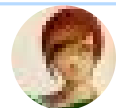


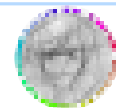


Introduction to Galaxy and BCO submission

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Nicola Soranzo

📅 Updated: Sep 13, 2022

📺 [View video slides for this lecture](#)

📄 [Plain-text slides](#)

Tip: press P to view the presenter notes



② Questions

- What is Galaxy?
- Why should I use Galaxy?
- How do I use Galaxy?
- Can I export my analyses as BCOs?



What is Galaxy?



Galaxy

Data Intensive *analysis* for everyone

- **Data Analysis** platform
- Web-based
- **Easy** to use
- **Free** and Open Source
- Many tools (~8000)
- Popular (>11,000 [publications](#))
- Extensive [tutorials](#) available



Homepage: galaxyproject.org



Why use Galaxy?

- It's **easy**!
 - No installation, all you need is a browser.
 - No complex commands, just point and click!
- Makes your research **reproducible**
 - Galaxy keeps track of all analysis details
- **Cross-domain**: bioinformatics, chemistry, ecology, climate science, ..





How do I use Galaxy?



Find a Galaxy server

- **The Big Three:** Galaxy Main (usegalaxy.org), Galaxy Europe (usegalaxy.eu), Galaxy Australia (usegalaxy.org.au)



- Many other smaller, often domain-specific Galaxies available
 - List of all public Galaxies (130+): galaxyproject.org/use



The Galaxy Interface

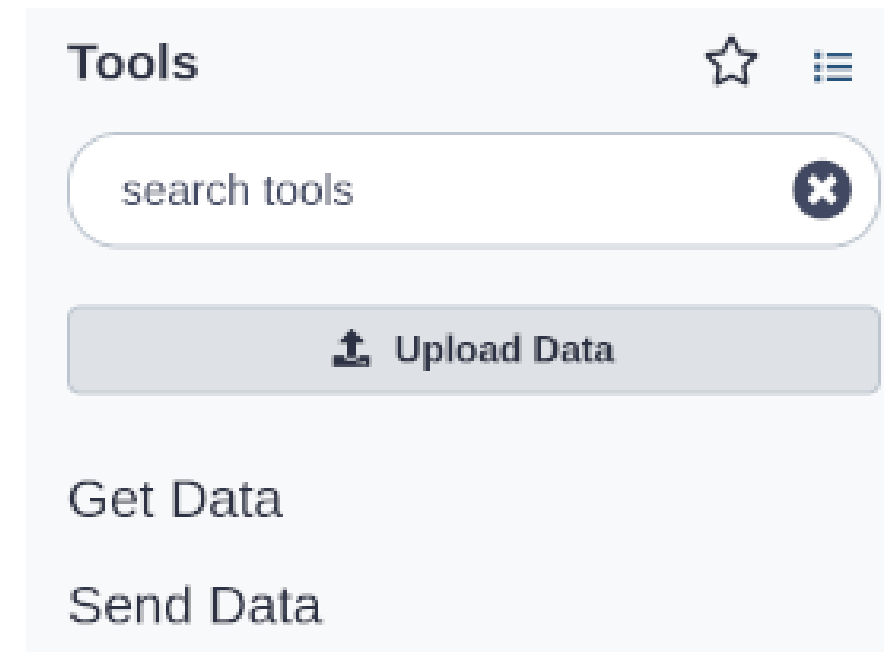
- Three main panels
 - **Left:** Available Tools
 - **Middle:** View your data and run tools
 - **Right:** Full record of your analysis **history**







Uploading data

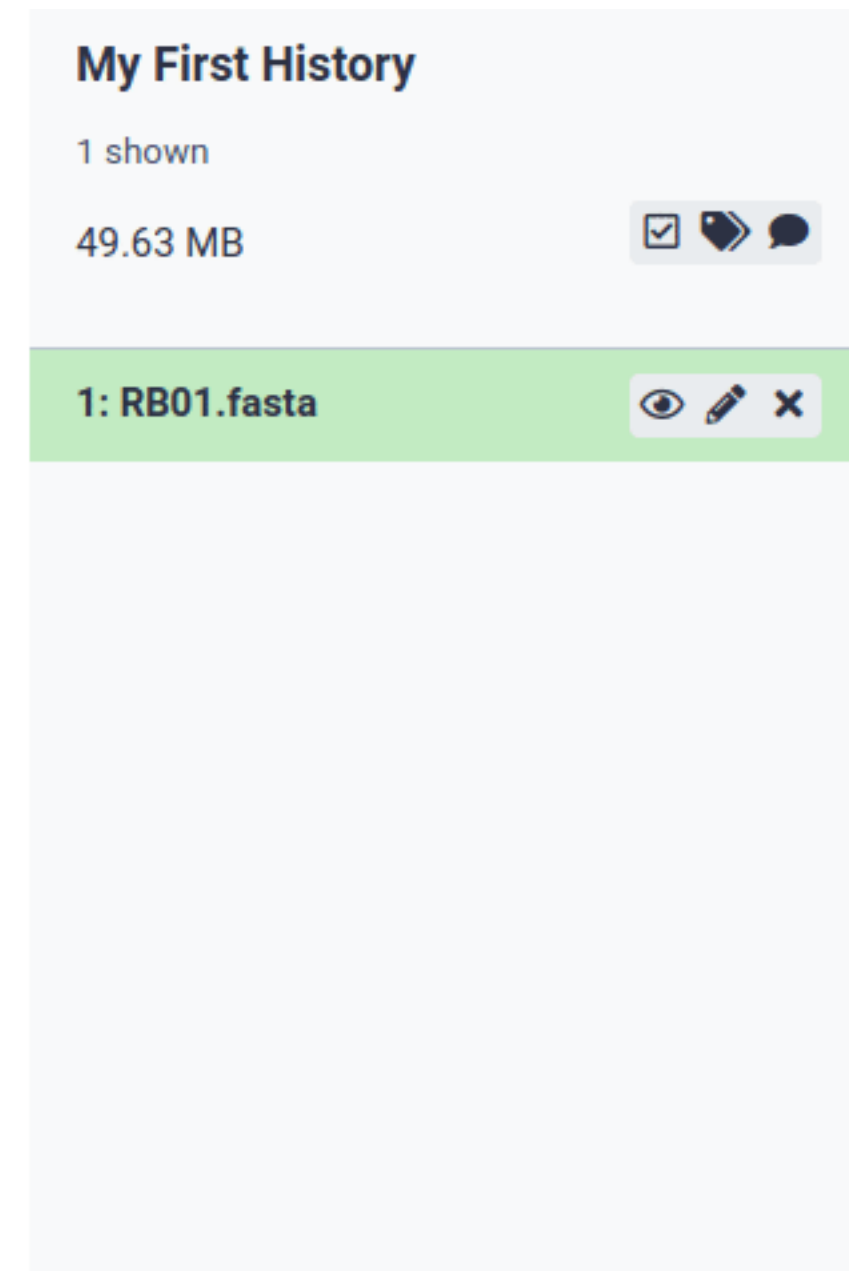
- Upload from **your computer**
- Import files **from URL**
- Import from **public data stores**
 - UCSC, NCBI, ENA, many more..





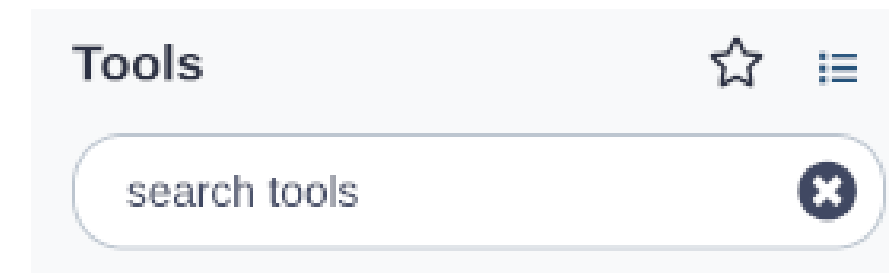
History

- The **history** collects all the files of your analysis
- Three buttons
 -  **View** the file
 -  **Edit attributes**
 - e.g. change name
 - **✕ Delete file**
- Click to **expand**
 - file information
 - format, size, ..
 - file preview
 - file options
 - download, visualize, ..

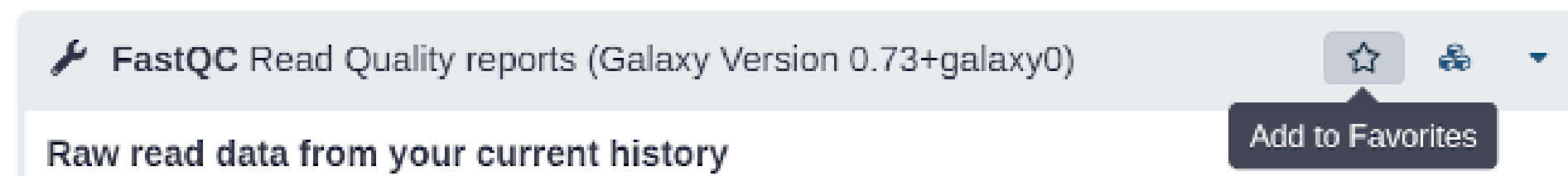


Finding a tool

- Explore tool panel sections
- Enter name in **Tool search** box



- ☆ **Star** you favorite tools to make them easier to find





Running a tool

- Choose **input files**
- Set tool **parameters**
- **Execute**
- Below tool form:
 - Help information
 - Tool citation

Sort data in ascending or descending order (Galaxy Version 1.2.0)

Sort Dataset

1: 1.bed

on column

with flavor

Numerical sort

everything in

Descending order

Column selection

Insert Column selection

Number of header lines to skip

0

characters are already considered as comments and kept

Email notification

☒ No

Send an email notification when the job completes.

Execute

TIP: If your data is not TAB delimited, use *Text Manipulation->Convert*

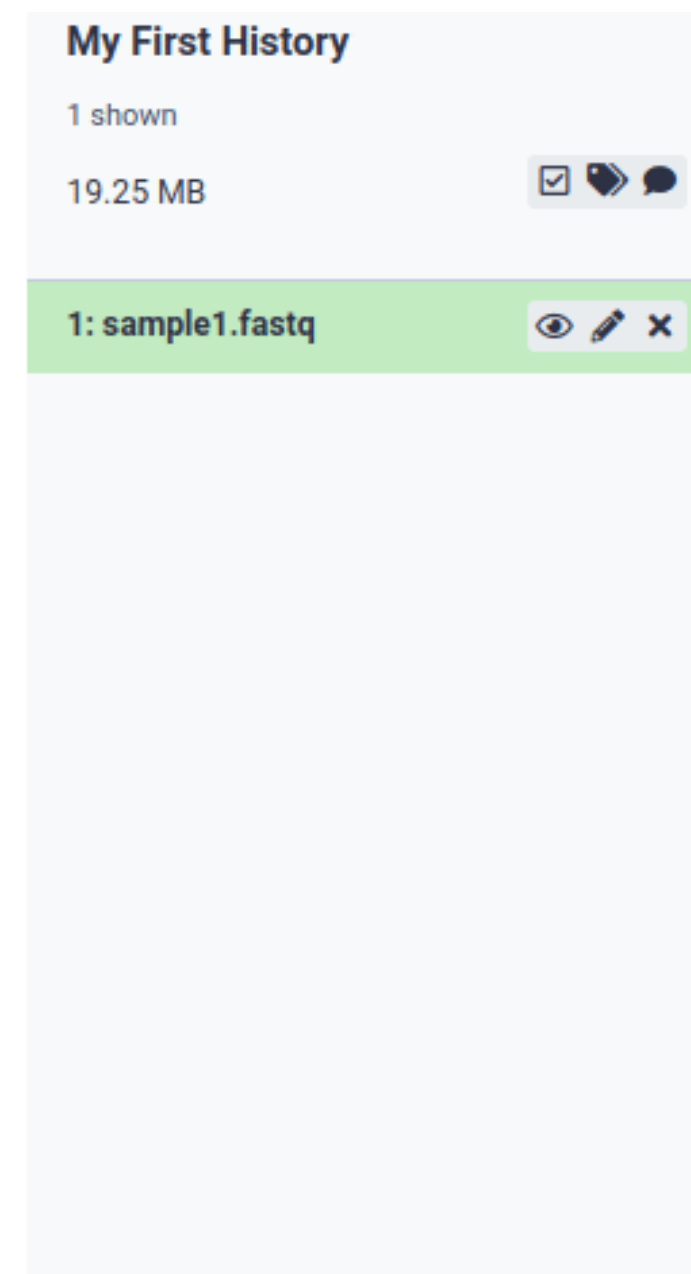
Syntax

This tool sorts the dataset on any number of columns in either ascending or descending order.

- **Numerical sort** orders numbers by their magnitude, ignores all characters besides numbers, and evaluates a string of numbers to the value they signify.

Analysis Results

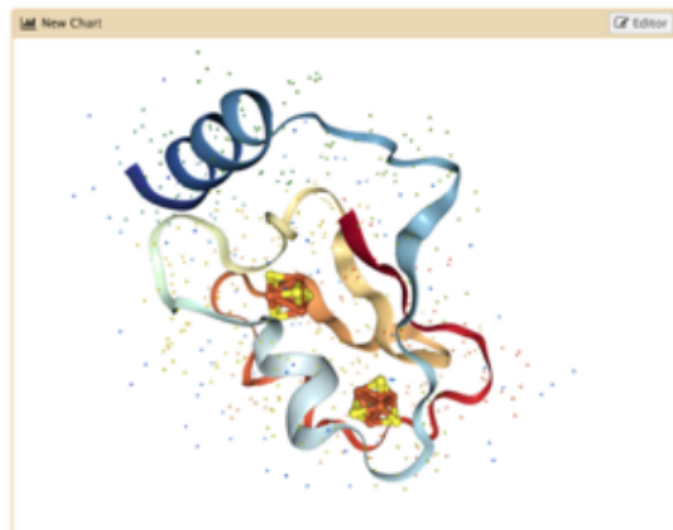
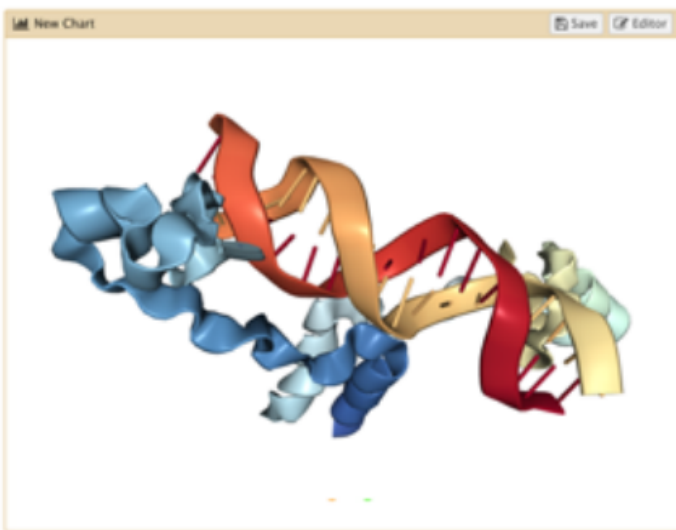
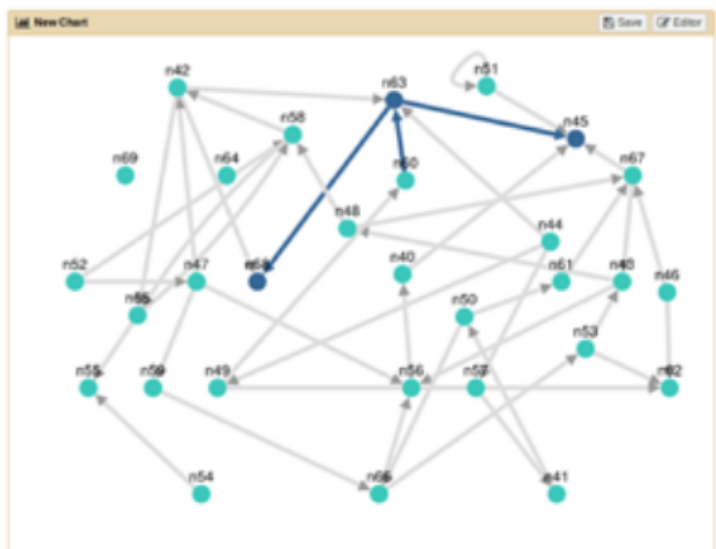
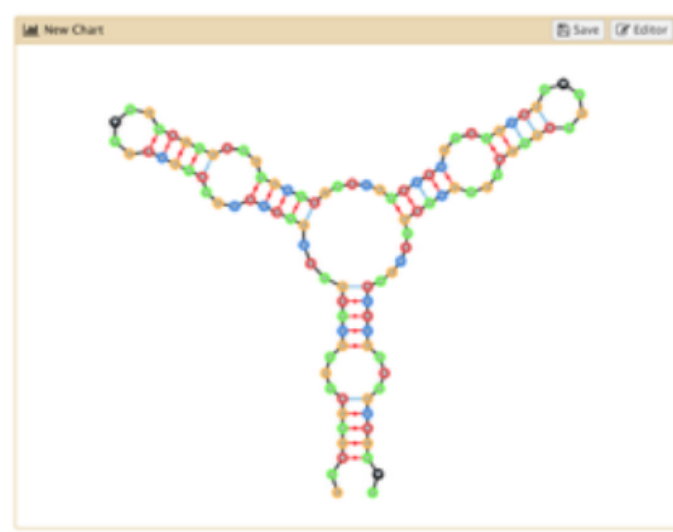
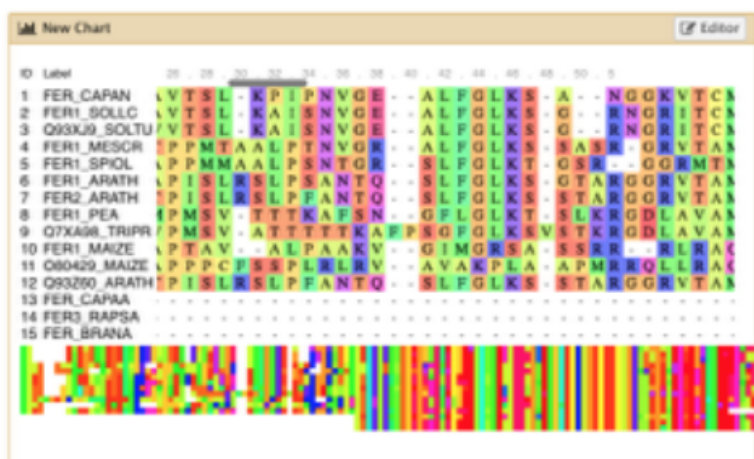
- Tool outputs are added to the history
- Different dataset states
 - waiting, running, success, failed
- Expand for more options
 - **Download** dataset
 - **Information** about tool run
 - **Reload** tool with the same parameters
 - **Visualize** dataset
- Red dataset?
 - Click Bug icon
 - view error message
 - submit error report





Visualisations

- Galaxy has many options to visualize data





Multiple Analyses

- Starting a new analysis? Create a new history +
- You can have as many histories as you want
- Overview of all your histories ▢
- Good names for your histories help to keep track of your analyses

Galaxy / Europe

Analyze DataWorkflowVisualizeShared DataHelpUser

Using 64.2 GB

search histories

search all datasets

Create new

Current History

Switch to

Switch to

Switch to

Workflow extract error

6 shown, 16 deleted, 3 hidden

10.83 KB

search datasets

Drag datasets here to copy them to the current history

24: data 7 (flattened)

a list with 1 item

x

23: Venn on collection 1: svg

a nested list with 1 / 1 jobs in error

x

22: Venn on collection 1: sharedotus

a nested list with 1 / 1 jobs in error

x

5: Venn on collection 1: svg

a nested list with 1 item

x

4: Venn on collection 1: sharedotus

a nested list with 1 item

x

1: Sub.sample on data 76: subsample.shared

a list with 1 item

x

Unnamed history

86 shown, 3 deleted, 44 hidden

910.45 MB

search datasets

127: Heatmap.sim on collection 86: heatmap.sim.svg

a list with 6 items

x

119: Plotting tool on collection 83

a list with 1 item

x

113: Classify.seqs on data 48, data 9, and others: tree.sum

eye edit x

112: Classify.seqs on data 48, data 9, and others: tax.summary

eye edit x

87: Rarefaction.single on data 79: rarefaction curves

a list with 1 item

x

86: Dist.shared on data 76: dist files

a list with 6 items

x

85: Summary.single on data 76: summary

eye edit x

84: Summary.single on data 76: ave-std.summary

eye edit x

83: Rarefaction.single on data 76: rarefaction curves

a list with 1 item

x

82: Sub.sample on data 76: subsample.shared

a list with 6 items

x

Training: 16S rRNA sequencing with mothur

134 shown, 54 deleted, 56 hidden

1.05 GB

search datasets

236: Krona pie chart on data 235: HTML

eye edit x

234: Taxonomy-to-Krona on collection 184: krona-formatted taxonomy file

a list with 1 item

x

232: Make.biom on collection 189 and collection 184: biom files

a nested list with 1 item

x

231: Newick Display on data 218: Tree Graph

eye edit x

217: Tree.shared on collection 199: tre

a list with 6 items

x

214: Venn on collection 189: svg

a nested list with 1 item

x

213: Venn on collection 189: sharedotus

a nested list with 1 item

x

206: Heatmap.sim on collection 199: heatmap.sim.svg

a list with 6 items

x

199: Dist.shared on data 182: dist files

a list with 6 items

x

Unnamed history

41 shown

163.07 MB

search datasets

41: samples

a list of pairs with 20 items

x

40: https://zenodo.org/record/800651/files/Mock_R2.fastq

eye edit x

39: https://zenodo.org/record/800651/files/Mock_R1.fastq

eye edit x

38: https://zenodo.org/record/800651/files/F3D9_R2.fastq

eye edit x

37: https://zenodo.org/record/800651/files/F3D9_R1.fastq

eye edit x

36: https://zenodo.org/record/800651/files/F3D8_R2.fastq

eye edit x

35: https://zenodo.org/record/800651/files/F3D8_R1.fastq

eye edit x

34: https://zenodo.org/record/800651/files/F3D7_R2.fastq

eye edit x

33: https://zenodo.org/record/800651/files/F3D7_R1.fastq

eye edit x

32: https://zenodo.org/record/800651/files/F3D6_R2.fastq

eye edit x

31: https://zenodo.org/record/800651/files/F3D6_R1.fastq

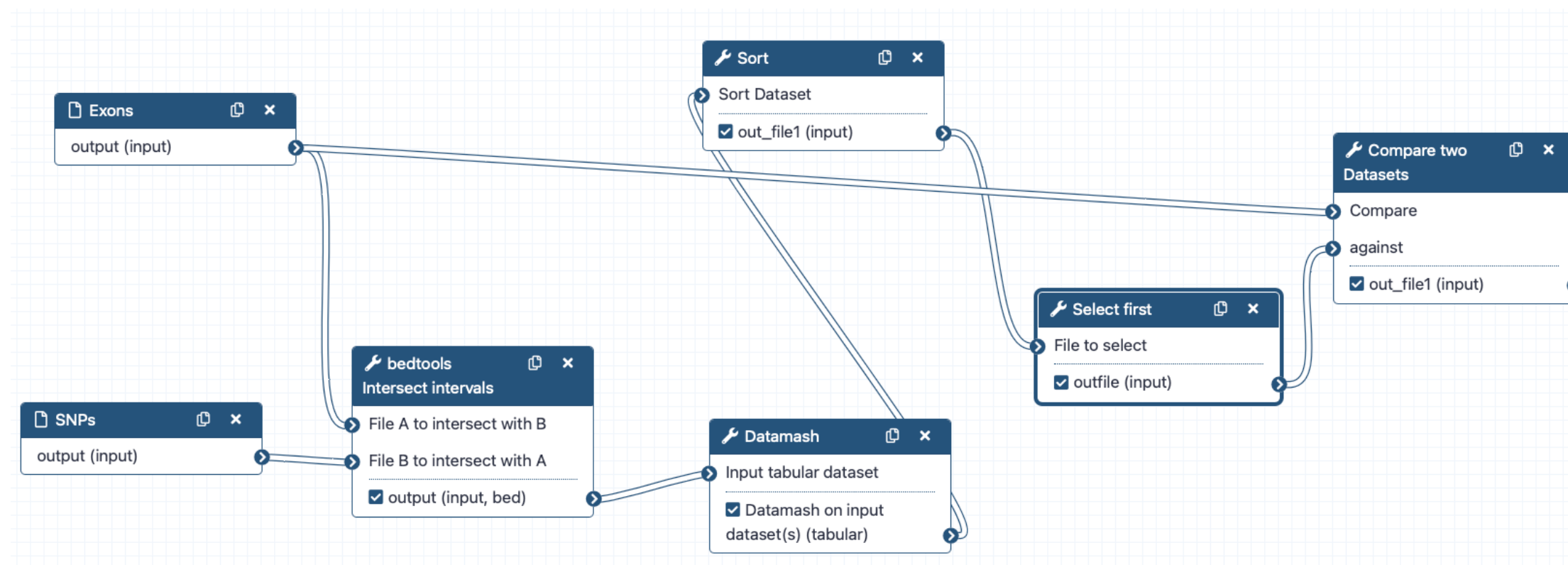
eye edit x

Galaxy



Workflows

- Run **end-to-end analyses** with one click

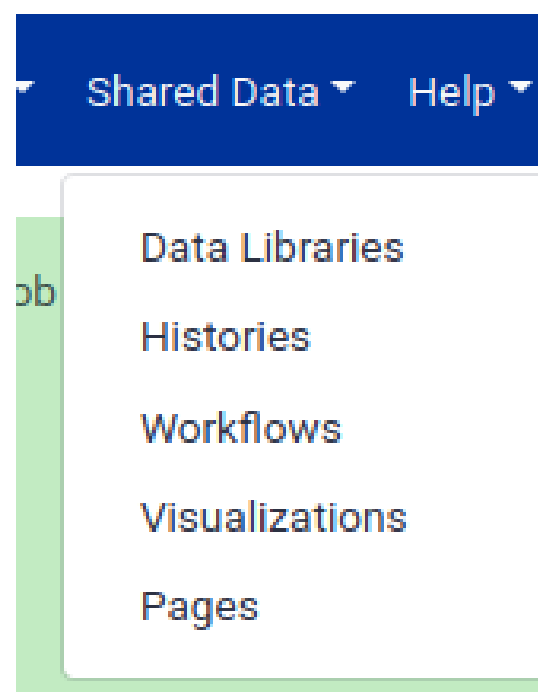


- **Extract** from a history
- **Build manually** with workflow editor
- **Import** a shared workflow



Sharing

- You can share everything you do in Galaxy
 - Histories, Workflows, Visualizations
- Sharing options
 - Share with specific users
 - Share via link
 - *Publish* to make it visible to everybody





Learning Galaxy

- Galaxy Training Materials (training.galaxyproject.org)

28

Topics

277

Tutorials

267

Contributors


7.2

Years



Getting Help

- **Help Forum** (help.galaxyproject.org)

 **GalaxyHelp**

Sign Up

Log In









all categories ▾

all tags ▾

Latest

Top

Categories












Topic	Category	Users	Replies	Views	Activity
<div><div> </div><div>Troubleshooting resources for errors or unexpected results</div><div>Start by reviewing the troubleshooting FAQ. Common reasons and solutions for tool errors are explained. Most job errors can be resolved by correcting your input data's format/content. Others indicate a tool setting/param... read more</div></div>	<div> usegalaxy.org support</div>	<div></div>	1	85	7d
<div><div> </div><div>Welcome to Galaxy Community Help</div><div>For assistance with a specific Galaxy server please post into appropriate category.</div></div>		<div> </div>	1	75	15d

- **Chat on Matrix**
 - [Main Chat](#)
 - [Galaxy Training Chat](#)
 - Many more channels (scientific domains, developers, admins)



Join an event

- Many Galaxy events across the globe
- Event Horizon: galaxyproject.org/events

Date	Topic/Event	Venue/Location	Contact
October 29th 2020	Galaxy Developer Roundtable	Online	 Dannon Baker, John Chilton, Marius van den Beek
October 29th 2020	Next Generation Sequencing (NGS) Introduction	Germantown, Maryland, United States	 Sijung Yun
October 28th 2020	مقدمه ای در تجزیه و تحلیل توالی آر.ان.آ. انسان و موش با استفاده از نرم افزار گالکسی	University of Isfahan, Isfahan, Iran	 Maryam Kay, Fariba Dehghanian, Alireza Khanteymoori 
October 27th 2020	GWAS Analysis with Galaxy on the Analysis Visualization Integrated Lab-space (AnVIL)	ASHG 2020, Online	 Dave Clements, Alex Ostrovsky 
October 26th 2020	Functionally Assembled Terrestrial Ecosystem Simulator (FATES)	Norway, Online	 Anne Fouilloux 
October 26th 2020	Machine Learning in Bioinformatics using Galaxy	ISCB-LA SolBio BioNetMX 2020, Mexico, Online	 Alireza Khanteymoori, Björn Grüning, Anup Kumar 
October 21st 2020	Galaxy Paper Cuts Day	Global, online	 Community



Export a Galaxy analysis as BCO

- It's possible to export a completed workflow **invocation** as a BioCompute Object
- Before running the workflow, it's recommended to annotate it following the Galaxy [best practices](#)

The screenshot shows the Galaxy interface with a dark navigation bar at the top containing links: Workflow, Visualize, Shared Data, Admin, Help, User, and icons for a graduation cap, a bell, and a grid. Below the navigation bar is the 'Workflow Invocations' section. It features a table with columns: Workflow, History, Invoked, and a status column. The table lists four workflow invocations, each with a dropdown arrow on the left and a play button on the right. A user menu is open over the table, showing options: Logged in as hadley_king, Preferences, Custom Builds, Logout, Datasets, Histories, Histories shared with me, Pages, Workflow Invocations (highlighted), and Visualizations.

	Workflow	History	Invoked	
▼	Galaxy BioComput Object Developm...	BioCompute Te...	about 2 months	▶
▼	Galaxy BioComput Object Developm...	BioCompute Te...	about 2 months	▶
▼	Galaxy BioComput Object Developm...	BioCompute Te...	3 months ago	▶
▼	Galaxy BioComput Object Developm...	BioCompute Te...	4 months ago	▶



Download a workflow invocation as BCO

- After expanding an invocation, BCO export options are available from the "Export" tab
- It's possible to either Download the BCO or Submit it to a BCODB
- Can be downloaded also from the Galaxy API:
`/api/workflows/<workflow_id>/invocations/<invocation_id>/biocompute`

Workflow Invocations

Workflow	History	Invoked	Updated	State
Galaxy BioCompute Object Developm...	BioCompute Te...	about 2 months ago	about 2 months ago	scheduled

Summary Details **Export**

Invocation: ebfb8f50c6abde6d

BioCompute Object

A BioCompute Object (BCO) is the unofficial name for a JSON object that adheres to the [IEEE-2791-2020 standard](#). A BCO is designed to communicate High-throughput Sequencing (HTS) analysis results, data set creation, data curation, and bioinformatics verification protocols.

[Learn more about BioCompute Objects.](#)

[Instructions for creating a BCO using Galaxy.](#)

[Download](#) [Submit To BCODB](#)

Download BCO



Submit a draft BCO to a BCODB

- The user needs to specify the BCODB's URL and their username and API key
- After submission, the draft BCO can be modified and published by going to the BCO DB website.
- More details in the [BCO Galaxy export guide](#)

Workflow Invocations

Workflow

History

Invoked

Updated

State

Galaxy BioComput Object Developm...

BioCompute Te...

about 2 months ago

about 2 months ago

scheduled

▶

Summary

Details

Export

Invocation: ebfb8f50c6abde6d

BioCompute Object

A BioCompute Object (BCO) is the unofficial name for a JSON object that adheres to the IEEE-2791-2020 standard. A BCO is designed to communicate High-throughput Sequencing (HTS) analysis results, data set creation, data curation, and bioinformatics verification protocols.

Learn more about BioCompute Objects.

Instructions for creating a BCO using Galaxy.

Download

Submit To BCODB

To submit to a BCODB you need to already have an authenticated account. Instructions on submitting a BCO from Galaxy are available [here](#).

BCO DB URL (example: https://biocomputeobject.org)

https://biocomputeobject.org

User API Key

.....

Prefix

GALAXY

User Name

test5d

Submit

BioCompute Object DB

Select server to search.

http://127.0.0.1:8000 - BCO Server (Default)

Search Type:

My BCOs

Prefix Search

Search BCO_ID

BCO_000015

SEARCH

BCO Accession

Name

BCO_000015DRAFT

"Galaxy BioComput Object Development Test"



Key points

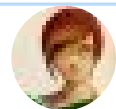
- Galaxy lets you perform complex data analysis right from your browser
- These analyses are *reproducible*; Galaxy keeps track of all the details of your analysis
- Galaxy has a very large and active user community
- There are many training materials available to learn Galaxy
- Workflow invocations can be easily submitted to a BCODB



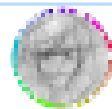
Thank You!

This material is the result of a collaborative work. Thanks to the [Galaxy Training Network](#) and all the contributors!

Authors:



Saskia Hiltemann



Helena Rasche



Charles Hadley King



Nicola Soranzo



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