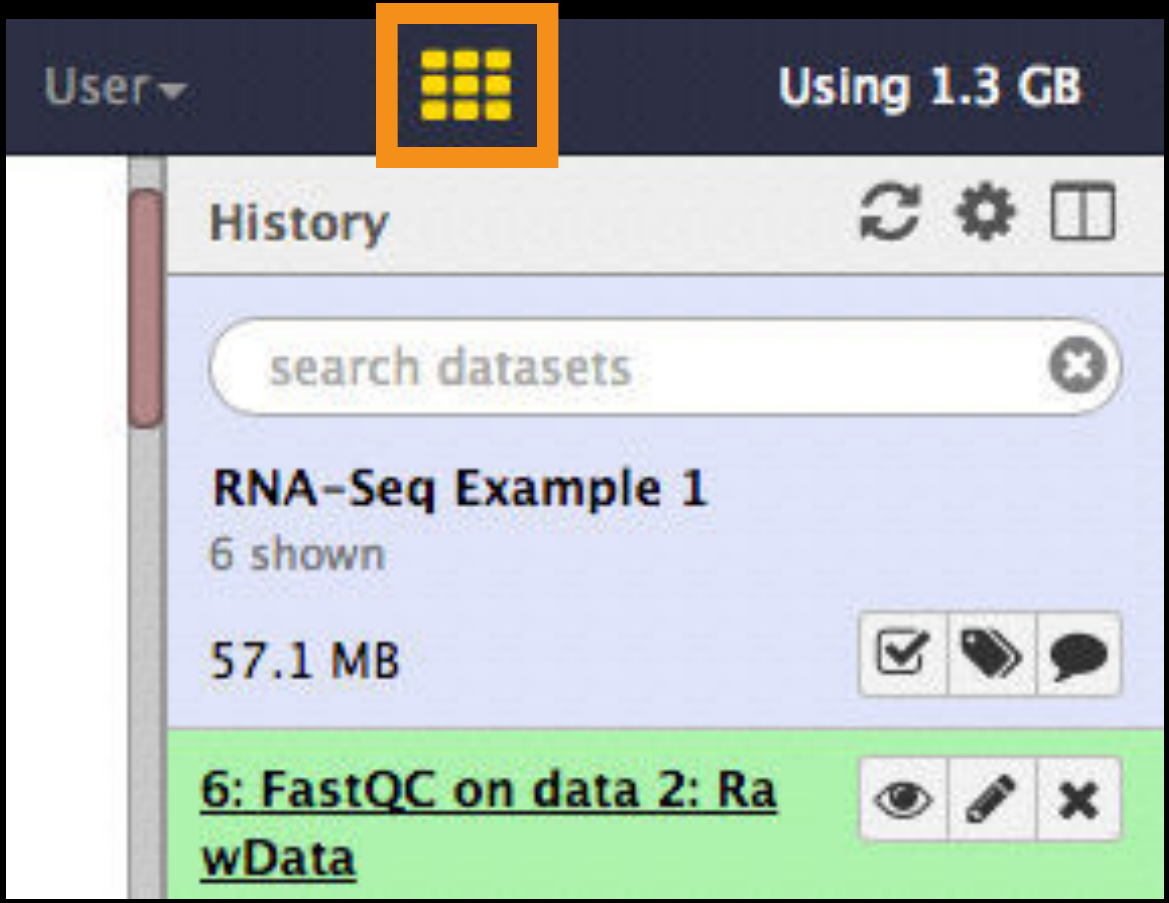
Please wait...11 out of 12 remaining.

Name	Size	Type	Genome	Settings	Status	
MeOH_REP1_R1.fastq	28.2 MB	fastqsanger	----- Additional S...	⚙	100%	✓
MeOH_REP1_R2.fastq	28.2 MB	fastqsanger	----- Additional S...	⚙	72%	
MeOH_REP2_R1.fastq	28.9 MB	fastqsanger	----- Additional S...	⚙	0%	
MeOH_REP2_R2.fastq	28.9 MB	fastqsanger	----- Additional S...	⚙	0%	
MeOH_REP3_R1.fastq	28.9 MB	fastqsanger	----- Additional S...	⚙	0%	
MeOH_REP3_R2.fastq	28.9 MB	fastqsanger	----- Additional S...	⚙	0%	
R3G_REP1_R1.fastq	23.5 MB	fastqsanger	----- Additional S...	⚙	0%	
R3G_REP1_R2.fastq	23.5 MB	fastqsanger	Additional S...	⚙		

Type (set all): fastqsanger

Genome (set all): ----- Additional Species ...

Scratchbook: View multiple datasets



And the icon turns **yellow**!

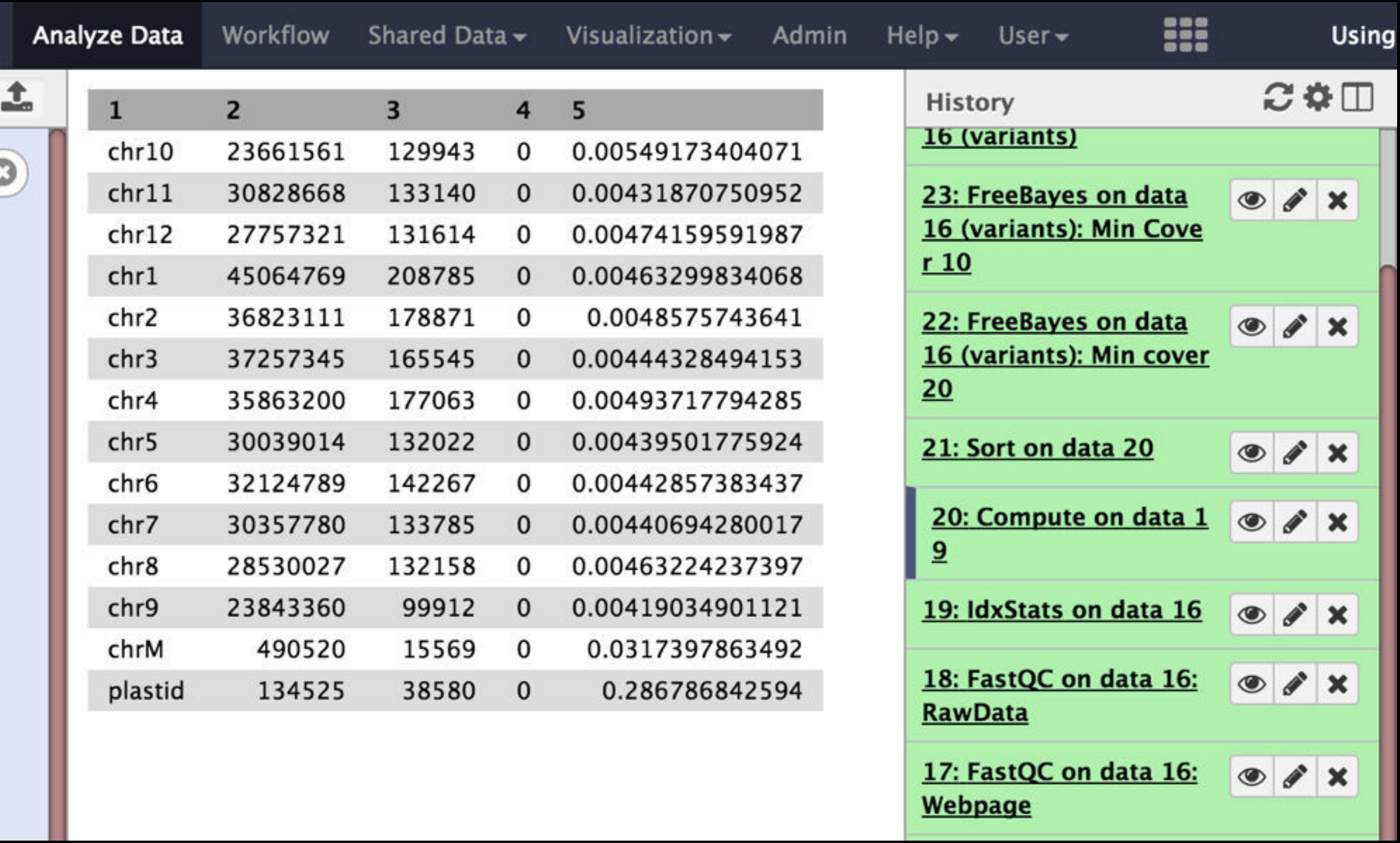
Now, poke one dataset in the eye,
and then another dataset in the eye.

And after some resizing and scrolling you see this

And lots of subtle, and sometimes sweeping changes

- Shift from HTML to JavaScript rendering
    - Which enables a new tool form rendering engine
        - And a generally smoother, and much more responsive interface

And lots of subtle changes



1	2	3	4	5
chr10	23661561	129943	0	0.00549173404071
chr11	30828668	133140	0	0.00431870750952
chr12	27757321	131614	0	0.00474159591987
chr1	45064769	208785	0	0.00463299834068
chr2	36823111	178871	0	0.0048575743641
chr3	37257345	165545	0	0.00444328494153
chr4	35863200	177063	0	0.00493717794285
chr5	30039014	132022	0	0.00439501775924
chr6	32124789	142267	0	0.00442857383437
chr7	30357780	133785	0	0.00440694280017
chr8	28530027	132158	0	0.00463224237397
chr9	23843360	99912	0	0.00419034901121
chrM	490520	15569	0	0.0317397863492
plastid	134525	38580	0	0.286786842594

16 (variants)

23: FreeBayes on data 16 (variants): Min Cover 10

22: FreeBayes on data 16 (variants): Min cover 20

21: Sort on data 20

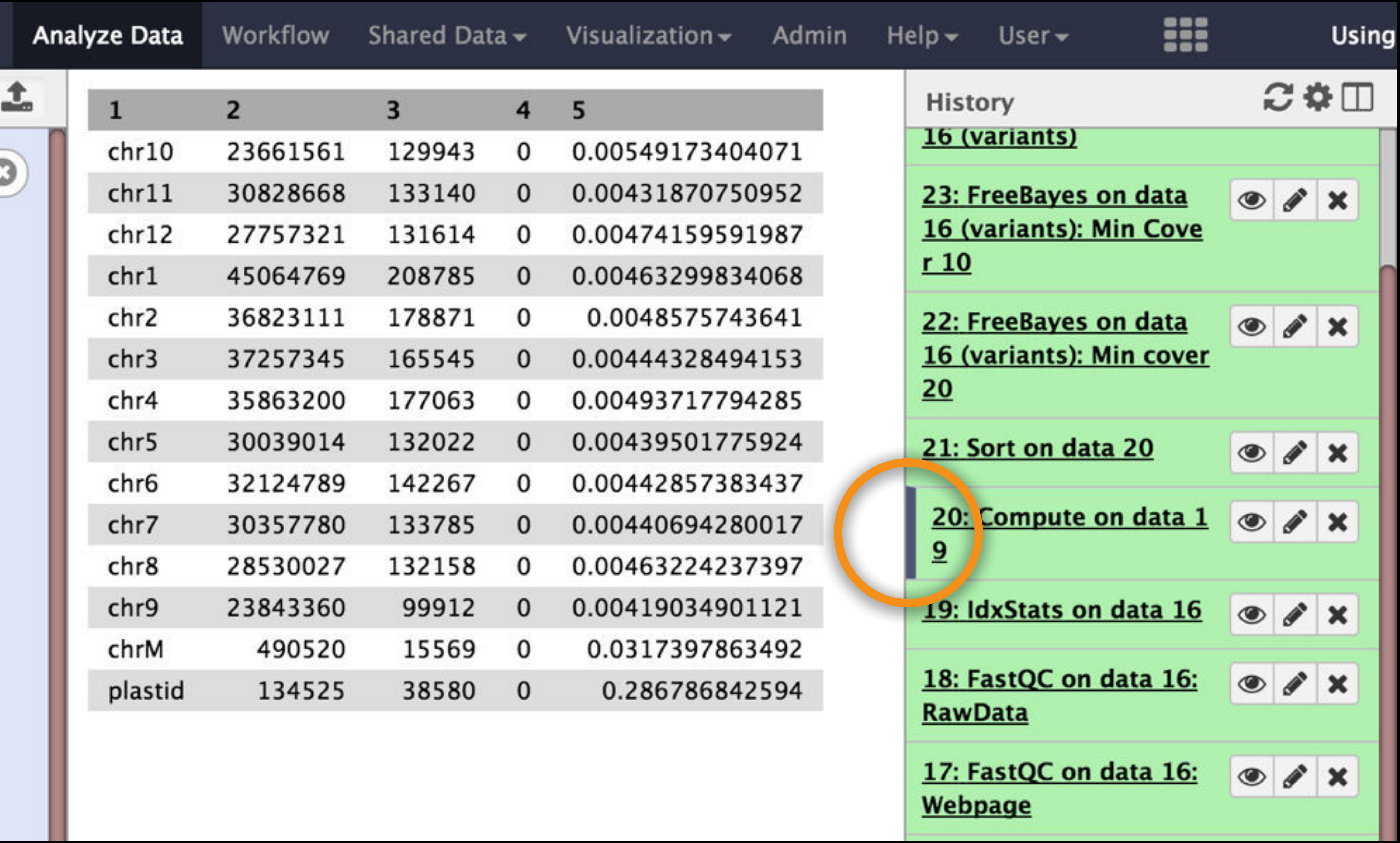
20: Compute on data 19

19: IdxStats on data 16

18: FastQC on data 16: RawData

17: FastQC on data 16: Webpage

And lots of subtle changes



1	2	3	4	5
chr10	23661561	129943	0	0.00549173404071
chr11	30828668	133140	0	0.00431870750952
chr12	27757321	131614	0	0.00474159591987
chr1	45064769	208785	0	0.00463299834068
chr2	36823111	178871	0	0.0048575743641
chr3	37257345	165545	0	0.00444328494153
chr4	35863200	177063	0	0.00493717794285
chr5	30039014	132022	0	0.00439501775924
chr6	32124789	142267	0	0.00442857383437
chr7	30357780	133785	0	0.00440694280017
chr8	28530027	132158	0	0.00463224237397
chr9	23843360	99912	0	0.00419034901121
chrM	490520	15569	0	0.0317397863492
plastid	134525	38580	0	0.286786842594

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17: FastQC on data 16: Webpage

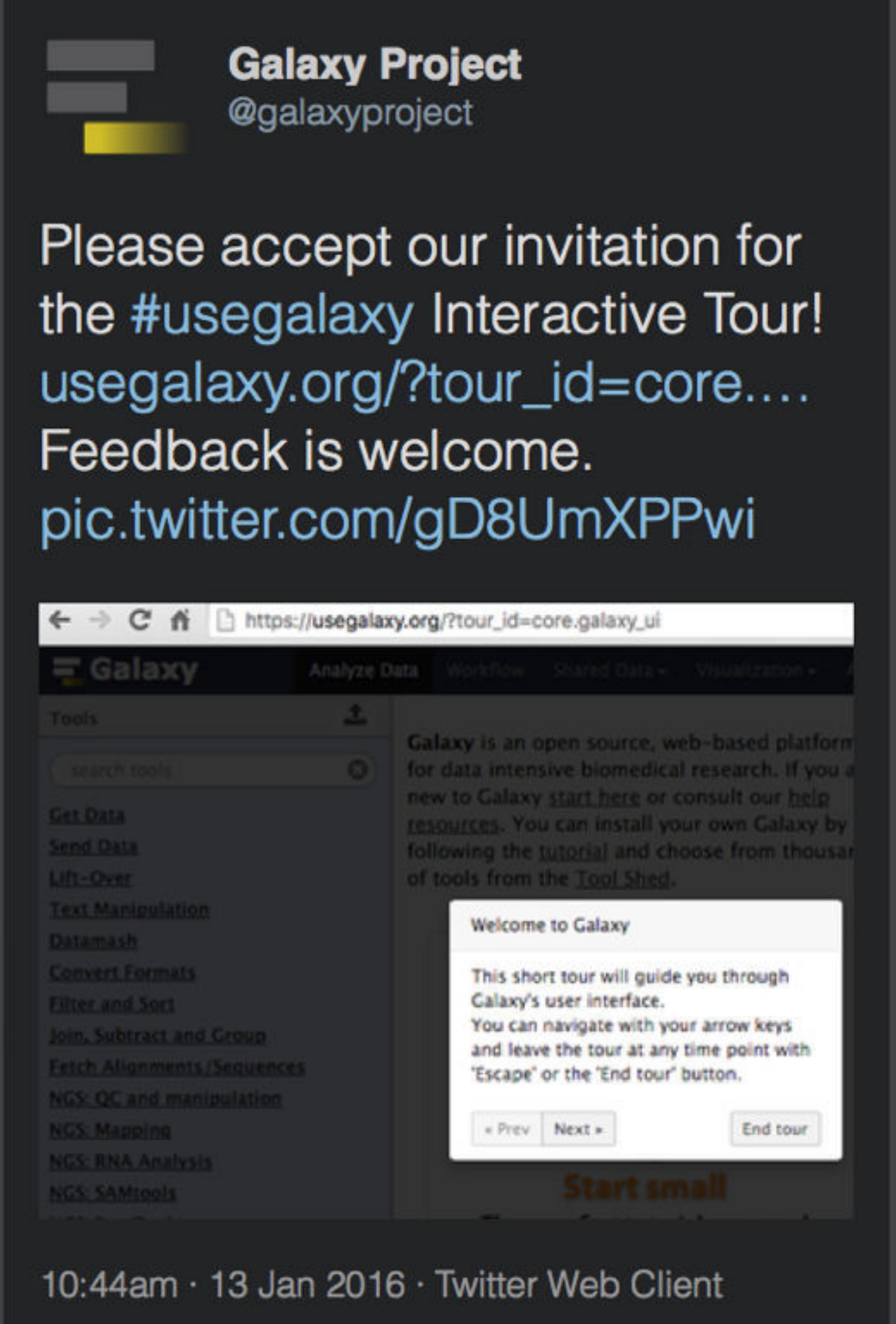
Interactive Environment Support: IPython Notebooks and RStudio in Galaxy

IP[y]: Notebook

RStudio®

Late breaking news

(during Nathan's Apollo talk)



Galaxy Project
@galaxyproject

Please accept our invitation for the #usegalaxy Interactive Tour! usegalaxy.org/?tour_id=core.… Feedback is welcome. pic.twitter.com/gD8UmXPPwi

https://usegalaxy.org/?tour_id=core.galaxy_ui

Galaxy is an open source, web-based platfor for data intensive biomedical research. If you a new to Galaxy start here or consult our help resources. You can install your own Galaxy by following the tutorial and choose from thousa of tools from the Tool Shed.

Welcome to Galaxy

This short tour will guide you through Galaxy's user interface.
You can navigate with your arrow keys and leave the tour at any time point with 'Escape' or the 'End tour' button.

10:44am · 13 Jan 2016 · Twitter Web Client

Agenda

A quick stroll through the Galaxy

User Facing Features

Admin / Developer Features

Galaxy Ecosystem Update

http://galaxyproject.org

PLANEMO

Command line utilities to assist in building and publishing Galaxy tools

```
% planemo lint mytool.xml

% planemo test --galaxy_root=../myTestServer mytool.xml

% planemo serve mytool.xml
```

https://github.com/galaxyproject/planemo

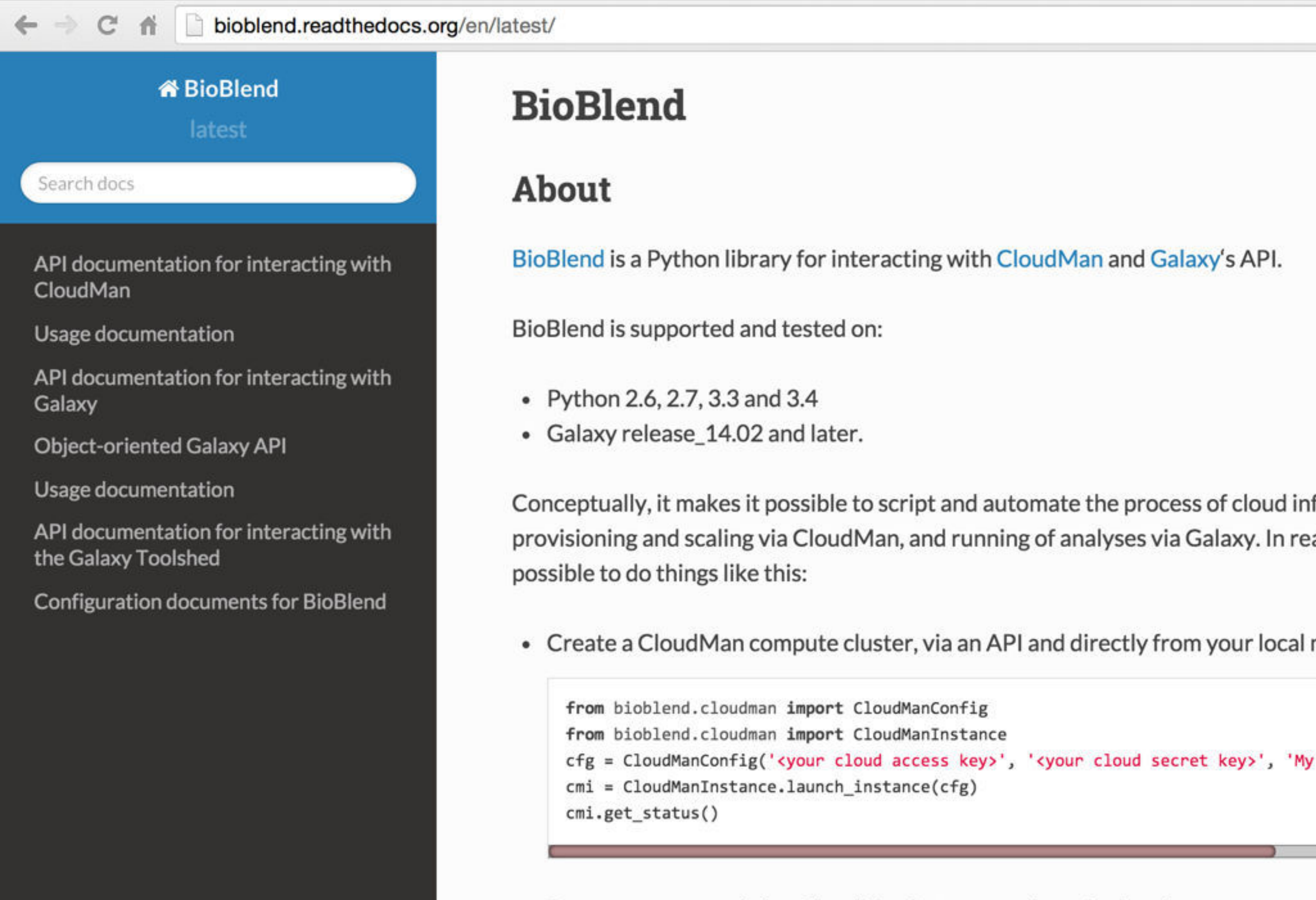
PLANEMO

Provides varying degrees of support for

Publishing tools to Galaxy ToolShed(s)
TravisCI integration
Running tools in Docker containers
Dependency resolution with Brew
Common Workflow Language (CWL) tools

https://github.com/galaxyproject/planemo

BioBlend



- API documentation for interacting with CloudMan
- Usage documentation
- API documentation for interacting with Galaxy
- Object-oriented Galaxy API
- Usage documentation
- API documentation for interacting with the Galaxy Toolshed
- Configuration documents for BioBlend

BioBlend

About

BioBlend is a Python library for interacting with CloudMan and Galaxy's API.

BioBlend is supported and tested on:

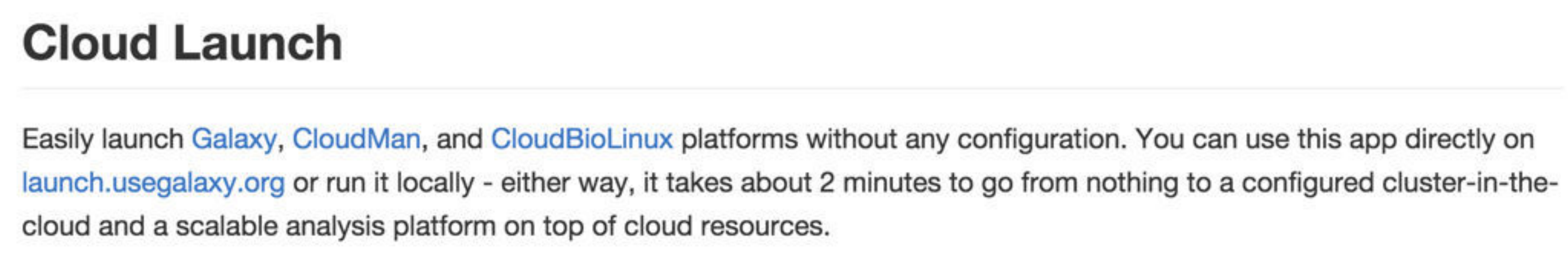
- Python 2.6, 2.7, 3.3 and 3.4
- Galaxy release_14.02 and later.

Conceptually, it makes it possible to script and automate the process of cloud inf provisioning and scaling via CloudMan, and running of analyses via Galaxy. In rea possible to do things like this:

- Create a CloudMan compute cluster, via an API and directly from your local r

```
from bioblend.cloudman import CloudManConfig
from bioblend.cloudman import CloudManInstance
cfg = CloudManConfig('<your cloud access key>', '<your cloud secret key>', 'My
cmi = CloudManInstance.launch_instance(cfg)
cmi.get_status()
```

CloudLaunch



Cloud Launch

Easily launch Galaxy, CloudMan, and CloudBioLinux platforms without any configuration. You can use this app directly on launch.usegalaxy.org or run it locally - either way, it takes about 2 minutes to go from nothing to a configured cluster-in-the-cloud and a scalable analysis platform on top of cloud resources.

https://github.com/galaxyproject/cloudlaunch

Ansible for managing Galaxy server deployments

- Ansible Galaxy
  - Ansible role for managing a Galaxy server
  - https://github.com/galaxyproject/ansible-galaxy
- Ansible Galaxy Tools
  - For working with ToolSheds
  - https://github.com/galaxyproject/ansible-galaxy-tools
- And many more ...
  - https://github.com/galaxyproject

Please note: Ansible Galaxy ≠ Ansible Galaxy

And the list goes on ...

Galaxy PROJECT

Data intensive science *for everyone.*

Open Source Software Projects

The Galaxy Project has produced numerous open source software offerings to help you build your science analysis infrastructure. Our software covers the gamut from helping you integrate new software into our platform, to a production-ready engine to run those programs in complex MapReduce workflows.

Human-Friendly Science

Galaxy PROJECT

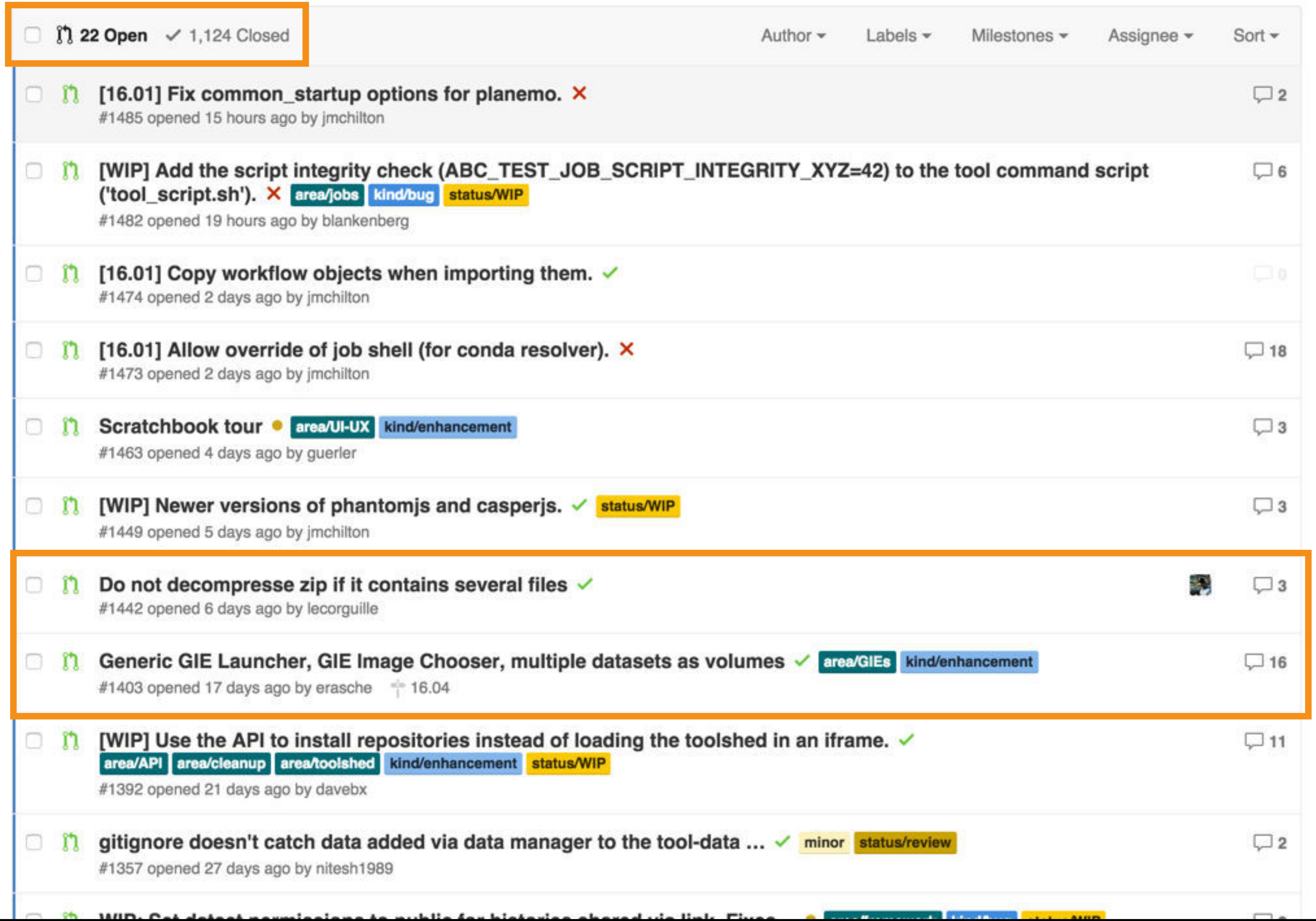
Galaxy is our first and primary product, an open source (AFL) workflow engine enabling rapid analysis on your compute infrastructure. Galaxy itself enables you or your researchers to do reproducible analyses, an absolute necessity in the realm of science.

Galaxy additionally allows design and execution of complex MapReduce-type

http://galaxyproject.github.io/ https://github.com/galaxyproject

GitHub

https://github.com/galaxyproject



☐ [16.01] Fix common_startup options for planemo. ✕ 2
#1485 opened 15 hours ago by jmchilton

☐ [WIP] Add the script integrity check (ABC_TEST_JOB_SCRIPT_INTEGRITY_XYZ=42) to the tool command script ('tool_script.sh'). ✕ area/jobs kind/bug status/WIP 6
#1482 opened 19 hours ago by blankenberg

☐ [16.01] Copy workflow objects when importing them. ✓ 0
#1474 opened 2 days ago by jmchilton

☐ [16.01] Allow override of job shell (for conda resolver). ✕ 18
#1473 opened 2 days ago by jmchilton

☐ Scratchbook tour ● area/UI-UX kind/enhancement 3
#1463 opened 4 days ago by guerler

☐ [WIP] Newer versions of phantomjs and casperjs. ✓ status/WIP 3
#1449 opened 5 days ago by jmchilton

☐ Do not decompresse zip if it contains several files ✓ 3
#1442 opened 6 days ago by lecorguille

☐ Generic GIE Launcher, GIE Image Chooser, multiple datasets as volumes ✓ area/GIEs kind/enhancement 16
#1403 opened 17 days ago by erasche 16.04

☐ [WIP] Use the API to install repositories instead of loading the toolshed in an iframe. ✓ 11
area/API area/cleanup area/toolshed kind/enhancement status/WIP
#1392 opened 21 days ago by davebx

☐ gitignore doesn't catch data added via data manager to the tool-data ... ✓ minor status/review 2
#1357 opened 27 days ago by nitesh1989

Hackathons

- Annual in person hackathon started at GCC2014
- Data hackathon added at GCC2015
- Community sponsored hackathons in France & Michigan
- Virtual online hackathons have become a regular event.

The next one is

RADSeq Tools and Workflows
7-8 March 2016

https://github.com/galaxyproject/tools-iuc/issues/422
(http://bit.ly/gxyradseqhack)

Agenda

A quick stroll through the Galaxy

User Facing Features

Admin / Developer Features

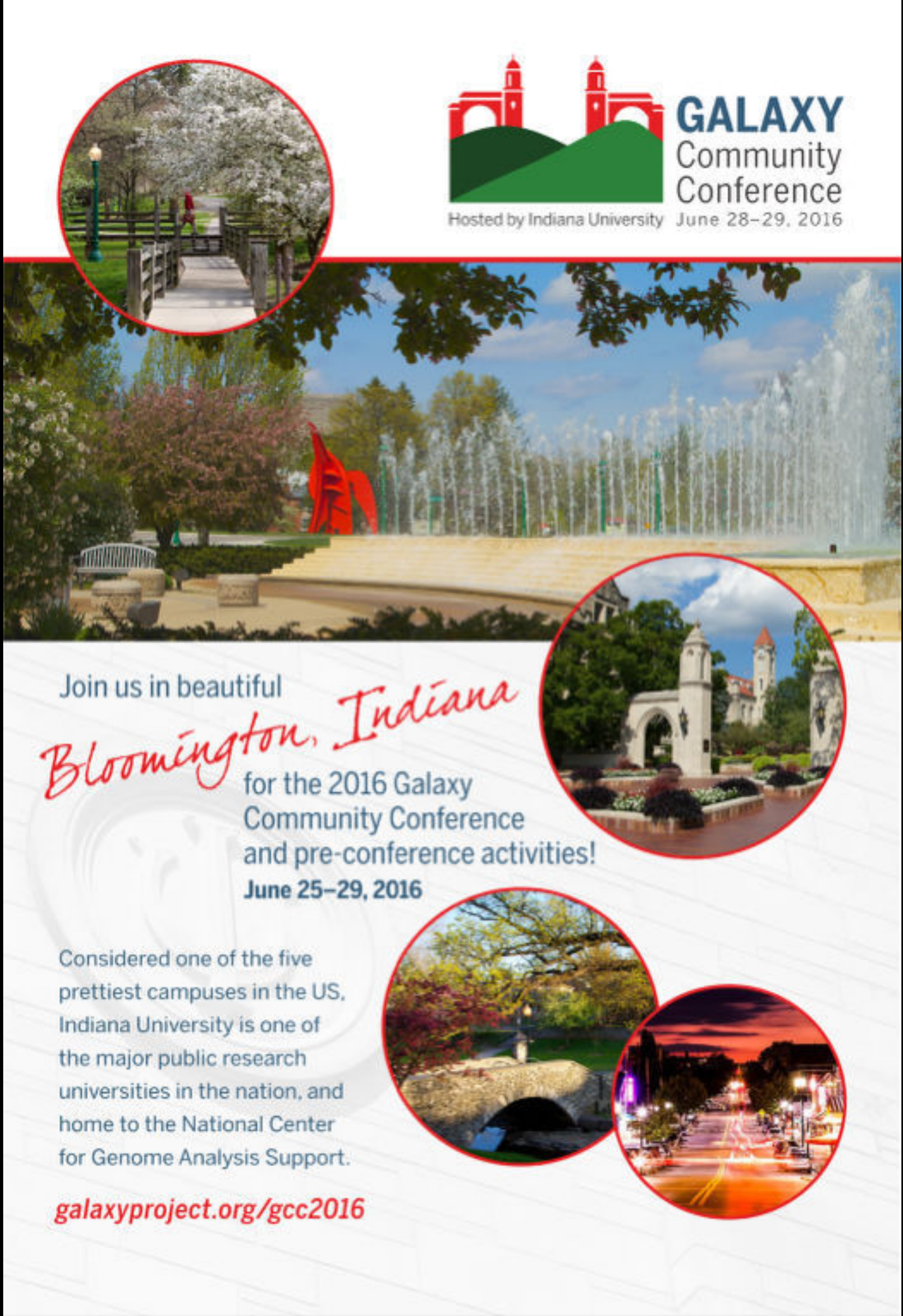
Galaxy Ecosystem Update

http://galaxyproject.org

2016 Galaxy Community Conference (GCC2016)

June 25-29, 2016
Bloomington, Indiana

galaxyproject.org/GCC2016



GALAXY
Community
Conference

Hosted by Indiana University
June 28–29, 2016

Join us in beautiful
Bloomington, Indiana
for the 2016 Galaxy
Community Conference
and pre-conference activities!
June 25–29, 2016

Considered one of the five prettiest campuses in the US, Indiana University is one of the major public research universities in the nation, and home to the National Center for Genome Analysis Support.

galaxyproject.org/gcc2016

Galaxy Community Resources: Galaxy Biostar

Tens of thousands of users leads to a lot of questions.

Absolutely have to encourage community support.

Project traditionally used mailing list

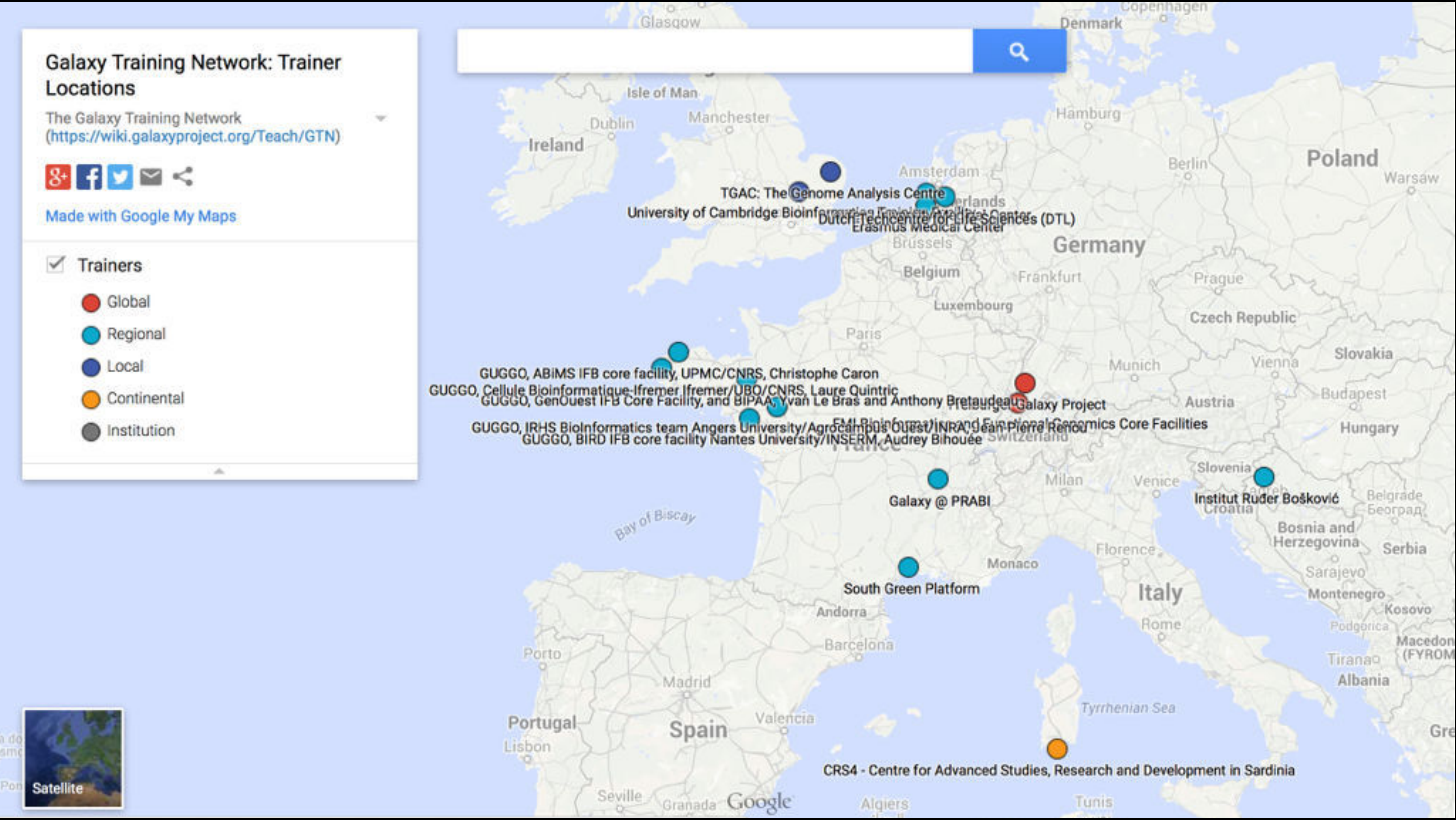
Moved the user support list to Galaxy Biostar, an online forum, that uses the Biostar platform

Want help?
Get answers.

Biostars
GALAXY EXPLAINED

https://biostar.usegalaxy.org/

Scaling **Training**



Galaxy Training Network: Trainer Locations

The Galaxy Training Network
(https://wiki.galaxyproject.org/Teach/GTN)

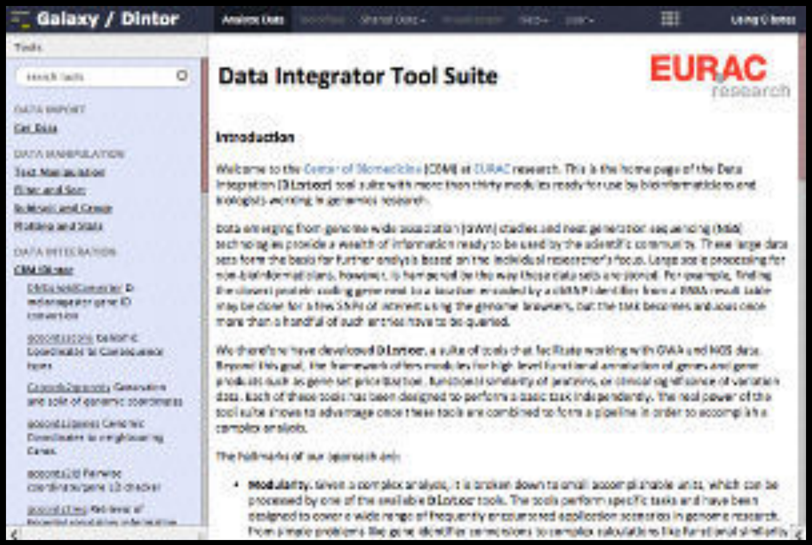
Made with Google My Maps

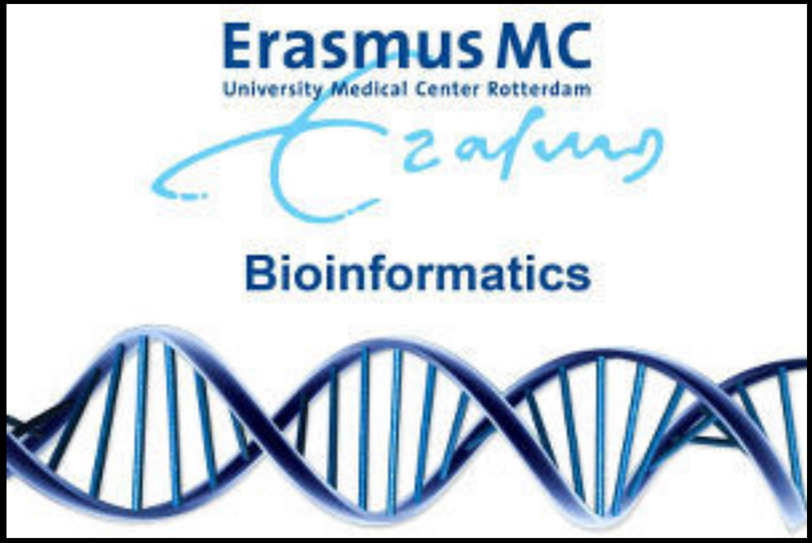
☑ Trainers

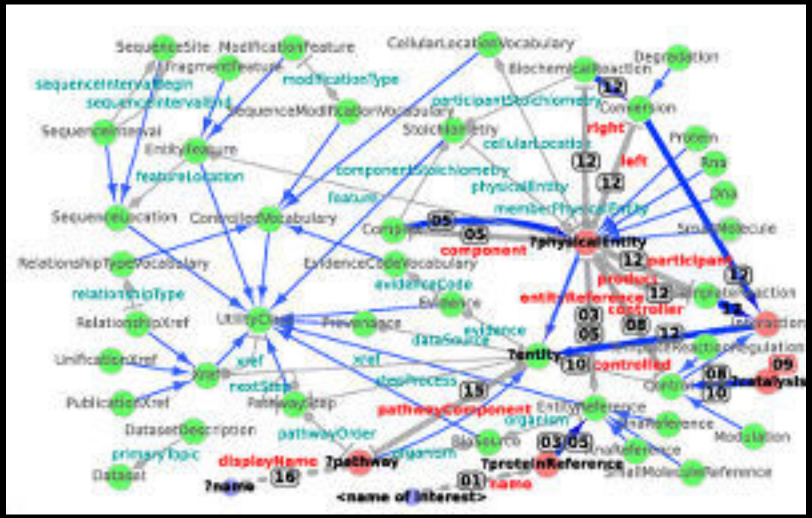
- ● Global
- ● Regional
- ● Local
- ● Continental
- ● Institution

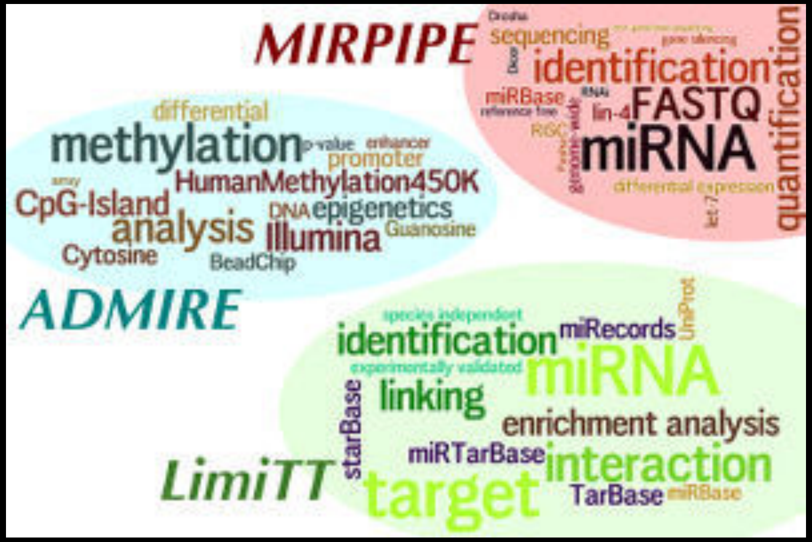
Galaxy Training Network launched In October 2014.

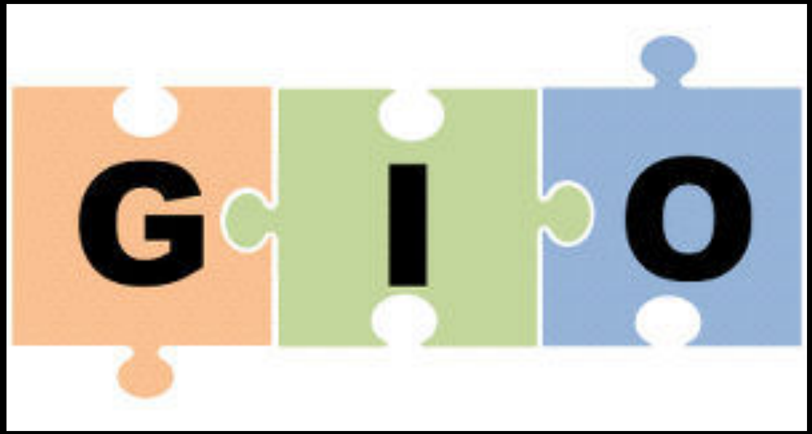
bit.ly/gxygtn

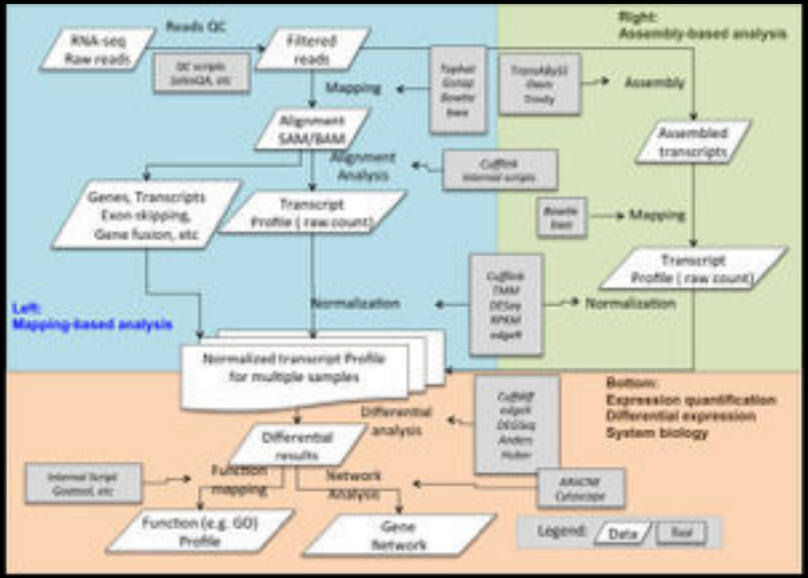


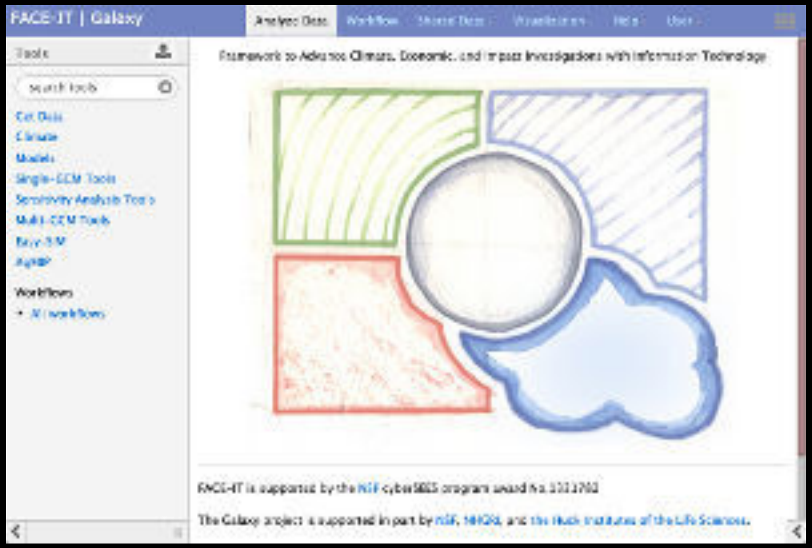




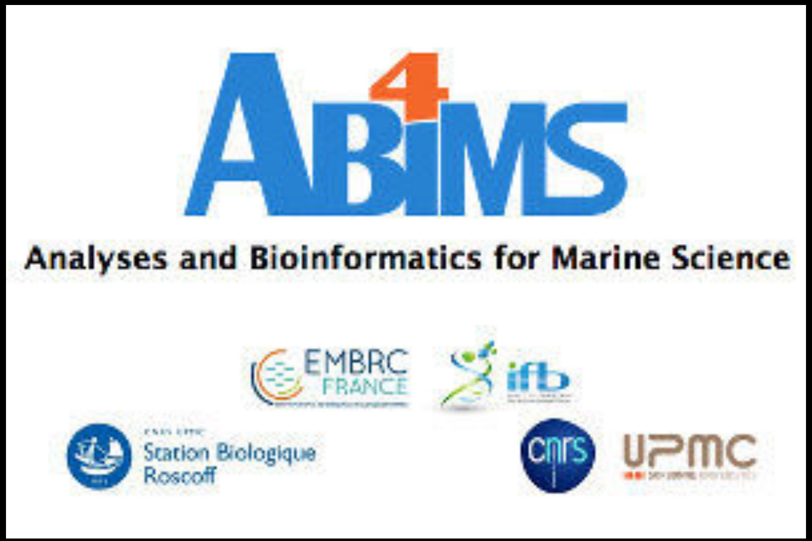








Proteomics
Metabolomics
Natural Language
Image Analysis
Climate Change
Social Science
Cosmology



The Galaxy Team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Nate Coraor


Carl Eberhard


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Jen Jackson


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Nick Stoler


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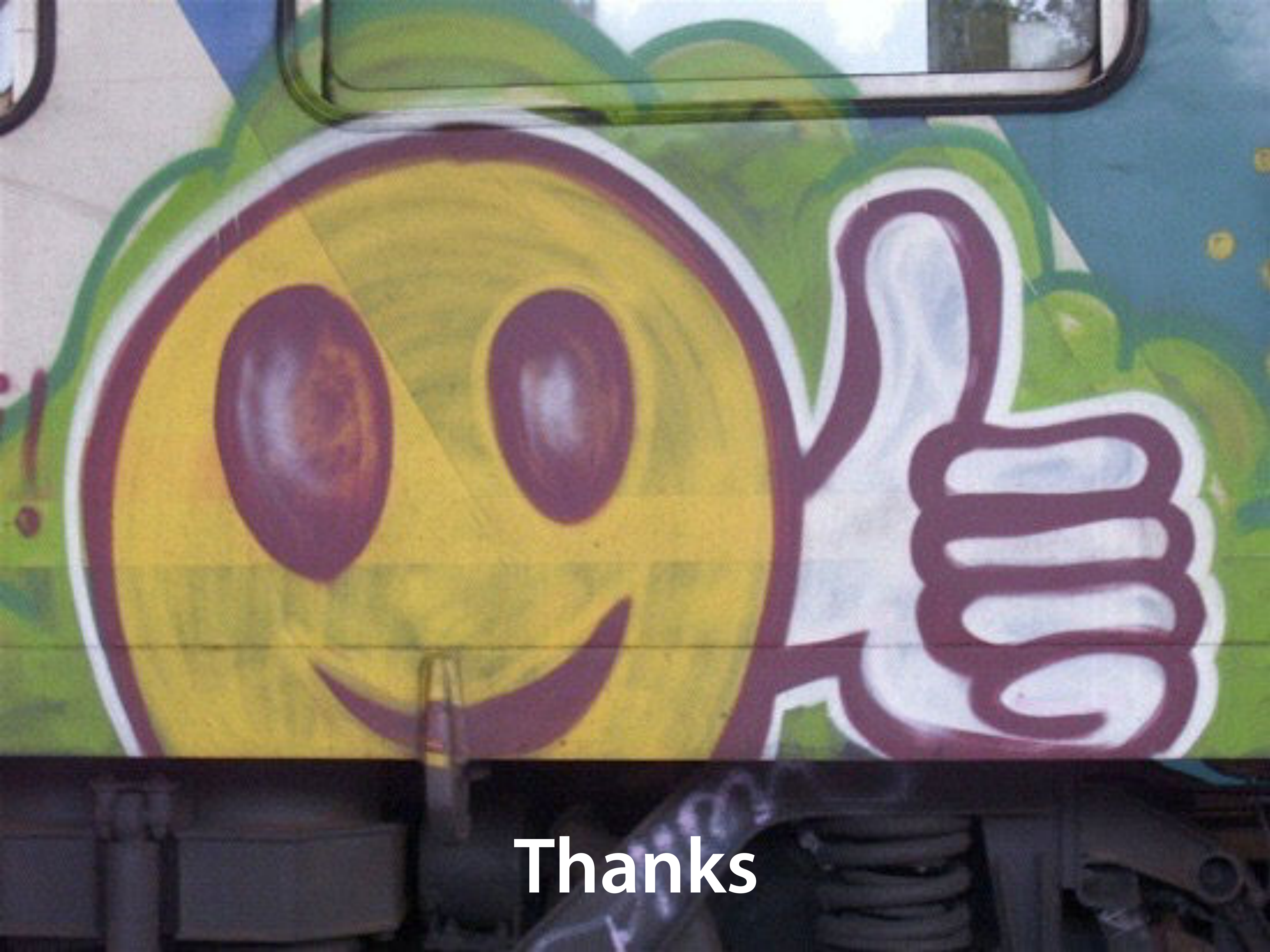
http://wiki.galaxyproject.org/GalaxyTeam

Acknowledgements

You

Scott Cain

PAG
NIH
Johns Hopkins University
Penn State University



Thanks